

Date	2012/03/06 @ 13:07:01
EasyProt version	v2.2 (build 452)
#Jobs	1
FDR	5
MinUniqPepCount	2
Reporters	114 115 116 117
Ratios	116/114 117/115 116/117
Tolerance	0,05
Intensity normalization with internal standard	No
Global normalization	Median log peptide ratios = 0
Confidence	95 %
Isotopic purity correction	iTRAQ 4-plex Batch Applied Biosystems 070406 $i114 = 1.0722661143666323 * I114 + -0.021481$ $i115 = -0.06366037221582475 * I114 + 1.08008$ $i116 = 0.0014071154479143215 * I114 + -0.060$ $i117 = 2.8132929466527135E-7 * I114 + 0.0016$

i2 (Used: 114 115 116 117)

1417611045946 * I115 + 6.446362097163709E-4 * I116 + -4.304030777608941E-6 * I117

380843649168 * I115 + -0.03241238085268591 * I116 + 2.1640714974252142E-4 * I117

045125760183586 * I115 + 1.0797543752969976 * I116 + -0.04312972375427809 * I117

5427466736954693 * I115 + -0.048601691521348966 * I116 + 1.0789424249141801 * I117

Job Title	Nuclei_fractions
Job ID	1330977477981
User	anf
Submission date	2012/03/05 @ 20:57:57
Databases	uniprot_sprot (2011_02 of 08-Feb-2011)
Taxonomies	Homo sapiens (9606)
Instrument Type	ESI-LTQ-Orbitrap
Scoring Model	CID_LTQ_scan_LTQ
	Round 1
Enzyme	Trypsin_(KR)
Missed Cleavage	1 normal
Precursor Error Tolerance	25.0 ppm
Min. Peptide Length	6
Min. Peptide z-Score	3
Extended PTM Search	FALSO
Modifications	Cys_CAM (fixed all) iTRAQ_K (fixed all) iTRAQ_Nterm (fixed all) Oxidation_M (variable none)
Peaklist File	Nuclei.idj.gz

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91	Q92945.FUBP2_HUMAN	Far upstrea	64,65	14,79	9	8	1
91	Q92945.FUBP2_HUMAN	Far upstrea	64,65	14,79	9	8	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
92	P36578.RL4_HUMAN	60S ribosom	63,94	30,05	15	9	1
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
93	P22314.UBA1_HUMAN	Ubiquitin-li	62,914	11,44	12	9	0
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
94	P11940.PABP1_HUMAN	Polyadenyl:	62,016	20,66	15	9	2
95	P60842.IF4A1_HUMAN	Eukaryotic i	61,929	22,66	17	9	2
95	P60842.IF4A1_HUMAN	Eukaryotic i	61,929	22,66	17	9	2
95	P60842.IF4A1_HUMAN	Eukaryotic i	61,929	22,66	17	9	2
95	P60842.IF4A1_HUMAN	Eukaryotic i	61,929	22,66	17	9	2

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104	P23396_RS3_HUMAN	40S ribosom	57,491	41,32	16	9	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
105	P46940_IQGA1_HUMAN	Ras GTPase	56,774	6,04	10	8	1
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
106	O00571_DDX3X_HUMAN	ATP-depen	56,082	14,37	10	7	2
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
107	P62805_H4_HUMAN	Histone H4	55,944	63,73	24	8	1
108	P20700_LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700_LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700_LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1

108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
108	P20700.LMNB1_HUMAN	Lamin-B1 [C	55,856	11,86	15	8	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
109	P55072.TERA_HUMAN	Transitiona	55,816	12,8	11	7	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
110	P50990.TCPQ_HUMAN	T-complex j	55,638	15,36	10	6	1
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
111	Q9NQC3.RTN4_HUMAN	Reticulon-4	55,377	19,3	13	6	5
112	P08865.RSSA_HUMAN	40S ribosor	55,13	25,51	12	7	1
112	P08865.RSSA_HUMAN	40S ribosor	55,13	25,51	12	7	1

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162	P00338.LDHA_HUMAN	L-lactate de	44,779	23,26	11	7	2
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
163	P26038.MOES_HUMAN	Moesin [CH	44,634	11,98	12	7	1
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
164	P00387.NB5R3_HUMAN	NADH-cyto	44,504	28,73	6	6	3
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
165	P62701.RS4X_HUMAN	40S riboso	44,27	24,81	13	6	5
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
166	O00148.DDX39_HUMAN	ATP-depen	44,084	16,9	10	7	1
167	P23246.SFPQ_HUMAN	Splicing fac	43,94	9,76	7	6	1
167	P23246.SFPQ_HUMAN	Splicing fac	43,94	9,76	7	6	1
167	P23246.SFPQ_HUMAN	Splicing fac	43,94	9,76	7	6	1
167	P23246.SFPQ_HUMAN	Splicing fac	43,94	9,76	7	6	1
167	P23246.SFPQ_HUMAN	Splicing fac	43,94	9,76	7	6	1

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171	O43852	CALU_HUMAN	Calumenin	43,486	25	10	6	2
171	O43852	CALU_HUMAN	Calumenin	43,486	25	10	6	2
171	O43852	CALU_HUMAN	Calumenin	43,486	25	10	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
172	P52272	HNRPM_HUMAN	Heterogene	43,265	10,71	11	6	2
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
173	P21291	CSRP1_HUMAN	Cysteine an	43,05	34,9	9	5	1
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
174	P13674	P4HA1_HUMAN	Prolyl 4-hyc	42,64	14,7	9	6	2
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
175	P16403	H12_HUMAN	Histone H1.	42,605	23,58	11	7	9
176	Q9H0U4	RAB1B_HUMAN	Ras-related	42,605	29,85	11	6	5
176	Q9H0U4	RAB1B_HUMAN	Ras-related	42,605	29,85	11	6	5
176	Q9H0U4	RAB1B_HUMAN	Ras-related	42,605	29,85	11	6	5
176	Q9H0U4	RAB1B_HUMAN	Ras-related	42,605	29,85	11	6	5

[illegible]

181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
181	Q32P28.P3H1_HUMAN	Prolyl 3-hyc	41,39	8,26	9	5	3
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
182	P51149.RAB7A_HUMAN	Ras-related	41,34	29,47	8	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
183	P62753.RS6_HUMAN	40S ribosom	41,321	17,67	10	5	0
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
184	P05141.ADT2_HUMAN	ADP/ATP tr	40,96	22,9	12	6	1
185	O60716.CTND1_HUMAN	Catenin del	40,83	12,71	5	5	31
185	O60716.CTND1_HUMAN	Catenin del	40,83	12,71	5	5	31
185	O60716.CTND1_HUMAN	Catenin del	40,83	12,71	5	5	31
185	O60716.CTND1_HUMAN	Catenin del	40,83	12,71	5	5	31
185	O60716.CTND1_HUMAN	Catenin del	40,83	12,71	5	5	31
186	Q08043.ACTN3_HUMAN	Alpha-actin	40,747	7,1	11	6	0
186	Q08043.ACTN3_HUMAN	Alpha-actin	40,747	7,1	11	6	0

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

218	P21980	TGM2_HUMAN	Protein-gluc	35,308	10,33	8	5	1
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
219	Q9NVI7	ATD3A_HUMAN	ATPase fam	35,301	10,75	7	5	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
220	P67809	YBOX1_HUMAN	Nuclease-se	35,242	19,5	12	4	5
221	P69849	NOMO3_HUMAN	Nodal mod	35,218	5,12	5	5	6
221	P69849	NOMO3_HUMAN	Nodal mod	35,218	5,12	5	5	6
221	P69849	NOMO3_HUMAN	Nodal mod	35,218	5,12	5	5	6
221	P69849	NOMO3_HUMAN	Nodal mod	35,218	5,12	5	5	6
221	P69849	NOMO3_HUMAN	Nodal mod	35,218	5,12	5	5	6
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
222	P62081	RS7_HUMAN	40S ribosom	35,161	27,32	9	5	0
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
223	P07910	HNRPC_HUMAN	Heterogene	35,1	18	10	5	1
224	P35749	MYH11_HUMAN	Myosin-11	35,056	3,19	11	5	0
224	P35749	MYH11_HUMAN	Myosin-11	35,056	3,19	11	5	0

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240	P10606_COX5B_HUMAN	Cytochrome	33,628	52,04	10	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
241	Q96AY3_FKB10_HUMAN	Peptidyl-pro	33,623	10,07	7	5	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
242	Q07020_RL18_HUMAN	60S ribosom	33,613	25,67	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
243	P62873_GBB1_HUMAN	Guanine nu	33,56	16,52	9	4	1
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
244	P08195_4F2_HUMAN	4F2 cell-sur	33,529	11,34	8	5	3
245	P54886_P5CS_HUMAN	Delta-1-pyr	33,428	6,56	4	4	1
245	P54886_P5CS_HUMAN	Delta-1-pyr	33,428	6,56	4	4	1
245	P54886_P5CS_HUMAN	Delta-1-pyr	33,428	6,56	4	4	1
245	P54886_P5CS_HUMAN	Delta-1-pyr	33,428	6,56	4	4	1
246	Q86UP2_KTN1_HUMAN	Kinectin [IS	33,332	7,08	5	5	1
246	Q86UP2_KTN1_HUMAN	Kinectin [IS	33,332	7,08	5	5	1
246	Q86UP2_KTN1_HUMAN	Kinectin [IS	33,332	7,08	5	5	1
246	Q86UP2_KTN1_HUMAN	Kinectin [IS	33,332	7,08	5	5	1
246	Q86UP2_KTN1_HUMAN	Kinectin [IS	33,332	7,08	5	5	1
247	Q92841_DDX17_HUMAN	Probable A	33,014	9,38	9	5	3
247	Q92841_DDX17_HUMAN	Probable A	33,014	9,38	9	5	3

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280	P30044_PRDX5_HUMAN	Peroxiredoxin 5	30,144	22,22	9	4	2
280	P30044_PRDX5_HUMAN	Peroxiredoxin 5	30,144	22,22	9	4	2
281	P49327_FAS_HUMAN	Fatty acid synthase	30,144	3,11	4	4	0
281	P49327_FAS_HUMAN	Fatty acid synthase	30,144	3,11	4	4	0
281	P49327_FAS_HUMAN	Fatty acid synthase	30,144	3,11	4	4	0
281	P49327_FAS_HUMAN	Fatty acid synthase	30,144	3,11	4	4	0
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
282	P62906_RL10A_HUMAN	60S ribosomal protein L10A	29,886	25,46	6	4	1
283	O94925_GLSK_HUMAN	Glutaminase	29,755	11,04	4	4	3
283	O94925_GLSK_HUMAN	Glutaminase	29,755	11,04	4	4	3
283	O94925_GLSK_HUMAN	Glutaminase	29,755	11,04	4	4	3
283	O94925_GLSK_HUMAN	Glutaminase	29,755	11,04	4	4	3
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
284	P41091_IF2G_HUMAN	Eukaryotic initiation factor 2 gamma	29,745	16,77	7	5	4
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
285	P53396_ACLY_HUMAN	ATP-citrate lyase	29,527	5,36	6	4	0
286	O95782_AP2A1_HUMAN	AP-2 complex subunit alpha 1	29,354	4,82	5	5	1
286	O95782_AP2A1_HUMAN	AP-2 complex subunit alpha 1	29,354	4,82	5	5	1
286	O95782_AP2A1_HUMAN	AP-2 complex subunit alpha 1	29,354	4,82	5	5	1
286	O95782_AP2A1_HUMAN	AP-2 complex subunit alpha 1	29,354	4,82	5	5	1
286	O95782_AP2A1_HUMAN	AP-2 complex subunit alpha 1	29,354	4,82	5	5	1
287	Q16891_IMMT_HUMAN	Mitochondrial inner membrane protein	29,349	11,57	5	5	2
287	Q16891_IMMT_HUMAN	Mitochondrial inner membrane protein	29,349	11,57	5	5	2
287	Q16891_IMMT_HUMAN	Mitochondrial inner membrane protein	29,349	11,57	5	5	2
287	Q16891_IMMT_HUMAN	Mitochondrial inner membrane protein	29,349	11,57	5	5	2
287	Q16891_IMMT_HUMAN	Mitochondrial inner membrane protein	29,349	11,57	5	5	2
288	Q15019_SEPT2_HUMAN	Septin-2 (N-terminal)	29,323	14,96	5	4	1
288	Q15019_SEPT2_HUMAN	Septin-2 (N-terminal)	29,323	14,96	5	4	1
288	Q15019_SEPT2_HUMAN	Septin-2 (N-terminal)	29,323	14,96	5	4	1
288	Q15019_SEPT2_HUMAN	Septin-2 (N-terminal)	29,323	14,96	5	4	1
288	Q15019_SEPT2_HUMAN	Septin-2 (N-terminal)	29,323	14,96	5	4	1

289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
289	P07737_PROF1_HUMAN	Profilin-1 [C	29,274	28,78	14	4	1
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
290	Q99613 EIF3C_HUMAN	Eukaryotic t	29,244	5,15	6	5	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
291	Q969G5_PRDBP_HUMAN	Protein kin	29,229	17,24	7	4	0
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
292	P16188_1A30_HUMAN	HLA class II	29,11	16,13	6	4	38
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
293	P52597_HNRPF_HUMAN	Heterogene	29,06	12,56	8	4	1
294	P27824_CALX_HUMAN	Calnexin [C	29,047	8,92	5	4	1
294	P27824_CALX_HUMAN	Calnexin [C	29,047	8,92	5	4	1
294	P27824_CALX_HUMAN	Calnexin [C	29,047	8,92	5	4	1
294	P27824_CALX_HUMAN	Calnexin [C	29,047	8,92	5	4	1
294	P27824_CALX_HUMAN	Calnexin [C	29,047	8,92	5	4	1

295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
295	Q06830	PRDX1_HUMAN	Peroxiredo	29,032	19,6	6	4	0
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
296	P55769	NH2L1_HUMAN	NHP2-like p	29,001	28,35	6	4	1
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
297	P04899	GNAI2_HUMAN	Guanine nu	28,999	14,41	7	4	9
298	P62491	RB11A_HUMAN	Ras-related	28,933	19,81	5	4	3
298	P62491	RB11A_HUMAN	Ras-related	28,933	19,81	5	4	3
298	P62491	RB11A_HUMAN	Ras-related	28,933	19,81	5	4	3
298	P62491	RB11A_HUMAN	Ras-related	28,933	19,81	5	4	3
298	P62491	RB11A_HUMAN	Ras-related	28,933	19,81	5	4	3
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
299	P62280	RS11_HUMAN	40S ribosor	28,821	26,11	9	5	1
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
300	Q99714	HCD2_HUMAN	3-hydroxya	28,773	23,85	6	4	2
301	Q15717	ELAV1_HUMAN	ELAV-like p	28,77	14,11	5	4	0
301	Q15717	ELAV1_HUMAN	ELAV-like p	28,77	14,11	5	4	0
301	Q15717	ELAV1_HUMAN	ELAV-like p	28,77	14,11	5	4	0
301	Q15717	ELAV1_HUMAN	ELAV-like p	28,77	14,11	5	4	0
301	Q15717	ELAV1_HUMAN	ELAV-like p	28,77	14,11	5	4	0

302	O15460.P4HA2_HUMAN	Prolyl 4-hyc	28,489	11,48	5	4	2
302	O15460.P4HA2_HUMAN	Prolyl 4-hyc	28,489	11,48	5	4	2
302	O15460.P4HA2_HUMAN	Prolyl 4-hyc	28,489	11,48	5	4	2
302	O15460.P4HA2_HUMAN	Prolyl 4-hyc	28,489	11,48	5	4	2
302	O15460.P4HA2_HUMAN	Prolyl 4-hyc	28,489	11,48	5	4	2
303	Q9Y3F4.STRAP_HUMAN	Serine-thre	28,481	12,86	5	4	0
303	Q9Y3F4.STRAP_HUMAN	Serine-thre	28,481	12,86	5	4	0
303	Q9Y3F4.STRAP_HUMAN	Serine-thre	28,481	12,86	5	4	0
303	Q9Y3F4.STRAP_HUMAN	Serine-thre	28,481	12,86	5	4	0
303	Q9Y3F4.STRAP_HUMAN	Serine-thre	28,481	12,86	5	4	0
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
304	P04216.THY1_HUMAN	Thy-1 mem	28,315	35,14	9	3	1
305	Q9P258.RCC2_HUMAN	Protein RCC	27,867	9,58	4	4	0
305	Q9P258.RCC2_HUMAN	Protein RCC	27,867	9,58	4	4	0
305	Q9P258.RCC2_HUMAN	Protein RCC	27,867	9,58	4	4	0
305	Q9P258.RCC2_HUMAN	Protein RCC	27,867	9,58	4	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
306	P83731.RL24_HUMAN	60S ribosor	27,857	24,84	6	4	0
307	Q92616.GCN1L_HUMAN	Translation.	27,834	2,4	4	4	1
307	Q92616.GCN1L_HUMAN	Translation.	27,834	2,4	4	4	1
307	Q92616.GCN1L_HUMAN	Translation.	27,834	2,4	4	4	1
307	Q92616.GCN1L_HUMAN	Translation.	27,834	2,4	4	4	1
308	P00505.AATM_HUMAN	Aspartate a	27,639	12,22	4	3	1
308	P00505.AATM_HUMAN	Aspartate a	27,639	12,22	4	3	1
308	P00505.AATM_HUMAN	Aspartate a	27,639	12,22	4	3	1
308	P00505.AATM_HUMAN	Aspartate a	27,639	12,22	4	3	1
309	P49756.RBM25_HUMAN	RNA-bindin	27,47	6,76	5	4	2
309	P49756.RBM25_HUMAN	RNA-bindin	27,47	6,76	5	4	2
309	P49756.RBM25_HUMAN	RNA-bindin	27,47	6,76	5	4	2
309	P49756.RBM25_HUMAN	RNA-bindin	27,47	6,76	5	4	2
309	P49756.RBM25_HUMAN	RNA-bindin	27,47	6,76	5	4	2
310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1
310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1

310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1
310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1
310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1
310	Q16658.FSCN1_HUMAN	Fascin [CHA	27,452	10,77	6	4	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
311	O75396.SC22B_HUMAN	Vesicle-traf	27,389	15,89	6	3	1
312	P13647.K2C5_HUMAN	Keratin, typ	27,318	7,12	5	4	8
312	P13647.K2C5_HUMAN	Keratin, typ	27,318	7,12	5	4	8
312	P13647.K2C5_HUMAN	Keratin, typ	27,318	7,12	5	4	8
312	P13647.K2C5_HUMAN	Keratin, typ	27,318	7,12	5	4	8
312	P13647.K2C5_HUMAN	Keratin, typ	27,318	7,12	5	4	8
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
313	P59998.ARPC4_HUMAN	Actin-relate	27,312	29,34	8	4	1
314	Q92499.DDX1_HUMAN	ATP-depen	27,24	8,38	5	4	0
314	Q92499.DDX1_HUMAN	ATP-depen	27,24	8,38	5	4	0
314	Q92499.DDX1_HUMAN	ATP-depen	27,24	8,38	5	4	0
314	Q92499.DDX1_HUMAN	ATP-depen	27,24	8,38	5	4	0
314	Q92499.DDX1_HUMAN	ATP-depen	27,24	8,38	5	4	0
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
315	P62269.RS18_HUMAN	40S ribosom	27,213	23,84	8	5	1
316	O75367.H2AY_HUMAN	Core histon	27,068	12,47	5	4	3
316	O75367.H2AY_HUMAN	Core histon	27,068	12,47	5	4	3
316	O75367.H2AY_HUMAN	Core histon	27,068	12,47	5	4	3
316	O75367.H2AY_HUMAN	Core histon	27,068	12,47	5	4	3
316	O75367.H2AY_HUMAN	Core histon	27,068	12,47	5	4	3
317	P61247.RS3A_HUMAN	40S ribosom	26,895	16,73	5	4	1
317	P61247.RS3A_HUMAN	40S ribosom	26,895	16,73	5	4	1
317	P61247.RS3A_HUMAN	40S ribosom	26,895	16,73	5	4	1
317	P61247.RS3A_HUMAN	40S ribosom	26,895	16,73	5	4	1

[illegible]

325	Q9Y262 EIF3L_HUMAN	Eukaryotic t	26,117	7,82	4	4	1
325	Q9Y262 EIF3L_HUMAN	Eukaryotic t	26,117	7,82	4	4	1
325	Q9Y262 EIF3L_HUMAN	Eukaryotic t	26,117	7,82	4	4	1
325	Q9Y262 EIF3L_HUMAN	Eukaryotic t	26,117	7,82	4	4	1
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
326	P62851_RS25_HUMAN	40S ribosom	25,942	24,8	9	4	0
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
327	P43243_MATR3_HUMAN	Matrin-3 [C	25,859	6,86	10	4	1
328	Q9UBV2_SE1L1_HUMAN	Protein sel-	25,78	7,24	4	3	2
328	Q9UBV2_SE1L1_HUMAN	Protein sel-	25,78	7,24	4	3	2
328	Q9UBV2_SE1L1_HUMAN	Protein sel-	25,78	7,24	4	3	2
328	Q9UBV2_SE1L1_HUMAN	Protein sel-	25,78	7,24	4	3	2
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
329	P13797_PLST_HUMAN	Plastin-3	25,74	10,16	6	4	1
330	Q9UHD8_SEPT9_HUMAN	Septin-9 (M	25,683	7,58	4	4	7
330	Q9UHD8_SEPT9_HUMAN	Septin-9 (M	25,683	7,58	4	4	7
330	Q9UHD8_SEPT9_HUMAN	Septin-9 (M	25,683	7,58	4	4	7
330	Q9UHD8_SEPT9_HUMAN	Septin-9 (M	25,683	7,58	4	4	7
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
331	P63010_AP2B1_HUMAN	AP-2 compl	25,565	5,76	6	4	1
332	P06744_G6PI_HUMAN	Glucose-6- π	25,396	7,9	5	3	1

332	P06744_G6PI_HUMAN	Glucose-6- ϕ	25,396	7,9	5	3	1
332	P06744_G6PI_HUMAN	Glucose-6- ϕ	25,396	7,9	5	3	1
332	P06744_G6PI_HUMAN	Glucose-6- ϕ	25,396	7,9	5	3	1
332	P06744_G6PI_HUMAN	Glucose-6- ϕ	25,396	7,9	5	3	1
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
333	P07602_SAP_HUMAN	Proactivato	25,374	8,59	7	4	2
334	O43143_DHX15_HUMAN	Putative pri	25,313	5,79	4	4	0
334	O43143_DHX15_HUMAN	Putative pri	25,313	5,79	4	4	0
334	O43143_DHX15_HUMAN	Putative pri	25,313	5,79	4	4	0
334	O43143_DHX15_HUMAN	Putative pri	25,313	5,79	4	4	0
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
335	P20073_ANXA7_HUMAN	Annexin A7	25,282	9,01	7	4	1
336	Q86Y82_STX12_HUMAN	Syntaxin-12	25,159	16,67	5	3	0
336	Q86Y82_STX12_HUMAN	Syntaxin-12	25,159	16,67	5	3	0
336	Q86Y82_STX12_HUMAN	Syntaxin-12	25,159	16,67	5	3	0
336	Q86Y82_STX12_HUMAN	Syntaxin-12	25,159	16,67	5	3	0
336	Q86Y82_STX12_HUMAN	Syntaxin-12	25,159	16,67	5	3	0
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
337	Q9UKM9_RALY_HUMAN	RNA-bindin	25,157	13,1	6	4	1
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
338	P34931_HS71L_HUMAN	Heat shock	25,105	6,24	9	3	0
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4

339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
339	P62136_PP1A_HUMAN	Serine/thre	24,918	16,72	7	4	4
340	Q8NC51_PAIRB_HUMAN	Plasminoge	24,837	15,5	4	4	4
340	Q8NC51_PAIRB_HUMAN	Plasminoge	24,837	15,5	4	4	4
340	Q8NC51_PAIRB_HUMAN	Plasminoge	24,837	15,5	4	4	4
340	Q8NC51_PAIRB_HUMAN	Plasminoge	24,837	15,5	4	4	4
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
341	P11279_LAMP1_HUMAN	Lysosome-α	24,695	9,25	6	3	1
342	O00469_PLOD2_HUMAN	Procollager	24,69	5,76	5	4	2
342	O00469_PLOD2_HUMAN	Procollager	24,69	5,76	5	4	2
342	O00469_PLOD2_HUMAN	Procollager	24,69	5,76	5	4	2
342	O00469_PLOD2_HUMAN	Procollager	24,69	5,76	5	4	2
342	O00469_PLOD2_HUMAN	Procollager	24,69	5,76	5	4	2
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
343	P40939_ECHA_HUMAN	Trifunction:	24,597	5,5	6	3	1
344	P16401_H15_HUMAN	Histone H1.	24,528	17,33	5	4	1
344	P16401_H15_HUMAN	Histone H1.	24,528	17,33	5	4	1
344	P16401_H15_HUMAN	Histone H1.	24,528	17,33	5	4	1
344	P16401_H15_HUMAN	Histone H1.	24,528	17,33	5	4	1
344	P16401_H15_HUMAN	Histone H1.	24,528	17,33	5	4	1
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
345	P62140_PP1B_HUMAN	Serine/thre	24,524	18,4	7	4	4
346	P30153_2AAA_HUMAN	Serine/thre	24,492	9,51	5	4	1
346	P30153_2AAA_HUMAN	Serine/thre	24,492	9,51	5	4	1
346	P30153_2AAA_HUMAN	Serine/thre	24,492	9,51	5	4	1
346	P30153_2AAA_HUMAN	Serine/thre	24,492	9,51	5	4	1
346	P30153_2AAA_HUMAN	Serine/thre	24,492	9,51	5	4	1
347	POCG39_POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	POCG39_POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0

347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
347	P0CG39	POTEJ_HUMAN	POTE ankyr	24,45	3,28	14	3	0
348	P12111	_CO6A3_HUMAN	Collagen al	24,41	1,68	5	4	2
348	P12111	_CO6A3_HUMAN	Collagen al	24,41	1,68	5	4	2
348	P12111	_CO6A3_HUMAN	Collagen al	24,41	1,68	5	4	2
348	P12111	_CO6A3_HUMAN	Collagen al	24,41	1,68	5	4	2
348	P12111	_CO6A3_HUMAN	Collagen al	24,41	1,68	5	4	2
349	P25205	_MCM3_HUMAN	DNA replica	24,384	3,47	4	3	1
349	P25205	_MCM3_HUMAN	DNA replica	24,384	3,47	4	3	1
349	P25205	_MCM3_HUMAN	DNA replica	24,384	3,47	4	3	1
349	P25205	_MCM3_HUMAN	DNA replica	24,384	3,47	4	3	1
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
350	Q9Y5M8	SRPRB_HUMAN	Signal reco	24,03	14,39	6	3	0
351	Q6P2Q9	PRP8_HUMAN	Pre-mRNA-	23,955	2,01	4	4	1
351	Q6P2Q9	PRP8_HUMAN	Pre-mRNA-	23,955	2,01	4	4	1
351	Q6P2Q9	PRP8_HUMAN	Pre-mRNA-	23,955	2,01	4	4	1
351	Q6P2Q9	PRP8_HUMAN	Pre-mRNA-	23,955	2,01	4	4	1
352	Q13740	CD166_HUMAN	CD166 anti	23,899	9,35	4	4	2
352	Q13740	CD166_HUMAN	CD166 anti	23,899	9,35	4	4	2
352	Q13740	CD166_HUMAN	CD166 anti	23,899	9,35	4	4	2
352	Q13740	CD166_HUMAN	CD166 anti	23,899	9,35	4	4	2
353	Q13505	MTX1_HUMAN	Metaxin-1	23,894	10,52	4	4	2
353	Q13505	MTX1_HUMAN	Metaxin-1	23,894	10,52	4	4	2
353	Q13505	MTX1_HUMAN	Metaxin-1	23,894	10,52	4	4	2
353	Q13505	MTX1_HUMAN	Metaxin-1	23,894	10,52	4	4	2
354	Q16181	SEPT7_HUMAN	Septin-7 [IS	23,85	10,09	3	3	1
354	Q16181	SEPT7_HUMAN	Septin-7 [IS	23,85	10,09	3	3	1
354	Q16181	SEPT7_HUMAN	Septin-7 [IS	23,85	10,09	3	3	1
355	Q99497	PARK7_HUMAN	Protein DJ-	23,827	28,57	4	3	0
355	Q99497	PARK7_HUMAN	Protein DJ-	23,827	28,57	4	3	0

355	Q99497	PARK7_HUMAN	Protein DJ-	23,827	28,57	4	3	0
355	Q99497	PARK7_HUMAN	Protein DJ-	23,827	28,57	4	3	0
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
356	O15260	SURF4_HUMAN	Surfeit locu	23,788	23,27	7	3	1
357	P19105	ML12A_HUMAN	Myosin reg	23,764	27,65	4	4	3
357	P19105	ML12A_HUMAN	Myosin reg	23,764	27,65	4	4	3
357	P19105	ML12A_HUMAN	Myosin reg	23,764	27,65	4	4	3
357	P19105	ML12A_HUMAN	Myosin reg	23,764	27,65	4	4	3
358	O60568	PLOD3_HUMAN	Procollager	23,725	5,6	5	3	1
358	O60568	PLOD3_HUMAN	Procollager	23,725	5,6	5	3	1
358	O60568	PLOD3_HUMAN	Procollager	23,725	5,6	5	3	1
358	O60568	PLOD3_HUMAN	Procollager	23,725	5,6	5	3	1
358	O60568	PLOD3_HUMAN	Procollager	23,725	5,6	5	3	1
359	P46777	RL5_HUMAN	60S riboson	23,541	13,18	4	3	1
359	P46777	RL5_HUMAN	60S riboson	23,541	13,18	4	3	1
359	P46777	RL5_HUMAN	60S riboson	23,541	13,18	4	3	1
359	P46777	RL5_HUMAN	60S riboson	23,541	13,18	4	3	1
360	P12277	KCRB_HUMAN	Creatine kir	23,428	10,79	4	3	1
360	P12277	KCRB_HUMAN	Creatine kir	23,428	10,79	4	3	1
360	P12277	KCRB_HUMAN	Creatine kir	23,428	10,79	4	3	1
360	P12277	KCRB_HUMAN	Creatine kir	23,428	10,79	4	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
361	P50914	RL14_HUMAN	60S riboson	23,32	16,36	8	3	1
362	P62495	ERF1_HUMAN	Eukaryotic	23,144	8,03	4	3	1
362	P62495	ERF1_HUMAN	Eukaryotic	23,144	8,03	4	3	1
362	P62495	ERF1_HUMAN	Eukaryotic	23,144	8,03	4	3	1
362	P62495	ERF1_HUMAN	Eukaryotic	23,144	8,03	4	3	1
363	P42704	LPPRC_HUMAN	Leucine-ricl	22,988	2,77	3	3	1
363	P42704	LPPRC_HUMAN	Leucine-ricl	22,988	2,77	3	3	1
363	P42704	LPPRC_HUMAN	Leucine-ricl	22,988	2,77	3	3	1
364	O00203	AP3B1_HUMAN	AP-3 compl	22,947	4,2	3	3	0
364	O00203	AP3B1_HUMAN	AP-3 compl	22,947	4,2	3	3	0

364	O00203	AP3B1_HUMAN	AP-3 compl	22,947	4,2	3	3	0
365	P51659	DHB4_HUMAN	Enoyl-CoA l	22,828	5,99	4	3	2
365	P51659	DHB4_HUMAN	Enoyl-CoA l	22,828	5,99	4	3	2
365	P51659	DHB4_HUMAN	Enoyl-CoA l	22,828	5,99	4	3	2
365	P51659	DHB4_HUMAN	Enoyl-CoA l	22,828	5,99	4	3	2
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
366	P35637	FUS_HUMAN	RNA-bindin	22,8	6,29	7	3	1
367	P52907	CAZA1_HUMAN	F-actin-capl	22,763	15,79	4	3	1
367	P52907	CAZA1_HUMAN	F-actin-capl	22,763	15,79	4	3	1
367	P52907	CAZA1_HUMAN	F-actin-capl	22,763	15,79	4	3	1
367	P52907	CAZA1_HUMAN	F-actin-capl	22,763	15,79	4	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
368	P60866	RS20_HUMAN	40S ribosor	22,762	22,88	6	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
369	Q9UBG0	MRC2_HUMAN	C-type man	22,629	2,9	8	3	1
370	Q96AE4	FUBP1_HUMAN	Far upstrea	22,423	5,6	4	3	2
370	Q96AE4	FUBP1_HUMAN	Far upstrea	22,423	5,6	4	3	2
370	Q96AE4	FUBP1_HUMAN	Far upstrea	22,423	5,6	4	3	2
370	Q96AE4	FUBP1_HUMAN	Far upstrea	22,423	5,6	4	3	2
371	Q9UMS4	PRP19_HUMAN	Pre-mRNA-	22,339	7,55	5	3	1
371	Q9UMS4	PRP19_HUMAN	Pre-mRNA-	22,339	7,55	5	3	1
371	Q9UMS4	PRP19_HUMAN	Pre-mRNA-	22,339	7,55	5	3	1
371	Q9UMS4	PRP19_HUMAN	Pre-mRNA-	22,339	7,55	5	3	1
371	Q9UMS4	PRP19_HUMAN	Pre-mRNA-	22,339	7,55	5	3	1
372	P16615	AT2A2_HUMAN	Sarcoplasm	22,33	4,81	3	3	4
372	P16615	AT2A2_HUMAN	Sarcoplasm	22,33	4,81	3	3	4
372	P16615	AT2A2_HUMAN	Sarcoplasm	22,33	4,81	3	3	4
373	P61604	CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1

373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
373	P61604.CH10_HUMAN	10 kDa hea	22,288	35,64	7	3	1
374	P48047.ATPO_HUMAN	ATP syntha	22,245	18,42	4	3	1
374	P48047.ATPO_HUMAN	ATP syntha	22,245	18,42	4	3	1
374	P48047.ATPO_HUMAN	ATP syntha	22,245	18,42	4	3	1
374	P48047.ATPO_HUMAN	ATP syntha	22,245	18,42	4	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
375	P61158.ARP3_HUMAN	Actin-relate	22,193	10,79	6	3	1
376	P99999.CYC_HUMAN	Cytochrom	22,051	22,12	4	3	1
376	P99999.CYC_HUMAN	Cytochrom	22,051	22,12	4	3	1
376	P99999.CYC_HUMAN	Cytochrom	22,051	22,12	4	3	1
376	P99999.CYC_HUMAN	Cytochrom	22,051	22,12	4	3	1
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
377	P15259.PGAM2_HUMAN	Phosphogly	21,903	13,89	6	3	4
378	P61006.RAB8A_HUMAN	Ras-related	21,876	14,71	5	3	10
378	P61006.RAB8A_HUMAN	Ras-related	21,876	14,71	5	3	10
378	P61006.RAB8A_HUMAN	Ras-related	21,876	14,71	5	3	10
378	P61006.RAB8A_HUMAN	Ras-related	21,876	14,71	5	3	10
378	P61006.RAB8A_HUMAN	Ras-related	21,876	14,71	5	3	10
379	P26640.SYVC_HUMAN	Valine--tRN	21,709	2,77	3	3	1
379	P26640.SYVC_HUMAN	Valine--tRN	21,709	2,77	3	3	1
379	P26640.SYVC_HUMAN	Valine--tRN	21,709	2,77	3	3	1
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
380	P40429.RL13A_HUMAN	60S ribosom	21,698	18,32	7	4	2
381	Q02818.NUCB1_HUMAN	Nucleobind	21,683	5,75	4	3	1
381	Q02818.NUCB1_HUMAN	Nucleobind	21,683	5,75	4	3	1
381	Q02818.NUCB1_HUMAN	Nucleobind	21,683	5,75	4	3	1

381	Q02818.NUCB1_HUMAN	Nucleobind	21,683	5,75	4	3	1
382	P08648.ITA5_HUMAN	Integrin alp	21,595	5,74	4	3	2
382	P08648.ITA5_HUMAN	Integrin alp	21,595	5,74	4	3	2
382	P08648.ITA5_HUMAN	Integrin alp	21,595	5,74	4	3	2
382	P08648.ITA5_HUMAN	Integrin alp	21,595	5,74	4	3	2
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
383	Q92520.FAM3C_HUMAN	Protein FAM	21,568	8,37	6	2	1
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
384	P62879.GBB2_HUMAN	Guanine nu	21,527	12,98	7	3	3
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
385	O95302.FKBP9_HUMAN	Peptidyl-pri	21,497	5,86	6	3	1
386	P17066.HSP76_HUMAN	Heat shock	21,365	5,29	5	3	1
386	P17066.HSP76_HUMAN	Heat shock	21,365	5,29	5	3	1
386	P17066.HSP76_HUMAN	Heat shock	21,365	5,29	5	3	1
386	P17066.HSP76_HUMAN	Heat shock	21,365	5,29	5	3	1
386	P17066.HSP76_HUMAN	Heat shock	21,365	5,29	5	3	1
387	P38919.IF4A3_HUMAN	Eukaryotic i	21,34	9,76	4	4	1
387	P38919.IF4A3_HUMAN	Eukaryotic i	21,34	9,76	4	4	1
387	P38919.IF4A3_HUMAN	Eukaryotic i	21,34	9,76	4	4	1
387	P38919.IF4A3_HUMAN	Eukaryotic i	21,34	9,76	4	4	1
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
388	P18206.VINC_HUMAN	Vinculin [IS	21,329	4,6	10	3	2
389	P46459.NSF_HUMAN	Vesicle-fusi	21,167	3,63	3	3	0

389	P46459	NSF_HUMAN	Vesicle-fusi	21,167	3,63	3	3	0
389	P46459	NSF_HUMAN	Vesicle-fusi	21,167	3,63	3	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
390	Q99584	S10AD_HUMAN	Protein S10	21,158	33,67	7	3	0
391	Q96N66	MBOA7_HUMAN	Lysophosph	21,108	9,75	3	3	2
391	Q96N66	MBOA7_HUMAN	Lysophosph	21,108	9,75	3	3	2
391	Q96N66	MBOA7_HUMAN	Lysophosph	21,108	9,75	3	3	2
392	P61160	ARP2_HUMAN	Actin-relate	21,09	10,66	3	3	0
392	P61160	ARP2_HUMAN	Actin-relate	21,09	10,66	3	3	0
392	P61160	ARP2_HUMAN	Actin-relate	21,09	10,66	3	3	0
393	Q13492	PICAL_HUMAN	Phosphatid	21,09	7,54	3	3	2
393	Q13492	PICAL_HUMAN	Phosphatid	21,09	7,54	3	3	2
393	Q13492	PICAL_HUMAN	Phosphatid	21,09	7,54	3	3	2
394	P12109	CO6A1_HUMAN	Collagen al	21,066	3,79	3	3	1
394	P12109	CO6A1_HUMAN	Collagen al	21,066	3,79	3	3	1
394	P12109	CO6A1_HUMAN	Collagen al	21,066	3,79	3	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
395	P08708	RS17_HUMAN	40S ribosom	21,053	32,84	11	3	1
396	P32969	RL9_HUMAN	60S ribosom	20,982	20,83	5	3	0
396	P32969	RL9_HUMAN	60S ribosom	20,982	20,83	5	3	0
396	P32969	RL9_HUMAN	60S ribosom	20,982	20,83	5	3	0
396	P32969	RL9_HUMAN	60S ribosom	20,982	20,83	5	3	0
396	P32969	RL9_HUMAN	60S ribosom	20,982	20,83	5	3	0
397	Q14444	CAPR1_HUMAN	Caprin-1 (G	20,92	5,48	5	3	1
397	Q14444	CAPR1_HUMAN	Caprin-1 (G	20,92	5,48	5	3	1
397	Q14444	CAPR1_HUMAN	Caprin-1 (G	20,92	5,48	5	3	1
397	Q14444	CAPR1_HUMAN	Caprin-1 (G	20,92	5,48	5	3	1
397	Q14444	CAPR1_HUMAN	Caprin-1 (G	20,92	5,48	5	3	1
398	P51571	SSRD_HUMAN	Translocon	20,897	26,67	3	3	1

398	P51571_SSRD_HUMAN	Translocon-	20,897	26,67	3	3	1
398	P51571_SSRD_HUMAN	Translocon-	20,897	26,67	3	3	1
399	P60891_PRPS1_HUMAN	Ribose-pho	20,894	12,62	3	3	3
399	P60891_PRPS1_HUMAN	Ribose-pho	20,894	12,62	3	3	3
399	P60891_PRPS1_HUMAN	Ribose-pho	20,894	12,62	3	3	3
400	P61803_DAD1_HUMAN	Dolichyl-diç	20,842	28,57	4	3	1
400	P61803_DAD1_HUMAN	Dolichyl-diç	20,842	28,57	4	3	1
400	P61803_DAD1_HUMAN	Dolichyl-diç	20,842	28,57	4	3	1
400	P61803_DAD1_HUMAN	Dolichyl-diç	20,842	28,57	4	3	1
401	P24844_MYL9_HUMAN	Myosin reg	20,831	33,33	4	4	1
401	P24844_MYL9_HUMAN	Myosin reg	20,831	33,33	4	4	1
401	P24844_MYL9_HUMAN	Myosin reg	20,831	33,33	4	4	1
401	P24844_MYL9_HUMAN	Myosin reg	20,831	33,33	4	4	1
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
402	Q01105_SET_HUMAN	Protein SET	20,824	13,36	6	3	2
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
403	P62829_RL23_HUMAN	60S riboso	20,625	25,71	7	3	0
404	P47897_SYQ_HUMAN	Glutamine-	20,613	4,39	3	3	1
404	P47897_SYQ_HUMAN	Glutamine-	20,613	4,39	3	3	1
404	P47897_SYQ_HUMAN	Glutamine-	20,613	4,39	3	3	1
405	Q5SSJ5_HP1B3_HUMAN	Heterochro	20,575	5,07	3	3	2
405	Q5SSJ5_HP1B3_HUMAN	Heterochro	20,575	5,07	3	3	2
405	Q5SSJ5_HP1B3_HUMAN	Heterochro	20,575	5,07	3	3	2
406	P31930_QCR1_HUMAN	Cytochrom	20,559	6,5	3	3	1
406	P31930_QCR1_HUMAN	Cytochrom	20,559	6,5	3	3	1
406	P31930_QCR1_HUMAN	Cytochrom	20,559	6,5	3	3	1
407	P09211_GSTP1_HUMAN	Glutathione	20,537	19,62	3	3	1
407	P09211_GSTP1_HUMAN	Glutathione	20,537	19,62	3	3	1
407	P09211_GSTP1_HUMAN	Glutathione	20,537	19,62	3	3	1
408	P49591_SYSC_HUMAN	Seryl-tRNA	20,47	7,59	3	3	1
408	P49591_SYSC_HUMAN	Seryl-tRNA	20,47	7,59	3	3	1
408	P49591_SYSC_HUMAN	Seryl-tRNA	20,47	7,59	3	3	1

409	Q13151	ROAO_HUMAN	Heterogene	20,435	13,44	5	3	0
409	Q13151	ROAO_HUMAN	Heterogene	20,435	13,44	5	3	0
409	Q13151	ROAO_HUMAN	Heterogene	20,435	13,44	5	3	0
409	Q13151	ROAO_HUMAN	Heterogene	20,435	13,44	5	3	0
409	Q13151	ROAO_HUMAN	Heterogene	20,435	13,44	5	3	0
410	O00567	NOP56_HUMAN	Nucleolar p	20,423	5,39	3	3	0
410	O00567	NOP56_HUMAN	Nucleolar p	20,423	5,39	3	3	0
410	O00567	NOP56_HUMAN	Nucleolar p	20,423	5,39	3	3	0
411	Q9Y6C9	MTCH2_HUMAN	Mitochondi	20,327	10,93	4	3	1
411	Q9Y6C9	MTCH2_HUMAN	Mitochondi	20,327	10,93	4	3	1
411	Q9Y6C9	MTCH2_HUMAN	Mitochondi	20,327	10,93	4	3	1
411	Q9Y6C9	MTCH2_HUMAN	Mitochondi	20,327	10,93	4	3	1
412	Q9H299	SH3L3_HUMAN	SH3 domair	20,193	32,26	4	3	0
412	Q9H299	SH3L3_HUMAN	SH3 domair	20,193	32,26	4	3	0
412	Q9H299	SH3L3_HUMAN	SH3 domair	20,193	32,26	4	3	0
412	Q9H299	SH3L3_HUMAN	SH3 domair	20,193	32,26	4	3	0
413	P06756	ITAV_HUMAN	Integrin alp	20,046	4,15	3	3	3
413	P06756	ITAV_HUMAN	Integrin alp	20,046	4,15	3	3	3
413	P06756	ITAV_HUMAN	Integrin alp	20,046	4,15	3	3	3
414	Q9NSD9	SYFB_HUMAN	Phenylalan	20,042	5,26	3	3	0
414	Q9NSD9	SYFB_HUMAN	Phenylalan	20,042	5,26	3	3	0
414	Q9NSD9	SYFB_HUMAN	Phenylalan	20,042	5,26	3	3	0
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
415	O43175	SERA_HUMAN	D-3-phosph	19,997	6,2	6	3	1
416	O75694	NU155_HUMAN	Nuclear por	19,918	3,83	3	3	1
416	O75694	NU155_HUMAN	Nuclear por	19,918	3,83	3	3	1
416	O75694	NU155_HUMAN	Nuclear por	19,918	3,83	3	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
417	P60953	CDC42_HUMAN	Cell divisior	19,818	21,28	6	3	1
418	P33993	MCM7_HUMAN	DNA replica	19,803	5,71	5	3	1
418	P33993	MCM7_HUMAN	DNA replica	19,803	5,71	5	3	1
418	P33993	MCM7_HUMAN	DNA replica	19,803	5,71	5	3	1
418	P33993	MCM7_HUMAN	DNA replica	19,803	5,71	5	3	1
418	P33993	MCM7_HUMAN	DNA replica	19,803	5,71	5	3	1

419	Q15233	NONO_HUMAN	Non-POU d	19,791	9,77	3	3	0
419	Q15233	NONO_HUMAN	Non-POU d	19,791	9,77	3	3	0
419	Q15233	NONO_HUMAN	Non-POU d	19,791	9,77	3	3	0
420	Q15286	RAB35_HUMAN	Ras-related	19,751	15,42	5	3	1
420	Q15286	RAB35_HUMAN	Ras-related	19,751	15,42	5	3	1
420	Q15286	RAB35_HUMAN	Ras-related	19,751	15,42	5	3	1
420	Q15286	RAB35_HUMAN	Ras-related	19,751	15,42	5	3	1
420	Q15286	RAB35_HUMAN	Ras-related	19,751	15,42	5	3	1
421	P52292	IMA2_HUMAN	Importin su	19,728	7,95	3	3	1
421	P52292	IMA2_HUMAN	Importin su	19,728	7,95	3	3	1
421	P52292	IMA2_HUMAN	Importin su	19,728	7,95	3	3	1
422	P30041	PRDX6_HUMAN	Peroxiredo	19,725	17,04	3	3	1
422	P30041	PRDX6_HUMAN	Peroxiredo	19,725	17,04	3	3	1
422	P30041	PRDX6_HUMAN	Peroxiredo	19,725	17,04	3	3	1
423	P36542	ATPG_HUMAN	ATP syntha	19,603	12,09	5	3	2
423	P36542	ATPG_HUMAN	ATP syntha	19,603	12,09	5	3	2
423	P36542	ATPG_HUMAN	ATP syntha	19,603	12,09	5	3	2
423	P36542	ATPG_HUMAN	ATP syntha	19,603	12,09	5	3	2
423	P36542	ATPG_HUMAN	ATP syntha	19,603	12,09	5	3	2
424	A1L0T0	ILVBL_HUMAN	Acetolactat	19,589	9,49	3	3	1
424	A1L0T0	ILVBL_HUMAN	Acetolactat	19,589	9,49	3	3	1
424	A1L0T0	ILVBL_HUMAN	Acetolactat	19,589	9,49	3	3	1
425	P05023	AT1A1_HUMAN	Sodium/poi	19,557	2,85	3	3	2
425	P05023	AT1A1_HUMAN	Sodium/poi	19,557	2,85	3	3	2
425	P05023	AT1A1_HUMAN	Sodium/poi	19,557	2,85	3	3	2
426	P29590	PML_HUMAN	Probable tr	19,387	4,52	3	3	3
426	P29590	PML_HUMAN	Probable tr	19,387	4,52	3	3	3
426	P29590	PML_HUMAN	Probable tr	19,387	4,52	3	3	3
427	P30086	PEBP1_HUMAN	Phosphatid	19,372	19,35	4	3	1
427	P30086	PEBP1_HUMAN	Phosphatid	19,372	19,35	4	3	1
427	P30086	PEBP1_HUMAN	Phosphatid	19,372	19,35	4	3	1
427	P30086	PEBP1_HUMAN	Phosphatid	19,372	19,35	4	3	1
428	P06748	NPM_HUMAN	Nucleophos	19,328	13,21	4	3	1
428	P06748	NPM_HUMAN	Nucleophos	19,328	13,21	4	3	1
428	P06748	NPM_HUMAN	Nucleophos	19,328	13,21	4	3	1
428	P06748	NPM_HUMAN	Nucleophos	19,328	13,21	4	3	1
429	P02768	ALBU_HUMAN	Serum albu	19,309	8,39	3	3	2
429	P02768	ALBU_HUMAN	Serum albu	19,309	8,39	3	3	2
429	P02768	ALBU_HUMAN	Serum albu	19,309	8,39	3	3	2
430	P31947	1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947	1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1

430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
430	P31947_1433S_HUMAN	14-3-3 prot	19,213	12,5	19	3	1
431	Q13247_SRSF6_HUMAN	Serine/argi	19,153	7,46	4	3	1
431	Q13247_SRSF6_HUMAN	Serine/argi	19,153	7,46	4	3	1
431	Q13247_SRSF6_HUMAN	Serine/argi	19,153	7,46	4	3	1
431	Q13247_SRSF6_HUMAN	Serine/argi	19,153	7,46	4	3	1
432	P62910_RL32_HUMAN	60S ribosom	19,148	27,41	3	3	1
432	P62910_RL32_HUMAN	60S ribosom	19,148	27,41	3	3	1
432	P62910_RL32_HUMAN	60S ribosom	19,148	27,41	3	3	1
433	P17813_EGLN_HUMAN	Endoglin [C	19,127	6,32	4	3	2
433	P17813_EGLN_HUMAN	Endoglin [C	19,127	6,32	4	3	2
433	P17813_EGLN_HUMAN	Endoglin [C	19,127	6,32	4	3	2
433	P17813_EGLN_HUMAN	Endoglin [C	19,127	6,32	4	3	2
434	P36871_PGM1_HUMAN	Phosphoglu	19,077	6,24	3	3	2
434	P36871_PGM1_HUMAN	Phosphoglu	19,077	6,24	3	3	2
434	P36871_PGM1_HUMAN	Phosphoglu	19,077	6,24	3	3	2
435	Q9NYL9_TM0D3_HUMAN	Tropomodul	19,075	9,38	3	3	0
435	Q9NYL9_TM0D3_HUMAN	Tropomodul	19,075	9,38	3	3	0
435	Q9NYL9_TM0D3_HUMAN	Tropomodul	19,075	9,38	3	3	0
436	Q13263_TIF1B_HUMAN	Transcripti	19,071	5,84	3	3	2
436	Q13263_TIF1B_HUMAN	Transcripti	19,071	5,84	3	3	2
436	Q13263_TIF1B_HUMAN	Transcripti	19,071	5,84	3	3	2
437	P46977_STT3A_HUMAN	Dolichyl-di	19,044	3,83	3	3	0
437	P46977_STT3A_HUMAN	Dolichyl-di	19,044	3,83	3	3	0
437	P46977_STT3A_HUMAN	Dolichyl-di	19,044	3,83	3	3	0
438	Q15185_TEBP_HUMAN	Prostaglanc	18,93	20	3	3	0
438	Q15185_TEBP_HUMAN	Prostaglanc	18,93	20	3	3	0
438	Q15185_TEBP_HUMAN	Prostaglanc	18,93	20	3	3	0

439	P51114_FXR1_HUMAN	Fragile X m	18,781	5,97	2	2	3
439	P51114_FXR1_HUMAN	Fragile X m	18,781	5,97	2	2	3
440	P08729_K2C7_HUMAN	Keratin, typ	18,771	6,41	4	3	3
440	P08729_K2C7_HUMAN	Keratin, typ	18,771	6,41	4	3	3
440	P08729_K2C7_HUMAN	Keratin, typ	18,771	6,41	4	3	3
440	P08729_K2C7_HUMAN	Keratin, typ	18,771	6,41	4	3	3
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
441	P35241_RADI_HUMAN	Radixin	18,737	3,43	7	3	0
442	Q9UNX3_RL26L_HUMAN	60S ribosom	18,694	11,81	4	3	2
442	Q9UNX3_RL26L_HUMAN	60S ribosom	18,694	11,81	4	3	2
442	Q9UNX3_RL26L_HUMAN	60S ribosom	18,694	11,81	4	3	2
442	Q9UNX3_RL26L_HUMAN	60S ribosom	18,694	11,81	4	3	2
443	P50402_EMD_HUMAN	Emerin	18,646	12,2	4	3	0
443	P50402_EMD_HUMAN	Emerin	18,646	12,2	4	3	0
443	P50402_EMD_HUMAN	Emerin	18,646	12,2	4	3	0
443	P50402_EMD_HUMAN	Emerin	18,646	12,2	4	3	0
444	P43304_GPDM_HUMAN	Glycerol-3- β	18,563	5,82	5	3	2
444	P43304_GPDM_HUMAN	Glycerol-3- β	18,563	5,82	5	3	2
444	P43304_GPDM_HUMAN	Glycerol-3- β	18,563	5,82	5	3	2
444	P43304_GPDM_HUMAN	Glycerol-3- β	18,563	5,82	5	3	2
444	P43304_GPDM_HUMAN	Glycerol-3- β	18,563	5,82	5	3	2
445	Q13283_G3BP1_HUMAN	Ras GTPase	18,542	6,45	2	2	1
445	Q13283_G3BP1_HUMAN	Ras GTPase	18,542	6,45	2	2	1
446	P18085_ARF4_HUMAN	ADP-ribosyl	18,54	22,91	5	3	1
446	P18085_ARF4_HUMAN	ADP-ribosyl	18,54	22,91	5	3	1
446	P18085_ARF4_HUMAN	ADP-ribosyl	18,54	22,91	5	3	1
446	P18085_ARF4_HUMAN	ADP-ribosyl	18,54	22,91	5	3	1
446	P18085_ARF4_HUMAN	ADP-ribosyl	18,54	22,91	5	3	1
447	P14923_PLAK_HUMAN	Junction pla	18,513	4,43	3	3	1
447	P14923_PLAK_HUMAN	Junction pla	18,513	4,43	3	3	1
447	P14923_PLAK_HUMAN	Junction pla	18,513	4,43	3	3	1
448	P49411_EFTU_HUMAN	Elongation f	18,481	6,36	2	2	1
448	P49411_EFTU_HUMAN	Elongation f	18,481	6,36	2	2	1
449	Q92688_AN32B_HUMAN	Acidic leuci	18,408	20,51	3	3	1
449	Q92688_AN32B_HUMAN	Acidic leuci	18,408	20,51	3	3	1
449	Q92688_AN32B_HUMAN	Acidic leuci	18,408	20,51	3	3	1

450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
450	P63092_GNAS2_HUMAN	Guanine nu	18,4	7,65	6	3	5
451	P31942_HNRH3_HUMAN	Heterogene	18,381	19,42	3	2	1
451	P31942_HNRH3_HUMAN	Heterogene	18,381	19,42	3	2	1
451	P31942_HNRH3_HUMAN	Heterogene	18,381	19,42	3	2	1
452	P23528_COF1_HUMAN	Cofilin-1 (p:	18,335	32,12	5	3	1
452	P23528_COF1_HUMAN	Cofilin-1 (p:	18,335	32,12	5	3	1
452	P23528_COF1_HUMAN	Cofilin-1 (p:	18,335	32,12	5	3	1
452	P23528_COF1_HUMAN	Cofilin-1 (p:	18,335	32,12	5	3	1
452	P23528_COF1_HUMAN	Cofilin-1 (p:	18,335	32,12	5	3	1
453	P14866_HNRPL_HUMAN	Heterogene	18,323	5,26	3	3	0
453	P14866_HNRPL_HUMAN	Heterogene	18,323	5,26	3	3	0
453	P14866_HNRPL_HUMAN	Heterogene	18,323	5,26	3	3	0
454	P55010_IF5_HUMAN	Eukaryotic t	18,314	7,19	4	3	0
454	P55010_IF5_HUMAN	Eukaryotic t	18,314	7,19	4	3	0
454	P55010_IF5_HUMAN	Eukaryotic t	18,314	7,19	4	3	0
454	P55010_IF5_HUMAN	Eukaryotic t	18,314	7,19	4	3	0
455	Q9Y4L1_HYOU1_HUMAN	Hypoxia up	18,264	3,52	4	3	1
455	Q9Y4L1_HYOU1_HUMAN	Hypoxia up	18,264	3,52	4	3	1
455	Q9Y4L1_HYOU1_HUMAN	Hypoxia up	18,264	3,52	4	3	1
455	Q9Y4L1_HYOU1_HUMAN	Hypoxia up	18,264	3,52	4	3	1
456	P34932_HSP74_HUMAN	Heat shock	18,249	3,93	3	3	0
456	P34932_HSP74_HUMAN	Heat shock	18,249	3,93	3	3	0
456	P34932_HSP74_HUMAN	Heat shock	18,249	3,93	3	3	0
457	Q9H853_TBA4B_HUMAN	Putative tul	18,189	10,79	5	2	0
457	Q9H853_TBA4B_HUMAN	Putative tul	18,189	10,79	5	2	0
457	Q9H853_TBA4B_HUMAN	Putative tul	18,189	10,79	5	2	0
457	Q9H853_TBA4B_HUMAN	Putative tul	18,189	10,79	5	2	0
457	Q9H853_TBA4B_HUMAN	Putative tul	18,189	10,79	5	2	0
458	O75390_CISY_HUMAN	Citrate synt	18,154	7,06	5	3	1
458	O75390_CISY_HUMAN	Citrate synt	18,154	7,06	5	3	1
458	O75390_CISY_HUMAN	Citrate synt	18,154	7,06	5	3	1
458	O75390_CISY_HUMAN	Citrate synt	18,154	7,06	5	3	1
458	O75390_CISY_HUMAN	Citrate synt	18,154	7,06	5	3	1
459	O15400_STX7_HUMAN	Syntaxin-7	18,126	10,04	4	2	2
459	O15400_STX7_HUMAN	Syntaxin-7	18,126	10,04	4	2	2
459	O15400_STX7_HUMAN	Syntaxin-7	18,126	10,04	4	2	2
459	O15400_STX7_HUMAN	Syntaxin-7	18,126	10,04	4	2	2

[illegible]

471	Q8NBJ5_GT251_HUMAN	Procollagen	17,637	4,22	3	3	1
471	Q8NBJ5_GT251_HUMAN	Procollagen	17,637	4,22	3	3	1
471	Q8NBJ5_GT251_HUMAN	Procollagen	17,637	4,22	3	3	1
472	Q0ZGT2_NEXN_HUMAN	Nexilin [ISO	17,565	6,95	3	3	2
472	Q0ZGT2_NEXN_HUMAN	Nexilin [ISO	17,565	6,95	3	3	2
472	Q0ZGT2_NEXN_HUMAN	Nexilin [ISO	17,565	6,95	3	3	2
473	P14868_SYDC_HUMAN	Aspartate--	17,542	6,79	4	3	0
473	P14868_SYDC_HUMAN	Aspartate--	17,542	6,79	4	3	0
473	P14868_SYDC_HUMAN	Aspartate--	17,542	6,79	4	3	0
473	P14868_SYDC_HUMAN	Aspartate--	17,542	6,79	4	3	0
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
474	P56134_ATPK_HUMAN	ATP syntha:	17,538	27,27	7	2	2
475	P40227_TCPZ_HUMAN	T-complex	17,481	6,23	5	3	1
475	P40227_TCPZ_HUMAN	T-complex	17,481	6,23	5	3	1
475	P40227_TCPZ_HUMAN	T-complex	17,481	6,23	5	3	1
475	P40227_TCPZ_HUMAN	T-complex	17,481	6,23	5	3	1
475	P40227_TCPZ_HUMAN	T-complex	17,481	6,23	5	3	1
476	Q9BWM7_SFXN3_HUMAN	Sideroflexir	17,457	9,54	2	2	0
476	Q9BWM7_SFXN3_HUMAN	Sideroflexir	17,457	9,54	2	2	0
477	Q14566_MCM6_HUMAN	DNA replica	17,35	4,51	3	3	0
477	Q14566_MCM6_HUMAN	DNA replica	17,35	4,51	3	3	0
477	Q14566_MCM6_HUMAN	DNA replica	17,35	4,51	3	3	0
478	Q07021_C1QBP_HUMAN	Complemer	17,336	16,27	4	2	1
478	Q07021_C1QBP_HUMAN	Complemer	17,336	16,27	4	2	1
478	Q07021_C1QBP_HUMAN	Complemer	17,336	16,27	4	2	1
478	Q07021_C1QBP_HUMAN	Complemer	17,336	16,27	4	2	1
479	P35268_RL22_HUMAN	60S ribosom	17,317	18,9	4	2	1
479	P35268_RL22_HUMAN	60S ribosom	17,317	18,9	4	2	1
479	P35268_RL22_HUMAN	60S ribosom	17,317	18,9	4	2	1
479	P35268_RL22_HUMAN	60S ribosom	17,317	18,9	4	2	1
480	Q15758_AAAT_HUMAN	Neutral am	17,309	4,44	3	2	0
480	Q15758_AAAT_HUMAN	Neutral am	17,309	4,44	3	2	0
480	Q15758_AAAT_HUMAN	Neutral am	17,309	4,44	3	2	0
481	Q01813_K6PP_HUMAN	6-phosphof	17,3	4,85	4	2	0
481	Q01813_K6PP_HUMAN	6-phosphof	17,3	4,85	4	2	0
481	Q01813_K6PP_HUMAN	6-phosphof	17,3	4,85	4	2	0
481	Q01813_K6PP_HUMAN	6-phosphof	17,3	4,85	4	2	0

482	P07996.TSP1_HUMAN	Thrombosp	17,272	2	3	2	1
482	P07996.TSP1_HUMAN	Thrombosp	17,272	2	3	2	1
482	P07996.TSP1_HUMAN	Thrombosp	17,272	2	3	2	1
483	P30533.AMRP_HUMAN	Alpha-2-ma	17,244	10,22	4	3	1
483	P30533.AMRP_HUMAN	Alpha-2-ma	17,244	10,22	4	3	1
483	P30533.AMRP_HUMAN	Alpha-2-ma	17,244	10,22	4	3	1
483	P30533.AMRP_HUMAN	Alpha-2-ma	17,244	10,22	4	3	1
484	P50991.TCPD_HUMAN	T-complex j	17,203	4,83	5	2	1
484	P50991.TCPD_HUMAN	T-complex j	17,203	4,83	5	2	1
484	P50991.TCPD_HUMAN	T-complex j	17,203	4,83	5	2	1
484	P50991.TCPD_HUMAN	T-complex j	17,203	4,83	5	2	1
484	P50991.TCPD_HUMAN	T-complex j	17,203	4,83	5	2	1
485	P34897.GLYM_HUMAN	Serine hydr	17,096	9,47	3	3	1
485	P34897.GLYM_HUMAN	Serine hydr	17,096	9,47	3	3	1
485	P34897.GLYM_HUMAN	Serine hydr	17,096	9,47	3	3	1
486	Q16555.DPYL2_HUMAN	Dihydropyr	17,09	4,02	2	2	0
486	Q16555.DPYL2_HUMAN	Dihydropyr	17,09	4,02	2	2	0
487	P61769.B2MG_HUMAN	Beta-2-micr	16,997	32,65	3	2	2
487	P61769.B2MG_HUMAN	Beta-2-micr	16,997	32,65	3	2	2
487	P61769.B2MG_HUMAN	Beta-2-micr	16,997	32,65	3	2	2
488	Q9UBQ0.VPS29_HUMAN	Vacuolar pr	16,988	17,03	3	3	1
488	Q9UBQ0.VPS29_HUMAN	Vacuolar pr	16,988	17,03	3	3	1
488	Q9UBQ0.VPS29_HUMAN	Vacuolar pr	16,988	17,03	3	3	1
489	P49755.TMEDA_HUMAN	Transmemt	16,938	16,49	3	3	1
489	P49755.TMEDA_HUMAN	Transmemt	16,938	16,49	3	3	1
489	P49755.TMEDA_HUMAN	Transmemt	16,938	16,49	3	3	1
490	P22087.FBRL_HUMAN	rRNA 2'-O-r	16,918	13,4	3	3	0
490	P22087.FBRL_HUMAN	rRNA 2'-O-r	16,918	13,4	3	3	0
490	P22087.FBRL_HUMAN	rRNA 2'-O-r	16,918	13,4	3	3	0
491	Q8N556.AFAP1_HUMAN	Actin filame	16,824	5,48	3	3	0
491	Q8N556.AFAP1_HUMAN	Actin filame	16,824	5,48	3	3	0
491	Q8N556.AFAP1_HUMAN	Actin filame	16,824	5,48	3	3	0
492	Q14554.PDIA5_HUMAN	Protein disu	16,739	5,42	3	3	1
492	Q14554.PDIA5_HUMAN	Protein disu	16,739	5,42	3	3	1
492	Q14554.PDIA5_HUMAN	Protein disu	16,739	5,42	3	3	1
493	P12270.TPR_HUMAN	Nucleoprot	16,734	1,23	3	2	1
493	P12270.TPR_HUMAN	Nucleoprot	16,734	1,23	3	2	1
493	P12270.TPR_HUMAN	Nucleoprot	16,734	1,23	3	2	1
494	Q9HDC9.APMAP_HUMAN	Adipocyte p	16,733	12,11	3	3	1

494	Q9HDC9	APMAP_HUMAN	Adipocyte p	16,733	12,11	3	3	1
494	Q9HDC9	APMAP_HUMAN	Adipocyte p	16,733	12,11	3	3	1
495	P24539	AT5F1_HUMAN	ATP syntha	16,728	14,49	3	3	1
495	P24539	AT5F1_HUMAN	ATP syntha	16,728	14,49	3	3	1
495	P24539	AT5F1_HUMAN	ATP syntha	16,728	14,49	3	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
496	P38159	HNRPG_HUMAN	Heterogene	16,708	7,44	6	3	1
497	P20618	PSB1_HUMAN	Proteasome	16,691	12,68	2	2	1
497	P20618	PSB1_HUMAN	Proteasome	16,691	12,68	2	2	1
498	P07099	HYEP_HUMAN	Epoxide hyd	16,644	4,84	3	3	0
498	P07099	HYEP_HUMAN	Epoxide hyd	16,644	4,84	3	3	0
498	P07099	HYEP_HUMAN	Epoxide hyd	16,644	4,84	3	3	0
499	Q9UKV3	ACINU_HUMAN	Apoptotic c	16,638	2,09	4	3	2
499	Q9UKV3	ACINU_HUMAN	Apoptotic c	16,638	2,09	4	3	2
499	Q9UKV3	ACINU_HUMAN	Apoptotic c	16,638	2,09	4	3	2
499	Q9UKV3	ACINU_HUMAN	Apoptotic c	16,638	2,09	4	3	2
500	P37108	SRP14_HUMAN	Signal reco	16,576	20	3	2	1
500	P37108	SRP14_HUMAN	Signal reco	16,576	20	3	2	1
500	P37108	SRP14_HUMAN	Signal reco	16,576	20	3	2	1
501	Q70UQ0	IKIP_HUMAN	Inhibitor of	16,545	6,86	5	3	0
501	Q70UQ0	IKIP_HUMAN	Inhibitor of	16,545	6,86	5	3	0
501	Q70UQ0	IKIP_HUMAN	Inhibitor of	16,545	6,86	5	3	0
501	Q70UQ0	IKIP_HUMAN	Inhibitor of	16,545	6,86	5	3	0
501	Q70UQ0	IKIP_HUMAN	Inhibitor of	16,545	6,86	5	3	0
502	Q9NVD7	PARVA_HUMAN	Alpha-parvi	16,541	5,91	2	2	0
502	Q9NVD7	PARVA_HUMAN	Alpha-parvi	16,541	5,91	2	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
503	P13987	CD59_HUMAN	CD59 glyco	16,53	35,06	6	2	0
504	Q99439	CNN2_HUMAN	Calponin-2	16,507	9,09	3	2	1
504	Q99439	CNN2_HUMAN	Calponin-2	16,507	9,09	3	2	1
504	Q99439	CNN2_HUMAN	Calponin-2	16,507	9,09	3	2	1
505	Q9Y5X1	SNX9_HUMAN	Sorting nex	16,421	4,2	2	2	0
505	Q9Y5X1	SNX9_HUMAN	Sorting nex	16,421	4,2	2	2	0

506	O75380	NDUS6_HUMAN	NADH dehy	16,364	31,25	4	2	1
506	O75380	NDUS6_HUMAN	NADH dehy	16,364	31,25	4	2	1
506	O75380	NDUS6_HUMAN	NADH dehy	16,364	31,25	4	2	1
506	O75380	NDUS6_HUMAN	NADH dehy	16,364	31,25	4	2	1
507	P09669	COX6C_HUMAN	Cytochrome	16,3	21,62	4	3	1
507	P09669	COX6C_HUMAN	Cytochrome	16,3	21,62	4	3	1
507	P09669	COX6C_HUMAN	Cytochrome	16,3	21,62	4	3	1
507	P09669	COX6C_HUMAN	Cytochrome	16,3	21,62	4	3	1
508	Q9Y2D5	AKAP2_HUMAN	A-kinase an	16,298	3,96	2	2	4
508	Q9Y2D5	AKAP2_HUMAN	A-kinase an	16,298	3,96	2	2	4
509	Q13641	TPBG_HUMAN	Trophoblas	16,291	10,28	3	3	1
509	Q13641	TPBG_HUMAN	Trophoblas	16,291	10,28	3	3	1
509	Q13641	TPBG_HUMAN	Trophoblas	16,291	10,28	3	3	1
510	P09525	ANXA4_HUMAN	Annexin A4	16,283	6,92	2	2	1
510	P09525	ANXA4_HUMAN	Annexin A4	16,283	6,92	2	2	1
511	P09661	RU2A_HUMAN	U2 small nu	16,195	9,06	2	2	1
511	P09661	RU2A_HUMAN	U2 small nu	16,195	9,06	2	2	1
512	Q6IAA8	PDRO_HUMAN	Ragulator c	16,19	15	3	2	1
512	Q6IAA8	PDRO_HUMAN	Ragulator c	16,19	15	3	2	1
512	Q6IAA8	PDRO_HUMAN	Ragulator c	16,19	15	3	2	1
513	P62888	RL30_HUMAN	60S ribosom	16,189	24,56	4	2	1
513	P62888	RL30_HUMAN	60S ribosom	16,189	24,56	4	2	1
513	P62888	RL30_HUMAN	60S ribosom	16,189	24,56	4	2	1
513	P62888	RL30_HUMAN	60S ribosom	16,189	24,56	4	2	1
514	P07093	GDN_HUMAN	Glia-derive	16,141	5,8	2	2	2
514	P07093	GDN_HUMAN	Glia-derive	16,141	5,8	2	2	2
515	O75534	CSDE1_HUMAN	Cold shock	16,099	3,52	4	3	1
515	O75534	CSDE1_HUMAN	Cold shock	16,099	3,52	4	3	1
515	O75534	CSDE1_HUMAN	Cold shock	16,099	3,52	4	3	1
515	O75534	CSDE1_HUMAN	Cold shock	16,099	3,52	4	3	1
516	Q10713	MPPA_HUMAN	Mitochondi	16,075	7,32	3	3	1
516	Q10713	MPPA_HUMAN	Mitochondi	16,075	7,32	3	3	1
516	Q10713	MPPA_HUMAN	Mitochondi	16,075	7,32	3	3	1
517	Q92598	HS105_HUMAN	Heat shock	16,065	5,04	3	3	2
517	Q92598	HS105_HUMAN	Heat shock	16,065	5,04	3	3	2
517	Q92598	HS105_HUMAN	Heat shock	16,065	5,04	3	3	2
518	O00231	PSD11_HUMAN	26S proteas	16,032	6,18	3	3	1
518	O00231	PSD11_HUMAN	26S proteas	16,032	6,18	3	3	1
518	O00231	PSD11_HUMAN	26S proteas	16,032	6,18	3	3	1

519	P30049_ATPD_HUMAN	ATP syntha:	16,017	16,44	5	2	1
519	P30049_ATPD_HUMAN	ATP syntha:	16,017	16,44	5	2	1
519	P30049_ATPD_HUMAN	ATP syntha:	16,017	16,44	5	2	1
519	P30049_ATPD_HUMAN	ATP syntha:	16,017	16,44	5	2	1
519	P30049_ATPD_HUMAN	ATP syntha:	16,017	16,44	5	2	1
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
520	P62913_RL11_HUMAN	60S ribosom	15,872	12,99	8	2	2
521	Q15436_SC23A_HUMAN	Protein trar	15,84	2,88	2	2	1
521	Q15436_SC23A_HUMAN	Protein trar	15,84	2,88	2	2	1
522	P30443_1A01_HUMAN	HLA class II	15,81	7,33	5	2	3
522	P30443_1A01_HUMAN	HLA class II	15,81	7,33	5	2	3
522	P30443_1A01_HUMAN	HLA class II	15,81	7,33	5	2	3
522	P30443_1A01_HUMAN	HLA class II	15,81	7,33	5	2	3
522	P30443_1A01_HUMAN	HLA class II	15,81	7,33	5	2	3
523	Q53GQ0_DHB12_HUMAN	Estradiol 17	15,808	9,62	3	2	0
523	Q53GQ0_DHB12_HUMAN	Estradiol 17	15,808	9,62	3	2	0
523	Q53GQ0_DHB12_HUMAN	Estradiol 17	15,808	9,62	3	2	0
524	Q53FA7_QORX_HUMAN	Quinone ox	15,743	5,12	2	2	0
524	Q53FA7_QORX_HUMAN	Quinone ox	15,743	5,12	2	2	0
525	P04632_CPNS1_HUMAN	Calpain sm:	15,742	11,94	3	2	0
525	P04632_CPNS1_HUMAN	Calpain sm:	15,742	11,94	3	2	0
525	P04632_CPNS1_HUMAN	Calpain sm:	15,742	11,94	3	2	0
526	P41250_SYG_HUMAN	Glycine--tRl	15,732	3,52	2	2	0
526	P41250_SYG_HUMAN	Glycine--tRl	15,732	3,52	2	2	0
527	Q8IVL6_P3H3_HUMAN	Prolyl 3-hyc	15,705	3,21	2	2	1
527	Q8IVL6_P3H3_HUMAN	Prolyl 3-hyc	15,705	3,21	2	2	1
528	P02533_K1C14_HUMAN	Keratin, typ	15,694	5,1	5	2	1
528	P02533_K1C14_HUMAN	Keratin, typ	15,694	5,1	5	2	1
528	P02533_K1C14_HUMAN	Keratin, typ	15,694	5,1	5	2	1
528	P02533_K1C14_HUMAN	Keratin, typ	15,694	5,1	5	2	1
528	P02533_K1C14_HUMAN	Keratin, typ	15,694	5,1	5	2	1
529	Q8N4C6_NIN_HUMAN	Ninein (hNi	15,674	2,43	3	3	7
529	Q8N4C6_NIN_HUMAN	Ninein (hNi	15,674	2,43	3	3	7
529	Q8N4C6_NIN_HUMAN	Ninein (hNi	15,674	2,43	3	3	7

530	Q96I24_FUBP3_HUMAN	Far upstrea	15,609	5,6	2	2	1
530	Q96I24_FUBP3_HUMAN	Far upstrea	15,609	5,6	2	2	1
531	Q70UQ0 IKIP_HUMAN	Inhibitor of	15,571	7,16	3	3	0
531	Q70UQ0 IKIP_HUMAN	Inhibitor of	15,571	7,16	3	3	0
531	Q70UQ0 IKIP_HUMAN	Inhibitor of	15,571	7,16	3	3	0
532	Q00688.FKBP3_HUMAN	Peptidyl-pro	15,57	16,14	3	3	1
532	Q00688.FKBP3_HUMAN	Peptidyl-pro	15,57	16,14	3	3	1
532	Q00688.FKBP3_HUMAN	Peptidyl-pro	15,57	16,14	3	3	1
533	Q15393.SF3B3_HUMAN	Splicing fac	15,554	2,38	2	2	0
533	Q15393.SF3B3_HUMAN	Splicing fac	15,554	2,38	2	2	0
534	Q16630.CPSF6_HUMAN	Cleavage ar	15,53	8,79	3	2	2
534	Q16630.CPSF6_HUMAN	Cleavage ar	15,53	8,79	3	2	2
534	Q16630.CPSF6_HUMAN	Cleavage ar	15,53	8,79	3	2	2
535	P49748.ACADV_HUMAN	Very long-c	15,518	4,39	2	2	2
535	P49748.ACADV_HUMAN	Very long-c	15,518	4,39	2	2	2
536	Q9BUJ2_HNRL1_HUMAN	Heterogene	15,492	4,92	2	2	3
536	Q9BUJ2_HNRL1_HUMAN	Heterogene	15,492	4,92	2	2	3
537	P21281.VATB2_HUMAN	V-type prot	15,453	6,65	3	2	1
537	P21281.VATB2_HUMAN	V-type prot	15,453	6,65	3	2	1
537	P21281.VATB2_HUMAN	V-type prot	15,453	6,65	3	2	1
538	Q969X5.ERGI1_HUMAN	Endoplasmic	15,436	19,19	2	2	1
538	Q969X5.ERGI1_HUMAN	Endoplasmic	15,436	19,19	2	2	1
539	P08779.K1C16_HUMAN	Keratin, typ	15,408	4,87	3	2	1
539	P08779.K1C16_HUMAN	Keratin, typ	15,408	4,87	3	2	1
539	P08779.K1C16_HUMAN	Keratin, typ	15,408	4,87	3	2	1
540	Q9UQ80.PA2G4_HUMAN	Proliferatio	15,299	7,12	3	2	1
540	Q9UQ80.PA2G4_HUMAN	Proliferatio	15,299	7,12	3	2	1
540	Q9UQ80.PA2G4_HUMAN	Proliferatio	15,299	7,12	3	2	1
541	P60033.CD81_HUMAN	CD81 antigen	15,287	16,53	3	2	0
541	P60033.CD81_HUMAN	CD81 antigen	15,287	16,53	3	2	0
541	P60033.CD81_HUMAN	CD81 antigen	15,287	16,53	3	2	0
542	Q15459.SF3A1_HUMAN	Splicing fac	15,264	3,91	2	2	0
542	Q15459.SF3A1_HUMAN	Splicing fac	15,264	3,91	2	2	0
543	Q9Y230.RUVB2_HUMAN	RuvB-like 2	15,233	5,63	2	2	1
543	Q9Y230.RUVB2_HUMAN	RuvB-like 2	15,233	5,63	2	2	1
544	P62826.RAN_HUMAN	GTP-binding	15,23	9,77	3	2	1
544	P62826.RAN_HUMAN	GTP-binding	15,23	9,77	3	2	1
544	P62826.RAN_HUMAN	GTP-binding	15,23	9,77	3	2	1

545	P09874_PARP1_HUMAN	Poly [ADP-r	15,22	2,67	3	2	1
545	P09874_PARP1_HUMAN	Poly [ADP-r	15,22	2,67	3	2	1
545	P09874_PARP1_HUMAN	Poly [ADP-r	15,22	2,67	3	2	1
546	Q92791_SC65_HUMAN	Synaptoner	15,201	6,64	3	2	0
546	Q92791_SC65_HUMAN	Synaptoner	15,201	6,64	3	2	0
546	Q92791_SC65_HUMAN	Synaptoner	15,201	6,64	3	2	0
547	P62917_RL8_HUMAN	60S ribosom	15,117	6,64	4	2	1
547	P62917_RL8_HUMAN	60S ribosom	15,117	6,64	4	2	1
547	P62917_RL8_HUMAN	60S ribosom	15,117	6,64	4	2	1
547	P62917_RL8_HUMAN	60S ribosom	15,117	6,64	4	2	1
548	P20674_COX5A_HUMAN	Cytochrom	15,041	9,17	3	2	1
548	P20674_COX5A_HUMAN	Cytochrom	15,041	9,17	3	2	1
548	P20674_COX5A_HUMAN	Cytochrom	15,041	9,17	3	2	1
549	P24534_EF1B_HUMAN	Elongation	15,02	9,82	4	2	1
549	P24534_EF1B_HUMAN	Elongation	15,02	9,82	4	2	1
549	P24534_EF1B_HUMAN	Elongation	15,02	9,82	4	2	1
549	P24534_EF1B_HUMAN	Elongation	15,02	9,82	4	2	1
550	Q93008_USP9X_HUMAN	Probable ul	14,997	0,82	2	2	1
550	Q93008_USP9X_HUMAN	Probable ul	14,997	0,82	2	2	1
551	Q14019_COTL1_HUMAN	Coactosin-li	14,982	15,6	3	2	1
551	Q14019_COTL1_HUMAN	Coactosin-li	14,982	15,6	3	2	1
551	Q14019_COTL1_HUMAN	Coactosin-li	14,982	15,6	3	2	1
552	O76094_SRP72_HUMAN	Signal recoğ	14,877	4,03	2	2	1
552	O76094_SRP72_HUMAN	Signal recoğ	14,877	4,03	2	2	1
553	Q13423_NNTM_HUMAN	NAD transh	14,836	2,97	2	2	1
553	Q13423_NNTM_HUMAN	NAD transh	14,836	2,97	2	2	1
554	O14602_IF1AY_HUMAN	Eukaryotic t	14,835	10,49	2	2	3
554	O14602_IF1AY_HUMAN	Eukaryotic t	14,835	10,49	2	2	3
555	P46063_RECQ1_HUMAN	ATP-depen	14,834	4,94	3	2	1
555	P46063_RECQ1_HUMAN	ATP-depen	14,834	4,94	3	2	1
555	P46063_RECQ1_HUMAN	ATP-depen	14,834	4,94	3	2	1
556	P54136_SYRC_HUMAN	Arginyl-tRN	14,818	4,08	2	2	1
556	P54136_SYRC_HUMAN	Arginyl-tRN	14,818	4,08	2	2	1
557	Q6NYC8_PHTNS_HUMAN	Phostensin	14,797	6,53	2	2	0
557	Q6NYC8_PHTNS_HUMAN	Phostensin	14,797	6,53	2	2	0
558	Q9Y4P3_TBL2_HUMAN	Transducin	14,795	5,59	2	2	0
558	Q9Y4P3_TBL2_HUMAN	Transducin	14,795	5,59	2	2	0

559	O94874.UFL1_HUMAN	E3 UFM1-pi	14,706	5,3	2	2	2
559	O94874.UFL1_HUMAN	E3 UFM1-pi	14,706	5,3	2	2	2
560	P28066.PSA5_HUMAN	Proteasome	14,703	12,86	4	2	0
560	P28066.PSA5_HUMAN	Proteasome	14,703	12,86	4	2	0
560	P28066.PSA5_HUMAN	Proteasome	14,703	12,86	4	2	0
560	P28066.PSA5_HUMAN	Proteasome	14,703	12,86	4	2	0
561	Q4VXU2.PAP1L_HUMAN	Polyadenyl	14,694	3,26	4	2	0
561	Q4VXU2.PAP1L_HUMAN	Polyadenyl	14,694	3,26	4	2	0
561	Q4VXU2.PAP1L_HUMAN	Polyadenyl	14,694	3,26	4	2	0
561	Q4VXU2.PAP1L_HUMAN	Polyadenyl	14,694	3,26	4	2	0
562	P54920.SNAA_HUMAN	Alpha-solut	14,423	8,81	2	2	0
562	P54920.SNAA_HUMAN	Alpha-solut	14,423	8,81	2	2	0
563	P11177.ODPB_HUMAN	Pyruvate de	14,414	9,73	3	2	2
563	P11177.ODPB_HUMAN	Pyruvate de	14,414	9,73	3	2	2
563	P11177.ODPB_HUMAN	Pyruvate de	14,414	9,73	3	2	2
564	Q16795.NDUA9_HUMAN	NADH dehy	14,412	7,31	2	2	1
564	Q16795.NDUA9_HUMAN	NADH dehy	14,412	7,31	2	2	1
565	Q9Y3B3.TMED7_HUMAN	Transmembr	14,403	11,58	3	2	1
565	Q9Y3B3.TMED7_HUMAN	Transmembr	14,403	11,58	3	2	1
565	Q9Y3B3.TMED7_HUMAN	Transmembr	14,403	11,58	3	2	1
566	P09622.DLDH_HUMAN	Dihydrolipo	14,403	6,12	3	2	1
566	P09622.DLDH_HUMAN	Dihydrolipo	14,403	6,12	3	2	1
566	P09622.DLDH_HUMAN	Dihydrolipo	14,403	6,12	3	2	1
567	P04181.OAT_HUMAN	Ornithine a	14,403	5,2	2	2	2
567	P04181.OAT_HUMAN	Ornithine a	14,403	5,2	2	2	2
568	Q15043.S39AE_HUMAN	Zinc transp	14,387	6,93	2	2	0
568	Q15043.S39AE_HUMAN	Zinc transp	14,387	6,93	2	2	0
569	O75131.CPNE3_HUMAN	Copine-3 [C	14,376	4,66	4	2	1
569	O75131.CPNE3_HUMAN	Copine-3 [C	14,376	4,66	4	2	1
569	O75131.CPNE3_HUMAN	Copine-3 [C	14,376	4,66	4	2	1
569	O75131.CPNE3_HUMAN	Copine-3 [C	14,376	4,66	4	2	1
570	O14776.TCRG1_HUMAN	Transcripti	14,37	2,04	2	2	1
570	O14776.TCRG1_HUMAN	Transcripti	14,37	2,04	2	2	1
571	P98179.RBM3_HUMAN	Putative RN	14,354	21,02	2	2	0
571	P98179.RBM3_HUMAN	Putative RN	14,354	21,02	2	2	0
572	P18621.RL17_HUMAN	60S ribosom	14,345	16,39	3	2	1
572	P18621.RL17_HUMAN	60S ribosom	14,345	16,39	3	2	1
572	P18621.RL17_HUMAN	60S ribosom	14,345	16,39	3	2	1

573	Q08431.MFGM_HUMAN	Lactadherin	14,318	8,97	2	2	3
573	Q08431.MFGM_HUMAN	Lactadherin	14,318	8,97	2	2	3
574	Q04837.SSBP_HUMAN	Single-strand	14,311	22,73	3	2	0
574	Q04837.SSBP_HUMAN	Single-strand	14,311	22,73	3	2	0
574	Q04837.SSBP_HUMAN	Single-strand	14,311	22,73	3	2	0
575	Q16881.TRXR1_HUMAN	Thioredoxin	14,284	6,81	2	2	5
575	Q16881.TRXR1_HUMAN	Thioredoxin	14,284	6,81	2	2	5
576	P24752.THIL_HUMAN	Acetyl-CoA	14,26	6,35	3	2	1
576	P24752.THIL_HUMAN	Acetyl-CoA	14,26	6,35	3	2	1
576	P24752.THIL_HUMAN	Acetyl-CoA	14,26	6,35	3	2	1
577	Q14676.MDC1_HUMAN	Mediator of	14,253	3,75	2	2	3
577	Q14676.MDC1_HUMAN	Mediator of	14,253	3,75	2	2	3
578	P61221.ABCE1_HUMAN	ATP-binding	14,238	4,67	3	2	0
578	P61221.ABCE1_HUMAN	ATP-binding	14,238	4,67	3	2	0
578	P61221.ABCE1_HUMAN	ATP-binding	14,238	4,67	3	2	0
579	Q6UVK1.CSPG4_HUMAN	Chondroitin	14,21	1,66	2	2	1
579	Q6UVK1.CSPG4_HUMAN	Chondroitin	14,21	1,66	2	2	1
580	P08574.CY1_HUMAN	Cytochrome	14,204	11,62	2	2	1
580	P08574.CY1_HUMAN	Cytochrome	14,204	11,62	2	2	1
581	P59190.RAB15_HUMAN	Ras-related	14,184	10,58	4	2	1
581	P59190.RAB15_HUMAN	Ras-related	14,184	10,58	4	2	1
581	P59190.RAB15_HUMAN	Ras-related	14,184	10,58	4	2	1
581	P59190.RAB15_HUMAN	Ras-related	14,184	10,58	4	2	1
582	Q9UJZ1.STML2_HUMAN	Stomatin-lil	14,18	7,58	3	2	0
582	Q9UJZ1.STML2_HUMAN	Stomatin-lil	14,18	7,58	3	2	0
582	Q9UJZ1.STML2_HUMAN	Stomatin-lil	14,18	7,58	3	2	0
583	Q13243.SRSF5_HUMAN	Serine/argin	14,177	8,55	4	2	1
583	Q13243.SRSF5_HUMAN	Serine/argin	14,177	8,55	4	2	1
583	Q13243.SRSF5_HUMAN	Serine/argin	14,177	8,55	4	2	1
583	Q13243.SRSF5_HUMAN	Serine/argin	14,177	8,55	4	2	1
584	P10321.1C07_HUMAN	HLA class II	14,173	6,73	2	2	5
584	P10321.1C07_HUMAN	HLA class II	14,173	6,73	2	2	5
585	Q03135.CAV1_HUMAN	Caveolin-1	14,162	21,09	3	2	2
585	Q03135.CAV1_HUMAN	Caveolin-1	14,162	21,09	3	2	2
585	Q03135.CAV1_HUMAN	Caveolin-1	14,162	21,09	3	2	2
586	Q9NX63.CHCH3_HUMAN	Coiled-coil-	14,148	6,17	2	2	0
586	Q9NX63.CHCH3_HUMAN	Coiled-coil-	14,148	6,17	2	2	0
587	P42766.RL35_HUMAN	60S ribosom	14,131	18,85	5	2	1

587	P42766_RL35_HUMAN	60S ribosom	14,131	18,85	5	2	1
587	P42766_RL35_HUMAN	60S ribosom	14,131	18,85	5	2	1
587	P42766_RL35_HUMAN	60S ribosom	14,131	18,85	5	2	1
587	P42766_RL35_HUMAN	60S ribosom	14,131	18,85	5	2	1
588	Q15008.PSMD6_HUMAN	26S proteas	14,117	6,19	2	2	1
588	Q15008.PSMD6_HUMAN	26S proteas	14,117	6,19	2	2	1
589	Q9Y265_RUVB1_HUMAN	RuvB-like 1	14,088	6,14	3	2	0
589	Q9Y265_RUVB1_HUMAN	RuvB-like 1	14,088	6,14	3	2	0
589	Q9Y265_RUVB1_HUMAN	RuvB-like 1	14,088	6,14	3	2	0
590	O75531_BAF_HUMAN	Barrier-to-a	14,052	14,61	3	2	0
590	O75531_BAF_HUMAN	Barrier-to-a	14,052	14,61	3	2	0
590	O75531_BAF_HUMAN	Barrier-to-a	14,052	14,61	3	2	0
591	P49257_LMAN1_HUMAN	Protein ERC	13,992	5,42	4	2	0
591	P49257_LMAN1_HUMAN	Protein ERC	13,992	5,42	4	2	0
591	P49257_LMAN1_HUMAN	Protein ERC	13,992	5,42	4	2	0
591	P49257_LMAN1_HUMAN	Protein ERC	13,992	5,42	4	2	0
592	O75368_SH3L1_HUMAN	SH3 domair	13,986	13,16	4	2	0
592	O75368_SH3L1_HUMAN	SH3 domair	13,986	13,16	4	2	0
592	O75368_SH3L1_HUMAN	SH3 domair	13,986	13,16	4	2	0
592	O75368_SH3L1_HUMAN	SH3 domair	13,986	13,16	4	2	0
593	P49773_HINT1_HUMAN	Histidine tri	13,976	19,2	2	2	1
593	P49773_HINT1_HUMAN	Histidine tri	13,976	19,2	2	2	1
594	P33176_KINH_HUMAN	Kinesin-1 h	13,968	1,98	2	2	1
594	P33176_KINH_HUMAN	Kinesin-1 h	13,968	1,98	2	2	1
595	Q15293.RCN1_HUMAN	Reticulocall	13,965	6,95	2	2	1
595	Q15293.RCN1_HUMAN	Reticulocall	13,965	6,95	2	2	1
596	P30084_ECHM_HUMAN	Enoyl-CoA l	13,962	14,83	3	2	1
596	P30084_ECHM_HUMAN	Enoyl-CoA l	13,962	14,83	3	2	1
596	P30084_ECHM_HUMAN	Enoyl-CoA l	13,962	14,83	3	2	1
597	P17301_ITA2_HUMAN	Integrin alp	13,951	2,26	2	2	1
597	P17301_ITA2_HUMAN	Integrin alp	13,951	2,26	2	2	1
598	O14737.PDCD5_HUMAN	Programme	13,949	19,35	3	2	1
598	O14737.PDCD5_HUMAN	Programme	13,949	19,35	3	2	1
598	O14737.PDCD5_HUMAN	Programme	13,949	19,35	3	2	1
599	Q14344_GNA13_HUMAN	Guanine nu	13,901	5,57	4	2	0
599	Q14344_GNA13_HUMAN	Guanine nu	13,901	5,57	4	2	0
599	Q14344_GNA13_HUMAN	Guanine nu	13,901	5,57	4	2	0
599	Q14344_GNA13_HUMAN	Guanine nu	13,901	5,57	4	2	0
600	O14653_GOSR2_HUMAN	Golgi SNAP	13,895	14,62	2	2	1

600	O14653	GOSR2_HUMAN	Golgi SNAP	13,895	14,62	2	2	1
601	P22102	PUR2_HUMAN	Trifunction:	13,886	2,57	2	2	1
601	P22102	PUR2_HUMAN	Trifunction:	13,886	2,57	2	2	1
602	Q13895	BYST_HUMAN	Bystin	13,847	6,64	2	2	0
602	Q13895	BYST_HUMAN	Bystin	13,847	6,64	2	2	0
603	Q16666	IF16_HUMAN	Gamma-int	13,844	6,76	2	2	3
603	Q16666	IF16_HUMAN	Gamma-int	13,844	6,76	2	2	3
604	Q10567	AP1B1_HUMAN	AP-1 compl	13,792	3,83	4	2	2
604	Q10567	AP1B1_HUMAN	AP-1 compl	13,792	3,83	4	2	2
604	Q10567	AP1B1_HUMAN	AP-1 compl	13,792	3,83	4	2	2
604	Q10567	AP1B1_HUMAN	AP-1 compl	13,792	3,83	4	2	2
605	P14927	QCR7_HUMAN	Cytochrom	13,746	19,09	3	2	1
605	P14927	QCR7_HUMAN	Cytochrom	13,746	19,09	3	2	1
605	P14927	QCR7_HUMAN	Cytochrom	13,746	19,09	3	2	1
606	Q13177	PAK2_HUMAN	PAK-2p34 (I	13,734	8,96	2	2	1
606	Q13177	PAK2_HUMAN	PAK-2p34 (I	13,734	8,96	2	2	1
607	P62249	RS16_HUMAN	40S ribosom	13,725	14,48	5	2	1
607	P62249	RS16_HUMAN	40S ribosom	13,725	14,48	5	2	1
607	P62249	RS16_HUMAN	40S ribosom	13,725	14,48	5	2	1
607	P62249	RS16_HUMAN	40S ribosom	13,725	14,48	5	2	1
607	P62249	RS16_HUMAN	40S ribosom	13,725	14,48	5	2	1
608	O43294	TGFI1_HUMAN	Transformin	13,72	2,39	2	2	1
608	O43294	TGFI1_HUMAN	Transformin	13,72	2,39	2	2	1
609	A0FGR8	ESYT2_HUMAN	Extended sy	13,718	4,55	3	2	3
609	A0FGR8	ESYT2_HUMAN	Extended sy	13,718	4,55	3	2	3
609	A0FGR8	ESYT2_HUMAN	Extended sy	13,718	4,55	3	2	3
610	Q9Y512	SAM50_HUMAN	Sorting and	13,716	4,26	2	2	0
610	Q9Y512	SAM50_HUMAN	Sorting and	13,716	4,26	2	2	0
611	Q8WUM4	PDC6L_HUMAN	Programme	13,711	2,54	2	2	1
611	Q8WUM4	PDC6L_HUMAN	Programme	13,711	2,54	2	2	1
612	P09496	CLCA_HUMAN	Clathrin lig	13,68	8,26	2	2	2
612	P09496	CLCA_HUMAN	Clathrin lig	13,68	8,26	2	2	2
613	P63000	RAC1_HUMAN	Ras-related	13,66	11,98	2	2	1
613	P63000	RAC1_HUMAN	Ras-related	13,66	11,98	2	2	1
614	P68402	PA1B2_HUMAN	Platelet-act	13,631	12,66	2	2	0
614	P68402	PA1B2_HUMAN	Platelet-act	13,631	12,66	2	2	0
615	O15145	ARPC3_HUMAN	Actin-relate	13,615	10,17	3	2	1

615	O15145_ARPC3_HUMAN	Actin-relate	13,615	10,17	3	2	1
615	O15145_ARPC3_HUMAN	Actin-relate	13,615	10,17	3	2	1
616	P26368_U2AF2_HUMAN	Splicing fac	13,614	3,82	5	2	2
616	P26368_U2AF2_HUMAN	Splicing fac	13,614	3,82	5	2	2
616	P26368_U2AF2_HUMAN	Splicing fac	13,614	3,82	5	2	2
616	P26368_U2AF2_HUMAN	Splicing fac	13,614	3,82	5	2	2
616	P26368_U2AF2_HUMAN	Splicing fac	13,614	3,82	5	2	2
617	O43684_BUB3_HUMAN	Mitotic che	13,6	7,06	2	2	1
617	O43684_BUB3_HUMAN	Mitotic che	13,6	7,06	2	2	1
618	P13073_COX41_HUMAN	Cytochrom	13,554	14,29	2	2	1
618	P13073_COX41_HUMAN	Cytochrom	13,554	14,29	2	2	1
619	P62995_TRA2B_HUMAN	Transforme	13,525	12,23	2	2	1
619	P62995_TRA2B_HUMAN	Transforme	13,525	12,23	2	2	1
620	P26373_RL13_HUMAN	60S ribosom	13,5	10	4	2	1
620	P26373_RL13_HUMAN	60S ribosom	13,5	10	4	2	1
620	P26373_RL13_HUMAN	60S ribosom	13,5	10	4	2	1
620	P26373_RL13_HUMAN	60S ribosom	13,5	10	4	2	1
621	O75844_FACE1_HUMAN	CAAX preny	13,491	6,74	2	2	0
621	O75844_FACE1_HUMAN	CAAX preny	13,491	6,74	2	2	0
622	Q9UKM7_MA1B1_HUMAN	Endoplasmic	13,474	3,15	2	2	0
622	Q9UKM7_MA1B1_HUMAN	Endoplasmic	13,474	3,15	2	2	0
623	P29992_GNA11_HUMAN	Guanine nu	13,473	7,8	2	2	0
623	P29992_GNA11_HUMAN	Guanine nu	13,473	7,8	2	2	0
624	P62750_RL23A_HUMAN	60S ribosom	13,416	15,48	3	2	1
624	P62750_RL23A_HUMAN	60S ribosom	13,416	15,48	3	2	1
624	P62750_RL23A_HUMAN	60S ribosom	13,416	15,48	3	2	1
625	P42224_STAT1_HUMAN	Signal trans	13,402	3,93	2	2	1
625	P42224_STAT1_HUMAN	Signal trans	13,402	3,93	2	2	1
626	P30837_AL1B1_HUMAN	Aldehyde d	13,362	4,2	3	2	1
626	P30837_AL1B1_HUMAN	Aldehyde d	13,362	4,2	3	2	1
626	P30837_AL1B1_HUMAN	Aldehyde d	13,362	4,2	3	2	1
627	Q9H930_LY10L_HUMAN	Nuclear box	13,331	4,96	3	2	1
627	Q9H930_LY10L_HUMAN	Nuclear box	13,331	4,96	3	2	1
627	Q9H930_LY10L_HUMAN	Nuclear box	13,331	4,96	3	2	1
628	Q9UHX1_PUF60_HUMAN	Poly(U)-bin	13,318	8,22	2	2	5
628	Q9UHX1_PUF60_HUMAN	Poly(U)-bin	13,318	8,22	2	2	5
629	Q9NP72_RAB18_HUMAN	Ras-related	13,312	11,33	2	2	1
629	Q9NP72_RAB18_HUMAN	Ras-related	13,312	11,33	2	2	1

630	Q9UJS0	CMC2_HUMAN	Calcium-bir	13,273	5,63	2	2	0
630	Q9UJS0	CMC2_HUMAN	Calcium-bir	13,273	5,63	2	2	0
631	Q9UL25	RAB21_HUMAN	Ras-related	13,262	9,95	3	2	1
631	Q9UL25	RAB21_HUMAN	Ras-related	13,262	9,95	3	2	1
631	Q9UL25	RAB21_HUMAN	Ras-related	13,262	9,95	3	2	1
632	O75915	PRAF3_HUMAN	PRA1 family	13,254	13,83	4	2	0
632	O75915	PRAF3_HUMAN	PRA1 family	13,254	13,83	4	2	0
632	O75915	PRAF3_HUMAN	PRA1 family	13,254	13,83	4	2	0
632	O75915	PRAF3_HUMAN	PRA1 family	13,254	13,83	4	2	0
633	P62244	RS15A_HUMAN	40S ribosom	13,248	10,85	4	2	1
633	P62244	RS15A_HUMAN	40S ribosom	13,248	10,85	4	2	1
633	P62244	RS15A_HUMAN	40S ribosom	13,248	10,85	4	2	1
633	P62244	RS15A_HUMAN	40S ribosom	13,248	10,85	4	2	1
634	Q9P0L0	VAPA_HUMAN	Vesicle-assc	13,248	13,31	4	2	2
634	Q9P0L0	VAPA_HUMAN	Vesicle-assc	13,248	13,31	4	2	2
634	Q9P0L0	VAPA_HUMAN	Vesicle-assc	13,248	13,31	4	2	2
634	Q9P0L0	VAPA_HUMAN	Vesicle-assc	13,248	13,31	4	2	2
635	P14314	GLU2B_HUMAN	Glucosidase	13,212	7	4	2	1
635	P14314	GLU2B_HUMAN	Glucosidase	13,212	7	4	2	1
635	P14314	GLU2B_HUMAN	Glucosidase	13,212	7	4	2	1
635	P14314	GLU2B_HUMAN	Glucosidase	13,212	7	4	2	1
636	P62899	RL31_HUMAN	60S ribosom	13,182	17,6	5	2	0
636	P62899	RL31_HUMAN	60S ribosom	13,182	17,6	5	2	0
636	P62899	RL31_HUMAN	60S ribosom	13,182	17,6	5	2	0
636	P62899	RL31_HUMAN	60S ribosom	13,182	17,6	5	2	0
636	P62899	RL31_HUMAN	60S ribosom	13,182	17,6	5	2	0
637	P46776	RL27A_HUMAN	60S ribosom	13,169	14,29	4	2	1
637	P46776	RL27A_HUMAN	60S ribosom	13,169	14,29	4	2	1
637	P46776	RL27A_HUMAN	60S ribosom	13,169	14,29	4	2	1
637	P46776	RL27A_HUMAN	60S ribosom	13,169	14,29	4	2	1
638	P51572	BAP31_HUMAN	B-cell recep	13,147	9,8	4	2	1
638	P51572	BAP31_HUMAN	B-cell recep	13,147	9,8	4	2	1
638	P51572	BAP31_HUMAN	B-cell recep	13,147	9,8	4	2	1
638	P51572	BAP31_HUMAN	B-cell recep	13,147	9,8	4	2	1
639	O75340	PDCD6_HUMAN	Programme	13,141	10,99	2	2	0
639	O75340	PDCD6_HUMAN	Programme	13,141	10,99	2	2	0
640	Q969H8	CS010_HUMAN	UPF0556 pr	13,119	17,61	3	2	1
640	Q969H8	CS010_HUMAN	UPF0556 pr	13,119	17,61	3	2	1
640	Q969H8	CS010_HUMAN	UPF0556 pr	13,119	17,61	3	2	1
641	Q01844	EWS_HUMAN	RNA-bindin	13,082	4,97	4	2	1

641	Q01844.EWS_HUMAN	RNA-bindin	13,082	4,97	4	2	1
641	Q01844.EWS_HUMAN	RNA-bindin	13,082	4,97	4	2	1
641	Q01844.EWS_HUMAN	RNA-bindin	13,082	4,97	4	2	1
642	Q9UJ70.NAGK_HUMAN	N-acetyl-D-	13,076	6,41	2	2	1
642	Q9UJ70.NAGK_HUMAN	N-acetyl-D-	13,076	6,41	2	2	1
643	P12004.PCNA_HUMAN	Proliferatin	13,062	8,43	4	2	0
643	P12004.PCNA_HUMAN	Proliferatin	13,062	8,43	4	2	0
643	P12004.PCNA_HUMAN	Proliferatin	13,062	8,43	4	2	0
643	P12004.PCNA_HUMAN	Proliferatin	13,062	8,43	4	2	0
644	P35221.CTNA1_HUMAN	Catenin alp	13,056	2,76	3	2	2
644	P35221.CTNA1_HUMAN	Catenin alp	13,056	2,76	3	2	2
644	P35221.CTNA1_HUMAN	Catenin alp	13,056	2,76	3	2	2
645	P16152.CBR1_HUMAN	Carbonyl re	13,056	6,88	2	2	1
645	P16152.CBR1_HUMAN	Carbonyl re	13,056	6,88	2	2	1
646	A2RRP1.NBAS_HUMAN	Neuroblast	13,035	0,84	2	2	1
646	A2RRP1.NBAS_HUMAN	Neuroblast	13,035	0,84	2	2	1
647	Q14498.RBM39_HUMAN	RNA-bindin	13,001	4,39	4	2	2
647	Q14498.RBM39_HUMAN	RNA-bindin	13,001	4,39	4	2	2
647	Q14498.RBM39_HUMAN	RNA-bindin	13,001	4,39	4	2	2
647	Q14498.RBM39_HUMAN	RNA-bindin	13,001	4,39	4	2	2
648	Q99805.TM9S2_HUMAN	Transmemk	12,976	4,09	2	2	1
648	Q99805.TM9S2_HUMAN	Transmemk	12,976	4,09	2	2	1
649	Q9Y2W2.WBP11_HUMAN	WW domai	12,928	4,52	2	2	0
649	Q9Y2W2.WBP11_HUMAN	WW domai	12,928	4,52	2	2	0
650	P35613.BASI_HUMAN	Basigin (EM	12,914	8,55	3	2	2
650	P35613.BASI_HUMAN	Basigin (EM	12,914	8,55	3	2	2
650	P35613.BASI_HUMAN	Basigin (EM	12,914	8,55	3	2	2
651	O75489.NDUS3_HUMAN	NADH dehy	12,888	12,28	2	2	1
651	O75489.NDUS3_HUMAN	NADH dehy	12,888	12,28	2	2	1
652	Q9BXP5.SRRT_HUMAN	Serrate RN/	12,874	1,67	2	2	4
652	Q9BXP5.SRRT_HUMAN	Serrate RN/	12,874	1,67	2	2	4
653	Q8N163.K1967_HUMAN	Protein KIA	12,856	2,38	2	2	1
653	Q8N163.K1967_HUMAN	Protein KIA	12,856	2,38	2	2	1
654	O94905.ERLN2_HUMAN	Erlin-2 (SPF	12,813	9,44	2	2	0
654	O94905.ERLN2_HUMAN	Erlin-2 (SPF	12,813	9,44	2	2	0
655	O43747.AP1G1_HUMAN	AP-1 compl	12,809	2,31	2	2	2
655	O43747.AP1G1_HUMAN	AP-1 compl	12,809	2,31	2	2	2

656	P84103	SRSF3_HUMAN	Serine/argi	12,685	14,02	3	2	0
656	P84103	SRSF3_HUMAN	Serine/argi	12,685	14,02	3	2	0
656	P84103	SRSF3_HUMAN	Serine/argi	12,685	14,02	3	2	0
657	O00629	IMA4_HUMAN	Importin su	12,667	5,77	2	2	1
657	O00629	IMA4_HUMAN	Importin su	12,667	5,77	2	2	1
658	O94826	TOM70_HUMAN	Mitochondi	12,649	3,29	2	2	1
658	O94826	TOM70_HUMAN	Mitochondi	12,649	3,29	2	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
659	P60903	S10AA_HUMAN	Protein S10	12,621	28,12	6	2	1
660	P10301	RRAS_HUMAN	Ras-related	12,59	8,84	2	2	1
660	P10301	RRAS_HUMAN	Ras-related	12,59	8,84	2	2	1
661	P11387	TOP1_HUMAN	DNA topois	12,59	3,66	2	2	1
661	P11387	TOP1_HUMAN	DNA topois	12,59	3,66	2	2	1
662	Q96CW1	AP2M1_HUMAN	AP-2 compl	12,586	3,91	3	2	1
662	Q96CW1	AP2M1_HUMAN	AP-2 compl	12,586	3,91	3	2	1
662	Q96CW1	AP2M1_HUMAN	AP-2 compl	12,586	3,91	3	2	1
663	Q9HBRO	S38AA_HUMAN	Putative sor	12,573	3,35	2	2	1
663	Q9HBRO	S38AA_HUMAN	Putative sor	12,573	3,35	2	2	1
664	Q16698	DECR_HUMAN	2,4-dienoyl	12,556	7,97	2	2	1
664	Q16698	DECR_HUMAN	2,4-dienoyl	12,556	7,97	2	2	1
665	Q92804	RBP56_HUMAN	TATA-bindin	12,543	3,04	2	2	1
665	Q92804	RBP56_HUMAN	TATA-bindin	12,543	3,04	2	2	1
666	P23634	AT2B4_HUMAN	Plasma mer	12,532	1,34	3	2	7
666	P23634	AT2B4_HUMAN	Plasma mer	12,532	1,34	3	2	7
666	P23634	AT2B4_HUMAN	Plasma mer	12,532	1,34	3	2	7
667	P26639	SYTC_HUMAN	Threonyl-tR	12,485	2,63	2	2	0
667	P26639	SYTC_HUMAN	Threonyl-tR	12,485	2,63	2	2	0
668	O15144	ARPC2_HUMAN	Actin-relate	12,421	6,67	3	2	0
668	O15144	ARPC2_HUMAN	Actin-relate	12,421	6,67	3	2	0
668	O15144	ARPC2_HUMAN	Actin-relate	12,421	6,67	3	2	0
669	Q9P0K7	RAI14_HUMAN	Ankycorbin	12,398	1,44	2	2	2
669	Q9P0K7	RAI14_HUMAN	Ankycorbin	12,398	1,44	2	2	2
670	P39687	AN32A_HUMAN	Acidic leuci	12,341	10,84	2	2	0
670	P39687	AN32A_HUMAN	Acidic leuci	12,341	10,84	2	2	0

671	P63173	RL38_HUMAN	60S ribosom	12,328	28,57	4	2	1
671	P63173	RL38_HUMAN	60S ribosom	12,328	28,57	4	2	1
671	P63173	RL38_HUMAN	60S ribosom	12,328	28,57	4	2	1
671	P63173	RL38_HUMAN	60S ribosom	12,328	28,57	4	2	1
672	Q9H0S4	DDX47_HUMAN	Probable A	12,327	6,17	2	2	1
672	Q9H0S4	DDX47_HUMAN	Probable A	12,327	6,17	2	2	1
673	Q9Y3I0	CV028_HUMAN	UPF0027 pr	12,321	7,72	2	2	0
673	Q9Y3I0	CV028_HUMAN	UPF0027 pr	12,321	7,72	2	2	0
674	P63167	DYL1_HUMAN	Dynein ligh	12,3	24,72	3	2	1
674	P63167	DYL1_HUMAN	Dynein ligh	12,3	24,72	3	2	1
674	P63167	DYL1_HUMAN	Dynein ligh	12,3	24,72	3	2	1
675	Q12797	ASPH_HUMAN	Aspartyl/as	12,295	3,69	2	2	0
675	Q12797	ASPH_HUMAN	Aspartyl/as	12,295	3,69	2	2	0
676	Q9Y3U8	RL36_HUMAN	60S ribosom	12,234	18,27	3	2	1
676	Q9Y3U8	RL36_HUMAN	60S ribosom	12,234	18,27	3	2	1
676	Q9Y3U8	RL36_HUMAN	60S ribosom	12,234	18,27	3	2	1
677	Q8TAQ2	SMRC2_HUMAN	SWI/SNF co	12,23	1,95	2	2	1
677	Q8TAQ2	SMRC2_HUMAN	SWI/SNF co	12,23	1,95	2	2	1
678	P26196	DDX6_HUMAN	Probable A	12,223	5,18	3	2	0
678	P26196	DDX6_HUMAN	Probable A	12,223	5,18	3	2	0
678	P26196	DDX6_HUMAN	Probable A	12,223	5,18	3	2	0
679	P16949	STMN1_HUMAN	Stathmin (C	12,222	7,38	3	2	1
679	P16949	STMN1_HUMAN	Stathmin (C	12,222	7,38	3	2	1
679	P16949	STMN1_HUMAN	Stathmin (C	12,222	7,38	3	2	1
680	P36957	ODO2_HUMAN	Dihydrolipo	12,218	5,7	2	2	1
680	P36957	ODO2_HUMAN	Dihydrolipo	12,218	5,7	2	2	1
681	Q02880	TOP2B_HUMAN	DNA topois	12,187	1,17	2	2	1
681	Q02880	TOP2B_HUMAN	DNA topois	12,187	1,17	2	2	1
682	P42892	ECE1_HUMAN	Endothelin-	12,186	5,17	2	2	3
682	P42892	ECE1_HUMAN	Endothelin-	12,186	5,17	2	2	3
683	P05161	ISG15_HUMAN	Ubiquitin-li	12,179	14,1	3	2	1
683	P05161	ISG15_HUMAN	Ubiquitin-li	12,179	14,1	3	2	1
683	P05161	ISG15_HUMAN	Ubiquitin-li	12,179	14,1	3	2	1
684	Q15417	CNN3_HUMAN	Calponin-3	12,168	9,12	5	2	0
684	Q15417	CNN3_HUMAN	Calponin-3	12,168	9,12	5	2	0
684	Q15417	CNN3_HUMAN	Calponin-3	12,168	9,12	5	2	0
684	Q15417	CNN3_HUMAN	Calponin-3	12,168	9,12	5	2	0
684	Q15417	CNN3_HUMAN	Calponin-3	12,168	9,12	5	2	0

685	P49821_NDUV1_HUMAN	NADH dehy	12,1	3,38	2	2	2
685	P49821_NDUV1_HUMAN	NADH dehy	12,1	3,38	2	2	2
686	P25786_PSA1_HUMAN	Proteasome	12,098	7,98	2	2	1
686	P25786_PSA1_HUMAN	Proteasome	12,098	7,98	2	2	1
687	O95816_BAG2_HUMAN	BAG family	12,086	11,85	2	2	0
687	O95816_BAG2_HUMAN	BAG family	12,086	11,85	2	2	0
688	Q7L014_DDX46_HUMAN	Probable A	12,046	1,84	3	2	0
688	Q7L014_DDX46_HUMAN	Probable A	12,046	1,84	3	2	0
688	Q7L014_DDX46_HUMAN	Probable A	12,046	1,84	3	2	0
689	P46939_UTRO_HUMAN	Utrophin (C	12,041	0,61	2	2	0
689	P46939_UTRO_HUMAN	Utrophin (C	12,041	0,61	2	2	0
690	Q13425_SNTB2_HUMAN	Beta-2-synt	12,01	4,26	3	2	0
690	Q13425_SNTB2_HUMAN	Beta-2-synt	12,01	4,26	3	2	0
690	Q13425_SNTB2_HUMAN	Beta-2-synt	12,01	4,26	3	2	0
691	P28370_SMCA1_HUMAN	Probable gl	11,999	2,02	2	2	2
691	P28370_SMCA1_HUMAN	Probable gl	11,999	2,02	2	2	2
692	Q8WUJ3_K1199_HUMAN	Protein KIA	11,895	1,35	2	2	1
692	Q8WUJ3_K1199_HUMAN	Protein KIA	11,895	1,35	2	2	1
693	Q9H3N1_TMX1_HUMAN	Thioredoxin	11,869	8,66	2	2	1
693	Q9H3N1_TMX1_HUMAN	Thioredoxin	11,869	8,66	2	2	1
694	P62318_SMD3_HUMAN	Small nucle	11,858	15,08	3	2	0
694	P62318_SMD3_HUMAN	Small nucle	11,858	15,08	3	2	0
694	P62318_SMD3_HUMAN	Small nucle	11,858	15,08	3	2	0
695	P08727_K1C19_HUMAN	Keratin, typ	11,854	4,75	3	2	0
695	P08727_K1C19_HUMAN	Keratin, typ	11,854	4,75	3	2	0
695	P08727_K1C19_HUMAN	Keratin, typ	11,854	4,75	3	2	0
696	P13473_LAMP2_HUMAN	Lysosome-a	11,815	5,5	2	2	2
696	P13473_LAMP2_HUMAN	Lysosome-a	11,815	5,5	2	2	2
697	Q99733_NP1L4_HUMAN	Nucleosom	11,803	5,35	2	2	1
697	Q99733_NP1L4_HUMAN	Nucleosom	11,803	5,35	2	2	1
698	P46783_RS10_HUMAN	40S ribosom	11,789	14,55	4	2	0
698	P46783_RS10_HUMAN	40S ribosom	11,789	14,55	4	2	0
698	P46783_RS10_HUMAN	40S ribosom	11,789	14,55	4	2	0
698	P46783_RS10_HUMAN	40S ribosom	11,789	14,55	4	2	0
699	P02042_HBD_HUMAN	Hemoglobin	11,772	13,01	2	2	1
699	P02042_HBD_HUMAN	Hemoglobin	11,772	13,01	2	2	1

700	Q13242	SRSF9_HUMAN	Serine/argi	11,746	10,41	3	2	0
700	Q13242	SRSF9_HUMAN	Serine/argi	11,746	10,41	3	2	0
700	Q13242	SRSF9_HUMAN	Serine/argi	11,746	10,41	3	2	0
701	Q6P1M0	S27A4_HUMAN	Long-chain	11,729	3,42	2	2	0
701	Q6P1M0	S27A4_HUMAN	Long-chain	11,729	3,42	2	2	0
702	P17655	CAN2_HUMAN	Calpain-2 c	11,638	3,82	2	2	1
702	P17655	CAN2_HUMAN	Calpain-2 c	11,638	3,82	2	2	1
703	P23526	SAHH_HUMAN	Adenosylhc	11,545	3,94	2	2	1
703	P23526	SAHH_HUMAN	Adenosylhc	11,545	3,94	2	2	1
704	P61353	RL27_HUMAN	60S riboso	11,54	13,24	2	2	1
704	P61353	RL27_HUMAN	60S riboso	11,54	13,24	2	2	1
705	P48735	IDHP_HUMAN	Isocitrate d	11,522	5,33	2	2	1
705	P48735	IDHP_HUMAN	Isocitrate d	11,522	5,33	2	2	1
706	Q8TCS8	PNPT1_HUMAN	Polyribonuc	11,514	2,98	2	2	1
706	Q8TCS8	PNPT1_HUMAN	Polyribonuc	11,514	2,98	2	2	1
707	Q08945	SSRP1_HUMAN	FACT comp	11,504	2,97	2	2	1
707	Q08945	SSRP1_HUMAN	FACT comp	11,504	2,97	2	2	1
708	O43854	EDIL3_HUMAN	EGF-like re	11,394	4,09	3	2	2
708	O43854	EDIL3_HUMAN	EGF-like re	11,394	4,09	3	2	2
708	O43854	EDIL3_HUMAN	EGF-like re	11,394	4,09	3	2	2
709	O00410	IPO5_HUMAN	Importin-5	11,371	1,55	2	2	2
709	O00410	IPO5_HUMAN	Importin-5	11,371	1,55	2	2	2
710	Q12841	FSTL1_HUMAN	Follistatin-r	11,337	6,25	2	2	1
710	Q12841	FSTL1_HUMAN	Follistatin-r	11,337	6,25	2	2	1
711	Q00325	MPCP_HUMAN	Phosphate	11,298	6,39	3	2	2
711	Q00325	MPCP_HUMAN	Phosphate	11,298	6,39	3	2	2
711	Q00325	MPCP_HUMAN	Phosphate	11,298	6,39	3	2	2
712	Q86UX6	ST32C_HUMAN	Serine/thre	11,293	4,32	2	2	0
712	Q86UX6	ST32C_HUMAN	Serine/thre	11,293	4,32	2	2	0
713	P41223	BUD31_HUMAN	Protein BUI	11,283	12,5	2	2	0
713	P41223	BUD31_HUMAN	Protein BUI	11,283	12,5	2	2	0
714	P20908	CO5A1_HUMAN	Collagen al	11,161	2,04	2	2	1
714	P20908	CO5A1_HUMAN	Collagen al	11,161	2,04	2	2	1
715	P52943	CRIP2_HUMAN	Cysteine-ric	11,05	11,06	2	2	0
715	P52943	CRIP2_HUMAN	Cysteine-ric	11,05	11,06	2	2	0
716	Q9BVK6	TMED9_HUMAN	Transmembr	10,99	10	5	2	1

716	Q9BVK6	TMED9_HUMAN	Transmemt	10,99	10	5	2	1
716	Q9BVK6	TMED9_HUMAN	Transmemt	10,99	10	5	2	1
716	Q9BVK6	TMED9_HUMAN	Transmemt	10,99	10	5	2	1
716	Q9BVK6	TMED9_HUMAN	Transmemt	10,99	10	5	2	1
717	Q12904	AIMP1_HUMAN	Endothelial	10,986	6,09	3	2	0
717	Q12904	AIMP1_HUMAN	Endothelial	10,986	6,09	3	2	0
717	Q12904	AIMP1_HUMAN	Endothelial	10,986	6,09	3	2	0
718	P07942	LAMB1_HUMAN	Laminin su	10,979	1,18	2	2	1
718	P07942	LAMB1_HUMAN	Laminin su	10,979	1,18	2	2	1
719	Q07666	KHDR1_HUMAN	KH domain-	10,861	5,74	2	2	1
719	Q07666	KHDR1_HUMAN	KH domain-	10,861	5,74	2	2	1
720	P05783	K1C18_HUMAN	Keratin, typ	10,859	3,73	2	2	1
720	P05783	K1C18_HUMAN	Keratin, typ	10,859	3,73	2	2	1
721	P37235	HPCL1_HUMAN	Hippocalcin	10,811	9,38	3	2	1
721	P37235	HPCL1_HUMAN	Hippocalcin	10,811	9,38	3	2	1
721	P37235	HPCL1_HUMAN	Hippocalcin	10,811	9,38	3	2	1
722	P55265	DSRAD_HUMAN	Double-str	10,81	3,54	2	2	4
722	P55265	DSRAD_HUMAN	Double-str	10,81	3,54	2	2	4
723	Q9Y2H6	FND3A_HUMAN	Fibronectin	10,753	1,23	2	2	1
723	Q9Y2H6	FND3A_HUMAN	Fibronectin	10,753	1,23	2	2	1
724	Q9P035	HACD3_HUMAN	Very-long-c	10,679	8,84	2	2	0
724	Q9P035	HACD3_HUMAN	Very-long-c	10,679	8,84	2	2	0
725	Q9NSK0	KLC4_HUMAN	Kinesin ligh	10,648	3,14	2	2	1
725	Q9NSK0	KLC4_HUMAN	Kinesin ligh	10,648	3,14	2	2	1
726	Q04637	IF4G1_HUMAN	Eukaryotic i	10,513	1,43	2	2	4
726	Q04637	IF4G1_HUMAN	Eukaryotic i	10,513	1,43	2	2	4
727	P36776	LONM_HUMAN	Lon proteas	10,477	2,8	3	2	1
727	P36776	LONM_HUMAN	Lon proteas	10,477	2,8	3	2	1
727	P36776	LONM_HUMAN	Lon proteas	10,477	2,8	3	2	1
728	Q13561	DCTN2_HUMAN	Dynactin su	10,448	4,5	2	2	3
728	Q13561	DCTN2_HUMAN	Dynactin su	10,448	4,5	2	2	3
729	P11413	G6PD_HUMAN	Glucose-6-p	10,41	4,67	3	2	3
729	P11413	G6PD_HUMAN	Glucose-6-p	10,41	4,67	3	2	3
729	P11413	G6PD_HUMAN	Glucose-6-p	10,41	4,67	3	2	3
730	Q9Y6M1	IF2B2_HUMAN	Insulin-like	10,378	6,29	2	2	1
730	Q9Y6M1	IF2B2_HUMAN	Insulin-like	10,378	6,29	2	2	1
731	O95573	ACSL3_HUMAN	Long-chain-	10,339	4,03	2	2	0

731	O95573	ACSL3_HUMAN	Long-chain-	10,339	4,03	2	2	0
732	Q06323	PSME1_HUMAN	Proteasome	10,253	6,83	3	2	0
732	Q06323	PSME1_HUMAN	Proteasome	10,253	6,83	3	2	0
732	Q06323	PSME1_HUMAN	Proteasome	10,253	6,83	3	2	0
733	Q13557	KCC2D_HUMAN	Calcium/cal	10,241	4,22	2	2	2
733	Q13557	KCC2D_HUMAN	Calcium/cal	10,241	4,22	2	2	2
734	Q9BS26	ERP44_HUMAN	Endoplasmic	10,135	4,51	2	2	1
734	Q9BS26	ERP44_HUMAN	Endoplasmic	10,135	4,51	2	2	1
735	Q96AC1	FERM2_HUMAN	Fermitin fam	10,101	4,58	2	2	1
735	Q96AC1	FERM2_HUMAN	Fermitin fam	10,101	4,58	2	2	1
736	O15042	SR140_HUMAN	U2-associat	10,084	3,5	2	2	1
736	O15042	SR140_HUMAN	U2-associat	10,084	3,5	2	2	1
737	Q6NUQ4	TM214_HUMAN	Transmembr	10,03	2,03	2	2	0
737	Q6NUQ4	TM214_HUMAN	Transmembr	10,03	2,03	2	2	0
738	P56385	ATP5I_HUMAN	ATP synthas	9,963	26,47	2	2	1
738	P56385	ATP5I_HUMAN	ATP synthas	9,963	26,47	2	2	1
739	Q14534	ERG1_HUMAN	Squalene m	9,952	4,53	2	2	0
739	Q14534	ERG1_HUMAN	Squalene m	9,952	4,53	2	2	0
740	P78357	CNTP1_HUMAN	Contactin-a	9,951	1,32	2	2	1
740	P78357	CNTP1_HUMAN	Contactin-a	9,951	1,32	2	2	1
741	Q16851	UGPA_HUMAN	UTP--glucos	9,938	4,83	2	2	2
741	Q16851	UGPA_HUMAN	UTP--glucos	9,938	4,83	2	2	2
742	Q12849	GRSF1_HUMAN	G-rich sequ	9,935	3,75	2	2	0
742	Q12849	GRSF1_HUMAN	G-rich sequ	9,935	3,75	2	2	0
743	Q8TF01	SFR18_HUMAN	Arginine/se	9,804	2,86	2	2	0
743	Q8TF01	SFR18_HUMAN	Arginine/se	9,804	2,86	2	2	0
744	Q07157	ZO1_HUMAN	Tight juncti	9,726	1,2	2	2	1
744	Q07157	ZO1_HUMAN	Tight juncti	9,726	1,2	2	2	1
745	O60762	DPM1_HUMAN	Dolichol-ph	9,711	6,18	2	2	1
745	O60762	DPM1_HUMAN	Dolichol-ph	9,711	6,18	2	2	1
746	Q99459	CDC5L_HUMAN	Cell divisio	9,653	2,37	2	2	0
746	Q99459	CDC5L_HUMAN	Cell divisio	9,653	2,37	2	2	0

Sub-protein: Sequence	Sequence + iPTMs	Position (rel z-score	Prec m/z	Scan Name	Job Title
P21333_CH AFGPGLQC [iTRAQ_N1		1 1072-1087	9,85	787,415	2012_02_2 Nuclei_frac
P21333_CH AFGPGLQC [iTRAQ_N1		1 1072-1087	8,276	525,279	2012_02_2 Nuclei_frac
P21333_CH AGNNMLL\ [iTRAQ_N1		2 2577-2590	6,1	532,292	2012_02_2 Nuclei_frac
P21333_CH AHVVPCFL [iTRAQ_N1		3 1152-1162	6,869	759,903	2012_02_2 Nuclei_frac
P21333_CH AHVVPCFL [iTRAQ_N1		3 1152-1162	6,291	506,938	2012_02_2 Nuclei_frac
P21333_CH ALGALVD\$ [iTRAQ_N1		4 197-226	5,587	1173,245	2012_02_2 Nuclei_frac
P21333_CH ALTQTGGF [iTRAQ_N1		2 1284-1294	6,591	466,278	2012_02_2 Nuclei_frac
P21333_CH ALTQTGGF [iTRAQ_N1		2 1284-1294	5,677	466,275	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	9,027	861,97	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	8,803	861,969	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	8,037	861,97	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	7,218	574,983	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	7,134	574,981	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	6,831	574,982	2012_02_2 Nuclei_frac
P21333_CH ANLPQSFC [iTRAQ_N1		2 1465-1477	6,324	574,982	2012_02_2 Nuclei_frac
P21333_CH APSVANV\ [iTRAQ_N1		3 2142-2157	8,322	648,348	2012_02_2 Nuclei_frac
P21333_CH ASGPGLNT [iTRAQ_N1		2 1550-1573	8,191	1315,72	2012_02_2 Nuclei_frac
P21333_CH ASGPGLNT [iTRAQ_N1		2 1550-1573	6,62	877,485	2012_02_2 Nuclei_frac
P21333_CH ATCAPQH\ [iTRAQ_N1		3 2533-2551	8,449	693,352	2012_02_2 Nuclei_frac
P21333_CH AVPTGDA\$ [iTRAQ_N1		2 1636-1644	6,006	567,326	2012_02_2 Nuclei_frac
P21333_CH AWGPGLE\ [iTRAQ_N1		2 581-593	8,592	757,932	2012_02_2 Nuclei_frac
P21333_CH AWGPGLE\ [iTRAQ_N1		2 581-593	8,547	757,934	2012_02_2 Nuclei_frac
P21333_CH AWGPGLE\ [iTRAQ_N1		2 581-593	4,753	505,624	2012_02_2 Nuclei_frac
P21333_CH AWGPGLE\ [iTRAQ_N1		2 581-593	4,74	505,624	2012_02_2 Nuclei_frac
P21333_CH AYGPGIEP\ [iTRAQ_N1		3 286-299	5,858	579,975	2012_02_2 Nuclei_frac
P21333_CH AYGPGIEP\ [iTRAQ_N1		3 286-299	5,202	579,975	2012_02_2 Nuclei_frac
P21333_CH DAGEGLLA [iTRAQ_N1		3 1574-1592	8,417	790,78	2012_02_2 Nuclei_frac
P21333_CH DAGEGLLA [iTRAQ_N1		3 1574-1592	8,378	790,78	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	5,981	571,638	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	5,623	428,981	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	5,581	428,981	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	5,198	428,981	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	5,128	428,981	2012_02_2 Nuclei_frac
P21333_CH DAPQDFHF [iTRAQ_N1		2 665-676	4,782	571,638	2012_02_2 Nuclei_frac
P21333_CH DKGEYTLV [iTRAQ_N1		3 2614-2623	5,372	528,65	2012_02_2 Nuclei_frac
P21333_CH DLAEDAPV [iTRAQ_N1		3 34-43	5,029	535,637	2012_02_2 Nuclei_frac
P21333_CH EATTEFSV [iTRAQ_N1		1 1273-1283	7,789	685,34	2012_02_2 Nuclei_frac
P21333_CH EATTEFSV [iTRAQ_N1		1 1273-1283	7,738	685,34	2012_02_2 Nuclei_frac
P21333_CH EEGPYEVE' [iTRAQ_N1		3 1037-1069	6,243	980,269	2012_02_2 Nuclei_frac
P21333_CH EGPYSISVL [iTRAQ_N1		1 1516-1532	9,242	1027,514	2012_02_2 Nuclei_frac
P21333_CH EGPYSISVL [iTRAQ_N1		1 1516-1532	4,782	685,343	2012_02_2 Nuclei_frac
P21333_CH FGGEHVPN [iTRAQ_N1		1 1718-1745	7,983	1030,536	2012_02_2 Nuclei_frac
P21333_CH FGGEHVPN [iTRAQ_N1		1 1718-1745	6,252	1030,541	2012_02_2 Nuclei_frac
P21333_CH FNEEHIPDS [iTRAQ_N1		1 2303-2325	7,05	871,105	2012_02_2 Nuclei_frac
P21333_CH FNEEHIPDS [iTRAQ_N1		1 2303-2325	6,892	871,104	2012_02_2 Nuclei_frac
P21333_CH FNEEHIPDS [iTRAQ_N1		1 2303-2325	4,845	871,102	2012_02_2 Nuclei_frac
P21333_CH FNGTHIPG\$ [iTRAQ_N1		2 2398-2409	5,847	530,628	2012_02_2 Nuclei_frac
P21333_CH FNGTHIPG\$ [iTRAQ_N1		2 2398-2409	5,844	530,626	2012_02_2 Nuclei_frac
P21333_CH FVPAEMGT [iTRAQ_N1		3 2194-2207	5,316	602,994	2012_02_2 Nuclei_frac
P21333_CH GAGTGGLC [iTRAQ_N1		2 1382-1399	11,219	930,01	2012_02_2 Nuclei_frac
P21333_CH GAGTGGLC [iTRAQ_N1		2 1382-1399	8,724	620,344	2012_02_2 Nuclei_frac

P21333_CH GKLDVQFS [iTRAQ_Ni	3 905-916	6,046	575,681	2012_02_2	Nuclei_frac
P21333_CH GKLDVQFS [iTRAQ_Ni	3 905-916	5,965	575,681	2012_02_2	Nuclei_frac
P21333_CH GKLDVQFS [iTRAQ_Ni	3 905-916	5,033	575,681	2012_02_2	Nuclei_frac
P21333_CH GKLDVQFS [iTRAQ_Ni	3 905-916	5,019	575,681	2012_02_2	Nuclei_frac
P21333_CH GQHVPGSF [iTRAQ_Ni	2 2210-2232	4,777	648,845	2012_02_2	Nuclei_frac
P21333_CH HTAMVSW [iTRAQ_Ni	2 743-760	8,463	701,69	2012_02_2	Nuclei_frac
P21333_CH IANLQTDL [iTRAQ_Ni	1 64-76	9,052	780,43	2012_02_2	Nuclei_frac
P21333_CH IKVSGLGEH [iTRAQ_Ni	3 974-982	5,238	454,962	2012_02_2	Nuclei_frac
P21333_CH IVGPSGAA [iTRAQ_Ni	3 1008-1019	7,811	722,416	2012_02_2	Nuclei_frac
P21333_CH IVGPSGAA [iTRAQ_Ni	3 1008-1019	7,708	722,415	2012_02_2	Nuclei_frac
P21333_CH KTHIQDNH [iTRAQ_Ni	2 1593-1615	4,856	719,623	2012_02_2	Nuclei_frac
P21333_CH LDVQFSGL [iTRAQ_Ni	2 907-916	7,12	698,41	2012_02_2	Nuclei_frac
P21333_CH LDVQFSGL [iTRAQ_Ni	2 907-916	6,471	698,41	2012_02_2	Nuclei_frac
P21333_CH LDVQFSGL [iTRAQ_Ni	2 907-916	5,901	698,41	2012_02_2	Nuclei_frac
P21333_CH LDVQFSGL [iTRAQ_Ni	2 907-916	5,606	465,942	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	2 77-87	7,95	757,993	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	2 77-87	7,897	757,99	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	2 77-87	7,872	757,993	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	2 77-87	6,792	505,665	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	2 77-87	5,857	505,664	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	3 77-88	8,769	596,397	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	3 77-88	8,476	894,092	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	3 77-88	7,02	894,092	2012_02_2	Nuclei_frac
P21333_CH LIALLEVLS [iTRAQ_Ni	3 77-88	6,852	596,393	2012_02_2	Nuclei_frac
P21333_CH LQVEPAVI [iTRAQ_Ni	2 1247-1272	8,76	969,82	2012_02_2	Nuclei_frac
P21333_CH LQVEPAVI [iTRAQ_Ni	2 1247-1272	8,663	969,82	2012_02_2	Nuclei_frac
P21333_CH LQVEPAVI [iTRAQ_Ni	2 1247-1272	5,936	727,616	2012_02_2	Nuclei_frac
P21333_CH LQVEPAVI [iTRAQ_Ni	2 1247-1272	5,437	1454,228	2012_02_2	Nuclei_frac
P21333_CH LQVEPAVI [iTRAQ_Ni	2 1247-1272	5,166	727,617	2012_02_2	Nuclei_frac
P21333_CH LSPFMADI [iTRAQ_Ni	2 656-664	5,039	605,326	2012_02_2	Nuclei_frac
P21333_CH LTVSSLQE [iTRAQ_Ni	2 2327-2338	7,049	775,455	2012_02_2	Nuclei_frac
P21333_CH LYSVSYLL [iTRAQ_Ni	2 2605-2613	6,157	458,614	2012_02_2	Nuclei_frac
P21333_CH LYSVSYLL [iTRAQ_Ni	2 2605-2613	5,609	687,418	2012_02_2	Nuclei_frac
P21333_CH NGHVGISF [iTRAQ_Ni	2 1996-2006	8,399	481,617	2012_02_2	Nuclei_frac
P21333_CH RLTVSSLQ [iTRAQ_Ni	2 2326-2338	8,339	853,509	2012_02_2	Nuclei_frac
P21333_CH RLTVSSLQ [iTRAQ_Ni	2 2326-2338	7,407	569,34	2012_02_2	Nuclei_frac
P21333_CH SAGQGEVI [iTRAQ_Ni	2 310-331	10,079	867,773	2012_02_2	Nuclei_frac
P21333_CH SAGQGEVI [iTRAQ_Ni	2 310-331	8,303	867,773	2012_02_2	Nuclei_frac
P21333_CH SPFSVAVS [iTRAQ_Ni	2 959-973	8,178	911,515	2012_02_2	Nuclei_frac
P21333_CH SPFSVAVS [iTRAQ_Ni	2 959-973	7,381	911,516	2012_02_2	Nuclei_frac
P21333_CH SPFSVAVS [iTRAQ_Ni	2 959-973	6,833	608,015	2012_02_2	Nuclei_frac
P21333_CH SPFSVAVS [iTRAQ_Ni	2 959-973	6,412	608,012	2012_02_2	Nuclei_frac
P21333_CH SPFSVAVS [iTRAQ_Ni	2 959-973	5,697	608,015	2012_02_2	Nuclei_frac
P21333_CH SPYTVTVG [iTRAQ_Ni	3 468-484	9,609	671,32	2012_02_2	Nuclei_frac
P21333_CH SPYTVTVG [iTRAQ_Ni	3 468-484	8,618	1006,477	2012_02_2	Nuclei_frac
P21333_CH TFSVWYVI [iTRAQ_Ni	2 341-355	7,212	680,364	2012_02_2	Nuclei_frac
P21333_CH TFSVWYVI [iTRAQ_Ni	2 341-355	6,212	510,526	2012_02_2	Nuclei_frac
P21333_CH TGVAVNKI [iTRAQ_Ni	3 685-700	5,86	693,734	2012_02_2	Nuclei_frac
P21333_CH TGVAVNKI [iTRAQ_Ni	3 685-700	4,742	693,733	2012_02_2	Nuclei_frac
P21333_CH TPCEEILVK [iTRAQ_Ni	3 2591-2599	5,387	688,889	2012_02_2	Nuclei_frac
P21333_CH VANPSGNI [iTRAQ_Ni	1 1297-1312	10,87	954,484	2012_02_2	Nuclei_frac
P21333_CH VANPSGNI [iTRAQ_Ni	1 1297-1312	7,219	636,657	2012_02_2	Nuclei_frac

P21333_CH VAQPTITD [iTRAQ_N1	2 1807-1823	9,366	701,728	2012_02_2	Nuclei_frac
P21333_CH VAQPTITD [iTRAQ_N1	2 1807-1823	8,613	701,728	2012_02_2	Nuclei_frac
P21333_CH VAQPTITD [iTRAQ_N1	2 1807-1823	7,984	701,729	2012_02_2	Nuclei_frac
P21333_CH VAQPTITD [iTRAQ_N1	2 1807-1823	6,574	701,729	2012_02_2	Nuclei_frac
P21333_CH VDVGKDQ [iTRAQ_N1	3 983-994	7,376	599,676	2012_02_2	Nuclei_frac
P21333_CH VDVGKDQ [iTRAQ_N1	3 983-994	6,706	599,677	2012_02_2	Nuclei_frac
P21333_CH VEPGLGAC [iTRAQ_N1	1 1020-1032	9,441	728,897	2012_02_2	Nuclei_frac
P21333_CH VGSAADIP [iTRAQ_N1	1 1957-1985	4,819	1013,223	2012_02_2	Nuclei_frac
P21333_CH VHGPQIQS [iTRAQ_N1	3 1360-1375	6,416	689,728	2012_02_2	Nuclei_frac
P21333_CH VHSPSGAL [iTRAQ_N1	3 2360-2383	5,989	764,384	2012_02_2	Nuclei_frac
P21333_CH VPVHDVTI [iTRAQ_N1	2 1440-1450	6,688	728,408	2012_02_2	Nuclei_frac
P21333_CH VPVHDVTI [iTRAQ_N1	2 1440-1450	6,499	728,409	2012_02_2	Nuclei_frac
P21333_CH VPVHDVTI [iTRAQ_N1	2 1440-1450	5,569	485,941	2012_02_2	Nuclei_frac
P21333_CH VQVQDNEI [iTRAQ_N1	3 709-724	7,893	691,701	2012_02_2	Nuclei_frac
P21333_CH VQVQDNEI [iTRAQ_N1	3 709-724	7,657	691,701	2012_02_2	Nuclei_frac
P21333_CH VQVQDNEI [iTRAQ_N1	3 709-724	6,288	691,702	2012_02_2	Nuclei_frac
P21333_CH VTAQGPGL [iTRAQ_N1	2 384-400	9,964	647,694	2012_02_2	Nuclei_frac
P21333_CH VTAQGPGL [iTRAQ_N1	2 384-400	8,078	647,694	2012_02_2	Nuclei_frac
P21333_CH VTAQGPGL [iTRAQ_N1	2 384-400	8,013	647,695	2012_02_2	Nuclei_frac
P21333_CH VTAQGPGL [iTRAQ_N1	2 384-400	6,762	647,694	2012_02_2	Nuclei_frac
P21333_CH VTAQGPGL [iTRAQ_N1	2 384-400	6,219	647,694	2012_02_2	Nuclei_frac
P21333_CH VTVLFGAC [iTRAQ_N1	2 356-367	7,663	786,48	2012_02_2	Nuclei_frac
P21333_CH VTVLFGAC [iTRAQ_N1	2 356-367	6,848	524,656	2012_02_2	Nuclei_frac
P21333_CH VTYTPMAF [iTRAQ_N1	3 2477-2492	6,858	1023,062	2012_02_2	Nuclei_frac
P21333_CH VTYTPMAF [iTRAQ_N1	3 2477-2492	6,475	682,38	2012_02_2	Nuclei_frac
P21333_CH YAPSEAGL [iTRAQ_N1	1 1824-1837	5,025	578,287	2012_02_2	Nuclei_frac
P21333_CH YGGDEIPFS [iTRAQ_N1	1 1622-1633	6,421	772,881	2012_02_2	Nuclei_frac
P21333_CH YGGPYHIG [iTRAQ_N1	2 2493-2505	6,592	556,631	2012_02_2	Nuclei_frac
P21333_CH YGGQPVPM [iTRAQ_N1	2 1235-1246	7,385	789,931	2012_02_2	Nuclei_frac
P21333_CH YNEQHVPC [iTRAQ_N1	1 1930-1943	5,524	582,961	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	9,324	858,799	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	8,395	858,8	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	8,292	858,8	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	8,034	858,802	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	7,684	1287,694	2012_02_2	Nuclei_frac
P21333_CH YTPVQQGF [iTRAQ_N1	2 937-958	7,496	858,803	2012_02_2	Nuclei_frac
Q15149_IS(AAAGKAEI [iTRAQ_N1	2 2074-2087	5,863	572,671	2012_02_2	Nuclei_frac
Q15149_IS(AALAHSEE [iTRAQ_N1	2 2744-2761	8,814	691,381	2012_02_2	Nuclei_frac
Q15149_IS(AALAHSEE [iTRAQ_N1	2 2744-2761	8,376	691,383	2012_02_2	Nuclei_frac
Q15149_IS(AELELELGI [iTRAQ_N1	1 2079-2087	6,634	587,333	2012_02_2	Nuclei_frac
Q15149_IS(AGLVGPEF [iTRAQ_N1	2 3221-3231	5,106	491,278	2012_02_2	Nuclei_frac
Q15149_IS(AGLVGPEF [iTRAQ_N1	2 3221-3231	5,096	491,279	2012_02_2	Nuclei_frac
Q15149_IS(AGTLSITEF [iTRAQ_N1	1 4361-4381	9,08	753,71	2012_02_2	Nuclei_frac
Q15149_IS(AIYEVLF [iTRAQ_N1	1 14-21	7,74	577,839	2012_02_2	Nuclei_frac
Q15149_IS(AIYEVLF [iTRAQ_N1	1 14-21	5,77	577,838	2012_02_2	Nuclei_frac
Q15149_IS(AKLEQLFQ [iTRAQ_N1	3 2651-2663	6,878	651,048	2012_02_2	Nuclei_frac
Q15149_IS(ALQALEEL [iTRAQ_N1	1 1671-1679	5,872	593,852	2012_02_2	Nuclei_frac
Q15149_IS(APVPASEL [iTRAQ_N1	1 3447-3462	8,832	856	2012_02_2	Nuclei_frac
Q15149_IS(AQAEAAQ [iTRAQ_N1	1 1274-1291	7,487	735,045	2012_02_2	Nuclei_frac
Q15149_IS(AQVEQEL [iTRAQ_N1	1 2319-2329	10,506	716,403	2012_02_2	Nuclei_frac
Q15149_IS(ARQEELYS [iTRAQ_N1	1 3356-3368	7,421	579,641	2012_02_2	Nuclei_frac

Q15149_IS(ATTAALLL [iTRAQ_Ni	1	3519-3540	5,037	791,45	2012_02_2	Nuclei_frac
Q15149_IS(ATVSAPFC [iTRAQ_Ni	2	3045-3053	5,668	583,345	2012_02_2	Nuclei_frac
Q15149_IS(AVTGYKDF [iTRAQ_Ni	3	4147-4158	5,836	573,322	2012_02_2	Nuclei_frac
Q15149_IS(EAIAELERE [iTRAQ_Ni	2	2587-2596	5,096	492,617	2012_02_2	Nuclei_frac
Q15149_IS(EAIAELERE [iTRAQ_Ni	2	2587-2596	4,901	492,618	2012_02_2	Nuclei_frac
Q15149_IS(ELAEQELE [iTRAQ_Ni	2	1825-1833	5,327	688,881	2012_02_2	Nuclei_frac
Q15149_IS(EQELQQTL [iTRAQ_Ni	1	2199-2224	7,276	1047,87	2012_02_2	Nuclei_frac
Q15149_IS(EQELQQTL [iTRAQ_Ni	1	2199-2224	6,667	786,154	2012_02_2	Nuclei_frac
Q15149_IS(FLEGTSCIA [iTRAQ_Ni	3	4065-4081	8,04	701,704	2012_02_2	Nuclei_frac
Q15149_IS(FRELAEEA [iTRAQ_Ni	1	1933-1942	9,138	668,364	2012_02_2	Nuclei_frac
Q15149_IS(FRELAEEA [iTRAQ_Ni	1	1933-1942	6,696	445,911	2012_02_2	Nuclei_frac
Q15149_IS(GANVIAGV [iTRAQ_Ni	2	3159-3174	7,491	644,027	2012_02_2	Nuclei_frac
Q15149_IS(GFFDPNTH [iTRAQ_Ni	1	2989-3007	8,301	817,755	2012_02_2	Nuclei_frac
Q15149_IS(GFFDPNTH [iTRAQ_Ni	1	3648-3661	7,554	618,969	2012_02_2	Nuclei_frac
Q15149_IS(GIYQSLEG/ [iTRAQ_Ni	2	478-493	6,34	650,704	2012_02_2	Nuclei_frac
Q15149_IS(GLHQSIEEF [iTRAQ_Ni	1	697-706	8,238	453,91	2012_02_2	Nuclei_frac
Q15149_IS(ILITIVEEVE [iTRAQ_Ni	1	3424-3436	7,567	558,005	2012_02_2	Nuclei_frac
Q15149_IS(ILITIVEEVE [iTRAQ_Ni	1	3424-3436	7,435	836,505	2012_02_2	Nuclei_frac
Q15149_IS(ILITIVEEVE [iTRAQ_Ni	1	3424-3439	6,564	695,742	2012_02_2	Nuclei_frac
Q15149_IS(LAAEQELIF [iTRAQ_Ni	1	1846-1854	5,162	593,852	2012_02_2	Nuclei_frac
Q15149_IS(LAEVEAAL [iTRAQ_Ni	2	1499-1508	5,629	454,269	2012_02_2	Nuclei_frac
Q15149_IS(LCFEGLR [iTRAQ_Ni	2	3109-3115	5,337	519,781	2012_02_2	Nuclei_frac
Q15149_IS(LGFHLPLE' [iTRAQ_Ni	1	3951-3963	8,833	843,973	2012_02_2	Nuclei_frac
Q15149_IS(LGFHLPLE' [iTRAQ_Ni	1	3951-3963	7,542	562,987	2012_02_2	Nuclei_frac
Q15149_IS(LGFHLPLE' [iTRAQ_Ni	1	3951-3963	7,315	562,986	2012_02_2	Nuclei_frac
Q15149_IS(LKAEAEEL [iTRAQ_Ni	3	2462-2473	5,953	916,058	2012_02_2	Nuclei_frac
Q15149_IS(LLEAAAQ\$ [iTRAQ_Ni	2	4600-4609	5,321	660,395	2012_02_2	Nuclei_frac
Q15149_IS(LLFNDVQT [iTRAQ_Ni	2	588-597	5,989	739,947	2012_02_2	Nuclei_frac
Q15149_IS(LLFNDVQT [iTRAQ_Ni	2	588-597	5,92	493,633	2012_02_2	Nuclei_frac
Q15149_IS(LQNVQIAL [iTRAQ_Ni	1	237-248	9,24	795,46	2012_02_2	Nuclei_frac
Q15149_IS(LQNVQIAL [iTRAQ_Ni	1	237-248	9,151	795,461	2012_02_2	Nuclei_frac
Q15149_IS(LQNVQIAL [iTRAQ_Ni	1	237-248	9,048	795,459	2012_02_2	Nuclei_frac
Q15149_IS(LQNVQIAL [iTRAQ_Ni	1	237-248	7,499	530,644	2012_02_2	Nuclei_frac
Q15149_IS(LREQQLL [iTRAQ_Ni	1	2731-2743	5,449	459,762	2012_02_2	Nuclei_frac
Q15149_IS(LRIEEIR [iTRAQ_Ni	1	1585-1592	6,093	401,24	2012_02_2	Nuclei_frac
Q15149_IS(LRIEEIR [iTRAQ_Ni	1	1585-1592	4,829	601,357	2012_02_2	Nuclei_frac
Q15149_IS(LSFSGLR [iTRAQ_Ni	1	3440-3446	6,623	462,276	2012_02_2	Nuclei_frac
Q15149_IS(LSIYNALK} [iTRAQ_Ni	3	3175-3183	5,643	494,652	2012_02_2	Nuclei_frac
Q15149_IS(LSYTQLLR [iTRAQ_Ni	1	3992-3999	6,895	569,342	2012_02_2	Nuclei_frac
Q15149_IS(LTVDEAVF [iTRAQ_Ni	2	3879-3887	4,772	440,27	2012_02_2	Nuclei_frac
Q15149_IS(NLLDEELQ [iTRAQ_Ni	1	2340-2348	5,905	637,347	2012_02_2	Nuclei_frac
Q15149_IS(NLVDNITG [iTRAQ_Ni	1	4438-4447	8,54	637,354	2012_02_2	Nuclei_frac
Q15149_IS(NLVDNITG [iTRAQ_Ni	1	4438-4447	7,459	637,353	2012_02_2	Nuclei_frac
Q15149_IS(QLLEEELA [iTRAQ_Ni	1	1867-1875	6,197	622,853	2012_02_2	Nuclei_frac
Q15149_IS(QLQLAQE/ [iTRAQ_Ni	2	2172-2183	7,959	557,998	2012_02_2	Nuclei_frac
Q15149_IS(QRELAEQE [iTRAQ_Ni	2	1823-1833	5,409	554,312	2012_02_2	Nuclei_frac
Q15149_IS(QVQVALE [iTRAQ_Ni	1	1699-1709	9,265	693,897	2012_02_2	Nuclei_frac
Q15149_IS(RQELEAEL [iTRAQ_Ni	2	1887-1896	5,974	492,289	2012_02_2	Nuclei_frac
Q15149_IS(RQELEAEL [iTRAQ_Ni	2	1887-1896	5,807	492,289	2012_02_2	Nuclei_frac
Q15149_IS(SELELTGI [iTRAQ_Ni	2	1202-1215	6,468	635,045	2012_02_2	Nuclei_frac
Q15149_IS(SIQEELQQI [iTRAQ_Ni	1	1554-1563	7,598	694,391	2012_02_2	Nuclei_frac
Q15149_IS(SLQEEHVA [iTRAQ_Ni	1	1732-1744	10,495	812,454	2012_02_2	Nuclei_frac

Q15149_IS(SLQEEHVA [iTRAQ_N1	1	1732-1744	7,257	541,971	2012_02_2	Nuclei_frac
Q15149_IS(SLQEEHVA [iTRAQ_N1	1	1732-1744	4,854	541,971	2012_02_2	Nuclei_frac
Q15149_IS(SLSAIYLEK [iTRAQ_N1	2	1216-1224	6,048	656,395	2012_02_2	Nuclei_frac
Q15149_IS(SLVPAAEI [iTRAQ_N1	1	3116-3127	6,544	714,915	2012_02_2	Nuclei_frac
Q15149_IS(SQVEEELF [iTRAQ_N1	1	2361-2371	9,123	733,885	2012_02_2	Nuclei_frac
Q15149_IS(SQVEEELF [iTRAQ_N1	1	2361-2371	8,306	733,885	2012_02_2	Nuclei_frac
Q15149_IS(SSIAGLLLK [iTRAQ_N1	2	2833-2841	4,917	595,392	2012_02_2	Nuclei_frac
Q15149_IS(SSSVGSSS [iTRAQ_N1	1	4384-4401	4,993	633,658	2012_02_2	Nuclei_frac
Q15149_IS(SWSLATFF [iTRAQ_N1	1	1045-1052	7,916	556,304	2012_02_2	Nuclei_frac
Q15149_IS(SWSLATFF [iTRAQ_N1	1	1045-1052	7,674	556,305	2012_02_2	Nuclei_frac
Q15149_IS(TISLVIR [iTRAQ_N1	1	1227-1233	6,566	473,315	2012_02_2	Nuclei_frac
Q15149_IS(TISLVIR [iTRAQ_N1	1	1227-1233	6,318	473,315	2012_02_2	Nuclei_frac
Q15149_IS(VLALPEPS [iTRAQ_N1	1	1187-1201	7,823	838,498	2012_02_2	Nuclei_frac
Q15149_IS(VLALPEPS [iTRAQ_N1	1	1187-1201	6,229	559,335	2012_02_2	Nuclei_frac
Q15149_IS(VPVDVAYI [iTRAQ_N1	1	3620-3628	6,099	595,838	2012_02_2	Nuclei_frac
Q15149_IS(VPVDVAYI [iTRAQ_N1	1	2961-2968	5,505	531,807	2012_02_2	Nuclei_frac
Q15149_IS(VTLVQTLE [iTRAQ_N1	1	2565-2575	8,99	722,44	2012_02_2	Nuclei_frac
Q15149_IS(VTLVQTLE [iTRAQ_N1	1	2565-2575	8,487	481,961	2012_02_2	Nuclei_frac
Q15149_IS(VTLVQTLE [iTRAQ_N1	1	2565-2575	7,698	481,962	2012_02_2	Nuclei_frac
P35579_CHADFCIIHYA [iTRAQ_N1	3	566-576	6,645	528,28	2012_02_2	Nuclei_frac
P35579_CHAGVLAHLE [iTRAQ_N1	1	765-775	7,311	684,376	2012_02_2	Nuclei_frac
P35579_CHAGVLAHLE [iTRAQ_N1	1	765-775	6,886	456,585	2012_02_2	Nuclei_frac
P35579_CHALEEAMEC [iTRAQ_N1	2	1484-1492	5,932	668,856	2012_02_2	Nuclei_frac
P35579_CHALELDSNL [iTRAQ_N1	1	746-755	6,825	669,359	2012_02_2	Nuclei_frac
P35579_CHALEQQVEE [iTRAQ_N1	2	1529-1538	6,421	746,901	2012_02_2	Nuclei_frac
P35579_CHANLQIDQI [iTRAQ_N1	1	1755-1770	11,17	1007,539	2012_02_2	Nuclei_frac
P35579_CHANLQIDQI [iTRAQ_N1	1	1755-1770	9,789	672,029	2012_02_2	Nuclei_frac
P35579_CHANLQIDQI [iTRAQ_N1	1	1755-1770	8,96	672,028	2012_02_2	Nuclei_frac
P35579_CHANLQIDQI [iTRAQ_N1	1	1755-1770	7,703	672,03	2012_02_2	Nuclei_frac
P35579_CHASITALEAI [iTRAQ_N1	2	1807-1815	6,845	596,365	2012_02_2	Nuclei_frac
P35579_CHASITALEAI [iTRAQ_N1	2	1807-1815	5,837	596,366	2012_02_2	Nuclei_frac
P35579_CHASITALEAI [iTRAQ_N1	2	1807-1815	5,674	596,365	2012_02_2	Nuclei_frac
P35579_CHASREEILAC [iTRAQ_N1	2	1659-1669	5,172	501,964	2012_02_2	Nuclei_frac
P35579_CHASREEILAC [iTRAQ_N1	2	1659-1669	4,782	501,964	2012_02_2	Nuclei_frac
P35579_CHDLQGRDEC [iTRAQ_N1	2	1572-1583	5,903	574,624	2012_02_2	Nuclei_frac
P35579_CHDVLLQVDI [iTRAQ_N1	1	1846-1856	9,224	501,275	2012_02_2	Nuclei_frac
P35579_CHDVLLQVDI [iTRAQ_N1	1	1846-1856	8,767	751,409	2012_02_2	Nuclei_frac
P35579_CHEDQSILCT [iTRAQ_N1	4	166-185	8,788	853,098	2012_02_2	Nuclei_frac
P35579_CHEDQSILCT [iTRAQ_N1	4	166-185	5,127	640,074	2012_02_2	Nuclei_frac
P35579_CHEMAELED [iTRAQ_N1	2	1593-1603	6,401	556,278	2012_02_2	Nuclei_frac
P35579_CHEQADFAIE [iTRAQ_N1	2	408-419	6,922	531,962	2012_02_2	Nuclei_frac
P35579_CHEQADFAIE [iTRAQ_N1	2	408-419	6,74	797,439	2012_02_2	Nuclei_frac
P35579_CHEQADFAIE [iTRAQ_N1	2	408-419	6,585	797,438	2012_02_2	Nuclei_frac
P35579_CHEQADFAIE [iTRAQ_N1	2	408-419	6,514	797,439	2012_02_2	Nuclei_frac
P35579_CHEQADFAIE [iTRAQ_N1	2	408-419	5,424	531,961	2012_02_2	Nuclei_frac
P35579_CHEQEVNLIK [iTRAQ_N1	3	1166-1174	6,009	511,652	2012_02_2	Nuclei_frac
P35579_CHEQEVNLIK [iTRAQ_N1	3	1166-1174	5,63	511,651	2012_02_2	Nuclei_frac
P35579_CHEQEVNLIK [iTRAQ_N1	3	1166-1174	5,344	766,974	2012_02_2	Nuclei_frac
P35579_CHFDQLLAE [iTRAQ_N1	2	1446-1454	4,782	690,886	2012_02_2	Nuclei_frac
P35579_CHHSQAVEEL [iTRAQ_N1	2	1194-1210	9,081	762,08	2012_02_2	Nuclei_frac
P35579_CHHSQAVEEL [iTRAQ_N1	2	1194-1210	5,476	571,809	2012_02_2	Nuclei_frac

P35579_CHIAEFTTNLT [iTRAQ_Ni	2 1001-1014	8,809	971,496	2012_02_2	Nuclei_frac
P35579_CHIAEFTTNLT [iTRAQ_Ni	2 1001-1014	7,206	648,002	2012_02_2	Nuclei_frac
P35579_CHIAEFTTNLT [iTRAQ_Ni	2 1001-1014	6,31	648	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	8,809	909,99	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	8,374	909,988	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	8,212	909,99	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	8,127	606,995	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	7,947	606,995	2012_02_2	Nuclei_frac
P35579_CHIAQLEEQLI [iTRAQ_Ni	2 1816-1828	7,855	606,995	2012_02_2	Nuclei_frac
P35579_CHIIGLDQVAC [iTRAQ_Ni	2 618-637	7,43	769,429	2012_02_2	Nuclei_frac
P35579_CHIIGLDQVAC [iTRAQ_Ni	2 618-637	7,174	769,427	2012_02_2	Nuclei_frac
P35579_CHIIGLDQVAC [iTRAQ_Ni	2 618-637	5,86	769,427	2012_02_2	Nuclei_frac
P35579_CHIRELESQIS [iTRAQ_Ni	1 1106-1124	9,344	816,418	2012_02_2	Nuclei_frac
P35579_CHIRELESQIS [iTRAQ_Ni	1 1106-1124	5,151	612,566	2012_02_2	Nuclei_frac
P35579_CHITDVIIGFQ [iTRAQ_Ni	3 779-791	8,706	848,937	2012_02_2	Nuclei_frac
P35579_CHITDVIIGFQ [iTRAQ_Ni	3 779-791	8,09	848,937	2012_02_2	Nuclei_frac
P35579_CHITDVIIGFQ [iTRAQ_Ni	3 779-791	6,87	566,293	2012_02_2	Nuclei_frac
P35579_CHITDVIIGFQ [iTRAQ_Ni	3 779-791	6,71	566,294	2012_02_2	Nuclei_frac
P35579_CHKANLQIDQ [iTRAQ_Ni	2 1754-1770	10,088	762,763	2012_02_2	Nuclei_frac
P35579_CHKANLQIDQ [iTRAQ_Ni	2 1754-1770	8,159	762,762	2012_02_2	Nuclei_frac
P35579_CHKEEELQAA [iTRAQ_Ni	2 1081-1091	7,342	773,446	2012_02_2	Nuclei_frac
P35579_CHKEEELQAA [iTRAQ_Ni	2 1081-1091	5,45	515,967	2012_02_2	Nuclei_frac
P35579_CHKLEEEQILI [iTRAQ_Ni	4 975-989	7,068	774,419	2012_02_2	Nuclei_frac
P35579_CHKLEGDSTD [iTRAQ_Ni	3 1052-1075	7,877	1016,556	2012_02_2	Nuclei_frac
P35579_CHKLVWVPSI [iTRAQ_Ni	3 30-38	5,373	752,467	2012_02_2	Nuclei_frac
P35579_CHKQEELEEIC [iTRAQ_Ni	3 910-923	9,848	686,69	2012_02_2	Nuclei_frac
P35579_CHKQEELEEIC [iTRAQ_Ni	3 910-923	7,138	515,27	2012_02_2	Nuclei_frac
P35579_CHKQEELEEIC [iTRAQ_Ni	3 910-923	6,54	515,27	2012_02_2	Nuclei_frac
P35579_CHKVEAQLQE [iTRAQ_Ni	3 1249-1260	5,755	615,713	2012_02_2	Nuclei_frac
P35579_CHKVEAQLQE [iTRAQ_Ni	3 1249-1260	5,618	615,711	2012_02_2	Nuclei_frac
P35579_CHKVIQYLAY [iTRAQ_Ni	3 186-199	6,475	680,405	2012_02_2	Nuclei_frac
P35579_CHKVIQYLAY [iTRAQ_Ni	3 186-199	4,785	510,554	2012_02_2	Nuclei_frac
P35579_CHLDPHLVLD [iTRAQ_Ni	1 683-693	5,777	731,93	2012_02_2	Nuclei_frac
P35579_CHLDPHLVLD [iTRAQ_Ni	1 683-693	5,165	488,289	2012_02_2	Nuclei_frac
P35579_CHLEVNLOAN [iTRAQ_Ni	3 1558-1566	5,666	675,391	2012_02_2	Nuclei_frac
P35579_CHLEVNLOAN [iTRAQ_Ni	3 1558-1566	4,743	450,596	2012_02_2	Nuclei_frac
P35579_CHLKDVLLQV [iTRAQ_Ni	2 1844-1855	6,146	577,668	2012_02_2	Nuclei_frac
P35579_CHLQEMEGTV [iTRAQ_Ni	2 1794-1802	5,419	661,867	2012_02_2	Nuclei_frac
P35579_CHLQQELDDL [iTRAQ_Ni	1 1418-1433	9,713	698,704	2012_02_2	Nuclei_frac
P35579_CHLQQELDDL [iTRAQ_Ni	1 1418-1433	9,66	698,703	2012_02_2	Nuclei_frac
P35579_CHLQQELDDL [iTRAQ_Ni	1 1418-1433	9,21	698,703	2012_02_2	Nuclei_frac
P35579_CHLQVELDN [iTRAQ_Ni	2 1278-1295	9,665	745,41	2012_02_2	Nuclei_frac
P35579_CHLQVELDN [iTRAQ_Ni	2 1278-1295	8,957	1117,613	2012_02_2	Nuclei_frac
P35579_CHLQVELDN [iTRAQ_Ni	2 1278-1295	7,422	745,411	2012_02_2	Nuclei_frac
P35579_CHLRLEVNLO [iTRAQ_Ni	3 1556-1566	6,202	540,324	2012_02_2	Nuclei_frac
P35579_CHLRLEVNLO [iTRAQ_Ni	2 1556-1566	5,479	534,992	2012_02_2	Nuclei_frac
P35579_CHLTEMETLQ [iTRAQ_Ni	2 868-882	6,254	680,692	2012_02_2	Nuclei_frac
P35579_CHLVWVPSDI [iTRAQ_Ni	2 31-38	5,357	616,367	2012_02_2	Nuclei_frac
P35579_CHLVWVPSDI [iTRAQ_Ni	2 31-38	5,053	616,369	2012_02_2	Nuclei_frac
P35579_CHNFINNPLA [iTRAQ_Ni	2 15-29	8,118	981,031	2012_02_2	Nuclei_frac
P35579_CHNFINNPLA [iTRAQ_Ni	2 15-29	8,024	981,029	2012_02_2	Nuclei_frac
P35579_CHNFINNPLA [iTRAQ_Ni	2 15-29	7,529	654,356	2012_02_2	Nuclei_frac

P35579_CH NFINNPLA([iTRAQ_Ni	2 15-29	6,937	654,355 2012_02_2 Nuclei_frac
P35579_CH NFINNPLA([iTRAQ_Ni	2 15-29	6,634	654,355 2012_02_2 Nuclei_frac
P35579_CH NFINNPLA([iTRAQ_Ni	2 15-29	6,457	654,354 2012_02_2 Nuclei_frac
P35579_CH NKHEAMIT([iTRAQ_Ni	3 1023-1035	6,69	630,66 2012_02_2 Nuclei_frac
P35579_CH QACVLMIK([iTRAQ_Ni	4 738-745	4,954	633,86 2012_02_2 Nuclei_frac
P35579_CH QAQQERDI([iTRAQ_Ni	2 1698-1716	10,234	793,066 2012_02_2 Nuclei_frac
P35579_CH QAQQERDI([iTRAQ_Ni	2 1698-1716	9,441	793,066 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	2 1358-1370	6,793	571,99 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	3 1358-1370	6,414	577,322 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	2 1358-1370	5,426	571,991 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	3 1358-1370	5,389	577,322 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	4 1358-1371	6,079	668,056 2012_02_2 Nuclei_frac
P35579_CH QIATLHAQ([iTRAQ_Ni	4 1358-1371	5,47	501,294 2012_02_2 Nuclei_frac
P35579_CH QLEEAEEE([iTRAQ_Ni	1 1878-1888	6,814	738,358 2012_02_2 Nuclei_frac
P35579_CH QLLQANPII([iTRAQ_Ni	2 210-225	8,519	1008,083 2012_02_2 Nuclei_frac
P35579_CH QLLQANPII([iTRAQ_Ni	2 210-225	8,427	1008,084 2012_02_2 Nuclei_frac
P35579_CH QLLQANPII([iTRAQ_Ni	2 210-225	6,921	672,39 2012_02_2 Nuclei_frac
P35579_CH QLLQANPII([iTRAQ_Ni	2 210-225	6,644	672,39 2012_02_2 Nuclei_frac
P35579_CH QLLQANPII([iTRAQ_Ni	2 210-225	5,777	672,389 2012_02_2 Nuclei_frac
P35579_CH QRYEILTPI([iTRAQ_Ni	2 719-731	6,821	616,359 2012_02_2 Nuclei_frac
P35579_CH QTLENERG([iTRAQ_Ni	2 1220-1234	6,492	673,365 2012_02_2 Nuclei_frac
P35579_CH QTLENERG([iTRAQ_Ni	2 1220-1234	6,067	673,366 2012_02_2 Nuclei_frac
P35579_CH RGDLPFVV([iTRAQ_Ni	1 1923-1932	9,153	650,388 2012_02_2 Nuclei_frac
P35579_CH RGDLPFVV([iTRAQ_Ni	1 1923-1932	7,263	433,927 2012_02_2 Nuclei_frac
P35579_CH SMEAEMIQ([iTRAQ_Ni	1 1677-1694	6,862	731,694 2012_02_2 Nuclei_frac
P35579_CH TDLLLEPYI([iTRAQ_Ni	2 290-299	6,176	747,426 2012_02_2 Nuclei_frac
P35579_CH TDLLLEPYI([iTRAQ_Ni	2 290-299	5,305	498,619 2012_02_2 Nuclei_frac
P35579_CH TRLQQELD([iTRAQ_Ni	1 1416-1433	7,891	784,424 2012_02_2 Nuclei_frac
P35579_CH TRLQQELD([iTRAQ_Ni	1 1416-1433	6,176	588,567 2012_02_2 Nuclei_frac
P35579_CH VIQYLAYV([iTRAQ_Ni	2 187-199	8,058	589,672 2012_02_2 Nuclei_frac
P35579_CH VISGVLQL([iTRAQ_Ni	2 342-355	8,064	888,056 2012_02_2 Nuclei_frac
P35579_CH VISGVLQL([iTRAQ_Ni	2 342-355	6,191	592,374 2012_02_2 Nuclei_frac
P35579_CH VISGVLQL([iTRAQ_Ni	3 342-356	9,385	683,104 2012_02_2 Nuclei_frac
P35579_CH VKPLLQVS([iTRAQ_Ni	2 834-842	5,078	443,293 2012_02_2 Nuclei_frac
P35579_CH VSHLLGIN([iTRAQ_Ni	1 374-387	8,183	572,657 2012_02_2 Nuclei_frac
P35579_CH VSHLLGIN([iTRAQ_Ni	1 374-387	7,806	858,482 2012_02_2 Nuclei_frac
P35579_CH VSHLLGIN([iTRAQ_Ni	1 374-387	7,488	572,657 2012_02_2 Nuclei_frac
P35579_CH VSHLLGIN([iTRAQ_Ni	1 374-387	7,443	572,658 2012_02_2 Nuclei_frac
P35579_CH VSHLLGIN([iTRAQ_Ni	1 374-387	6,744	572,657 2012_02_2 Nuclei_frac
P35579_CH VVFQEFR([iTRAQ_Ni	1 712-718	6,272	534,801 2012_02_2 Nuclei_frac
P35579_CH VVFQEFR([iTRAQ_Ni	1 712-718	5,843	534,803 2012_02_2 Nuclei_frac
P35579_CH VVFQEFR([iTRAQ_Ni	1 712-718	5,206	534,802 2012_02_2 Nuclei_frac
P35579_CH YLYVDKNF([iTRAQ_Ni	3 9-29	5,137	722,396 2012_02_2 Nuclei_frac
P08670,P17 DGQVINET([iTRAQ_Ni	1 450-465	6,414	660,973 2012_02_2 Nuclei_frac
P08670,P17 DGQVINET([iTRAQ_Ni	1 450-465	5,808	990,956 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	8,762	734,364 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	7,532	734,368 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	7,459	734,374 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	7,36	734,366 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	7,162	489,912 2012_02_2 Nuclei_frac
P08670,P17 EEAENTLQ([iTRAQ_Ni	1 196-206	6,626	489,912 2012_02_2 Nuclei_frac

P08670,P17 EEAENTLQ [iTRAQ_N1	1 196-206	6,488	734,365	2012_02_2	Nuclei_frac
P08670,P17 EEAENTLQ [iTRAQ_N1	1 196-206	5,393	734,365	2012_02_2	Nuclei_frac
P08670,P17 EEAENTLQ [iTRAQ_N1	1 196-216	7,032	846,417	2012_02_2	Nuclei_frac
P08670,P17 EKLQEEML [iTRAQ_N1	2 186-195	7,314	796,442	2012_02_2	Nuclei_frac
P08670,P17 EKLQEEML [iTRAQ_N1	2 186-195	6,446	531,297	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	10,814	653,023	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	9,841	653,023	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	9,798	653,024	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	9,632	653,024	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	8,607	653,024	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-438	8,487	653,023	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	12,128	1057,081	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	10,973	705,057	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	10,704	705,058	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	10,624	705,057	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	10,181	705,057	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	9,795	705,057	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	9,568	1057,081	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	9,091	705,058	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	5,152	529,045	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	5,13	529,045	2012_02_2	Nuclei_frac
P08670,P17 ETNLDSLPL [iTRAQ_N1	2 424-439	5,01	529,047	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	6,086	705,398	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	5,66	705,401	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	5,643	705,399	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	5,228	470,602	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	5,221	705,404	2012_02_2	Nuclei_frac
P08670,P17 EYQDLLNV [iTRAQ_N1	2 381-389	5,167	470,602	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	6,922	413,215	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	5,906	619,318	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	5,403	619,32	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	5,264	619,321	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	4,801	619,331	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-303	4,722	619,321	2012_02_2	Nuclei_frac
P08670,P17 FADLSEAA [iTRAQ_N1	1 294-309	5,233	640,994	2012_02_2	Nuclei_frac
P08670,P17 FANYIDK [iTRAQ_N1	2 113-119	4,866	579,826	2012_02_2	Nuclei_frac
P08670,P17 FANYIDK [iTRAQ_N1	2 113-119	4,813	579,826	2012_02_2	Nuclei_frac
P08670,P17 FANYIDKVI [iTRAQ_N1	2 113-121	6,853	471,943	2012_02_2	Nuclei_frac
P08670,P17 FANYIDKVI [iTRAQ_N1	2 113-121	6,499	707,411	2012_02_2	Nuclei_frac
P08670,P17 FANYIDKVI [iTRAQ_N1	2 113-121	5,598	471,942	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	2 129-138	5,005	729,467	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	2 129-138	4,724	729,466	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	8,309	986,617	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	8,168	986,617	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	8,138	986,619	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,985	986,618	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,965	986,617	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,918	986,616	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,907	986,616	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,73	986,616	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,665	986,617	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,6	986,616	2012_02_2	Nuclei_frac

P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,506	658,08	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	7,21	658,08	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,985	658,081	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,569	658,081	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,566	658,08	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,414	658,08	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,154	658,083	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,151	658,081	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	6,121	658,08	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,759	658,083	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,737	658,082	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,574	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,41	658,084	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,373	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,363	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,308	658,083	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	5,146	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	4,941	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	4,89	493,812	2012_02_2	Nuclei_frac
P08670,P17 ILLAELEQL [iTRAQ_N1	3 129-142	4,783	493,812	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	8,442	572,338	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	8,29	858,005	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	7,698	572,338	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	7,394	572,339	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	7,203	858,006	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	6,452	858,005	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	6,434	858,008	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	6,386	858,003	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	6,185	858,005	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	5,579	858,004	2012_02_2	Nuclei_frac
P08670,P17 ISLPLPNFS [iTRAQ_N1	1 410-423	5,305	572,336	2012_02_2	Nuclei_frac
P08670,P17 KLLEGEESI [iTRAQ_N1	2 401-409	7,146	450,263	2012_02_2	Nuclei_frac
P08670,P17 KLLEGEESI [iTRAQ_N1	2 401-409	6,978	450,263	2012_02_2	Nuclei_frac
P08670,P17 KVESLQEE [iTRAQ_N1	3 222-234	7,015	983,587	2012_02_2	Nuclei_frac
P08670,P17 KVESLQEE [iTRAQ_N1	3 222-234	6,77	983,587	2012_02_2	Nuclei_frac
P08670,P17 KVESLQEE [iTRAQ_N1	3 222-234	5,356	656,06	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	1 145-154	7,119	699,839	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	1 145-154	6,574	699,839	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	1 145-154	6,574	699,839	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	2 145-154	5,521	707,836	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	2 145-154	5,417	472,227	2012_02_2	Nuclei_frac
P08670,P17 LGDLYEEEE [iTRAQ_N1	1 145-157	8,421	599,638	2012_02_2	Nuclei_frac
P08670,P17 LHEEEIQEL [iTRAQ_N1	2 236-269	6,255	1053,558	2012_02_2	Nuclei_frac
P08670,P17 LHEEEIQEL [iTRAQ_N1	2 236-269	6,138	1053,566	2012_02_2	Nuclei_frac
P08670,P17 LHEEEIQEL [iTRAQ_N1	2 236-269	6,05	1053,561	2012_02_2	Nuclei_frac
P08670,P17 LQDEIQNM [iTRAQ_N1	3 364-372	5,685	711,88	2012_02_2	Nuclei_frac
P08670,P17 LQDEIQNM [iTRAQ_N1	2 364-372	5,607	469,591	2012_02_2	Nuclei_frac
P08670,P17 LQDEIQNM [iTRAQ_N1	2 364-372	4,856	703,882	2012_02_2	Nuclei_frac
P08670,P17 LQDEIQNM [iTRAQ_N1	2 364-377	7,272	675,012	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-195	5,95	595,821	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-195	5,432	595,821	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-206	8,628	832,417	2012_02_2	Nuclei_frac

P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-206	7,145	832,417	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	2 188-206	6,409	837,748	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-206	6,077	1248,119	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	1 188-206	5,768	624,564	2012_02_2	Nuclei_frac
P08670,P17 LQEEMLQR [iTRAQ_N1	2 188-206	5,255	837,746	2012_02_2	Nuclei_frac
P08670,P17 MALDIEIAT [iTRAQ_N1	1 390-400	8,69	720,389	2012_02_2	Nuclei_frac
P08670,P17 MALDIEIAT [iTRAQ_N1	2 390-400	5,911	728,389	2012_02_2	Nuclei_frac
P08670,P17 NLQEAEV [iTRAQ_N1	2 282-291	7,58	799,409	2012_02_2	Nuclei_frac
P08670,P17 NLQEAEV [iTRAQ_N1	2 282-291	6,576	799,412	2012_02_2	Nuclei_frac
P08670,P17 NLQEAEV [iTRAQ_N1	2 282-291	6,259	533,276	2012_02_2	Nuclei_frac
P08670,P17 QDVDNASI [iTRAQ_N1	1 207-216	7,358	616,823	2012_02_2	Nuclei_frac
P08670,P17 QDVDNASI [iTRAQ_N1	1 207-216	7,327	616,824	2012_02_2	Nuclei_frac
P08670,P17 QQYESVA/ [iTRAQ_N1	2 273-281	7,07	656,365	2012_02_2	Nuclei_frac
P08670,P17 QQYESVA/ [iTRAQ_N1	2 273-281	5,636	437,912	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-333	7,803	889,986	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-333	6,042	593,659	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-333	5,31	593,659	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-341	8,888	889,133	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-341	8,496	889,131	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-341	8,456	1333,19	2012_02_2	Nuclei_frac
P08670,P17 QVQSLTCE [iTRAQ_N1	3 321-341	6,516	667,101	2012_02_2	Nuclei_frac
P08670,P17 RQVDQLT [iTRAQ_N1	2 158-167	7,698	502,285	2012_02_2	Nuclei_frac
P08670,P17 RQVDQLT [iTRAQ_N1	2 158-167	7,604	502,286	2012_02_2	Nuclei_frac
P08670,P17 RQVDQLT [iTRAQ_N1	2 158-167	7,044	502,285	2012_02_2	Nuclei_frac
P08670,P17 RQVQSLTC [iTRAQ_N1	3 320-333	7,987	968,035	2012_02_2	Nuclei_frac
P08670,P17 RQVQSLTC [iTRAQ_N1	3 320-333	7,274	645,693	2012_02_2	Nuclei_frac
P08670,P17 SKFADLSE [iTRAQ_N1	2 292-303	7,112	532,96	2012_02_2	Nuclei_frac
P08670,P17 SSVPGVR [iTRAQ_N1	1 71-77	5,84	423,254	2012_02_2	Nuclei_frac
P08670,P17 TNEKVELC [iTRAQ_N1	2 100-112	7,608	938,507	2012_02_2	Nuclei_frac
P08670,P17 TNEKVELC [iTRAQ_N1	2 100-112	7,458	938,509	2012_02_2	Nuclei_frac
P08670,P17 TNEKVELC [iTRAQ_N1	2 100-112	7,215	626,008	2012_02_2	Nuclei_frac
P08670,P17 TNEKVELC [iTRAQ_N1	2 100-112	6,671	626,007	2012_02_2	Nuclei_frac
P08670,P17 TNEKVELC [iTRAQ_N1	2 100-112	5,478	626,006	2012_02_2	Nuclei_frac
P08670,P17 VELQELND [iTRAQ_N1	1 104-112	5,64	630,341	2012_02_2	Nuclei_frac
P08670,P17 VESLQEEI/ [iTRAQ_N1	2 223-234	7,255	847,489	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	1 170-183	7,784	611,648	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	2 170-183	7,672	924,967	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	1 170-183	7,508	916,968	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	1 170-183	7,269	916,97	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	1 170-183	7,136	611,648	2012_02_2	Nuclei_frac
P08670,P17 VEVERDNL [iTRAQ_N1	2 170-183	6,021	616,98	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	1 79-89	7,239	655,328	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	1 79-89	7,099	655,329	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	1 79-89	5,433	437,222	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	1 79-89	5,216	655,334	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	2 79-90	8,148	791,43	2012_02_2	Nuclei_frac
P02545_CH AAYEAELC [iTRAQ_N1	2 79-90	4,929	527,955	2012_02_2	Nuclei_frac
P02545_CH AGQVVTIV [iTRAQ_N1	2 491-515	10,527	941,18	2012_02_2	Nuclei_frac
P02545_CH AGQVVTIV [iTRAQ_N1	2 491-515	5,036	706,136	2012_02_2	Nuclei_frac
P02545_CH AQHEDQVI [iTRAQ_N1	3 250-261	6,005	484,514	2012_02_2	Nuclei_frac
P02545_CH AQNTWGC [iTRAQ_N1	2 516-527	9,02	754,364	2012_02_2	Nuclei_frac

P02545_CHAQNTWGC [iTRAQ_N1	2 516-527	7,182	503,245	2012_02_2	Nuclei_frac
P02545_CHARLQLELS [iTRAQ_N1	2 100-108	4,889	449,285	2012_02_2	Nuclei_frac
P02545_CHASASGSGA [iTRAQ_N1	1 598-624	11,252	1255,137	2012_02_2	Nuclei_frac
P02545_CHASASGSGA [iTRAQ_N1	1 598-624	10,278	837,093	2012_02_2	Nuclei_frac
P02545_CHASASGSGA [iTRAQ_N1	1 598-624	8,699	837,094	2012_02_2	Nuclei_frac
P02545_CHASASGSGA [iTRAQ_N1	1 598-624	5,085	628,072	2012_02_2	Nuclei_frac
P02545_CHDLEALLNS [iTRAQ_N1	2 136-144	5,997	430,922	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-155	6,423	469,938	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-155	6,211	704,403	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	10,117	782,453	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	9,669	782,453	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	9,408	782,454	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	9,262	521,971	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	8,243	521,971	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	7,535	521,971	2012_02_2	Nuclei_frac
P02545_CHEAALSTAL [iTRAQ_N1	2 145-156	6,747	521,97	2012_02_2	Nuclei_frac
P02545_CHGQVAKLEA [iTRAQ_N1	3 167-180	5,096	606,37	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	9,031	860	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	8,914	860,002	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	8,563	860,001	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	8,337	573,669	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	8,164	573,669	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	7,338	573,669	2012_02_2	Nuclei_frac
P02545_CHIDSLSAQLS [iTRAQ_N1	2 299-311	6,967	573,668	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	9,629	663,398	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	9,3	663,398	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	8,942	994,592	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	8,619	663,398	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	8,28	663,397	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	8,037	994,594	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	6,286	497,8	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	5,549	497,8	2012_02_2	Nuclei_frac
P02545_CHIRIDSLSAQ [iTRAQ_N1	2 297-311	4,749	497,8	2012_02_2	Nuclei_frac
P02545_CHITESEEVVS [iTRAQ_N1	1 63-72	9,351	646,846	2012_02_2	Nuclei_frac
P02545_CHITESEEVVS [iTRAQ_N1	1 63-72	7,28	646,845	2012_02_2	Nuclei_frac
P02545_CHLADALQEL [iTRAQ_N1	1 241-249	5,421	586,842	2012_02_2	Nuclei_frac
P02545_CHLALDMEIH [iTRAQ_N1	2 367-377	9,792	746,394	2012_02_2	Nuclei_frac
P02545_CHLALDMEIH [iTRAQ_N1	2 367-377	7,624	497,931	2012_02_2	Nuclei_frac
P02545_CHLALDMEIH [iTRAQ_N1	1 367-377	6,435	492,599	2012_02_2	Nuclei_frac
P02545_CHLAVYIDR [iTRAQ_N1	1 42-48	6,148	497,297	2012_02_2	Nuclei_frac
P02545_CHLAVYIDR [iTRAQ_N1	1 42-48	6,078	497,297	2012_02_2	Nuclei_frac
P02545_CHLAVYIDR [iTRAQ_N1	1 42-48	5,978	497,298	2012_02_2	Nuclei_frac
P02545_CHLAVYIDR [iTRAQ_N1	1 42-48	5,009	497,297	2012_02_2	Nuclei_frac
P02545_CHLAVYIDRVI [iTRAQ_N1	1 42-50	4,798	624,883	2012_02_2	Nuclei_frac
P02545_CHLEAALGEA [iTRAQ_N1	3 172-181	5,245	487,973	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	6,139	838,523	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	6,096	559,35	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	6,037	559,35	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	5,822	559,35	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	5,784	559,35	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	5,754	559,349	2012_02_2	Nuclei_frac
P02545_CHLKDLEALL [iTRAQ_N1	3 134-144	5,753	559,35	2012_02_2	Nuclei_frac

P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,715	559,349	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,691	838,522	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,603	559,35	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,5	838,521	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,436	559,35	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,318	838,521	2012_02_2	Nuclei_frac
P02545_CH LKDLEALL [iTRAQ_N1	3 134-144	5,308	838,522	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	7,028	959,509	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,877	959,51	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,863	959,51	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,561	640,009	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,346	640,009	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,229	640,009	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	6,193	640,009	2012_02_2	Nuclei_frac
P02545_CH LQEKEDLQ [iTRAQ_N1	2 29-41	5,966	640,008	2012_02_2	Nuclei_frac
P02545_CH LRDLEDSL [iTRAQ_N1	1 320-329	8,706	666,374	2012_02_2	Nuclei_frac
P02545_CH LRDLEDSL [iTRAQ_N1	1 320-329	7,536	444,586	2012_02_2	Nuclei_frac
P02545_CH LRITESEEV [iTRAQ_N1	1 61-72	10,292	521,294	2012_02_2	Nuclei_frac
P02545_CH LRLSPSPT [iTRAQ_N1	2 387-397	5,281	489,26	2012_02_2	Nuclei_frac
P02545_CH LRLSPSPT [iTRAQ_N1	2 387-397	4,98	733,387	2012_02_2	Nuclei_frac
P02545_CH LSPSPTSQ [iTRAQ_N1	1 389-397	6,522	558,811	2012_02_2	Nuclei_frac
P02545_CH MQQQQLDE [iTRAQ_N1	2 352-366	8,605	1091,571	2012_02_2	Nuclei_frac
P02545_CH MQQQQLDE [iTRAQ_N1	3 352-366	7,484	1099,567	2012_02_2	Nuclei_frac
P02545_CH MQQQQLDE [iTRAQ_N1	3 352-366	6,921	733,38	2012_02_2	Nuclei_frac
P02545_CH MQQQQLDE [iTRAQ_N1	2 352-366	5,928	728,05	2012_02_2	Nuclei_frac
P02545_CH NIYSEELR [iTRAQ_N1	1 209-216	5,366	584,311	2012_02_2	Nuclei_frac
P02545_CH NSNLVGA [iTRAQ_N1	1 281-296	11,599	632,995	2012_02_2	Nuclei_frac
P02545_CH NSNLVGA [iTRAQ_N1	1 281-296	11,167	632,995	2012_02_2	Nuclei_frac
P02545_CH NSNLVGA [iTRAQ_N1	1 281-296	9,796	948,988	2012_02_2	Nuclei_frac
P02545_CH NSNLVGA [iTRAQ_N1	1 281-296	9,383	632,993	2012_02_2	Nuclei_frac
P02545_CH RTLEGELH [iTRAQ_N1	1 156-166	6,052	494,943	2012_02_2	Nuclei_frac
P02545_CH TALINSTG [iTRAQ_N1	2 528-541	9,184	826,428	2012_02_2	Nuclei_frac
P02545_CH TALINSTG [iTRAQ_N1	2 528-541	8,747	551,287	2012_02_2	Nuclei_frac
P02545_CH TALINSTG [iTRAQ_N1	1 528-541	7,028	545,956	2012_02_2	Nuclei_frac
P02545_CH TLEGELHD [iTRAQ_N1	1 157-166	8,16	442,91	2012_02_2	Nuclei_frac
P02545_CH TLEGELHD [iTRAQ_N1	2 157-171	5,075	489,281	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-450	8,49	746,392	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-450	5,269	497,93	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-453	9,243	947,513	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-453	9,212	947,513	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-453	7,969	632,011	2012_02_2	Nuclei_frac
P02545_CH VAVEEVDE [iTRAQ_N1	2 440-453	5,502	474,26	2012_02_2	Nuclei_frac
Q13813,Q1 AALLELWE [iTRAQ_N1	1 450-459	7,954	679,402	2012_02_2	Nuclei_frac
Q13813,Q1 ALCAEADF [iTRAQ_N1	3 313-335	5,134	713,888	2012_02_2	Nuclei_frac
Q13813,Q1 AQLADSF [iTRAQ_N1	1 567-580	11,843	926,488	2012_02_2	Nuclei_frac
Q13813,Q1 DLAALGDI [iTRAQ_N1	2 1261-1278	6,344	716,393	2012_02_2	Nuclei_frac
Q13813,Q1 DLASVQAI [iTRAQ_N1	1 286-295	6,493	615,372	2012_02_2	Nuclei_frac
Q13813,Q1 DLASVQAI [iTRAQ_N1	1 286-295	6,483	615,371	2012_02_2	Nuclei_frac
Q13813,Q1 DLASVQAI [iTRAQ_N1	1 286-295	5,672	615,371	2012_02_2	Nuclei_frac
Q13813,Q1 DLSSVQTL [iTRAQ_N1	2 1987-1997	9,4	746,95	2012_02_2	Nuclei_frac
Q13813,Q1 DLSSVQTL [iTRAQ_N1	2 1987-1997	9,212	746,947	2012_02_2	Nuclei_frac

Q13813,Q1 DLSSVQTL [iTRAQ_N1	2	1987-1997	7,572	498,301	2012_02_2	Nuclei_frac
Q13813,Q1 DLSSVQTL [iTRAQ_N1	2	1987-1997	6,59	498,3	2012_02_2	Nuclei_frac
Q13813,Q1 DLTGVQNI [iTRAQ_N1	1	1775-1783	6,666	580,33	2012_02_2	Nuclei_frac
Q13813,Q1 DLTGVQNI [iTRAQ_N1	1	1775-1783	6,6	580,332	2012_02_2	Nuclei_frac
Q13813,Q1 DLTGVQNI [iTRAQ_N1	1	1775-1783	5,136	580,331	2012_02_2	Nuclei_frac
Q13813,Q1 DVTGAEAL [iTRAQ_N1	1	1350-1360	7,639	659,361	2012_02_2	Nuclei_frac
Q13813,Q1 EANELQQV [iTRAQ_N1	2	1079-1090	7,745	597,316	2012_02_2	Nuclei_frac
Q13813,Q1 ELPTAFDY [iTRAQ_N1	1	2435-2447	9,625	866,443	2012_02_2	Nuclei_frac
Q13813,Q1 FKELSTLR [iTRAQ_N1	2	29-36	5,176	427,931	2012_02_2	Nuclei_frac
Q13813,Q1 GKDLIGVQ [iTRAQ_N1	3	813-824	5,827	577,371	2012_02_2	Nuclei_frac
Q13813,Q1 GKDLIGVQ [iTRAQ_N1	3	813-824	5,342	577,371	2012_02_2	Nuclei_frac
Q13813,Q1 HQAFEAEAL [iTRAQ_N1	1	1572-1585	6,948	584,957	2012_02_2	Nuclei_frac
Q13813,Q1 HQAFEAEAL [iTRAQ_N1	1	1572-1585	6,063	438,971	2012_02_2	Nuclei_frac
Q13813,Q1 HQAFEAEAL [iTRAQ_N1	1	614-627	7,649	577,957	2012_02_2	Nuclei_frac
Q13813,Q1 IAALQAFAL [iTRAQ_N1	2	1481-1499	8,548	754,096	2012_02_2	Nuclei_frac
Q13813,Q1 KGDILTLLN [iTRAQ_N1	3	990-1002	7,187	617,042	2012_02_2	Nuclei_frac
Q13813,Q1 KGDILTLLN [iTRAQ_N1	3	990-1002	6,595	617,044	2012_02_2	Nuclei_frac
Q13813,Q1 KHQALQAI [iTRAQ_N1	2	825-839	5,359	494,029	2012_02_2	Nuclei_frac
Q13813,Q1 KLLVGSED [iTRAQ_N1	2	1764-1774	6,096	508,96	2012_02_2	Nuclei_frac
Q13813,Q1 KVEDLFLT [iTRAQ_N1	3	2068-2078	6,04	581,687	2012_02_2	Nuclei_frac
Q13813,Q1 LAALADQI [iTRAQ_N1	2	1613-1626	8,368	960,056	2012_02_2	Nuclei_frac
Q13813,Q1 LAALADQI [iTRAQ_N1	2	1613-1626	7,315	640,372	2012_02_2	Nuclei_frac
Q13813,Q1 LAALADQI [iTRAQ_N1	2	1613-1626	6,698	640,373	2012_02_2	Nuclei_frac
Q13813,Q1 LAALADQI [iTRAQ_N1	2	1613-1626	6,199	640,371	2012_02_2	Nuclei_frac
Q13813,Q1 LAQFVEHV [iTRAQ_N1	2	1825-1833	4,951	482,61	2012_02_2	Nuclei_frac
Q13813,Q1 LIQSHPEA [iTRAQ_N1	2	1279-1293	5,602	671,361	2012_02_2	Nuclei_frac
Q13813,Q1 LLEAQSHF [iTRAQ_N1	1	2059-2067	7,966	415,567	2012_02_2	Nuclei_frac
Q13813,Q1 LQQFLR [iTRAQ_N1	1	786-791	5,599	474,792	2012_02_2	Nuclei_frac
Q13813,Q1 LSDDNTIGI [iTRAQ_N1	2	1810-1824	6,849	678,696	2012_02_2	Nuclei_frac
Q13813,Q1 MQHNLEQI [iTRAQ_N1	2	2284-2295	6,165	552,618	2012_02_2	Nuclei_frac
Q13813,Q1 NQALNTDI [iTRAQ_N1	1	1233-1253	9,462	824,751	2012_02_2	Nuclei_frac
Q13813,Q1 QFQDAGHI [iTRAQ_N1	3	743-757	5,807	545,793	2012_02_2	Nuclei_frac
Q13813,Q1 QFQDAGHI [iTRAQ_N1	3	743-757	4,972	545,794	2012_02_2	Nuclei_frac
Q13813,Q1 RAQLADSF [iTRAQ_N1	1	566-580	5,099	502,772	2012_02_2	Nuclei_frac
Q13813,Q1 REELITNWI [iTRAQ_N1	1	336-347	7,235	577,65	2012_02_2	Nuclei_frac
Q13813,Q1 SLQQLAEE [iTRAQ_N1	1	1197-1205	6,86	609,336	2012_02_2	Nuclei_frac
Q13813,Q1 SLLGSAH [iTRAQ_N1	1	1206-1217	8,129	490,271	2012_02_2	Nuclei_frac
Q13813,Q1 SSEEIESAF [iTRAQ_N1	1	2385-2394	8,672	649,821	2012_02_2	Nuclei_frac
Q13813,Q1 TATDEAYK [iTRAQ_N1	3	595-610	6,905	724,053	2012_02_2	Nuclei_frac
Q13813,Q1 VLETAEDIK [iTRAQ_N1	1	8-18	7,384	723,879	2012_02_2	Nuclei_frac
O75369,O7 AGLAPLEV [iTRAQ_N1	1	1450-1458	6,558	535,329	2012_02_2	Nuclei_frac
O75369,O7 AGLAPLEV [iTRAQ_N1	1	1450-1458	6,34	535,328	2012_02_2	Nuclei_frac
O75369,O7 APLNVQFM [iTRAQ_N1	2	878-894	7,798	685,722	2012_02_2	Nuclei_frac
O75369,O7 DLAEDAPV [iTRAQ_N1	3	7-16	5,029	535,637	2012_02_2	Nuclei_frac
O75369,O7 EATTDFTV [iTRAQ_N1	2	1246-1267	6,571	669,603	2012_02_2	Nuclei_frac
O75369,O7 ERGDYVLA [iTRAQ_N1	2	2553-2562	5,53	479,949	2012_02_2	Nuclei_frac
O75369,O7 FADEHVPC [iTRAQ_N1	2	2051-2064	6,737	606,992	2012_02_2	Nuclei_frac
O75369,O7 GAGIGGLGI [iTRAQ_N1	2	1355-1372	7,822	639,691	2012_02_2	Nuclei_frac
O75369,O7 GAGTGGLG [iTRAQ_N1	3	1067-1084	7,206	654,681	2012_02_2	Nuclei_frac
O75369,O7 IAGPGLGS [iTRAQ_N1	1	1426-1436	7,943	564,336	2012_02_2	Nuclei_frac
O75369,O7 IFFAGDTIPI [iTRAQ_N1	2	430-439	6,624	698,908	2012_02_2	Nuclei_frac

O75369,O7 IGNLQTDL [iTRAQ_N1	1 37-49	8,442	773,423	2012_02_2	Nuclei_frac
O75369,O7 IKVFGPGIE [iTRAQ_N1	3 1231-1241	6,751	526,331	2012_02_2	Nuclei_frac
O75369,O7 IPYLPITNFI [iTRAQ_N1	2 153-169	8,154	779,416	2012_02_2	Nuclei_frac
O75369,O7 KGEITGEVI [iTRAQ_N1	4 1733-1746	7,713	640,022	2012_02_2	Nuclei_frac
O75369,O7 LDVTILSPS [iTRAQ_N1	1 977-986	7,682	622,87	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-60	7,95	757,993	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-60	7,897	757,99	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-60	7,872	757,993	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-60	6,792	505,665	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-60	5,857	505,664	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-61	8,016	836,043	2012_02_2	Nuclei_frac
O75369,O7 LIALLEVLS [iTRAQ_N1	2 50-61	6,205	557,698	2012_02_2	Nuclei_frac
O75369,O7 LVSPGSAN [iTRAQ_N1	1 2452-2471	9,366	1095,597	2012_02_2	Nuclei_frac
O75369,O7 LVSPGSAN [iTRAQ_N1	1 2452-2471	7,041	730,733	2012_02_2	Nuclei_frac
O75369,O7 SGCIVNNL [iTRAQ_N1	3 658-673	5,553	684,696	2012_02_2	Nuclei_frac
O75369,O7 SPFTVGVA [iTRAQ_N1	2 932-946	6,648	597,35	2012_02_2	Nuclei_frac
O75369,O7 VKVLPTYC [iTRAQ_N1	3 1509-1519	5,243	551,671	2012_02_2	Nuclei_frac
O75369,O7 VLFASQEIF [iTRAQ_N1	1 823-836	9,39	853,476	2012_02_2	Nuclei_frac
O75369,O7 VLFASQEIF [iTRAQ_N1	1 823-836	8,941	853,48	2012_02_2	Nuclei_frac
O75369,O7 VLFASQEIF [iTRAQ_N1	1 823-836	7,04	569,32	2012_02_2	Nuclei_frac
O75369,O7 VLFASQEIF [iTRAQ_N1	1 823-836	6,343	569,32	2012_02_2	Nuclei_frac
O75369,O7 VLPTYDAS [iTRAQ_N1	2 1511-1519	7,971	641,37	2012_02_2	Nuclei_frac
O75369,O7 VLQSFTVC [iTRAQ_N1	2 1439-1449	9,11	749,922	2012_02_2	Nuclei_frac
O75369,O7 VLQSFTVC [iTRAQ_N1	2 1439-1449	7,876	500,283	2012_02_2	Nuclei_frac
O75369,O7 VSYFPTVP [iTRAQ_N1	2 2035-2050	7,796	1023,084	2012_02_2	Nuclei_frac
O75369,O7 VSYFPTVP [iTRAQ_N1	2 2035-2050	6,777	682,391	2012_02_2	Nuclei_frac
O75369,O7 VTASGPGL [iTRAQ_N1	1 1520-1545	5,413	897,808	2012_02_2	Nuclei_frac
O75369,O7 VTVLFAGC [iTRAQ_N1	2 329-340	8,472	529,987	2012_02_2	Nuclei_frac
P02751_ISC DLQFVEVT [iTRAQ_N1	2 881-891	7,177	790,943	2012_02_2	Nuclei_frac
P02751_ISC DLQFVEVT [iTRAQ_N1	2 881-891	6,318	527,629	2012_02_2	Nuclei_frac
P02751_ISC EATIPGHLI [iTRAQ_N1	2 625-638	7,937	611,344	2012_02_2	Nuclei_frac
P02751_ISC FLATTPNS [iTRAQ_N1	1 1880-1896	9,059	1036,076	2012_02_2	Nuclei_frac
P02751_ISC FLATTPNS [iTRAQ_N1	1 1880-1896	7,362	691,053	2012_02_2	Nuclei_frac
P02751_ISC FTQVTPTS [iTRAQ_N1	1 1699-1722	10,063	946,164	2012_02_2	Nuclei_frac
P02751_ISC FTQVTPTS [iTRAQ_N1	1 1699-1722	8,677	1418,741	2012_02_2	Nuclei_frac
P02751_ISC FTQVTPTS [iTRAQ_N1	1 1699-1722	5,77	709,874	2012_02_2	Nuclei_frac
P02751_ISC GDSPASSK [iTRAQ_N1	2 1494-1508	6,667	627,342	2012_02_2	Nuclei_frac
P02751_ISC GDSPASSK [iTRAQ_N1	2 1494-1508	6,656	627,341	2012_02_2	Nuclei_frac
P02751_ISC GLKPGVVY [iTRAQ_N1	2 639-663	6,446	772,676	2012_02_2	Nuclei_frac
P02751_ISC GLKPGVVY [iTRAQ_N1	2 639-663	6,39	772,675	2012_02_2	Nuclei_frac
P02751_ISC HTSVQTTS [iTRAQ_N1	1 242-259	9,127	670,002	2012_02_2	Nuclei_frac
P02751_ISC HYQINQQV [iTRAQ_N1	1 27-36	7,858	773,387	2012_02_2	Nuclei_frac
P02751_ISC HYQINQQV [iTRAQ_N1	1 27-36	6,666	515,927	2012_02_2	Nuclei_frac
P02751_ISC IAWESPQG [iTRAQ_N1	1 1619-1630	8,189	751,398	2012_02_2	Nuclei_frac
P02751_ISC IITYGETGGI [iTRAQ_N1	2 1449-1469	6,419	819,425	2012_02_2	Nuclei_frac
P02751_ISC LGVRPSQC [iTRAQ_N1	1 1086-1098	6,166	489,944	2012_02_2	Nuclei_frac
P02751_ISC LLCQCLGF [iTRAQ_N1	3 2200-2213	8,996	599,3	2012_02_2	Nuclei_frac
P02751_ISC NLQPASEY [iTRAQ_N1	2 1024-1039	7,535	674,39	2012_02_2	Nuclei_frac
P02751_ISC NLQPASEY [iTRAQ_N1	2 1024-1039	5,717	674,39	2012_02_2	Nuclei_frac
P02751_ISC NLQPASEY [iTRAQ_N1	2 1024-1039	5,353	674,39	2012_02_2	Nuclei_frac
P02751_ISC NLQPASEY [iTRAQ_N1	2 1024-1039	4,956	674,392	2012_02_2	Nuclei_frac

P02751_ISC QYNVGPS\ [iTRAQ_Ni	2	1010-1023	8,97	632,692	2012_02_2	Nuclei_frac
P02751_ISC SSPVIDA\ [iTRAQ_Ni	1	1861-1879	8,477	1029,053	2012_02_2	Nuclei_frac
P02751_ISC STTPDITG\ [iTRAQ_Ni	1	1167-1176	8,463	627,827	2012_02_2	Nuclei_frac
P02751_ISC STTPDITG\ [iTRAQ_Ni	1	1167-1176	7,788	627,827	2012_02_2	Nuclei_frac
P02751_ISC STTPDITG\ [iTRAQ_Ni	1	1167-1176	7,538	627,827	2012_02_2	Nuclei_frac
P02751_ISC SYTITGLQF [iTRAQ_Ni	2	1836-1849	9,115	916,488	2012_02_2	Nuclei_frac
P02751_ISC SYTITGLQF [iTRAQ_Ni	2	1836-1849	5,074	611,328	2012_02_2	Nuclei_frac
P02751_ISC TYHVGEQV [iTRAQ_Ni	2	2270-2279	6,588	521,943	2012_02_2	Nuclei_frac
P02751_ISC VDVIPVNL [iTRAQ_Ni	1	908-922	7,988	887,492	2012_02_2	Nuclei_frac
P02751_ISC VDVIPVNL [iTRAQ_Ni	1	908-922	6,704	591,993	2012_02_2	Nuclei_frac
P02751_ISC VGDTYERP [iTRAQ_Ni	2	77-85	5,31	451,586	2012_02_2	Nuclei_frac
P02751_ISC VPGTSTSA [iTRAQ_Ni	1	2119-2133	9,361	803,449	2012_02_2	Nuclei_frac
P02751_ISC VPGTSTSA [iTRAQ_Ni	1	2119-2133	7,667	535,969	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	7,451	1035,58	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	7,069	690,723	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	6,795	690,723	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	6,495	690,724	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	5,973	1035,582	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	5,671	690,725	2012_02_2	Nuclei_frac
P02751_ISC VTWAPPP\ [iTRAQ_Ni	1	1254-1270	5,295	1035,586	2012_02_2	Nuclei_frac
P02751_ISC VVTPLSPP [iTRAQ_Ni	1	1139-1166	5,634	1062,904	2012_02_2	Nuclei_frac
P02751_ISC WLPSSSPV [iTRAQ_Ni	1	1531-1542	9,557	747,397	2012_02_2	Nuclei_frac
P02751_ISC WLPSSSPV [iTRAQ_Ni	1	1531-1542	6,307	498,602	2012_02_2	Nuclei_frac
P02751_ISC YSFCTDHT [iTRAQ_Ni	2	367-380	5,533	624,312	2012_02_2	Nuclei_frac
Q07065_ISC ASVSQVE\ [iTRAQ_Ni	2	541-551	6,68	717,908	2012_02_2	Nuclei_frac
Q07065_ISC DLSDGIHV [iTRAQ_Ni	2	214-223	6,62	685,9	2012_02_2	Nuclei_frac
Q07065_ISC DLSDGIHV [iTRAQ_Ni	2	214-223	5,435	457,602	2012_02_2	Nuclei_frac
Q07065_ISC ELVSLKQE [iTRAQ_Ni	3	327-339	6,241	660,722	2012_02_2	Nuclei_frac
Q07065_ISC ELVSLKQE [iTRAQ_Ni	3	327-339	5,729	660,722	2012_02_2	Nuclei_frac
Q07065_ISC ELVSLKQE [iTRAQ_Ni	3	327-339	4,95	660,723	2012_02_2	Nuclei_frac
Q07065_ISC ERDFTSLEI [iTRAQ_Ni	1	227-240	7,948	934,96	2012_02_2	Nuclei_frac
Q07065_ISC ERDFTSLEI [iTRAQ_Ni	1	227-240	7,018	623,643	2012_02_2	Nuclei_frac
Q07065_ISC GLLDDLRLN [iTRAQ_Ni	1	579-590	4,975	520,282	2012_02_2	Nuclei_frac
Q07065_ISC HSEAFEAL [iTRAQ_Ni	2	395-405	7,804	788,424	2012_02_2	Nuclei_frac
Q07065_ISC HSEAFEAL [iTRAQ_Ni	2	395-405	6,645	525,952	2012_02_2	Nuclei_frac
Q07065_ISC IETNENNLE [iTRAQ_Ni	2	567-578	8,833	825,435	2012_02_2	Nuclei_frac
Q07065_ISC IETNENNLE [iTRAQ_Ni	2	567-578	7,561	550,624	2012_02_2	Nuclei_frac
Q07065_ISC ISEVLQK [iTRAQ_Ni	2	200-206	5,436	552,848	2012_02_2	Nuclei_frac
Q07065_ISC ISEVLQK [iTRAQ_Ni	2	200-206	5,016	552,848	2012_02_2	Nuclei_frac
Q07065_ISC LALQALTE [iTRAQ_Ni	2	347-355	5,952	637,901	2012_02_2	Nuclei_frac
Q07065_ISC LALQALTE [iTRAQ_Ni	2	347-355	5,637	637,902	2012_02_2	Nuclei_frac
Q07065_ISC LALQALTE [iTRAQ_Ni	2	347-355	5,565	425,604	2012_02_2	Nuclei_frac
Q07065_ISC LALQALTE [iTRAQ_Ni	2	347-355	5,3	425,604	2012_02_2	Nuclei_frac
Q07065_ISC LPPQDFLD [iTRAQ_Ni	1	524-532	5,015	622,843	2012_02_2	Nuclei_frac
Q07065_ISC LQHVEDG\ [iTRAQ_Ni	2	413-429	8,48	667,35	2012_02_2	Nuclei_frac
Q07065_ISC LQHVEDG\ [iTRAQ_Ni	2	413-429	8,099	1000,525	2012_02_2	Nuclei_frac
Q07065_ISC LQHVEDG\ [iTRAQ_Ni	1	413-429	7,323	662,02	2012_02_2	Nuclei_frac
Q07065_ISC LSSLDNLK [iTRAQ_Ni	2	533-540	5,304	589,357	2012_02_2	Nuclei_frac
Q07065_ISC QREELGQG [iTRAQ_Ni	2	147-161	8,964	663,035	2012_02_2	Nuclei_frac
Q07065_ISC QTESLESLE [iTRAQ_Ni	2	430-440	8,002	761,935	2012_02_2	Nuclei_frac
Q07065_ISC QTESLESLE [iTRAQ_Ni	2	430-440	5,338	508,29	2012_02_2	Nuclei_frac

Q07065_IS(SEESVSRLI [iTRAQ_Ni	1 359-371	4,856	558,964	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-260	7,775	627,351	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	9,639	679,387	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	9,528	679,386	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	8,47	679,385	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	8,34	679,387	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	7,833	679,386	2012_02_2 Nuclei_frac
Q07065_IS(SINDNIAIF [iTRAQ_Ni	2 247-261	5,105	509,792	2012_02_2 Nuclei_frac
Q07065_IS(SLGETQLV [iTRAQ_Ni	2 474-491	10,737	779,769	2012_02_2 Nuclei_frac
Q07065_IS(SLGETQLV [iTRAQ_Ni	2 474-491	5,805	585,079	2012_02_2 Nuclei_frac
Q07065_IS(SREWDME [iTRAQ_Ni	1 302-311	5,962	479,576	2012_02_2 Nuclei_frac
Q07065_IS(SSSSSSAS [iTRAQ_Ni	2 79-102	10,042	745,342	2012_02_2 Nuclei_frac
Q07065_IS(SSSSSSAS [iTRAQ_Ni	2 79-102	9,401	1117,509	2012_02_2 Nuclei_frac
Q07065_IS(SSSSSSAS [iTRAQ_Ni	2 79-102	8,882	745,342	2012_02_2 Nuclei_frac
Q07065_IS(SSSSSSAS [iTRAQ_Ni	2 79-102	6,819	745,342	2012_02_2 Nuclei_frac
Q07065_IS(STLQTMES [iTRAQ_Ni	1 312-326	10,882	958,974	2012_02_2 Nuclei_frac
Q07065_IS(SVGELPST [iTRAQ_Ni	2 492-505	8,338	881,499	2012_02_2 Nuclei_frac
Q07065_IS(SVGELPST [iTRAQ_Ni	2 492-505	8,296	881,498	2012_02_2 Nuclei_frac
Q07065_IS(SVGELPST [iTRAQ_Ni	2 492-505	7,759	588,001	2012_02_2 Nuclei_frac
Q07065_IS(SVGELPST [iTRAQ_Ni	2 492-505	6,158	588	2012_02_2 Nuclei_frac
Q07065_IS(SVGELPST [iTRAQ_Ni	2 492-505	5,619	588,001	2012_02_2 Nuclei_frac
Q07065_IS(VASLEESE [iTRAQ_Ni	3 273-287	5,783	693,717	2012_02_2 Nuclei_frac
Q07065_IS(VQEQVHTI [iTRAQ_Ni	1 506-523	11,421	1083,58	2012_02_2 Nuclei_frac
Q07065_IS(VQEQVHTI [iTRAQ_Ni	1 506-523	8,182	722,721	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	11,799	971,03	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	11,585	971,034	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	10,993	647,691	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	10,411	971,035	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	9,415	647,692	2012_02_2 Nuclei_frac
Q07065_IS(VQSLQATF [iTRAQ_Ni	1 162-177	8,199	647,693	2012_02_2 Nuclei_frac
Q00610_C(ALEHFTDL [iTRAQ_Ni	2 626-637	4,76	584,987	2012_02_2 Nuclei_frac
Q00610_C(AVNYFSK [iTRAQ_Ni	2 1435-1441	5,281	558,818	2012_02_2 Nuclei_frac
Q00610_C(DPHLACVA [iTRAQ_Ni	2 913-923	4,877	492,246	2012_02_2 Nuclei_frac
Q00610_C(EAIDSYIK [iTRAQ_Ni	2 1123-1130	5,021	613,847	2012_02_2 Nuclei_frac
Q00610_C(EHLELFWS [iTRAQ_Ni	1 1334-1342	5,864	454,243	2012_02_2 Nuclei_frac
Q00610_C(FDVNTSA [iTRAQ_Ni	1 1075-1094	10,886	795,429	2012_02_2 Nuclei_frac
Q00610_C(HSSLAGCC [iTRAQ_Ni	2 145-157	8,4	554,955	2012_02_2 Nuclei_frac
Q00610_C(IHEGCEEP [iTRAQ_Ni	3 866-881	8,486	689,019	2012_02_2 Nuclei_frac
Q00610_C(ISGETIFVT [iTRAQ_Ni	2 298-321	5,17	693,143	2012_02_2 Nuclei_frac
Q00610_C(IVLDNSVF [iTRAQ_Ni	1 1011-1022	8,467	520,615	2012_02_2 Nuclei_frac
Q00610_C(KFDVNTSA [iTRAQ_Ni	2 1074-1094	8,083	886,163	2012_02_2 Nuclei_frac
Q00610_C(KFDVNTSA [iTRAQ_Ni	2 1074-1094	6,165	664,874	2012_02_2 Nuclei_frac
Q00610_C(KFDVNTSA [iTRAQ_Ni	2 1074-1094	5,665	664,874	2012_02_2 Nuclei_frac
Q00610_C(KFNALFAQ [iTRAQ_Ni	3 367-382	9,836	731,067	2012_02_2 Nuclei_frac
Q00610_C(KFNALFAQ [iTRAQ_Ni	3 367-382	9,37	731,067	2012_02_2 Nuclei_frac
Q00610_C(KFNALFAQ [iTRAQ_Ni	3 367-382	4,839	548,553	2012_02_2 Nuclei_frac
Q00610_C(KVGYPDPV [iTRAQ_Ni	2 507-519	7,078	632,704	2012_02_2 Nuclei_frac
Q00610_C(LASTLVHL [iTRAQ_Ni	1 1227-1245	7,684	705,717	2012_02_2 Nuclei_frac
Q00610_C(LHIIEVGTP [iTRAQ_Ni	2 228-245	7,377	745,091	2012_02_2 Nuclei_frac
Q00610_C(LHIIEVGTP [iTRAQ_Ni	2 228-245	7,266	745,091	2012_02_2 Nuclei_frac
Q00610_C(LHIIEVGTP [iTRAQ_Ni	2 228-245	6,125	745,092	2012_02_2 Nuclei_frac

Q00610_Cf LLLPWLEA [iTRAQ_Nt	1	857-865	7,122	627,889	2012_02_2	Nuclei_frac
Q00610_Cf LLLPWLEA [iTRAQ_Nt	1	857-865	6,518	627,89	2012_02_2	Nuclei_frac
Q00610_Cf LLLPWLEA [iTRAQ_Nt	1	857-865	5,489	418,929	2012_02_2	Nuclei_frac
Q00610_Cf LLYNNVSN [iTRAQ_Nt	1	1216-1226	7,249	720,89	2012_02_2	Nuclei_frac
Q00610_Cf NLQNLLIL [iTRAQ_Nt	2	1023-1034	7,897	821,531	2012_02_2	Nuclei_frac
Q00610_Cf NLQNLLIL [iTRAQ_Nt	2	1023-1034	6,211	548,022	2012_02_2	Nuclei_frac
Q00610_Cf NNLAGAEE [iTRAQ_Nt	1	355-366	9,843	724,886	2012_02_2	Nuclei_frac
Q00610_Cf NNLAGAEE [iTRAQ_Nt	1	355-366	9,202	724,886	2012_02_2	Nuclei_frac
Q00610_Cf RDPHLACV [iTRAQ_Nt	2	912-923	4,847	544,279	2012_02_2	Nuclei_frac
Q00610_Cf RPISADSAI [iTRAQ_Nt	3	64-78	5,751	621,34	2012_02_2	Nuclei_frac
Q00610_Cf SVNESLNN [iTRAQ_Nt	1	1462-1481	7,536	833,755	2012_02_2	Nuclei_frac
Q00610_Cf VANVELY [iTRAQ_Nt	1	1398-1406	6,936	635,85	2012_02_2	Nuclei_frac
Q00610_Cf VGYTPDWI [iTRAQ_Nt	1	508-519	9,676	812,459	2012_02_2	Nuclei_frac
Q00610_Cf VGYTPDWI [iTRAQ_Nt	1	508-519	9,662	812,459	2012_02_2	Nuclei_frac
Q00610_Cf VGYTPDWI [iTRAQ_Nt	1	508-519	5,9	541,973	2012_02_2	Nuclei_frac
Q00610_Cf VSQPIEGH [iTRAQ_Nt	2	190-205	5,932	669,03	2012_02_2	Nuclei_frac
Q00610_Cf WLLLTGIS [iTRAQ_Nt	1	164-176	9,279	822,477	2012_02_2	Nuclei_frac
Q00610_Cf WLLLTGIS [iTRAQ_Nt	1	164-176	7,17	548,65	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,443	588,669	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,358	882,502	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,329	882,501	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,299	882,503	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,247	882,502	2012_02_2	Nuclei_frac
P04264 FLEQQNQ [iTRAQ_Nt	2	199-210	6,225	588,67	2012_02_2	Nuclei_frac
P04264 FSSCGGG [iTRAQ_Nt	2	45-64	11,846	955,424	2012_02_2	Nuclei_frac
P04264 FSSCGGG [iTRAQ_Nt	2	45-64	9,798	637,284	2012_02_2	Nuclei_frac
P04264 FSSCGGG [iTRAQ_Nt	2	45-64	9,247	637,284	2012_02_2	Nuclei_frac
P04264 GGGGGGYC [iTRAQ_Nt	1	518-548	10,443	843,359	2012_02_2	Nuclei_frac
P04264 GSYGSGGS [iTRAQ_Nt	1	549-587	8,238	864,861	2012_02_2	Nuclei_frac
P04264 IEISELNR [iTRAQ_Nt	1	395-402	5,487	559,322	2012_02_2	Nuclei_frac
P04264 KQJSNLQQ [iTRAQ_Nt	2	416-431	9,002	711,724	2012_02_2	Nuclei_frac
P04264 LNDLEDAL [iTRAQ_Nt	2	443-454	9,717	823,46	2012_02_2	Nuclei_frac
P04264 LNDLEDAL [iTRAQ_Nt	2	443-454	6,241	549,306	2012_02_2	Nuclei_frac
P04264 LNDLEDAL [iTRAQ_Nt	2	443-459	8,02	744,072	2012_02_2	Nuclei_frac
P04264 LRSEIDNV [iTRAQ_Nt	2	407-415	5,491	454,607	2012_02_2	Nuclei_frac
P04264 LRSEIDNV [iTRAQ_Nt	2	407-415	5,433	454,606	2012_02_2	Nuclei_frac
P04264 MSGECAPN [iTRAQ_Nt	3	492-517	9,192	909,094	2012_02_2	Nuclei_frac
P04264 MSGECAPN [iTRAQ_Nt	3	492-517	8,788	909,094	2012_02_2	Nuclei_frac
P04264 NSKIEISEL [iTRAQ_Nt	2	392-402	5,819	530,974	2012_02_2	Nuclei_frac
P04264 QJSNLQQS [iTRAQ_Nt	1	417-431	12,667	930,981	2012_02_2	Nuclei_frac
P04264 SGGGFSSG [iTRAQ_Nt	1	12-28	8,277	601,304	2012_02_2	Nuclei_frac
P04264 SISISVAR [iTRAQ_Nt	1	74-81	7,926	488,801	2012_02_2	Nuclei_frac
P04264 SKAEAESL [iTRAQ_Nt	3	364-375	8,143	591,665	2012_02_2	Nuclei_frac
P04264 SLDLDSIIA [iTRAQ_Nt	2	343-354	6,708	795,964	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-196	7,759	557,973	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-196	7,633	557,972	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-196	7,453	836,454	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-196	6,455	557,972	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-198	11,041	643,028	2012_02_2	Nuclei_frac
P04264 SLNNQFAS [iTRAQ_Nt	2	185-198	5,207	482,522	2012_02_2	Nuclei_frac
P04264 SLVNLGGS [iTRAQ_Nt	2	65-73	7,211	581,856	2012_02_2	Nuclei_frac

P04264	THNLEPYF [iTRAQ_N1	1 223-238	8,951	713,37	2012_02_2	Nuclei_frac
P04264	THNLEPYF [iTRAQ_N1	1 223-238	6,043	1069,545	2012_02_2	Nuclei_frac
P04264	TNAENEFV [iTRAQ_N1	2 277-287	7,371	777,428	2012_02_2	Nuclei_frac
P04264	TNAENEFV [iTRAQ_N1	3 277-288	5,505	457,268	2012_02_2	Nuclei_frac
P04264	WELLQQVI [iTRAQ_N1	1 211-222	7,897	810,433	2012_02_2	Nuclei_frac
	AGTQIENIE [iTRAQ_N1	1 48-60	7,829	833,414	2012_02_2	Nuclei_frac
	AGTQIENIE [iTRAQ_N1	2 48-64	8,401	741,722	2012_02_2	Nuclei_frac
	AGTQIENIE [iTRAQ_N1	2 48-64	7,535	741,721	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 96-103	5,307	576,847	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 96-103	5,273	576,848	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 96-103	4,847	576,847	2012_02_2	Nuclei_frac
	ASFNHFDR [iTRAQ_N1	2 753-772	5,345	645,569	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 403-413	8,151	751,897	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 403-413	6,76	501,6	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 403-413	5,791	501,6	2012_02_2	Nuclei_frac
	CQLEINFN [iTRAQ_N1	3 332-344	7,515	633,01	2012_02_2	Nuclei_frac
	DGLGFCAL [iTRAQ_N1	2 175-185	9,947	701,874	2012_02_2	Nuclei_frac
	DGLGFCAL [iTRAQ_N1	2 175-185	6,114	468,251	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 134-147	7,428	609,332	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 134-147	7,153	913,495	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 377-387	7,607	783,408	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 377-387	7,41	783,407	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 377-387	6,589	783,406	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 377-387	5,258	522,608	2012_02_2	Nuclei_frac
	HRPELIDYC [iTRAQ_N1	2 186-195	5,309	505,956	2012_02_2	Nuclei_frac
	ICDQWDNL [iTRAQ_N1	3 479-492	8,317	975,504	2012_02_2	Nuclei_frac
	ICDQWDNL [iTRAQ_N1	3 479-492	7,518	975,503	2012_02_2	Nuclei_frac
	ICDQWDNL [iTRAQ_N1	3 479-492	7,463	650,671	2012_02_2	Nuclei_frac
	ICDQWDNL [iTRAQ_N1	3 479-492	6,836	650,672	2012_02_2	Nuclei_frac
	ILAGDKNYI [iTRAQ_N1	2 835-849	5,722	680,71	2012_02_2	Nuclei_frac
	ISIEMHGTL [iTRAQ_N1	2 656-672	4,826	535,531	2012_02_2	Nuclei_frac
	KDDPLTNL [iTRAQ_N1	3 198-214	8,666	775,087	2012_02_2	Nuclei_frac
	KDDPLTNL [iTRAQ_N1	3 198-214	7,798	775,089	2012_02_2	Nuclei_frac
	KQFGAQAI [iTRAQ_N1	3 633-649	6,698	773,449	2012_02_2	Nuclei_frac
	LAILGIHNE [iTRAQ_N1	2 566-577	6,963	791,482	2012_02_2	Nuclei_frac
	LAILGIHNE [iTRAQ_N1	2 566-577	5,61	527,99	2012_02_2	Nuclei_frac
	LASDLLEW [iTRAQ_N1	1 282-291	7,178	680,395	2012_02_2	Nuclei_frac
	LLETIDQLY [iTRAQ_N1	2 503-516	9,035	1000,565	2012_02_2	Nuclei_frac
	LLETIDQLY [iTRAQ_N1	2 503-516	7,568	667,379	2012_02_2	Nuclei_frac
	LLETIDQLY [iTRAQ_N1	2 503-517	6,813	719,414	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2 65-76	7,637	511,634	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	1 65-76	7,344	758,951	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2 65-76	7,344	766,947	2012_02_2	Nuclei_frac
	LSNRPAFM [iTRAQ_N1	1 347-359	6,524	535,948	2012_02_2	Nuclei_frac
	NVNIQNFH [iTRAQ_N1	2 163-174	7,299	596,664	2012_02_2	Nuclei_frac
	QKDYETA1 [iTRAQ_N1	3 419-431	5,747	653,37	2012_02_2	Nuclei_frac
	SIVNYKPK [iTRAQ_N1	3 677-684	4,803	690,932	2012_02_2	Nuclei_frac
	TINEVENQ [iTRAQ_N1	1 727-738	10,894	787,438	2012_02_2	Nuclei_frac
	TINEVENQ [iTRAQ_N1	1 727-738	10,591	525,294	2012_02_2	Nuclei_frac
	VGWEQLL [iTRAQ_N1	1 715-726	8,749	765,942	2012_02_2	Nuclei_frac
	VGWEQLL [iTRAQ_N1	1 715-726	8,542	765,943	2012_02_2	Nuclei_frac

VGWEQLL [iTRAQ_N1	1 715-726	8,428	765,942	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	8,029	510,964	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	7,941	765,942	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	7,389	765,943	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	6,746	510,965	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	6,342	510,965	2012_02_2	Nuclei_frac
VGWEQLL [iTRAQ_N1	1 715-726	6,146	765,945	2012_02_2	Nuclei_frac
AEGPEVDV [iTRAQ_N1	2 764-775	7,526	778,433	2012_02_2	Nuclei_frac
AEGPEVDV [iTRAQ_N1	2 764-775	5,296	519,291	2012_02_2	Nuclei_frac
AGAISASG [iTRAQ_N1	2 226-243	11,696	642,682	2012_02_2	Nuclei_frac
AGAISASG [iTRAQ_N1	2 226-243	11,662	642,681	2012_02_2	Nuclei_frac
AGAISASG [iTRAQ_N1	2 226-243	4,961	482,262	2012_02_2	Nuclei_frac
AVEVQGP [iTRAQ_N1	2 288-303	8,101	633,336	2012_02_2	Nuclei_frac
ELLLPNWC [iTRAQ_N1	1 9-28	10,253	774,422	2012_02_2	Nuclei_frac
ELLLPNWC [iTRAQ_N1	1 9-28	9,451	774,421	2012_02_2	Nuclei_frac
FSVSGLK [iTRAQ_N1	2 3482-3488	5,133	513,317	2012_02_2	Nuclei_frac
GGQIGLQA [iTRAQ_N1	2 5630-5655	12,124	902,823	2012_02_2	Nuclei_frac
GGQIGLQA [iTRAQ_N1	2 5630-5655	10,408	902,821	2012_02_2	Nuclei_frac
GKGGVTG [iTRAQ_N1	3 5724-5740	6,675	651,032	2012_02_2	Nuclei_frac
GSEVGFHG [iTRAQ_N1	2 5529-5544	8,799	620,338	2012_02_2	Nuclei_frac
GSEVGFHG [iTRAQ_N1	2 5529-5544	7,843	620,338	2012_02_2	Nuclei_frac
IKGDVDVS [iTRAQ_N1	3 2326-2336	6,57	520,984	2012_02_2	Nuclei_frac
IKGGADVS [iTRAQ_N1	3 5566-5591	5,787	721,409	2012_02_2	Nuclei_frac
ISIPDVL [iTRAQ_N1	3 4849-4862	5,771	648,06	2012_02_2	Nuclei_frac
ISIPDVGLH [iTRAQ_N1	2 1451-1461	6,4	493,978	2012_02_2	Nuclei_frac
ISMPDFDL [iTRAQ_N1	4 2579-2592	5,665	512,293	2012_02_2	Nuclei_frac
ISMPDFDL [iTRAQ_N1	4 2579-2592	4,772	512,292	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	3 818-828	6,642	524,631	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	3 818-828	6,306	524,63	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	3 818-828	6,109	524,63	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	3 818-828	5,626	524,63	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	4 1195-1208	5,205	500,293	2012_02_2	Nuclei_frac
ISMPDVL [iTRAQ_N1	4 1195-1208	5,119	500,292	2012_02_2	Nuclei_frac
LNVGAPD [iTRAQ_N1	1 5356-5366	7,165	649,883	2012_02_2	Nuclei_frac
LNVGAPD [iTRAQ_N1	1 5356-5366	6,953	649,883	2012_02_2	Nuclei_frac
LPSGSGAA [iTRAQ_N1	1 208-225	7,669	596,32	2012_02_2	Nuclei_frac
LPTGQISG [iTRAQ_N1	2 5513-5524	7,3	764,456	2012_02_2	Nuclei_frac
LPTGQISG [iTRAQ_N1	2 5513-5524	6,385	509,974	2012_02_2	Nuclei_frac
VDIDAPDV [iTRAQ_N1	2 731-748	6,157	579,803	2012_02_2	Nuclei_frac
VEGDLKGF [iTRAQ_N1	2 2988-3000	5,525	572,325	2012_02_2	Nuclei_frac
VHAPGLN [iTRAQ_N1	2 5324-5337	5,095	531,984	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 2131-2141	5,814	530,328	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 2131-2141	5,426	530,329	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 2131-2141	5,181	530,328	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 2131-2141	5,153	530,328	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 1209-1219	7,002	525,657	2012_02_2	Nuclei_frac
VKGDVDV [iTRAQ_N1	3 1209-1219	5,546	525,656	2012_02_2	Nuclei_frac
VKGEYDV [iTRAQ_N1	3 711-721	5,081	556,333	2012_02_2	Nuclei_frac
VSAPEVSV [iTRAQ_N1	2 331-341	6,963	466,606	2012_02_2	Nuclei_frac
VSAPEVSV [iTRAQ_N1	2 331-341	5,812	466,606	2012_02_2	Nuclei_frac
VSAPEVSV [iTRAQ_N1	2 331-341	5,73	466,607	2012_02_2	Nuclei_frac

VTAPDVDI [iTRAQ_N1	2	4916-4926	6,37	499,299	2012_02_2	Nuclei_frac
Q9P2E9_IS(ADAEKAQI [iTRAQ_N1	4	470-488	5,793	655,339	2012_02_2	Nuclei_frac
Q9P2E9_IS(AGIIQDTWI [iTRAQ_N1	2	245-254	7,375	728,909	2012_02_2	Nuclei_frac
Q9P2E9_IS(AGIIQDTWI [iTRAQ_N1	2	245-254	6,538	486,277	2012_02_2	Nuclei_frac
Q9P2E9_IS(AKVGAAEI [iTRAQ_N1	3	725-736	6,982	569,001	2012_02_2	Nuclei_frac
Q9P2E9_IS(AKVGAAEI [iTRAQ_N1	3	725-736	6,093	569,001	2012_02_2	Nuclei_frac
Q9P2E9_IS(AQEQQQQ [iTRAQ_N1	2	475-488	9,602	648,668	2012_02_2	Nuclei_frac
Q9P2E9_IS(DALNQAT[[iTRAQ_N1	2	374-386	9,941	839,948	2012_02_2	Nuclei_frac
Q9P2E9_IS(DALNQAT[[iTRAQ_N1	2	374-386	9,347	560,299	2012_02_2	Nuclei_frac
Q9P2E9_IS(HPPAPAEP [iTRAQ_N1	2	666-680	7,443	597,989	2012_02_2	Nuclei_frac
Q9P2E9_IS(HPPAPAEP [iTRAQ_N1	2	666-680	5,798	597,99	2012_02_2	Nuclei_frac
Q9P2E9_IS(LIEILSEK [iTRAQ_N1	2	237-244	5,032	411,596	2012_02_2	Nuclei_frac
Q9P2E9_IS(LKELESQV [iTRAQ_N1	3	556-568	6,948	631,376	2012_02_2	Nuclei_frac
Q9P2E9_IS(LKGELESSI [iTRAQ_N1	2	751-762	8,595	824,96	2012_02_2	Nuclei_frac
Q9P2E9_IS(LKGELESSI [iTRAQ_N1	2	751-762	7,82	824,96	2012_02_2	Nuclei_frac
Q9P2E9_IS(LKGELESSI [iTRAQ_N1	2	751-762	7,03	550,309	2012_02_2	Nuclei_frac
Q9P2E9_IS(LLATEQED [iTRAQ_N1	2	275-287	9,666	823,964	2012_02_2	Nuclei_frac
Q9P2E9_IS(LQQENSILF [iTRAQ_N1	1	365-373	5,74	622,859	2012_02_2	Nuclei_frac
Q9P2E9_IS(LREAEETQ [iTRAQ_N1	2	681-699	10,469	824,39	2012_02_2	Nuclei_frac
Q9P2E9_IS(LTAEFEEA [iTRAQ_N1	2	878-891	9,65	878,917	2012_02_2	Nuclei_frac
Q9P2E9_IS(NTDVAQSI [iTRAQ_N1	3	179-196	4,916	579,067	2012_02_2	Nuclei_frac
Q9P2E9_IS(QKLTAEFE [iTRAQ_N1	3	876-891	8,749	719,703	2012_02_2	Nuclei_frac
Q9P2E9_IS(QLLLESQS [iTRAQ_N1	2	795-808	6,136	611,352	2012_02_2	Nuclei_frac
Q9P2E9_IS(SIEALLEAC [iTRAQ_N1	1	526-537	7,792	701,403	2012_02_2	Nuclei_frac
Q9P2E9_IS(SIEALLEAC [iTRAQ_N1	1	526-537	6,899	467,934	2012_02_2	Nuclei_frac
Q9P2E9_IS(SILAETEGM [iTRAQ_N1	2	700-710	6,465	690,371	2012_02_2	Nuclei_frac
Q9P2E9_IS(SKCEELSGI [iTRAQ_N1	3	498-514	9,006	744,057	2012_02_2	Nuclei_frac
Q9P2E9_IS(SKCEELSGI [iTRAQ_N1	3	498-514	6,41	558,294	2012_02_2	Nuclei_frac
Q9P2E9_IS(SKCEELSGI [iTRAQ_N1	3	498-514	5,865	558,294	2012_02_2	Nuclei_frac
Q9P2E9_IS(SVEEEEQV [iTRAQ_N1	1	715-724	6,207	717,853	2012_02_2	Nuclei_frac
Q9P2E9_IS(TAGPLESS [iTRAQ_N1	2	901-917	6,264	689,022	2012_02_2	Nuclei_frac
Q9P2E9_IS(TAGPLESS [iTRAQ_N1	2	901-917	6,028	689,023	2012_02_2	Nuclei_frac
Q9P2E9_IS(TLVSTVGS [iTRAQ_N1	1	219-236	9,699	690,353	2012_02_2	Nuclei_frac
Q9P2E9_IS(VGAAEEEL [iTRAQ_N1	2	727-736	7,407	681,38	2012_02_2	Nuclei_frac
Q9P2E9_IS(VGAAEEEL [iTRAQ_N1	2	727-736	4,959	454,589	2012_02_2	Nuclei_frac
P08133 AINEAYKEI [iTRAQ_N1	3	471-482	7,283	638,343	2012_02_2	Nuclei_frac
P08133 AINEAYKEI [iTRAQ_N1	3	471-482	6,732	957,013	2012_02_2	Nuclei_frac
P08133 AINEAYKEI [iTRAQ_N1	3	471-482	4,923	479,01	2012_02_2	Nuclei_frac
P08133 ALIEILATR [iTRAQ_N1	1	456-464	8,186	572,365	2012_02_2	Nuclei_frac
P08133 ALIEILATR [iTRAQ_N1	1	456-464	7,691	572,366	2012_02_2	Nuclei_frac
P08133 ALIEILATR [iTRAQ_N1	1	456-464	7,588	572,365	2012_02_2	Nuclei_frac
P08133 ALIEILATR [iTRAQ_N1	1	456-464	6,827	572,365	2012_02_2	Nuclei_frac
P08133 ALIEILATR [iTRAQ_N1	1	456-464	6,725	572,365	2012_02_2	Nuclei_frac
P08133 CLIEILASR [iTRAQ_N1	2	113-121	7,872	609,855	2012_02_2	Nuclei_frac
P08133 CLIEILASR [iTRAQ_N1	2	113-121	7,254	609,854	2012_02_2	Nuclei_frac
P08133 DAFVAIVQ [iTRAQ_N1	2	587-597	8,007	732,94	2012_02_2	Nuclei_frac
P08133 DAFVAIVQ [iTRAQ_N1	2	587-597	7,763	732,938	2012_02_2	Nuclei_frac
P08133 DAFVAIVQ [iTRAQ_N1	2	587-597	6,629	488,961	2012_02_2	Nuclei_frac
P08133 DAFVAIVQ [iTRAQ_N1	2	587-597	5,362	488,961	2012_02_2	Nuclei_frac
P08133 DAFVAIVQ [iTRAQ_N1	2	587-597	4,792	488,961	2012_02_2	Nuclei_frac

P08133	DLEADIIGD [iTRAQ_N1	2 140-155	9,514	678,684	2012_02_2	Nuclei_frac
P08133	DLEADIIGD [iTRAQ_N1	2 140-155	8,106	678,686	2012_02_2	Nuclei_frac
P08133	EAILDIITSR [iTRAQ_N1	1 40-49	7,851	637,876	2012_02_2	Nuclei_frac
P08133	FMTILCTR [iTRAQ_N1	3 546-553	5,959	601,313	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	8,174	670,71	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	8,133	670,71	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	7,934	1005,563	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	7,659	1005,561	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	7,634	670,709	2012_02_2	Nuclei_frac
P08133	GFGSDKEA [iTRAQ_N1	2 34-49	5,035	503,284	2012_02_2	Nuclei_frac
P08133	GLGTDEDT [iTRAQ_N1	1 377-392	9,872	638,341	2012_02_2	Nuclei_frac
P08133	GTVRPANL [iTRAQ_N1	2 354-369	5,48	659,343	2012_02_2	Nuclei_frac
P08133	ILISLATGH [iTRAQ_N1	1 499-508	10,075	408,923	2012_02_2	Nuclei_frac
P08133	ILISLATGH [iTRAQ_N1	1 499-508	8,082	408,923	2012_02_2	Nuclei_frac
P08133	ILISLATGH [iTRAQ_N1	1 499-519	6,814	606,577	2012_02_2	Nuclei_frac
P08133	ILISLATGH [iTRAQ_N1	1 499-519	5,636	606,576	2012_02_2	Nuclei_frac
P08133	ILISLATGH [iTRAQ_N1	1 499-519	5,531	808,433	2012_02_2	Nuclei_frac
P08133	LILGLMMPH [iTRAQ_N1	4 427-441	5,893	664,03	2012_02_2	Nuclei_frac
P08133	LIVGLMRPH [iTRAQ_N1	4 84-98	5,787	670,037	2012_02_2	Nuclei_frac
P08133	LMLAVVK [iTRAQ_N1	3 240-246	4,755	539,35	2012_02_2	Nuclei_frac
P08133	LVFDEYLN [iTRAQ_N1	2 212-219	4,933	657,883	2012_02_2	Nuclei_frac
P08133	MLVVLLQK [iTRAQ_N1	1 156-165	7,706	637,392	2012_02_2	Nuclei_frac
P08133	MLVVLLQK [iTRAQ_N1	2 156-165	5,747	645,39	2012_02_2	Nuclei_frac
P08133	MTNYDVEH [iTRAQ_N1	4 568-579	5,71	482,513	2012_02_2	Nuclei_frac
P08133	MTNYDVEH [iTRAQ_N1	4 568-579	5,533	643,013	2012_02_2	Nuclei_frac
P08133	NKPLFFAD [iTRAQ_N1	3 598-606	4,85	756,451	2012_02_2	Nuclei_frac
P08133	RVFQEFIK [iTRAQ_N1	2 560-567	5,493	452,274	2012_02_2	Nuclei_frac
P08133	SEIDLLNIR [iTRAQ_N1	1 629-637	6,663	608,855	2012_02_2	Nuclei_frac
P08133	SLEDALSS [iTRAQ_N1	1 483-497	7,457	589,287	2012_02_2	Nuclei_frac
P08133	SLHQAIEGI [iTRAQ_N1	2 647-662	9,034	669,355	2012_02_2	Nuclei_frac
P08133	TNEQMHQI [iTRAQ_N1	3 122-134	5,434	612,988	2012_02_2	Nuclei_frac
P08133	VFQEFIK [iTRAQ_N1	2 561-567	4,803	599,858	2012_02_2	Nuclei_frac
P08133	VFQEFIK [iTRAQ_N1	2 561-567	4,78	599,857	2012_02_2	Nuclei_frac
	ACLISLGYI [iTRAQ_N1	2 792-813	6,663	900,767	2012_02_2	Nuclei_frac
	AGTQIENIC [iTRAQ_N1	2 67-83	7,088	737,049	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 115-122	5,307	576,847	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 115-122	5,273	576,848	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 115-122	4,847	576,847	2012_02_2	Nuclei_frac
	ASFNHFDK [iTRAQ_N1	3 772-791	6,265	659,589	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 422-432	8,151	751,897	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 422-432	6,76	501,6	2012_02_2	Nuclei_frac
	ASIHEAWT [iTRAQ_N1	2 422-432	5,791	501,6	2012_02_2	Nuclei_frac
	CQLEINFN [iTRAQ_N1	3 351-363	7,515	633,01	2012_02_2	Nuclei_frac
	DGLAFNAL [iTRAQ_N1	1 194-204	9,483	685,888	2012_02_2	Nuclei_frac
	DGLAFNAL [iTRAQ_N1	1 194-204	8,705	457,595	2012_02_2	Nuclei_frac
	EAILAIHK [iTRAQ_N1	2 585-592	5,687	591,876	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 153-166	7,428	609,332	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 153-166	7,153	913,495	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 396-406	7,607	783,408	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 396-406	7,41	783,407	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1 396-406	6,589	783,406	2012_02_2	Nuclei_frac

GYEEWLLN [iTRAQ_Ni	1 396-406	5,258	522,608	2012_02_2 Nuclei_frac
ICDQWDAL [iTRAQ_Ni	2 498-512	13,094	634,981	2012_02_2 Nuclei_frac
ICDQWDAL [iTRAQ_Ni	2 498-512	11,753	634,981	2012_02_2 Nuclei_frac
KDDPVTNI [iTRAQ_Ni	3 217-233	8,378	779,426	2012_02_2 Nuclei_frac
LASDLLEW [iTRAQ_Ni	1 301-310	7,178	680,395	2012_02_2 Nuclei_frac
LMLLLEVIS [iTRAQ_Ni	2 84-95	7,637	511,634	2012_02_2 Nuclei_frac
LMLLLEVIS [iTRAQ_Ni	1 84-95	7,344	758,951	2012_02_2 Nuclei_frac
LMLLLEVIS [iTRAQ_Ni	2 84-95	7,344	766,947	2012_02_2 Nuclei_frac
LSGSNPYT [iTRAQ_Ni	2 605-622	9,598	736,742	2012_02_2 Nuclei_frac
LSGSNPYT [iTRAQ_Ni	2 605-622	9,163	736,742	2012_02_2 Nuclei_frac
LSNRPAFM [iTRAQ_Ni	3 366-378	4,992	579,979	2012_02_2 Nuclei_frac
QFASQAN [iTRAQ_Ni	2 653-668	8,843	688,049	2012_02_2 Nuclei_frac
QLEAIDQL [iTRAQ_Ni	2 522-535	7,406	653,701	2012_02_2 Nuclei_frac
TINEVENQ [iTRAQ_Ni	1 746-757	10,894	787,438	2012_02_2 Nuclei_frac
TINEVENQ [iTRAQ_Ni	1 746-757	10,591	525,294	2012_02_2 Nuclei_frac
TIPWLEDR [iTRAQ_Ni	2 312-323	6,323	590,678	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	8,749	765,942	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	8,542	765,943	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	8,428	765,942	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	8,029	510,964	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	7,941	765,942	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	7,389	765,943	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	6,746	510,965	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	6,342	510,965	2012_02_2 Nuclei_frac
VGWEQLL [iTRAQ_Ni	1 734-745	6,146	765,945	2012_02_2 Nuclei_frac
VLAGDKNF [iTRAQ_Ni	2 854-868	8,693	982,562	2012_02_2 Nuclei_frac
VLAGDKNF [iTRAQ_Ni	2 854-868	8,526	655,375	2012_02_2 Nuclei_frac
VLAGDKNF [iTRAQ_Ni	2 854-868	6,776	655,374	2012_02_2 Nuclei_frac

P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	6,264	560,778	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,984	560,779	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,489	560,78	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,253	560,779	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,222	560,781	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,208	560,78	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	5,045	560,781	2012_02_2 Nuclei_frac
P63261_CH AGFAGDD [iTRAQ_Ni	1 18-27	4,84	560,78	2012_02_2 Nuclei_frac
P63261_CH AVFPSIVGI [iTRAQ_Ni	1 28-36	8,57	545,33	2012_02_2 Nuclei_frac
P63261_CH AVFPSIVGI [iTRAQ_Ni	1 28-36	8,103	545,331	2012_02_2 Nuclei_frac
P63261_CH AVFPSIVGI [iTRAQ_Ni	1 28-36	8,066	545,33	2012_02_2 Nuclei_frac
P63261_CH AVFPSIVGI [iTRAQ_Ni	1 28-36	8,028	545,33	2012_02_2 Nuclei_frac
P63261_CH AVFPSIVGI [iTRAQ_Ni	1 28-36	7,739	545,331	2012_02_2 Nuclei_frac
P63261_CH DLTDYLMK [iTRAQ_Ni	3 183-190	6,33	651,845	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	2 291-311	10,781	792,393	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	2 291-311	9,497	792,394	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	1 291-311	8,76	1180,091	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	2 291-311	8,689	1188,087	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	1 291-311	8,365	787,062	2012_02_2 Nuclei_frac
P63261_CH DLYANTVI [iTRAQ_Ni	2 291-311	6,936	792,394	2012_02_2 Nuclei_frac
P63261_CH DSYVGDEA [iTRAQ_Ni	2 50-61	8,537	548,282	2012_02_2 Nuclei_frac
P63261_CH DSYVGDEA [iTRAQ_Ni	2 50-61	8,118	548,282	2012_02_2 Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	2 315-325	7,722	725,415	2012_02_2 Nuclei_frac

P63261_CH EITALAPST [iTRAQ_Ni	3 315-325	7,448	733,413	2012_02_2	Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	2 315-325	6,541	725,416	2012_02_2	Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	3 315-325	6,239	733,413	2012_02_2	Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	3 315-325	5,742	733,414	2012_02_2	Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	3 315-325	4,998	489,278	2012_02_2	Nuclei_frac
P63261_CH EITALAPST [iTRAQ_Ni	3 315-325	4,993	489,279	2012_02_2	Nuclei_frac
P63261_CH EKLCYVAL [iTRAQ_Ni	4 213-237	6,944	1080,543	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	8,772	638,818	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	8,422	638,818	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	8,226	638,819	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	8,145	638,819	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	8,077	638,817	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	7,892	638,82	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	7,751	638,82	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	7,52	638,819	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	6,826	638,821	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	6,493	426,215	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	6,309	638,821	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	5,899	638,82	2012_02_2	Nuclei_frac
P63261_CH GYSFTTTA [iTRAQ_Ni	1 196-205	5,517	638,817	2012_02_2	Nuclei_frac
P63261_CH HQGVMVG [iTRAQ_Ni	4 39-49	8,368	497,927	2012_02_2	Nuclei_frac
P63261_CH HQGVMVG [iTRAQ_Ni	4 39-49	8,205	497,927	2012_02_2	Nuclei_frac
P63261_CH HQGVMVG [iTRAQ_Ni	4 39-49	6,049	497,929	2012_02_2	Nuclei_frac
P63261_CH HQGVMVG [iTRAQ_Ni	5 39-60	5,115	704,602	2012_02_2	Nuclei_frac
P63261_CH IAPPER [iTRAQ_Ni	1 328-334	5,107	470,292	2012_02_2	Nuclei_frac
P63261_CH IAPPER [iTRAQ_Ni	1 328-334	4,884	470,297	2012_02_2	Nuclei_frac
P63261_CH IAPPERK [iTRAQ_Ni	2 328-335	4,91	404,595	2012_02_2	Nuclei_frac
P63261_CH IWHHTFYN [iTRAQ_Ni	1 84-94	8,692	830,429	2012_02_2	Nuclei_frac
P63261_CH IWHHTFYN [iTRAQ_Ni	1 84-94	7,853	553,956	2012_02_2	Nuclei_frac
P63261_CH IWHHTFYN [iTRAQ_Ni	1 84-94	7,671	553,955	2012_02_2	Nuclei_frac
P63261_CH IWHHTFYN [iTRAQ_Ni	1 84-94	6,661	553,954	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	12,314	883,128	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	12,282	883,13	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	12,052	883,126	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	11,689	883,126	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	11,394	883,128	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	2 290-311	10,773	877,796	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	10,555	883,128	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	2 290-311	10,3	877,798	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	2 290-311	10,216	877,796	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	2 290-311	9,861	877,796	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	2 290-311	9,823	877,797	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	8,761	1324,187	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	8,541	1324,188	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	8,3	883,132	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	8,081	1324,186	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	6,479	662,597	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	6,377	662,598	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	5,787	662,598	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	5,613	662,598	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	5,421	662,598	2012_02_2	Nuclei_frac
P63261_CH KDLYANT\ [iTRAQ_Ni	3 290-311	5,352	662,598	2012_02_2	Nuclei_frac

P63261_CHKDLYANTV [iTRAQ_Ni	3 290-311	5,339	662,597	2012_02_2	Nuclei_frac
P63261_CHKDLYANTV [iTRAQ_Ni	2 290-311	5,133	658,599	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	9,349	1419,706	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	9,337	1419,693	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	9,087	946,799	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,717	946,803	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,704	946,798	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,695	946,8	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,464	946,798	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,4	946,793	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	8,263	946,801	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	4 215-237	8,051	1427,691	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,859	946,802	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,639	946,797	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,349	946,805	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,33	946,801	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,292	710,35	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	7,027	946,801	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	6,963	710,35	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	6,957	946,799	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	4 215-237	6,423	952,129	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	6,349	710,349	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	5,86	710,348	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	5,532	710,349	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	5,511	710,349	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	5,411	710,349	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	5,22	710,347	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	4,988	710,342	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	4,948	710,346	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	4 215-237	4,842	952,13	2012_02_2	Nuclei_frac
P63261_CHLCYVALDF [iTRAQ_Ni	3 215-237	4,812	710,352	2012_02_2	Nuclei_frac
P63261_CHQEYDESGP [iTRAQ_Ni	1 359-371	9,495	554,274	2012_02_2	Nuclei_frac
P63261_CHQEYDESGP [iTRAQ_Ni	1 359-371	5,931	554,276	2012_02_2	Nuclei_frac
P63261_CHSYELPDGQ [iTRAQ_Ni	1 238-253	12,535	968,001	2012_02_2	Nuclei_frac
P63261_CHSYELPDGQ [iTRAQ_Ni	1 238-253	11,152	968,005	2012_02_2	Nuclei_frac
P63261_CHSYELPDGQ [iTRAQ_Ni	1 238-253	9,834	645,67	2012_02_2	Nuclei_frac
P63261_CHSYELPDGQ [iTRAQ_Ni	1 238-253	8,819	645,67	2012_02_2	Nuclei_frac
P63261_CHSYELPDGQ [iTRAQ_Ni	1 238-253	6,31	968,006	2012_02_2	Nuclei_frac
P63261_CHTTGIVMDS [iTRAQ_Ni	1 147-176	5,493	832,687	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	8,668	748,095	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	8,635	748,096	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	8,388	748,095	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	8,058	748,096	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	8,033	748,096	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	7,985	748,095	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	7,411	1121,641	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,786	1121,64	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,564	1121,641	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,495	1121,638	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,493	1121,64	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,315	748,098	2012_02_2	Nuclei_frac
P63261_CHVAPEEHPV [iTRAQ_Ni	2 95-112	6,137	1121,641	2012_02_2	Nuclei_frac

P63261_CH VAPEEHPV [iTRAQ_N1	2 95-112	6,039	748,095	2012_02_2	Nuclei_frac
P63261_CH VAPEEHPV [iTRAQ_N1	2 95-112	4,997	748,096	2012_02_2	Nuclei_frac
P63261_CH VAPEEHPV [iTRAQ_N1	2 95-112	4,785	748,093	2012_02_2	Nuclei_frac
P63261_CH YPIEHGIVT [iTRAQ_N1	3 68-83	6,155	750,376	2012_02_2	Nuclei_frac
P63261_CH YPIEHGIVT [iTRAQ_N1	4 68-83	5,987	755,71	2012_02_2	Nuclei_frac
P63261_CH YPIEHGIVT [iTRAQ_N1	3 68-83	5,934	750,377	2012_02_2	Nuclei_frac
P63261_CH YPIEHGIVT [iTRAQ_N1	4 68-83	5,708	755,709	2012_02_2	Nuclei_frac
P63261_CH YPIEHGIVT [iTRAQ_N1	3 68-83	5,33	750,375	2012_02_2	Nuclei_frac
Q01082_IS(EIGQSVDE) [iTRAQ_N1	2 2044-2054	7,336	760,906	2012_02_2	Nuclei_frac
Q01082_IS(EIGQSVDE) [iTRAQ_N1	2 2044-2054	4,772	507,606	2012_02_2	Nuclei_frac
Q01082_IS(FANSLVG) [iTRAQ_N1	1 330-348	9,372	776,752	2012_02_2	Nuclei_frac
Q01082_IS(FATDGEGY) [iTRAQ_N1	3 594-610	5,34	747,712	2012_02_2	Nuclei_frac
Q01082_IS(HQILEQAV) [iTRAQ_N1	2 1634-1653	6,204	657,348	2012_02_2	Nuclei_frac
Q01082_IS(IDDIFER) [iTRAQ_N1	1 1541-1547	5,836	526,28	2012_02_2	Nuclei_frac
Q01082_IS(IHCLENVDI) [iTRAQ_N1	3 110-118	5,819	472,591	2012_02_2	Nuclei_frac
Q01082_IS(ITDLYTDLF) [iTRAQ_N1	1 75-83	6,04	627,348	2012_02_2	Nuclei_frac
Q01082_IS(LLEVLSGEI) [iTRAQ_N1	1 91-99	5,257	580,346	2012_02_2	Nuclei_frac
Q01082_IS(LQALDTGV) [iTRAQ_N1	2 1144-1156	10,735	605,001	2012_02_2	Nuclei_frac
Q01082_IS(LQQFLR) [iTRAQ_N1	1 1064-1069	4,985	474,792	2012_02_2	Nuclei_frac
Q01082_IS(LTTLELLE) [iTRAQ_N1	1 2079-2088	6,787	665,908	2012_02_2	Nuclei_frac
Q01082_IS(LTTLELLE) [iTRAQ_N1	1 2079-2088	6,539	444,275	2012_02_2	Nuclei_frac
Q01082_IS(LVDTGDKF) [iTRAQ_N1	2 1907-1915	5,26	446,927	2012_02_2	Nuclei_frac
Q01082_IS(LVSQDNFG) [iTRAQ_N1	2 444-462	6,099	770,744	2012_02_2	Nuclei_frac
Q01082_IS(QLWGLLIEI) [iTRAQ_N1	2 1572-1584	8,873	635,036	2012_02_2	Nuclei_frac
Q01082_IS(QLWGLLIEI) [iTRAQ_N1	2 1572-1584	8,004	635,038	2012_02_2	Nuclei_frac
Q01082_IS(QNLLSQSF) [iTRAQ_N1	1 1162-1176	9,892	659,686	2012_02_2	Nuclei_frac
Q01082_IS(TAASGIPYI) [iTRAQ_N1	2 2242-2258	7,634	682,05	2012_02_2	Nuclei_frac
Q01082_IS(TAASGIPYI) [iTRAQ_N1	2 2242-2258	6,957	682,049	2012_02_2	Nuclei_frac
Q01082_IS(TAASGIPYI) [iTRAQ_N1	2 2242-2258	6,493	682,05	2012_02_2	Nuclei_frac
Q01082_IS(TAGYPNV) [iTRAQ_N1	1 187-203	9,017	708,025	2012_02_2	Nuclei_frac
Q01082_IS(TALPAQSA) [iTRAQ_N1	1 2178-2191	11,156	756,437	2012_02_2	Nuclei_frac
Q01082_IS(TQILAASYI) [iTRAQ_N1	2 1798-1809	7,037	554,654	2012_02_2	Nuclei_frac
Q01082_IS(VAVVNQIA) [iTRAQ_N1	1 905-913	6,957	557,347	2012_02_2	Nuclei_frac
Q01082_IS(VQAVVAV) [iTRAQ_N1	1 478-486	6,1	528,836	2012_02_2	Nuclei_frac
Q01082_IS(VQAVVAV) [iTRAQ_N1	1 478-486	5,948	528,825	2012_02_2	Nuclei_frac
A6NNZ2,Q3 AILVDLEPC [iTRAQ_N1	2 63-77	8,943	888,472	2012_02_2	Nuclei_frac
A6NNZ2,Q3 AILVDLEPC [iTRAQ_N1	1 63-77	7,599	880,476	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ALTVPELT [iTRAQ_N1	2 283-297	8,325	650,039	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ALTVPELT [iTRAQ_N1	2 283-297	7,607	974,556	2012_02_2	Nuclei_frac
A6NNZ2,Q3 EIVHIQAGC [iTRAQ_N1	3 3-19	10,288	704,381	2012_02_2	Nuclei_frac
A6NNZ2,Q3 EIVHIQAGC [iTRAQ_N1	3 3-19	10,234	704,382	2012_02_2	Nuclei_frac
A6NNZ2,Q3 EVDEQMLN [iTRAQ_N1	2 325-336	7,481	867,95	2012_02_2	Nuclei_frac
A6NNZ2,Q3 EVDEQMLN [iTRAQ_N1	3 325-336	6,583	584,301	2012_02_2	Nuclei_frac
A6NNZ2,Q3 FPGQLNAC [iTRAQ_N1	1 242-251	6,113	637,854	2012_02_2	Nuclei_frac
A6NNZ2,Q3 FPGQLNAC [iTRAQ_N1	1 242-251	5,592	637,853	2012_02_2	Nuclei_frac
A6NNZ2,Q3 FPGQLNAC [iTRAQ_N1	1 242-251	5,557	637,854	2012_02_2	Nuclei_frac
A6NNZ2,Q3 FWEVISDEI [iTRAQ_N1	1 20-46	6,437	812,382	2012_02_2	Nuclei_frac
A6NNZ2,Q3 GHYTEGAE [iTRAQ_N1	1 104-121	7,555	701,7	2012_02_2	Nuclei_frac
A6NNZ2,Q3 GHYTEGAE [iTRAQ_N1	2 104-122	8,964	792,434	2012_02_2	Nuclei_frac
A6NNZ2,Q3 GHYTEGAE [iTRAQ_N1	2 104-122	6,128	594,577	2012_02_2	Nuclei_frac

A6NNZ2,Q3 IREEYPDR [iTRAQ_N1	1 155-162	5,507	407,884	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ISEQFTAMI [iTRAQ_N1	2 381-390	8,625	695,352	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ISEQFTAMI [iTRAQ_N1	2 381-390	7,303	695,351	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ISVYYNEA ⁺ [iTRAQ_N1	2 47-58	7,329	795,427	2012_02_2	Nuclei_frac
A6NNZ2,Q3 ISVYYNEA ⁺ [iTRAQ_N1	2 47-58	7,158	795,427	2012_02_2	Nuclei_frac
A6NNZ2,Q3 LAVNMVPI [iTRAQ_N1	2 253-262	6,896	652,37	2012_02_2	Nuclei_frac
A6NNZ2,Q3 LAVNMVPI [iTRAQ_N1	1 253-262	6,297	644,371	2012_02_2	Nuclei_frac
A6NNZ2,Q3 LHFFMPGF [iTRAQ_N1	2 263-276	5,964	594,316	2012_02_2	Nuclei_frac
A6NNZ2,Q3 LTTPTYGD [iTRAQ_N1	3 217-241	6,819	956,819	2012_02_2	Nuclei_frac
A6NNZ2,Q3 LTTPTYGD [iTRAQ_N1	3 217-241	6,433	956,816	2012_02_2	Nuclei_frac
A6NNZ2,Q3 MAVTFIGN [iTRAQ_N1	3 363-379	6,597	725,4	2012_02_2	Nuclei_frac
A6NNZ2,Q3 NSSYFVEV [iTRAQ_N1	2 337-350	8,31	993,024	2012_02_2	Nuclei_frac
A6NNZ2,Q3 NSSYFVEV [iTRAQ_N1	2 337-350	7,863	993,024	2012_02_2	Nuclei_frac
A6NNZ2,Q3 NSSYFVEV [iTRAQ_N1	2 337-350	5,527	662,353	2012_02_2	Nuclei_frac
A6NNZ2,Q3 NSSYFVEV [iTRAQ_N1	2 337-350	5,515	662,352	2012_02_2	Nuclei_frac
A6NNZ2,Q3 SGPFGQIFF [iTRAQ_N1	2 78-103	10,536	1029,519	2012_02_2	Nuclei_frac
A6NNZ2,Q3 SGPFGQIFF [iTRAQ_N1	2 78-103	9,809	1029,521	2012_02_2	Nuclei_frac
A6NNZ2,Q3 SGPFGQIFF [iTRAQ_N1	2 78-103	8,538	1029,521	2012_02_2	Nuclei_frac
A6NNZ2,Q3 SGPFGQIFF [iTRAQ_N1	2 78-103	4,903	772,393	2012_02_2	Nuclei_frac
A6NNZ2,Q3 YLTVAAVF [iTRAQ_N1	1 310-318	6,344	592,35	2012_02_2	Nuclei_frac
P06753_ISC AREQAEAE [iTRAQ_N1	1 41-54	10,316	844,449	2012_02_2	Nuclei_frac
P06753_ISC AREQAEAE [iTRAQ_N1	1 41-54	8,4	563,301	2012_02_2	Nuclei_frac
P06753_ISC CTKEEHLC [iTRAQ_N1	4 226-236	6,548	583,963	2012_02_2	Nuclei_frac
P06753_ISC EQAEAEV/ [iTRAQ_N1	1 43-54	8,775	730,878	2012_02_2	Nuclei_frac
P06753_ISC EQAEAEV/ [iTRAQ_N1	1 43-54	6,556	487,587	2012_02_2	Nuclei_frac
P06753_ISC EQAEAEV/ [iTRAQ_N1	1 43-55	7,145	539,621	2012_02_2	Nuclei_frac
P06753_ISC IQLVEEELL [iTRAQ_N1	1 56-65	7,322	463,257	2012_02_2	Nuclei_frac
P06753_ISC IQLVEEELL [iTRAQ_N1	1 56-65	6,486	694,383	2012_02_2	Nuclei_frac
P06753_ISC IQLVEEELL [iTRAQ_N1	1 56-69	8,6	624,67	2012_02_2	Nuclei_frac
P06753_ISC IQLVEEELL [iTRAQ_N1	1 56-69	6,843	936,504	2012_02_2	Nuclei_frac
P06753_ISC IQVLQQQA [iTRAQ_N1	1 14-27	10,125	893,957	2012_02_2	Nuclei_frac
P06753_ISC IQVLQQQA [iTRAQ_N1	1 14-27	8,4	596,307	2012_02_2	Nuclei_frac
P06753_ISC IQVLQQQA [iTRAQ_N1	1 14-30	7,089	715,037	2012_02_2	Nuclei_frac
P06753_ISC KIQVLQQQ [iTRAQ_N1	2 13-27	10,097	1030,058	2012_02_2	Nuclei_frac
P06753_ISC KIQVLQQQ [iTRAQ_N1	2 13-27	9,023	687,042	2012_02_2	Nuclei_frac
P06753_ISC KIQVLQQQ [iTRAQ_N1	2 13-27	8,895	687,041	2012_02_2	Nuclei_frac
P06753_ISC KIQVLQQQ [iTRAQ_N1	2 13-27	8,248	687,042	2012_02_2	Nuclei_frac
P06753_ISC KLVIIIGDL [iTRAQ_N1	2 132-142	6,838	786,985	2012_02_2	Nuclei_frac
P06753_ISC KLVIIIGDL [iTRAQ_N1	2 132-142	6,544	786,986	2012_02_2	Nuclei_frac
P06753_ISC KLVIIIGDL [iTRAQ_N1	2 132-142	5,633	524,993	2012_02_2	Nuclei_frac
P06753_ISC KYEEVAR [iTRAQ_N1	2 125-131	5,353	591,841	2012_02_2	Nuclei_frac
P06753_ISC LATALQK [iTRAQ_N1	2 70-76	4,993	516,837	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	6,675	938,563	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	6,419	938,564	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	5,98	626,045	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	5,915	938,562	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	5,474	626,044	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	5,117	626,043	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	5,034	626,045	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	4,917	626,044	2012_02_2	Nuclei_frac
P06753_ISC LATALQKL [iTRAQ_N1	3 70-82	4,868	626,044	2012_02_2	Nuclei_frac

P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	9,383	882,949	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	9,234	882,947	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	9,216	882,948	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	8,423	441,977	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	7,313	441,977	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	7,014	441,978	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	5,942	588,967	2012_02_2	Nuclei_frac
P06753_ISC LEEAEKAA [iTRAQ_N1	2 77-89	5,34	588,969	2012_02_2	Nuclei_frac
P06753_ISC LVIEGDLEI [iTRAQ_N1	1 133-142	6,17	650,883	2012_02_2	Nuclei_frac
P06753_ISC LVIEGDLEI [iTRAQ_N1	1 133-146	6,315	606,004	2012_02_2	Nuclei_frac
P06753_ISC RIQLVEEEL [iTRAQ_N1	1 55-65	9,479	772,433	2012_02_2	Nuclei_frac
P06753_ISC RIQLVEEEL [iTRAQ_N1	1 55-65	6,925	515,291	2012_02_2	Nuclei_frac
P06753_ISC TIDDEDKI [iTRAQ_N1	3 216-225	5,252	541,319	2012_02_2	Nuclei_frac
P06753_ISC TIDDEDKI [iTRAQ_N1	3 216-225	5,151	541,319	2012_02_2	Nuclei_frac
P06753_ISC TIDDEDKI [iTRAQ_N1	3 216-225	4,973	811,476	2012_02_2	Nuclei_frac
P06753_ISC TIDDEDKI [iTRAQ_N1	3 216-225	4,886	541,319	2012_02_2	Nuclei_frac
P06753_ISC TIDDEDKI [iTRAQ_N1	3 216-225	4,873	811,475	2012_02_2	Nuclei_frac
P07355,P07 AYTNFDAE [iTRAQ_N1	2 28-46	8,459	815,095	2012_02_2	Nuclei_frac
P07355,P07 AYTNFDAE [iTRAQ_N1	2 28-46	8,272	815,095	2012_02_2	Nuclei_frac
P07355,P07 AYTNFDAE [iTRAQ_N1	2 28-46	7,811	815,096	2012_02_2	Nuclei_frac
P07355,P07 AYTNFDAE [iTRAQ_N1	2 28-46	7,65	1222,139	2012_02_2	Nuclei_frac
P07355,P07 DALNIETAI [iTRAQ_N1	2 37-46	7,154	688,405	2012_02_2	Nuclei_frac
P07355,P07 DALNIETAI [iTRAQ_N1	2 37-46	5,976	459,272	2012_02_2	Nuclei_frac
P07355,P07 DIISDTSGD [iTRAQ_N1	2 157-168	8,338	547,961	2012_02_2	Nuclei_frac
P07355,P07 DIISDTSGD [iTRAQ_N1	2 157-168	8,034	821,439	2012_02_2	Nuclei_frac
P07355,P07 GDLENAFL [iTRAQ_N1	3 249-265	7,55	755,403	2012_02_2	Nuclei_frac
P07355,P07 GDLENAFL [iTRAQ_N1	3 249-272	9,885	1042,878	2012_02_2	Nuclei_frac
P07355,P07 GDLENAFL [iTRAQ_N1	3 249-272	6,13	782,411	2012_02_2	Nuclei_frac
P07355,P07 GVDEVTIV [iTRAQ_N1	1 49-62	8,645	562,988	2012_02_2	Nuclei_frac
P07355,P07 GVDEVTIV [iTRAQ_N1	1 49-62	8,539	843,977	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	8,742	711,709	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	8,272	711,709	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	8,077	711,707	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	7,553	711,708	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	7,509	1067,062	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	7,471	711,708	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	7,081	1067,059	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	6,364	1067,061	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	5,124	534,033	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	5,048	711,71	2012_02_2	Nuclei_frac
P07355,P07 LSLEGDHS [iTRAQ_N1	2 10-27	4,981	711,709	2012_02_2	Nuclei_frac
P07355,P07 QDIAFAYQ [iTRAQ_N1	1 68-76	8,577	628,331	2012_02_2	Nuclei_frac
P07355,P07 QDIAFAYQ [iTRAQ_N1	1 68-76	8,55	628,331	2012_02_2	Nuclei_frac
P07355,P07 QDIAFAYQ [iTRAQ_N1	1 68-76	7,538	628,331	2012_02_2	Nuclei_frac
P07355,P07 SALSGHLE [iTRAQ_N1	2 88-103	8,142	970,094	2012_02_2	Nuclei_frac
P07355,P07 SALSGHLE [iTRAQ_N1	2 88-103	5,838	647,066	2012_02_2	Nuclei_frac
P07355,P07 SLYYYIQQI [iTRAQ_N1	2 313-323	7,237	855,456	2012_02_2	Nuclei_frac
P07355,P07 SLYYYIQQI [iTRAQ_N1	2 313-323	7,007	855,455	2012_02_2	Nuclei_frac
P07355,P07 SLYYYIQQI [iTRAQ_N1	2 313-323	6,014	570,638	2012_02_2	Nuclei_frac
P07355,P07 SLYYYIQQI [iTRAQ_N1	2 313-323	5,951	570,638	2012_02_2	Nuclei_frac
P07355,P07 SNAQRQDI [iTRAQ_N1	1 63-76	6,916	604,648	2012_02_2	Nuclei_frac

P07355,P07 SYSPYDML [iTRAQ_N1	2 233-244	8,602	810,888	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	1 233-244	7,828	802,891	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	1 233-244	6,754	535,597	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	2 233-245	8,045	626,327	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	3 233-245	6,993	631,661	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	3 233-245	6,208	631,662	2012_02_2	Nuclei_frac
P07355,P07 SYSPYDML [iTRAQ_N1	3 233-245	5,575	631,661	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,596	700,693	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,455	1050,537	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,423	700,694	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,144	700,695	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,143	700,694	2012_02_2	Nuclei_frac
P07355,P07 TDLEKDIIS [iTRAQ_N1	2 152-167	7,063	1050,538	2012_02_2	Nuclei_frac
P07355,P07 TKGVDENV [iTRAQ_N1	2 47-62	6,649	687,401	2012_02_2	Nuclei_frac
P07355,P07 TPAQYDA5 [iTRAQ_N1	2 104-114	7,682	755,905	2012_02_2	Nuclei_frac
P07355,P07 TPAQYDA5 [iTRAQ_N1	2 104-114	6,467	504,271	2012_02_2	Nuclei_frac
P07355,P07 WISIMTER [iTRAQ_N1	2 212-219	6,479	598,319	2012_02_2	Nuclei_frac
P07355,P07 WISIMTER [iTRAQ_N1	2 212-219	5,572	598,32	2012_02_2	Nuclei_frac
P07355,P07 WISIMTER [iTRAQ_N1	1 212-219	4,736	590,322	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	6,264	560,778	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,984	560,779	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,489	560,78	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,253	560,779	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,222	560,781	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,208	560,78	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	5,045	560,781	2012_02_2	Nuclei_frac
P68032,P68 AGFAGDD1 [iTRAQ_N1	1 19-28	4,84	560,78	2012_02_2	Nuclei_frac
P68032,P68 AVFPSIVGI [iTRAQ_N1	1 29-37	8,57	545,33	2012_02_2	Nuclei_frac
P68032,P68 AVFPSIVGI [iTRAQ_N1	1 29-37	8,103	545,331	2012_02_2	Nuclei_frac
P68032,P68 AVFPSIVGI [iTRAQ_N1	1 29-37	8,066	545,33	2012_02_2	Nuclei_frac
P68032,P68 AVFPSIVGI [iTRAQ_N1	1 29-37	8,028	545,33	2012_02_2	Nuclei_frac
P68032,P68 AVFPSIVGI [iTRAQ_N1	1 29-37	7,739	545,331	2012_02_2	Nuclei_frac
P68032,P68 DLT DYLMK [iTRAQ_N1	3 184-191	6,33	651,845	2012_02_2	Nuclei_frac
P68032,P68 DSYVGDEA [iTRAQ_N1	2 51-62	8,537	548,282	2012_02_2	Nuclei_frac
P68032,P68 DSYVGDEA [iTRAQ_N1	2 51-62	8,118	548,282	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	2 316-326	7,722	725,415	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	3 316-326	7,448	733,413	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	2 316-326	6,541	725,416	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	3 316-326	6,239	733,413	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	3 316-326	5,742	733,414	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	3 316-326	4,998	489,278	2012_02_2	Nuclei_frac
P68032,P68 EITALAPST [iTRAQ_N1	3 316-326	4,993	489,279	2012_02_2	Nuclei_frac
P68032,P68 GYSFVTTA [iTRAQ_N1	1 197-206	8,643	637,827	2012_02_2	Nuclei_frac
P68032,P68 GYSFVTTA [iTRAQ_N1	1 197-206	7,892	637,829	2012_02_2	Nuclei_frac
P68032,P68 GYSFVTTA [iTRAQ_N1	1 197-206	7,366	637,828	2012_02_2	Nuclei_frac
P68032,P68 HQGVMVG [iTRAQ_N1	4 40-50	8,368	497,927	2012_02_2	Nuclei_frac
P68032,P68 HQGVMVG [iTRAQ_N1	4 40-50	8,205	497,927	2012_02_2	Nuclei_frac
P68032,P68 HQGVMVG [iTRAQ_N1	4 40-50	6,049	497,929	2012_02_2	Nuclei_frac
P68032,P68 HQGVMVG [iTRAQ_N1	5 40-61	5,115	704,602	2012_02_2	Nuclei_frac
P68032,P68 IAPPER [iTRAQ_N1	1 329-335	5,107	470,292	2012_02_2	Nuclei_frac
P68032,P68 IAPPER [iTRAQ_N1	1 329-335	4,884	470,297	2012_02_2	Nuclei_frac

P68032,P68 IAPPERK [iTRAQ_N1	2 329-336	4,91	404,595	2012_02_2	Nuclei_frac
P68032,P68 IWHHTFYN [iTRAQ_N1	1 85-95	8,692	830,429	2012_02_2	Nuclei_frac
P68032,P68 IWHHTFYN [iTRAQ_N1	1 85-95	7,853	553,956	2012_02_2	Nuclei_frac
P68032,P68 IWHHTFYN [iTRAQ_N1	1 85-95	7,671	553,955	2012_02_2	Nuclei_frac
P68032,P68 IWHHTFYN [iTRAQ_N1	1 85-95	6,661	553,954	2012_02_2	Nuclei_frac
P68032,P68 KDLYANN\ [iTRAQ_N1	3 291-312	10,684	887,453	2012_02_2	Nuclei_frac
P68032,P68 KDLYANN\ [iTRAQ_N1	3 291-312	9,094	887,458	2012_02_2	Nuclei_frac
P68032,P68 KDLYANN\ [iTRAQ_N1	3 291-312	8,74	887,457	2012_02_2	Nuclei_frac
P68032,P68 LCYVALDF [iTRAQ_N1	3 216-238	6,632	706,846	2012_02_2	Nuclei_frac
P68032,P68 LCYVALDF [iTRAQ_N1	3 216-238	6,438	942,127	2012_02_2	Nuclei_frac
P68032,P68 QEYDEAGF [iTRAQ_N1	1 360-372	8,875	548,941	2012_02_2	Nuclei_frac
P68032,P68 QEYDEAGF [iTRAQ_N1	1 360-372	8,35	822,909	2012_02_2	Nuclei_frac
P68032,P68 SYELPDGQ [iTRAQ_N1	1 239-254	12,535	968,001	2012_02_2	Nuclei_frac
P68032,P68 SYELPDGQ [iTRAQ_N1	1 239-254	11,152	968,005	2012_02_2	Nuclei_frac
P68032,P68 SYELPDGQ [iTRAQ_N1	1 239-254	9,834	645,67	2012_02_2	Nuclei_frac
P68032,P68 SYELPDGQ [iTRAQ_N1	1 239-254	8,819	645,67	2012_02_2	Nuclei_frac
P68032,P68 SYELPDGQ [iTRAQ_N1	1 239-254	6,31	968,006	2012_02_2	Nuclei_frac
P68032,P68 VAPEEHPT [iTRAQ_N1	2 96-113	8,59	748,755	2012_02_2	Nuclei_frac
P68032,P68 VAPEEHPT [iTRAQ_N1	2 96-113	6,511	748,755	2012_02_2	Nuclei_frac
P68032,P68 VAPEEHPT [iTRAQ_N1	2 96-113	6,244	748,754	2012_02_2	Nuclei_frac
P68032,P68 YPIEHGIITN [iTRAQ_N1	4 69-84	6,241	760,381	2012_02_2	Nuclei_frac
ADLEMQIE [iTRAQ_N1	4 267-285	8,372	891,496	2012_02_2	Nuclei_frac
ADLEMQIE [iTRAQ_N1	4 267-285	5,957	668,866	2012_02_2	Nuclei_frac
AETECQNT [iTRAQ_N1	3 423-439	5,642	791,061	2012_02_2	Nuclei_frac
ALEESNYE [iTRAQ_N1	2 166-177	8,648	835,43	2012_02_2	Nuclei_frac
ALEESNYE [iTRAQ_N1	2 166-177	8,559	835,43	2012_02_2	Nuclei_frac
DAEAWFN [iTRAQ_N1	2 335-343	4,72	699,353	2012_02_2	Nuclei_frac
GSLGGGFS [iTRAQ_N1	1 41-59	12,156	926,442	2012_02_2	Nuclei_frac
GSLGGGFS [iTRAQ_N1	1 41-59	7,075	617,964	2012_02_2	Nuclei_frac
GSSGGGCF [iTRAQ_N1	2 60-86	9,082	1244,05	2012_02_2	Nuclei_frac
GSSGGGCF [iTRAQ_N1	2 60-86	8,766	829,701	2012_02_2	Nuclei_frac
IRLENEIQT [iTRAQ_N1	1 440-450	6,586	526,963	2012_02_2	Nuclei_frac
LASYLDKV [iTRAQ_N1	2 157-165	6,521	451,61	2012_02_2	Nuclei_frac
LASYLDKV [iTRAQ_N1	2 157-165	5,626	676,913	2012_02_2	Nuclei_frac
LENEIQTYF [iTRAQ_N1	1 442-450	7,426	655,35	2012_02_2	Nuclei_frac
LKYENEVA [iTRAQ_N1	2 236-245	4,933	508,3	2012_02_2	Nuclei_frac
NQILNLTTI [iTRAQ_N1	1 208-228	8,9	837,795	2012_02_2	Nuclei_frac
NQILNLTTI [iTRAQ_N1	1 208-228	7,391	837,796	2012_02_2	Nuclei_frac
NVQALEIEI [iTRAQ_N1	2 371-386	6,889	695,746	2012_02_2	Nuclei_frac
QSLEASLA [iTRAQ_N1	1 387-399	10,306	767,896	2012_02_2	Nuclei_frac
QSVEADIN [iTRAQ_N1	1 246-257	6,434	501,28	2012_02_2	Nuclei_frac
RVLDELTL [iTRAQ_N1	2 257-266	5,38	492,64	2012_02_2	Nuclei_frac
SQYEQLAE [iTRAQ_N1	2 323-334	9,079	594,652	2012_02_2	Nuclei_frac
SQYEQLAE [iTRAQ_N1	2 323-334	7,493	594,652	2012_02_2	Nuclei_frac
SQYEQLAE [iTRAQ_N1	2 323-334	6,456	594,653	2012_02_2	Nuclei_frac
SQYEQLAE [iTRAQ_N1	2 323-334	6,22	594,652	2012_02_2	Nuclei_frac
SQYEQLAE [iTRAQ_N1	2 323-334	5,526	446,242	2012_02_2	Nuclei_frac
VLDELTLT [iTRAQ_N1	2 258-266	7,686	660,405	2012_02_2	Nuclei_frac
ATDAEAD\ [iTRAQ_N1	1 78-91	8,468	816,926	2012_02_2	Nuclei_frac
ATDAEAD\ [iTRAQ_N1	1 78-91	6,08	544,953	2012_02_2	Nuclei_frac

CGDLEEEI [iTRAQ_N1	3 190-198	5,513	690,852	2012_02_2	Nuclei_frac
CKQLEEEQ [iTRAQ_N1	4 36-48	6,321	688,713	2012_02_2	Nuclei_frac
GTEDEVEK [iTRAQ_N1	3 52-65	6,414	678,02	2012_02_2	Nuclei_frac
GTEDEVEK [iTRAQ_N1	3 52-65	6,384	678,02	2012_02_2	Nuclei_frac
GTEDEVEK [iTRAQ_N1	3 52-65	5,448	508,766	2012_02_2	Nuclei_frac
IQLVEEEL [iTRAQ_N1	1 92-101	7,322	463,257	2012_02_2	Nuclei_frac
IQLVEEEL [iTRAQ_N1	1 92-101	6,486	694,383	2012_02_2	Nuclei_frac
IQLVEEEL [iTRAQ_N1	1 92-105	8,6	624,67	2012_02_2	Nuclei_frac
IQLVEEEL [iTRAQ_N1	1 92-105	6,843	936,504	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	11,812	874,975	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	11,221	583,652	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	11,088	583,652	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	9,916	874,975	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	9,322	583,651	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	8,375	583,652	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	6,518	437,991	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	6,439	437,992	2012_02_2	Nuclei_frac
KATDAEAI [iTRAQ_N1	2 77-90	4,746	583,652	2012_02_2	Nuclei_frac
KLVILEGEL [iTRAQ_N1	2 168-178	6,915	529,663	2012_02_2	Nuclei_frac
KLVILEGEL [iTRAQ_N1	2 168-178	5,194	793,992	2012_02_2	Nuclei_frac
KYEEVAR [iTRAQ_N1	2 161-167	5,353	591,841	2012_02_2	Nuclei_frac
LATALQK [iTRAQ_N1	2 106-112	4,993	516,837	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,675	938,563	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,419	938,564	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,98	626,045	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,915	938,562	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,474	626,044	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,117	626,043	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,034	626,045	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	4,917	626,044	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	4,868	626,044	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,383	882,949	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,234	882,947	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,216	882,948	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	8,423	441,977	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	7,313	441,977	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	7,014	441,978	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	5,942	588,967	2012_02_2	Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	5,34	588,969	2012_02_2	Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-178	7,29	438,931	2012_02_2	Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-178	7,163	657,891	2012_02_2	Nuclei_frac
QLEEEQQA [iTRAQ_N1	2 38-48	6,247	544,639	2012_02_2	Nuclei_frac
QLEEEQQA [iTRAQ_N1	3 38-49	7,742	635,367	2012_02_2	Nuclei_frac
QLEEEQQA [iTRAQ_N1	3 38-49	6,935	635,366	2012_02_2	Nuclei_frac
QLEEEQQA [iTRAQ_N1	3 38-49	5,522	476,776	2012_02_2	Nuclei_frac
QLEEEQQA [iTRAQ_N1	3 38-49	4,891	476,777	2012_02_2	Nuclei_frac
RIQLVEEEL [iTRAQ_N1	1 91-101	9,479	772,433	2012_02_2	Nuclei_frac
RIQLVEEEL [iTRAQ_N1	1 91-101	6,925	515,291	2012_02_2	Nuclei_frac
SLEAQADK [iTRAQ_N1	3 206-217	8,842	591,665	2012_02_2	Nuclei_frac
SLEAQADK [iTRAQ_N1	3 206-217	6,269	591,666	2012_02_2	Nuclei_frac

P07951_ISC ATDAEAD [iTRAQ_N1 1 **78-91** 8,468 816,926 2012_02_2 Nuclei_frac

P07951_ISC ATDAEAD\ [iTRAQ_Ni	1 78-91	6,08	544,953	2012_02_2	Nuclei_frac
P07951_ISC CKQLEEEQ [iTRAQ_Ni	4 36-48	6,321	688,713	2012_02_2	Nuclei_frac
P07951_ISC GTEDEVEK [iTRAQ_Ni	3 52-65	6,414	678,02	2012_02_2	Nuclei_frac
P07951_ISC GTEDEVEK [iTRAQ_Ni	3 52-65	6,384	678,02	2012_02_2	Nuclei_frac
P07951_ISC GTEDEVEK [iTRAQ_Ni	3 52-65	5,448	508,766	2012_02_2	Nuclei_frac
P07951_ISC IQLVEEEL [iTRAQ_Ni	1 92-101	7,322	463,257	2012_02_2	Nuclei_frac
P07951_ISC IQLVEEEL [iTRAQ_Ni	1 92-101	6,486	694,383	2012_02_2	Nuclei_frac
P07951_ISC IQLVEEEL [iTRAQ_Ni	1 92-105	8,6	624,67	2012_02_2	Nuclei_frac
P07951_ISC IQLVEEEL [iTRAQ_Ni	1 92-105	6,843	936,504	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,812	874,975	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,221	583,652	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,088	583,652	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	9,916	874,975	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	9,322	583,651	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	8,375	583,652	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	6,518	437,991	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	6,439	437,992	2012_02_2	Nuclei_frac
P07951_ISC KATDAEAI [iTRAQ_Ni	2 77-90	4,746	583,652	2012_02_2	Nuclei_frac
P07951_ISC KLVILEGEL [iTRAQ_Ni	2 168-178	6,915	529,663	2012_02_2	Nuclei_frac
P07951_ISC KLVILEGEL [iTRAQ_Ni	2 168-178	5,194	793,992	2012_02_2	Nuclei_frac
P07951_ISC KYEEVAR [iTRAQ_Ni	2 161-167	5,353	591,841	2012_02_2	Nuclei_frac
P07951_ISC LATALQK [iTRAQ_Ni	2 106-112	4,993	516,837	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,675	938,563	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,419	938,564	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,98	626,045	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,915	938,562	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,474	626,044	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,117	626,043	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,034	626,045	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,917	626,044	2012_02_2	Nuclei_frac
P07951_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,868	626,044	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,383	882,949	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,234	882,947	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,216	882,948	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	8,423	441,977	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,313	441,977	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,014	441,978	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,942	588,967	2012_02_2	Nuclei_frac
P07951_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,34	588,969	2012_02_2	Nuclei_frac
P07951_ISC LVILEGELE [iTRAQ_Ni	1 169-178	7,29	438,931	2012_02_2	Nuclei_frac
P07951_ISC LVILEGELE [iTRAQ_Ni	1 169-178	7,163	657,891	2012_02_2	Nuclei_frac
P07951_ISC QLEEEQQA [iTRAQ_Ni	2 38-48	6,247	544,639	2012_02_2	Nuclei_frac
P07951_ISC QLEEEQQA [iTRAQ_Ni	3 38-49	7,742	635,367	2012_02_2	Nuclei_frac
P07951_ISC QLEEEQQA [iTRAQ_Ni	3 38-49	6,935	635,366	2012_02_2	Nuclei_frac
P07951_ISC QLEEEQQA [iTRAQ_Ni	3 38-49	5,522	476,776	2012_02_2	Nuclei_frac
P07951_ISC QLEEEQQA [iTRAQ_Ni	3 38-49	4,891	476,777	2012_02_2	Nuclei_frac
P07951_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	9,479	772,433	2012_02_2	Nuclei_frac
P07951_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	6,925	515,291	2012_02_2	Nuclei_frac
P07951_ISC SLMASEEE [iTRAQ_Ni	2 206-217	8,303	831,911	2012_02_2	Nuclei_frac
P07951_ISC SLMASEEE [iTRAQ_Ni	3 206-217	7,828	839,908	2012_02_2	Nuclei_frac
P07951_ISC TIDDLEETL [iTRAQ_Ni	2 252-264	6,039	565,307	2012_02_2	Nuclei_frac

P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	6,264	560,778	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,984	560,779	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,489	560,78	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,253	560,779	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,222	560,781	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,208	560,78	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	5,045	560,781	2012_02_2	Nuclei_frac
P62736_CH AGFAGDD/ [iTRAQ_N1	1 21-30	4,84	560,78	2012_02_2	Nuclei_frac
P62736_CH AVFPSIVGI [iTRAQ_N1	1 31-39	8,57	545,33	2012_02_2	Nuclei_frac
P62736_CH AVFPSIVGI [iTRAQ_N1	1 31-39	8,103	545,331	2012_02_2	Nuclei_frac
P62736_CH AVFPSIVGI [iTRAQ_N1	1 31-39	8,066	545,33	2012_02_2	Nuclei_frac
P62736_CH AVFPSIVGI [iTRAQ_N1	1 31-39	8,028	545,33	2012_02_2	Nuclei_frac
P62736_CH AVFPSIVGI [iTRAQ_N1	1 31-39	7,739	545,331	2012_02_2	Nuclei_frac
P62736_CH DLTDYLMK [iTRAQ_N1	3 186-193	6,33	651,845	2012_02_2	Nuclei_frac
P62736_CH DSYVGDE/ [iTRAQ_N1	2 53-64	8,537	548,282	2012_02_2	Nuclei_frac
P62736_CH DSYVGDE/ [iTRAQ_N1	2 53-64	8,118	548,282	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	2 318-328	7,722	725,415	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	3 318-328	7,448	733,413	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	2 318-328	6,541	725,416	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	3 318-328	6,239	733,413	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	3 318-328	5,742	733,414	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	3 318-328	4,998	489,278	2012_02_2	Nuclei_frac
P62736_CH EITALAPST [iTRAQ_N1	3 318-328	4,993	489,279	2012_02_2	Nuclei_frac
P62736_CH GYSFVTTA [iTRAQ_N1	1 199-208	8,643	637,827	2012_02_2	Nuclei_frac
P62736_CH GYSFVTTA [iTRAQ_N1	1 199-208	7,892	637,829	2012_02_2	Nuclei_frac
P62736_CH GYSFVTTA [iTRAQ_N1	1 199-208	7,366	637,828	2012_02_2	Nuclei_frac
P62736_CH HQGVMVG [iTRAQ_N1	4 42-52	8,368	497,927	2012_02_2	Nuclei_frac
P62736_CH HQGVMVG [iTRAQ_N1	4 42-52	8,205	497,927	2012_02_2	Nuclei_frac
P62736_CH HQGVMVG [iTRAQ_N1	4 42-52	6,049	497,929	2012_02_2	Nuclei_frac
P62736_CH HQGVMVG [iTRAQ_N1	5 42-63	5,115	704,602	2012_02_2	Nuclei_frac
P62736_CH IAPPER [iTRAQ_N1	1 331-337	5,107	470,292	2012_02_2	Nuclei_frac
P62736_CH IAPPER [iTRAQ_N1	1 331-337	4,884	470,297	2012_02_2	Nuclei_frac
P62736_CH IAPPERK [iTRAQ_N1	2 331-338	4,91	404,595	2012_02_2	Nuclei_frac
P62736_CH KDLYANN [iTRAQ_N1	3 293-314	10,684	887,453	2012_02_2	Nuclei_frac
P62736_CH KDLYANN [iTRAQ_N1	3 293-314	9,094	887,458	2012_02_2	Nuclei_frac
P62736_CH KDLYANN [iTRAQ_N1	3 293-314	8,74	887,457	2012_02_2	Nuclei_frac
P62736_CH LCYVALDF [iTRAQ_N1	3 218-240	6,632	706,846	2012_02_2	Nuclei_frac
P62736_CH LCYVALDF [iTRAQ_N1	3 218-240	6,438	942,127	2012_02_2	Nuclei_frac
P62736_CH QEYDEAGF [iTRAQ_N1	1 362-374	8,875	548,941	2012_02_2	Nuclei_frac
P62736_CH QEYDEAGF [iTRAQ_N1	1 362-374	8,35	822,909	2012_02_2	Nuclei_frac
P62736_CH SYELPDGQ [iTRAQ_N1	1 241-256	12,535	968,001	2012_02_2	Nuclei_frac
P62736_CH SYELPDGQ [iTRAQ_N1	1 241-256	11,152	968,005	2012_02_2	Nuclei_frac
P62736_CH SYELPDGQ [iTRAQ_N1	1 241-256	9,834	645,67	2012_02_2	Nuclei_frac
P62736_CH SYELPDGQ [iTRAQ_N1	1 241-256	8,819	645,67	2012_02_2	Nuclei_frac
P62736_CH SYELPDGQ [iTRAQ_N1	1 241-256	6,31	968,006	2012_02_2	Nuclei_frac
P62736_CH VAPEEHPT [iTRAQ_N1	2 98-115	8,59	748,755	2012_02_2	Nuclei_frac
P62736_CH VAPEEHPT [iTRAQ_N1	2 98-115	6,511	748,755	2012_02_2	Nuclei_frac
P62736_CH VAPEEHPT [iTRAQ_N1	2 98-115	6,244	748,754	2012_02_2	Nuclei_frac
P62736_CH YPIEHGITN [iTRAQ_N1	4 71-86	6,241	760,381	2012_02_2	Nuclei_frac
P14618 AGKPVICA [iTRAQ_N1	6 319-335	7,209	781,094	2012_02_2	Nuclei_frac
P14618 APIIAVTR [iTRAQ_N1	1 447-454	7,022	492,82	2012_02_2	Nuclei_frac

P14618	CCSGAIIVL [iTRAQ_N1	4 422-432	7,937	755,424	2012_02_2	Nuclei_frac
P14618	FGVEQDVI [iTRAQ_N1	2 230-245	7,622	674,004	2012_02_2	Nuclei_frac
P14618	GDLGIEIPA [iTRAQ_N1	2 294-304	6,045	715,412	2012_02_2	Nuclei_frac
P14618	GIFPVLCK [iTRAQ_N1	3 467-474	5,959	611,366	2012_02_2	Nuclei_frac
P14618	GIFPVLCKI [iTRAQ_N1	3 467-488	8,638	949,163	2012_02_2	Nuclei_frac
P14618	GIFPVLCKI [iTRAQ_N1	3 467-488	7,714	949,164	2012_02_2	Nuclei_frac
P14618	GIFPVLCKI [iTRAQ_N1	3 467-488	5,258	712,125	2012_02_2	Nuclei_frac
P14618	GIFPVLCKI [iTRAQ_N1	3 467-488	5,044	712,125	2012_02_2	Nuclei_frac
P14618	GVNLPGA/ [iTRAQ_N1	2 207-223	7,588	642,372	2012_02_2	Nuclei_frac
P14618	GVNLPGA/ [iTRAQ_N1	2 207-223	6,058	642,372	2012_02_2	Nuclei_frac
P14618	IYVDDGLIS [iTRAQ_N1	2 173-185	6,75	876,013	2012_02_2	Nuclei_frac
P14618	KGDVVIVL [iTRAQ_N1	2 504-515	5,945	544,332	2012_02_2	Nuclei_frac
P14618	KGVNLPGA/ [iTRAQ_N1	3 206-223	7,426	733,102	2012_02_2	Nuclei_frac
P14618	KGVNLPGA/ [iTRAQ_N1	3 206-223	6,819	733,103	2012_02_2	Nuclei_frac
P14618	LAPITSDP1 [iTRAQ_N1	2 400-421	8,34	821,779	2012_02_2	Nuclei_frac
P14618	LAPITSDP1 [iTRAQ_N1	2 400-421	7,951	1232,166	2012_02_2	Nuclei_frac
P14618	LAPITSDP1 [iTRAQ_N1	2 400-421	7,216	821,779	2012_02_2	Nuclei_frac
P14618	LAPITSDP1 [iTRAQ_N1	2 400-421	7,211	821,78	2012_02_2	Nuclei_frac
P14618	LAPITSDP1 [iTRAQ_N1	2 400-421	5,492	821,778	2012_02_2	Nuclei_frac
P14618	LDIDSPPIT, [iTRAQ_N1	1 32-42	7,751	671,378	2012_02_2	Nuclei_frac
P14618	LDIDSPPIT, [iTRAQ_N1	1 32-42	6,201	671,379	2012_02_2	Nuclei_frac
P14618	LDIDSPPIT, [iTRAQ_N1	1 32-42	5,042	671,379	2012_02_2	Nuclei_frac
P14618	LNFSHGTH [iTRAQ_N1	2 73-88	5,38	543,783	2012_02_2	Nuclei_frac
P14618	NTGIICTIGF [iTRAQ_N1	2 43-55	9,648	752,408	2012_02_2	Nuclei_frac
P14618	NTGIICTIGF [iTRAQ_N1	2 43-55	4,992	501,941	2012_02_2	Nuclei_frac
P14618	TATESFAS [iTRAQ_N1	2 92-114	6,351	689,13	2012_02_2	Nuclei_frac
P14618	TATESFAS [iTRAQ_N1	2 92-114	6,174	918,516	2012_02_2	Nuclei_frac
P14618	TATESFAS [iTRAQ_N1	2 92-114	5,459	918,515	2012_02_2	Nuclei_frac
P14618	VNFAMNV [iTRAQ_N1	3 489-497	5,931	642,356	2012_02_2	Nuclei_frac
P14618	VNFAMNV [iTRAQ_N1	3 489-497	4,996	428,572	2012_02_2	Nuclei_frac
Q9NZM1,Q	ANVTVLD* [iTRAQ_N1	1 700-710	7,98	687,398	2012_02_2	Nuclei_frac
Q9NZM1,Q	ANVTVLD* [iTRAQ_N1	1 700-710	7,42	687,399	2012_02_2	Nuclei_frac
Q9NZM1,Q	DHYIPNTLI [iTRAQ_N1	1 1578-1591	5,737	596,316	2012_02_2	Nuclei_frac
Q9NZM1,Q	DQLRPTQL [iTRAQ_N1	1 1656-1669	8,614	599,346	2012_02_2	Nuclei_frac
Q9NZM1,Q	GIPLDFSSS [iTRAQ_N1	2 56-70	5,187	612,036	2012_02_2	Nuclei_frac
Q9NZM1,Q	GPVGTVSE [iTRAQ_N1	1 168-180	9,502	714,906	2012_02_2	Nuclei_frac
Q9NZM1,Q	ILVELATFL [iTRAQ_N1	2 524-534	5,314	521,992	2012_02_2	Nuclei_frac
Q9NZM1,Q	KVDNELNF [iTRAQ_N1	2 37-55	7,959	877,805	2012_02_2	Nuclei_frac
Q9NZM1,Q	LIGTATVA [iTRAQ_N1	2 80-89	4,975	425,614	2012_02_2	Nuclei_frac
Q9NZM1,Q	LISLLNEK [iTRAQ_N1	2 103-110	5,907	609,39	2012_02_2	Nuclei_frac
Q9NZM1,Q	LQTNIEALI [iTRAQ_N1	2 654-662	5,818	659,404	2012_02_2	Nuclei_frac
Q9NZM1,Q	LTIYDWDR [iTRAQ_N1	1 440-447	7,197	613,319	2012_02_2	Nuclei_frac
Q9NZM1,Q	NANPEWN [iTRAQ_N1	2 416-430	6,728	685,713	2012_02_2	Nuclei_frac
Q9NZM1,Q	SIFSPVVK [iTRAQ_N1	2 1217-1224	5,054	582,865	2012_02_2	Nuclei_frac
Q9NZM1,Q	SIFSPVVK [iTRAQ_N1	2 1217-1224	4,969	582,864	2012_02_2	Nuclei_frac
Q9NZM1,Q	SLSQIHEA/ [iTRAQ_N1	1 716-726	7,454	452,257	2012_02_2	Nuclei_frac
Q9NZM1,Q	SLSQIHEA/ [iTRAQ_N1	1 716-726	5,531	452,257	2012_02_2	Nuclei_frac
Q9NZM1,Q	TLHSTFQP [iTRAQ_N1	2 1733-1746	7,766	616,007	2012_02_2	Nuclei_frac
Q9NZM1,Q	TQGLVPEH [iTRAQ_N1	1 1721-1732	7,398	503,944	2012_02_2	Nuclei_frac
Q9NZM1,Q	VGETIIDLE [iTRAQ_N1	1 1621-1631	8,444	701,887	2012_02_2	Nuclei_frac

P09493_ISC ATDAEAD\ [iTRAQ_Ni	1 78-91	8,468	816,926	2012_02_2	Nuclei_frac
P09493_ISC ATDAEAD\ [iTRAQ_Ni	1 78-91	6,08	544,953	2012_02_2	Nuclei_frac
P09493_ISC CAEEEEEL [iTRAQ_Ni	3 190-198	6,208	704,865	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL [iTRAQ_Ni	1 92-101	7,322	463,257	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL [iTRAQ_Ni	1 92-101	6,486	694,383	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL [iTRAQ_Ni	1 92-105	8,6	624,67	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL [iTRAQ_Ni	1 92-105	6,843	936,504	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,812	874,975	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,221	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	11,088	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	9,916	874,975	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	9,322	583,651	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	8,375	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	6,518	437,991	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	6,439	437,992	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI [iTRAQ_Ni	2 77-90	4,746	583,652	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL [iTRAQ_Ni	2 168-178	7,828	801,989	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL [iTRAQ_Ni	2 168-178	7,16	801,988	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL [iTRAQ_Ni	2 168-178	6,246	534,995	2012_02_2	Nuclei_frac
P09493_ISC KYEEVAR [iTRAQ_Ni	2 161-167	5,353	591,841	2012_02_2	Nuclei_frac
P09493_ISC LATALQK [iTRAQ_Ni	2 106-112	4,993	516,837	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,675	938,563	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,419	938,564	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,98	626,045	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,915	938,562	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,474	626,044	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,117	626,043	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,034	626,045	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,917	626,044	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,868	626,044	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,383	882,949	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,234	882,947	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,216	882,948	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	8,423	441,977	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,313	441,977	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,014	441,978	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,942	588,967	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,34	588,969	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-178	7,536	665,888	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	7,722	606,003	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	6,485	606,003	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	6,148	908,503	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	2 38-48	7,383	795,451	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	2 38-48	6,522	530,638	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	7,699	621,372	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	7,053	621,372	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	5,322	466,281	2012_02_2	Nuclei_frac
P09493_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	9,479	772,433	2012_02_2	Nuclei_frac
P09493_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	6,925	515,291	2012_02_2	Nuclei_frac
P09493_ISC ALMAAEDI [iTRAQ_Ni	4 206-217	6,031	601,662	2012_02_2	Nuclei_frac
P09493_ISC ALMAAEDI [iTRAQ_Ni	4 206-217	4,864	601,663	2012_02_2	Nuclei_frac

P09493_ISC ATDAEAD\ [iTRAQ_Ni	1 78-91	8,468	816,926	2012_02_2	Nuclei_frac
P09493_ISC ATDAEAD\ [iTRAQ_Ni	1 78-91	6,08	544,953	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL\ [iTRAQ_Ni	1 92-101	7,322	463,257	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL\ [iTRAQ_Ni	1 92-101	6,486	694,383	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL\ [iTRAQ_Ni	1 92-105	8,6	624,67	2012_02_2	Nuclei_frac
P09493_ISC IQLVEEEL\ [iTRAQ_Ni	1 92-105	6,843	936,504	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	11,812	874,975	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	11,221	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	11,088	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	9,916	874,975	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	9,322	583,651	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	8,375	583,652	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	6,518	437,991	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	6,439	437,992	2012_02_2	Nuclei_frac
P09493_ISC KATDAEAI\ [iTRAQ_Ni	2 77-90	4,746	583,652	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL\ [iTRAQ_Ni	2 168-178	7,828	801,989	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL\ [iTRAQ_Ni	2 168-178	7,16	801,988	2012_02_2	Nuclei_frac
P09493_ISC KLVIIESDL\ [iTRAQ_Ni	2 168-178	6,246	534,995	2012_02_2	Nuclei_frac
P09493_ISC KYEEVAR [iTRAQ_Ni	2 161-167	5,353	591,841	2012_02_2	Nuclei_frac
P09493_ISC LATALQK [iTRAQ_Ni	2 106-112	4,993	516,837	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,675	938,563	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	6,419	938,564	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,98	626,045	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,915	938,562	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,474	626,044	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,117	626,043	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	5,034	626,045	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,917	626,044	2012_02_2	Nuclei_frac
P09493_ISC LATALQKL [iTRAQ_Ni	3 106-118	4,868	626,044	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,383	882,949	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,234	882,947	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	9,216	882,948	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	8,423	441,977	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,313	441,977	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	7,014	441,978	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,942	588,967	2012_02_2	Nuclei_frac
P09493_ISC LEEAEKAA [iTRAQ_Ni	2 113-125	5,34	588,969	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-178	7,536	665,888	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	7,722	606,003	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	6,485	606,003	2012_02_2	Nuclei_frac
P09493_ISC LVIIESDLEI [iTRAQ_Ni	1 169-182	6,148	908,503	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	2 38-48	7,383	795,451	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	2 38-48	6,522	530,638	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	7,699	621,372	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	7,053	621,372	2012_02_2	Nuclei_frac
P09493_ISC QLEDELVS [iTRAQ_Ni	3 38-49	5,322	466,281	2012_02_2	Nuclei_frac
P09493_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	9,479	772,433	2012_02_2	Nuclei_frac
P09493_ISC RIQLVEEEL [iTRAQ_Ni	1 91-101	6,925	515,291	2012_02_2	Nuclei_frac
AGALQCSF [iTRAQ_Ni	4 1934-1948	7,479	677,029	2012_02_2	Nuclei_frac
ALSTDPAF [iTRAQ_Ni	2 1321-1332	7,028	743,442	2012_02_2	Nuclei_frac
AVASAAA [iTRAQ_Ni	2 674-685	4,894	458,297	2012_02_2	Nuclei_frac

	AVSSAIAQ [iTRAQ_N1	1 1097-1122	8,819	906,486	2012_02_2	Nuclei_frac
	AVSSAIAQ [iTRAQ_N1	1 1097-1122	6,604	1359,222	2012_02_2	Nuclei_frac
	GLAGAVSE [iTRAQ_N1	1 614-624	7,821	615,371	2012_02_2	Nuclei_frac
	GLAGAVSE [iTRAQ_N1	1 614-624	7,633	615,371	2012_02_2	Nuclei_frac
	IGITNHDEY [iTRAQ_N1	1 119-131	6,293	554,297	2012_02_2	Nuclei_frac
	ISIGNVVK [iTRAQ_N1	2 8-15	6,317	559,362	2012_02_2	Nuclei_frac
	ISIGNVVK [iTRAQ_N1	2 8-15	4,762	559,362	2012_02_2	Nuclei_frac
	LAQAAQS [iTRAQ_N1	1 2044-2057	9,302	520,966	2012_02_2	Nuclei_frac
	LLAALLED [iTRAQ_N1	2 593-613	6,994	804,137	2012_02_2	Nuclei_frac
	LNEAAAGL [iTRAQ_N1	1 1242-1261	7,847	724,389	2012_02_2	Nuclei_frac
	NLGTALAE [iTRAQ_N1	1 1026-1035	7,918	601,357	2012_02_2	Nuclei_frac
	SIAAATSA [iTRAQ_N1	2 2351-2361	6,296	440,61	2012_02_2	Nuclei_frac
	TLAESALQ [iTRAQ_N1	2 1767-1780	5,668	604,025	2012_02_2	Nuclei_frac
	VQELGHGC [iTRAQ_N1	3 1920-1933	4,722	590,996	2012_02_2	Nuclei_frac
	VSHVLAAL [iTRAQ_N1	1 1961-1973	9,283	493,955	2012_02_2	Nuclei_frac
	VVAPTISSI [iTRAQ_N1	2 722-741	9,254	762,076	2012_02_2	Nuclei_frac
P04843	ALTSEIALI [iTRAQ_N1	1 502-513	9,349	723,428	2012_02_2	Nuclei_frac
P04843	ALTSEIALI [iTRAQ_N1	1 502-513	9,083	723,426	2012_02_2	Nuclei_frac
P04843	ALTSEIALI [iTRAQ_N1	1 502-513	7,895	482,62	2012_02_2	Nuclei_frac
P04843	ALTSEIALI [iTRAQ_N1	1 502-513	7,469	482,62	2012_02_2	Nuclei_frac
P04843	APDELHYT [iTRAQ_N1	2 369-390	5,137	714,888	2012_02_2	Nuclei_frac
P04843	ATSFLAL [iTRAQ_N1	1 43-57	8,212	902,506	2012_02_2	Nuclei_frac
P04843	ATSFLAL [iTRAQ_N1	1 43-57	6,918	602,003	2012_02_2	Nuclei_frac
P04843	DVPAYSQI [iTRAQ_N1	2 182-192	7,185	779,901	2012_02_2	Nuclei_frac
P04843	FPLFGGWK [iTRAQ_N1	2 297-304	6,054	413,909	2012_02_2	Nuclei_frac
P04843	FVDHVFDE [iTRAQ_N1	2 332-348	6,364	760,409	2012_02_2	Nuclei_frac
P04843	IDHILDAL [iTRAQ_N1	1 577-584	6,313	527,307	2012_02_2	Nuclei_frac
P04843	ISVIVETVY [iTRAQ_N1	2 104-128	7,59	793,443	2012_02_2	Nuclei_frac
P04843	LAHLGVQ [iTRAQ_N1	2 58-66	5,713	418,272	2012_02_2	Nuclei_frac
P04843	LPVALDPG [iTRAQ_N1	2 94-103	5,251	634,895	2012_02_2	Nuclei_frac
P04843	NIEIDSPYEI [iTRAQ_N1	1 357-368	8,395	790,407	2012_02_2	Nuclei_frac
P04843	TILPAAAQ [iTRAQ_N1	1 259-271	7,238	812,944	2012_02_2	Nuclei_frac
P04843	TVDLSSHL [iTRAQ_N1	2 16-25	6,739	679,899	2012_02_2	Nuclei_frac
P04843	VACITEQV [iTRAQ_N1	3 452-466	6,921	678,066	2012_02_2	Nuclei_frac
P04843	VHYENNSF [iTRAQ_N1	2 193-209	7,428	724,029	2012_02_2	Nuclei_frac
P04843	VTAEVVL [iTRAQ_N1	1 26-42	9,777	899,502	2012_02_2	Nuclei_frac
P04843	VTAEVVL [iTRAQ_N1	1 26-42	8,318	600,004	2012_02_2	Nuclei_frac
P04350,A6I	EIVHLQAG [iTRAQ_N1	3 3-19	10,262	704,381	2012_02_2	Nuclei_frac
P04350,A6I	EIVHLQAG [iTRAQ_N1	3 3-19	10,222	704,382	2012_02_2	Nuclei_frac
P04350,A6I	EVDEQMLN [iTRAQ_N1	2 325-336	7,481	867,95	2012_02_2	Nuclei_frac
P04350,A6I	EVDEQMLN [iTRAQ_N1	3 325-336	6,583	584,301	2012_02_2	Nuclei_frac
P04350,A6I	FPGQLNAC [iTRAQ_N1	1 242-251	6,113	637,854	2012_02_2	Nuclei_frac
P04350,A6I	FPGQLNAC [iTRAQ_N1	1 242-251	5,592	637,853	2012_02_2	Nuclei_frac
P04350,A6I	FPGQLNAC [iTRAQ_N1	1 242-251	5,557	637,854	2012_02_2	Nuclei_frac
P04350,A6I	FWEVISDEI [iTRAQ_N1	1 20-46	7,412	815,885	2012_02_2	Nuclei_frac
P04350,A6I	GHYTEGAE [iTRAQ_N1	1 104-121	7,555	701,7	2012_02_2	Nuclei_frac
P04350,A6I	GHYTEGAE [iTRAQ_N1	2 104-122	8,964	792,434	2012_02_2	Nuclei_frac
P04350,A6I	GHYTEGAE [iTRAQ_N1	2 104-122	6,128	594,577	2012_02_2	Nuclei_frac
P04350,A6I	INVYYNEA [iTRAQ_N1	2 47-58	5,666	539,624	2012_02_2	Nuclei_frac
P04350,A6I	IREEYPDR [iTRAQ_N1	1 155-162	5,507	407,884	2012_02_2	Nuclei_frac

P04350,A6I ISEQFTAMI [iTRAQ_N1	2 381-390	8,625	695,352	2012_02_2 Nuclei_frac
P04350,A6I ISEQFTAMI [iTRAQ_N1	2 381-390	7,303	695,351	2012_02_2 Nuclei_frac
P04350,A6I LAVNMVPI [iTRAQ_N1	2 253-262	6,896	652,37	2012_02_2 Nuclei_frac
P04350,A6I LAVNMVPI [iTRAQ_N1	1 253-262	6,297	644,371	2012_02_2 Nuclei_frac
P04350,A6I LHFFMPGF [iTRAQ_N1	2 263-276	5,964	594,316	2012_02_2 Nuclei_frac
P04350,A6I LTTPTYGD [iTRAQ_N1	3 217-241	6,819	956,819	2012_02_2 Nuclei_frac
P04350,A6I LTTPTYGD [iTRAQ_N1	3 217-241	6,433	956,816	2012_02_2 Nuclei_frac
P04350,A6I NSSYFVEV [iTRAQ_N1	2 337-350	8,31	993,024	2012_02_2 Nuclei_frac
P04350,A6I NSSYFVEV [iTRAQ_N1	2 337-350	7,863	993,024	2012_02_2 Nuclei_frac
P04350,A6I NSSYFVEV [iTRAQ_N1	2 337-350	5,527	662,353	2012_02_2 Nuclei_frac
P04350,A6I NSSYFVEV [iTRAQ_N1	2 337-350	5,515	662,352	2012_02_2 Nuclei_frac
P04350,A6I SGPFGQIFF [iTRAQ_N1	2 78-103	10,536	1029,519	2012_02_2 Nuclei_frac
P04350,A6I SGPFGQIFF [iTRAQ_N1	2 78-103	9,809	1029,521	2012_02_2 Nuclei_frac
P04350,A6I SGPFGQIFF [iTRAQ_N1	2 78-103	8,538	1029,521	2012_02_2 Nuclei_frac
P04350,A6I SGPFGQIFF [iTRAQ_N1	2 78-103	4,903	772,393	2012_02_2 Nuclei_frac
P04350,A6I YLTVAAVF [iTRAQ_N1	1 310-318	6,344	592,35	2012_02_2 Nuclei_frac
P50454 AVLSAEQL [iTRAQ_N1	1 77-85	6,7	565,837	2012_02_2 Nuclei_frac
P50454 AVLSAEQL [iTRAQ_N1	1 77-85	6,433	565,837	2012_02_2 Nuclei_frac
P50454 AVLSAEQL [iTRAQ_N1	1 77-98	7,965	850,469	2012_02_2 Nuclei_frac
P50454 AVLSAEQL [iTRAQ_N1	1 77-98	7,828	638,102	2012_02_2 Nuclei_frac
P50454 AVLSAEQL [iTRAQ_N1	1 77-98	5,401	638,101	2012_02_2 Nuclei_frac
P50454 DEEVHAGL [iTRAQ_N1	1 86-98	7,25	527,95	2012_02_2 Nuclei_frac
P50454 DQAVENIL [iTRAQ_N1	2 43-68	6,773	947,217	2012_02_2 Nuclei_frac
P50454 DQAVENIL [iTRAQ_N1	2 43-68	6,02	1420,322	2012_02_2 Nuclei_frac
P50454 DTQSGSLL [iTRAQ_N1	1 376-387	9,206	719,395	2012_02_2 Nuclei_frac
P50454 DTQSGSLL [iTRAQ_N1	1 376-387	8,686	719,395	2012_02_2 Nuclei_frac
P50454 GVVEVTHI [iTRAQ_N1	2 291-301	7,72	756,936	2012_02_2 Nuclei_frac
P50454 GVVEVTHI [iTRAQ_N1	2 291-301	7,447	756,937	2012_02_2 Nuclei_frac
P50454 GVVEVTHI [iTRAQ_N1	2 291-301	6,382	504,959	2012_02_2 Nuclei_frac
P50454 HLAGLGLT [iTRAQ_N1	2 302-314	6,56	542,653	2012_02_2 Nuclei_frac
P50454 HLAGLGLT [iTRAQ_N1	3 302-316	7,219	671,401	2012_02_2 Nuclei_frac
P50454 HLAGLGLT [iTRAQ_N1	3 302-316	7,166	671,4	2012_02_2 Nuclei_frac
P50454 HLAGLGLT [iTRAQ_N1	3 302-316	5,983	503,803	2012_02_2 Nuclei_frac
P50454 KAVAISLPI [iTRAQ_N1	3 282-290	5,851	453,641	2012_02_2 Nuclei_frac
P50454 KAVAISLPI [iTRAQ_N1	3 282-290	5,305	679,955	2012_02_2 Nuclei_frac
P50454 LFYADHPF [iTRAQ_N1	1 363-375	7,9	891,498	2012_02_2 Nuclei_frac
P50454 LFYADHPF [iTRAQ_N1	1 363-375	5,498	594,666	2012_02_2 Nuclei_frac
P50454 LQIVEMPL [iTRAQ_N1	2 235-245	6,811	522,984	2012_02_2 Nuclei_frac
P50454 LQIVEMPL [iTRAQ_N1	3 235-245	5,942	528,311	2012_02_2 Nuclei_frac
P50454 LSSLILMPI [iTRAQ_N1	2 246-262	7,071	715,406	2012_02_2 Nuclei_frac
P50454 LYGPSSVS [iTRAQ_N1	1 116-130	10,154	902,455	2012_02_2 Nuclei_frac
P50454 LYGPSSVS [iTRAQ_N1	1 116-130	7,69	601,973	2012_02_2 Nuclei_frac
P50454 SALQSINE\ [iTRAQ_N1	3 150-172	7,421	973,862	2012_02_2 Nuclei_frac
P50454 TGLYNYYD [iTRAQ_N1	3 222-234	7,664	690,684	2012_02_2 Nuclei_frac
P50454 TGLYNYYD [iTRAQ_N1	3 222-234	6,572	690,685	2012_02_2 Nuclei_frac
DIENQYET([iTRAQ_N1	2 340-368	8,573	1184,914	2012_02_2 Nuclei_frac
EIETYHNLL [iTRAQ_N1	2 450-472	7,546	933,446	2012_02_2 Nuclei_frac
GGGGSFGY [iTRAQ_N1	1 64-95	8,318	950,428	2012_02_2 Nuclei_frac
GGSGGSHC [iTRAQ_N1	2 580-619	6,211	878,63	2012_02_2 Nuclei_frac
GGSGGSYC [iTRAQ_N1	1 491-513	9,851	645,949	2012_02_2 Nuclei_frac

HGVQELEII [iTRAQ_N1	2 375-390	5,341	709,398	2012_02_2 Nuclei_frac
IKFEMEONI [iTRAQ_N1	2 241-250	5,738	532,635	2012_02_2 Nuclei_frac
IQDWYDKK [iTRAQ_N1	3 185-192	4,964	509,958	2012_02_2 Nuclei_frac
LASYLDKV [iTRAQ_N1	3 164-184	8,615	937,172	2012_02_2 Nuclei_frac
NYSPPYNT [iTRAQ_N1	3 200-224	5,046	834,435	2012_02_2 Nuclei_frac
QFSSSYLSI [iTRAQ_N1	1 5-13	7,473	609,816	2012_02_2 Nuclei_frac
QGVDAIDN [iTRAQ_N1	1 251-261	9,101	651,351	2012_02_2 Nuclei_frac
TLLDIDNTI [iTRAQ_N1	1 225-233	6,814	602,838	2012_02_2 Nuclei_frac
VQALEEAN [iTRAQ_N1	2 171-184	7,97	625,663	2012_02_2 Nuclei_frac
YCGQLQMI [iTRAQ_N1	3 405-427	8,748	966,481	2012_02_2 Nuclei_frac

ASDAEGD\ [iTRAQ_N1	1 78-91	7,326	530,276	2012_02_2 Nuclei_frac
CGDLEELI [iTRAQ_N1	3 190-198	5,513	690,852	2012_02_2 Nuclei_frac
CGDLEELI [iTRAQ_N1	4 190-205	6,326	770,081	2012_02_2 Nuclei_frac
CGDLEELI [iTRAQ_N1	4 190-205	4,743	577,812	2012_02_2 Nuclei_frac
IQLVEEELI [iTRAQ_N1	1 92-101	7,322	463,257	2012_02_2 Nuclei_frac
IQLVEEELI [iTRAQ_N1	1 92-101	6,486	694,383	2012_02_2 Nuclei_frac
IQLVEEELI [iTRAQ_N1	1 92-105	8,6	624,67	2012_02_2 Nuclei_frac
IQLVEEELI [iTRAQ_N1	1 92-105	6,843	936,504	2012_02_2 Nuclei_frac
KASDAEGI [iTRAQ_N1	2 77-90	7,647	568,978	2012_02_2 Nuclei_frac
KLVIIEGEL [iTRAQ_N1	2 168-178	6,915	529,663	2012_02_2 Nuclei_frac
KLVIIEGEL [iTRAQ_N1	2 168-178	5,194	793,992	2012_02_2 Nuclei_frac
KYEEVAR [iTRAQ_N1	2 161-167	5,353	591,841	2012_02_2 Nuclei_frac
LATALQK [iTRAQ_N1	2 106-112	4,993	516,837	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,675	938,563	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,419	938,564	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,98	626,045	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,915	938,562	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,474	626,044	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,117	626,043	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,034	626,045	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	4,917	626,044	2012_02_2 Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	4,868	626,044	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,383	882,949	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,234	882,947	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	9,216	882,948	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	8,423	441,977	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	7,313	441,977	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	7,014	441,978	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	5,942	588,967	2012_02_2 Nuclei_frac
LEEAEKAA [iTRAQ_N1	2 113-125	5,34	588,969	2012_02_2 Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-178	7,29	438,931	2012_02_2 Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-178	7,163	657,891	2012_02_2 Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-182	6,76	900,505	2012_02_2 Nuclei_frac
LVILEGELE [iTRAQ_N1	1 169-182	5,944	600,672	2012_02_2 Nuclei_frac
NVTNNLK [iTRAQ_N1	2 199-205	4,919	545,829	2012_02_2 Nuclei_frac
QVEEELTH [iTRAQ_N1	2 38-48	5,76	547,975	2012_02_2 Nuclei_frac
RIQLVEEEL [iTRAQ_N1	1 91-101	9,479	772,433	2012_02_2 Nuclei_frac
RIQLVEEEL [iTRAQ_N1	1 91-101	6,925	515,291	2012_02_2 Nuclei_frac

P78527_CHAQEPESGL [iTRAQ_N1	2 4060-4074	5,375	640,666	2012_02_2 Nuclei_frac
P78527_CHEIFNFVLK [iTRAQ_N1	2 247-254	5,877	649,393	2012_02_2 Nuclei_frac

P78527_CH ELLNPVVE [iTRAQ_Ni	2	2453-2470	10,178	743,722	2012_02_2	Nuclei_frac
P78527_CH GLSSLLCN [iTRAQ_Ni	3	226-236	6,994	764,427	2012_02_2	Nuclei_frac
P78527_CH GLSSLLCN [iTRAQ_Ni	3	226-236	4,784	509,954	2012_02_2	Nuclei_frac
P78527_CH GQAVTLLF [iTRAQ_Ni	1	1690-1711	6,245	827,459	2012_02_2	Nuclei_frac
P78527_CH KAALSALE [iTRAQ_Ni	3	310-321	4,894	570,689	2012_02_2	Nuclei_frac
P78527_CH LATTILQH [iTRAQ_Ni	2	1618-1627	5,822	500,302	2012_02_2	Nuclei_frac
P78527_CH LGASLAFN [iTRAQ_Ni	1	1076-1087	9,039	741,913	2012_02_2	Nuclei_frac
P78527_CH LLALNSLY [iTRAQ_Ni	2	2539-2549	7,441	502,976	2012_02_2	Nuclei_frac
P78527_CH LLQDFNR [iTRAQ_Ni	1	2836-2842	5,343	525,296	2012_02_2	Nuclei_frac
P78527_CH LSAVPFR [iTRAQ_Ni	1	892-899	6,716	540,821	2012_02_2	Nuclei_frac
P78527_CH NCISTVVH [iTRAQ_Ni	2	477-489	5,964	547,641	2012_02_2	Nuclei_frac
P78527_CH QLFSSLFS [iTRAQ_Ni	2	2807-2818	5,964	814,49	2012_02_2	Nuclei_frac
P78527_CH SLGTIQQC [iTRAQ_Ni	4	1120-1136	9,298	731,01	2012_02_2	Nuclei_frac
P78527_CH TVGALQVI [iTRAQ_Ni	2	1275-1292	5,747	701,748	2012_02_2	Nuclei_frac
P78527_CH YAVPSAGL [iTRAQ_Ni	1	265-273	9,069	539,313	2012_02_2	Nuclei_frac
P67936_CGDLEEL [iTRAQ_Ni	3	153-161	5,513	690,852	2012_02_2	Nuclei_frac
P67936_CGDLEEL [iTRAQ_Ni	4	153-168	6,326	770,081	2012_02_2	Nuclei_frac
P67936_CGDLEEL [iTRAQ_Ni	4	153-168	4,743	577,812	2012_02_2	Nuclei_frac
P67936_IQALQQQA [iTRAQ_Ni	1	13-26	9,638	879,941	2012_02_2	Nuclei_frac
P67936_IQALQQQA [iTRAQ_Ni	1	13-26	6,797	586,963	2012_02_2	Nuclei_frac
P67936_IQLVEEEL [iTRAQ_Ni	1	55-64	7,322	463,257	2012_02_2	Nuclei_frac
P67936_IQLVEEEL [iTRAQ_Ni	1	55-64	6,486	694,383	2012_02_2	Nuclei_frac
P67936_IQLVEEEL [iTRAQ_Ni	1	55-68	8,6	624,67	2012_02_2	Nuclei_frac
P67936_IQLVEEEL [iTRAQ_Ni	1	55-68	6,843	936,504	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	10,693	677,698	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	9,449	1016,044	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	9,431	1016,043	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	9,388	677,697	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	8,631	677,697	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	8,539	677,697	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	7,718	1016,044	2012_02_2	Nuclei_frac
P67936_KIQALQQQ [iTRAQ_Ni	2	12-26	6,02	508,525	2012_02_2	Nuclei_frac
P67936_KLVILEGEL [iTRAQ_Ni	2	131-141	6,915	529,663	2012_02_2	Nuclei_frac
P67936_KLVILEGEL [iTRAQ_Ni	2	131-141	5,194	793,992	2012_02_2	Nuclei_frac
P67936_KYEEVAR [iTRAQ_Ni	2	124-130	5,353	591,841	2012_02_2	Nuclei_frac
P67936_LATALQK [iTRAQ_Ni	2	69-75	4,993	516,837	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	6,675	938,563	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	6,419	938,564	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	5,98	626,045	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	5,915	938,562	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	5,474	626,044	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	5,117	626,043	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	5,034	626,045	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	4,917	626,044	2012_02_2	Nuclei_frac
P67936_LATALQKL [iTRAQ_Ni	3	69-81	4,868	626,044	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	9,383	882,949	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	9,234	882,947	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	9,216	882,948	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	8,423	441,977	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	7,313	441,977	2012_02_2	Nuclei_frac
P67936_LEEAEKAA [iTRAQ_Ni	2	76-88	7,014	441,978	2012_02_2	Nuclei_frac

P67936	LEEAEKAA [iTRAQ_N1	2 76-88	5,942	588,967	2012_02_2	Nuclei_frac
P67936	LEEAEKAA [iTRAQ_N1	2 76-88	5,34	588,969	2012_02_2	Nuclei_frac
P67936	LVILEGELE [iTRAQ_N1	1 132-141	7,29	438,931	2012_02_2	Nuclei_frac
P67936	LVILEGELE [iTRAQ_N1	1 132-141	7,163	657,891	2012_02_2	Nuclei_frac
P67936	LVILEGELE [iTRAQ_N1	1 132-145	6,76	900,505	2012_02_2	Nuclei_frac
P67936	LVILEGELE [iTRAQ_N1	1 132-145	5,944	600,672	2012_02_2	Nuclei_frac
P67936	NVTNNLK [iTRAQ_N1	2 162-168	4,919	545,829	2012_02_2	Nuclei_frac
P67936	RIQLVEEEL [iTRAQ_N1	1 54-64	9,479	772,433	2012_02_2	Nuclei_frac
P67936	RIQLVEEEL [iTRAQ_N1	1 54-64	6,925	515,291	2012_02_2	Nuclei_frac
Q9BVA1,A6	AILVDLEPC [iTRAQ_N1	2 63-77	8,943	888,472	2012_02_2	Nuclei_frac
Q9BVA1,A6	AILVDLEPC [iTRAQ_N1	1 63-77	7,599	880,476	2012_02_2	Nuclei_frac
Q9BVA1,A6	EIVHIQAGC [iTRAQ_N1	3 3-19	10,288	704,381	2012_02_2	Nuclei_frac
Q9BVA1,A6	EIVHIQAGC [iTRAQ_N1	3 3-19	10,234	704,382	2012_02_2	Nuclei_frac
Q9BVA1,A6	EVDEQMLN [iTRAQ_N1	2 325-336	7,481	867,95	2012_02_2	Nuclei_frac
Q9BVA1,A6	EVDEQMLN [iTRAQ_N1	3 325-336	6,583	584,301	2012_02_2	Nuclei_frac
Q9BVA1,A6	FPGQLNAC [iTRAQ_N1	1 242-251	6,113	637,854	2012_02_2	Nuclei_frac
Q9BVA1,A6	FPGQLNAC [iTRAQ_N1	1 242-251	5,592	637,853	2012_02_2	Nuclei_frac
Q9BVA1,A6	FPGQLNAC [iTRAQ_N1	1 242-251	5,557	637,854	2012_02_2	Nuclei_frac
Q9BVA1,A6	GHYTEGAE [iTRAQ_N1	1 104-121	7,555	701,7	2012_02_2	Nuclei_frac
Q9BVA1,A6	GHYTEGAE [iTRAQ_N1	2 104-122	8,964	792,434	2012_02_2	Nuclei_frac
Q9BVA1,A6	GHYTEGAE [iTRAQ_N1	2 104-122	6,128	594,577	2012_02_2	Nuclei_frac
Q9BVA1,A6	IREEYPDR [iTRAQ_N1	1 155-162	5,507	407,884	2012_02_2	Nuclei_frac
Q9BVA1,A6	ISEQFTAMI [iTRAQ_N1	2 381-390	8,625	695,352	2012_02_2	Nuclei_frac
Q9BVA1,A6	ISEQFTAMI [iTRAQ_N1	2 381-390	7,303	695,351	2012_02_2	Nuclei_frac
Q9BVA1,A6	LAVNMVPI [iTRAQ_N1	2 253-262	6,896	652,37	2012_02_2	Nuclei_frac
Q9BVA1,A6	LAVNMVPI [iTRAQ_N1	1 253-262	6,297	644,371	2012_02_2	Nuclei_frac
Q9BVA1,A6	LHFFMPGF [iTRAQ_N1	2 263-276	5,964	594,316	2012_02_2	Nuclei_frac
Q9BVA1,A6	LTTPTYGD [iTRAQ_N1	3 217-241	6,819	956,819	2012_02_2	Nuclei_frac
Q9BVA1,A6	LTTPTYGD [iTRAQ_N1	3 217-241	6,433	956,816	2012_02_2	Nuclei_frac
Q9BVA1,A6	NSSYFVEV [iTRAQ_N1	2 337-350	8,31	993,024	2012_02_2	Nuclei_frac
Q9BVA1,A6	NSSYFVEV [iTRAQ_N1	2 337-350	7,863	993,024	2012_02_2	Nuclei_frac
Q9BVA1,A6	NSSYFVEV [iTRAQ_N1	2 337-350	5,527	662,353	2012_02_2	Nuclei_frac
Q9BVA1,A6	NSSYFVEV [iTRAQ_N1	2 337-350	5,515	662,352	2012_02_2	Nuclei_frac
Q9BVA1,A6	SGPFGQIFF [iTRAQ_N1	2 78-103	10,536	1029,519	2012_02_2	Nuclei_frac
Q9BVA1,A6	SGPFGQIFF [iTRAQ_N1	2 78-103	9,809	1029,521	2012_02_2	Nuclei_frac
Q9BVA1,A6	SGPFGQIFF [iTRAQ_N1	2 78-103	8,538	1029,521	2012_02_2	Nuclei_frac
Q9BVA1,A6	SGPFGQIFF [iTRAQ_N1	2 78-103	4,903	772,393	2012_02_2	Nuclei_frac
Q9BVA1,A6	YLTVA AIFI [iTRAQ_N1	1 310-318	7,363	599,362	2012_02_2	Nuclei_frac
P07900,P07	ADLINNLG [iTRAQ_N1	2 100-111	8,826	765,959	2012_02_2	Nuclei_frac
P07900,P07	ADLINNLG [iTRAQ_N1	2 100-111	8,779	765,96	2012_02_2	Nuclei_frac
P07900,P07	ADLINNLG [iTRAQ_N1	2 100-111	8,642	765,959	2012_02_2	Nuclei_frac
P07900,P07	ADLINNLG [iTRAQ_N1	2 100-111	7,488	510,975	2012_02_2	Nuclei_frac
P07900,P07	ADLINNLG [iTRAQ_N1	2 100-111	6,049	510,975	2012_02_2	Nuclei_frac
P07900,P07	ALLFVPR [iTRAQ_N1	1 338-344	5,977	480,312	2012_02_2	Nuclei_frac
P07900,P07	ELHINLIPNI [iTRAQ_N1	2 74-83	5,711	493,637	2012_02_2	Nuclei_frac
P07900,P07	ELHINLIPNI [iTRAQ_N1	2 74-86	6,241	470,276	2012_02_2	Nuclei_frac
P07900,P07	ELHINLIPNI [iTRAQ_N1	2 74-86	4,987	470,276	2012_02_2	Nuclei_frac
P07900,P07	ELISNSSDA [iTRAQ_N1	2 46-57	7,246	790,424	2012_02_2	Nuclei_frac
P07900,P07	ELISNSSDA [iTRAQ_N1	2 46-59	10,174	617,016	2012_02_2	Nuclei_frac
P07900,P07	FYEQFSK [iTRAQ_N1	2 436-442	5,096	618,83	2012_02_2	Nuclei_frac

P07900,P07	GVVDSEDI [iTRAQ_Ni	1	386-399	8,841	829,451	2012_02_2	Nuclei_frac
P07900,P07	HFSVEGQL [iTRAQ_Ni	1	327-337	9,363	498,261	2012_02_2	Nuclei_frac
P07900,P07	HFSVEGQL [iTRAQ_Ni	1	327-337	8,014	498,261	2012_02_2	Nuclei_frac
P07900,P07	HLEINPDH\$ [iTRAQ_Ni	1	632-646	5,899	483,518	2012_02_2	Nuclei_frac
P07900,P07	HLEINPDH\$ [iTRAQ_Ni	1	632-646	5,648	644,356	2012_02_2	Nuclei_frac
P07900,P07	HSQFIGYPI [iTRAQ_Ni	2	209-223	4,906	689,727	2012_02_2	Nuclei_frac
P07900,P07	KFYEQFSK [iTRAQ_Ni	3	435-442	5,319	503,621	2012_02_2	Nuclei_frac
P07900,P07	SLTNDWEI [iTRAQ_Ni	2	314-326	7,451	605,989	2012_02_2	Nuclei_frac
P07900,P07	TLTIVDTGI [iTRAQ_Ni	3	87-99	5,861	551,984	2012_02_2	Nuclei_frac
P07900,P07	YESLTDPSI [iTRAQ_Ni	3	60-73	4,906	658,026	2012_02_2	Nuclei_frac
P07900,P07	YIDQEELNH [iTRAQ_Ni	2	283-291	5,378	480,592	2012_02_2	Nuclei_frac
P07900,P07	YIDQEELNH [iTRAQ_Ni	2	283-291	5,375	720,386	2012_02_2	Nuclei_frac

P11021	AKFEELNM [iTRAQ_Ni	2	307-318	5,981	600,989	2012_02_2	Nuclei_frac
P11021	DAGTIAGL [iTRAQ_Ni	2	168-179	7,667	689,367	2012_02_2	Nuclei_frac
P11021	DAGTIAGL [iTRAQ_Ni	2	168-179	7,242	689,37	2012_02_2	Nuclei_frac
P11021	DAGTIAGL [iTRAQ_Ni	2	168-179	6,879	689,368	2012_02_2	Nuclei_frac
P11021	DAGTIAGL [iTRAQ_Ni	2	168-179	6,589	459,915	2012_02_2	Nuclei_frac
P11021	DAGTIAGL [iTRAQ_Ni	2	168-179	6,264	459,915	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	9,982	693,378	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	8,335	1039,566	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	7,267	693,378	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	7,266	693,378	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	6,459	693,38	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	5,795	693,38	2012_02_2	Nuclei_frac
P11021	DNHLLGTF [iTRAQ_Ni	1	457-474	4,809	693,377	2012_02_2	Nuclei_frac
P11021	ELEEIVQPII [iTRAQ_Ni	2	604-615	7,121	843,5	2012_02_2	Nuclei_frac
P11021	ELEEIVQPII [iTRAQ_Ni	2	604-615	6,473	843,501	2012_02_2	Nuclei_frac
P11021	ELEEIVQPII [iTRAQ_Ni	2	604-615	6,09	562,67	2012_02_2	Nuclei_frac
P11021	ELEEIVQPII [iTRAQ_Ni	2	604-615	5,785	562,67	2012_02_2	Nuclei_frac
P11021	ETAAYLG [iTRAQ_Ni	3	137-146	5,351	514,635	2012_02_2	Nuclei_frac
P11021	IEWLESHQ [iTRAQ_Ni	2	584-599	8,057	755,042	2012_02_2	Nuclei_frac
P11021	ITPSYVAFI [iTRAQ_Ni	1	43-56	9,854	855,946	2012_02_2	Nuclei_frac
P11021	ITPSYVAFI [iTRAQ_Ni	1	43-56	8,775	570,966	2012_02_2	Nuclei_frac
P11021	KSDIDEIVL [iTRAQ_Ni	2	335-349	8,712	626,359	2012_02_2	Nuclei_frac
P11021	KSDIDEIVL [iTRAQ_Ni	2	335-349	8,395	626,358	2012_02_2	Nuclei_frac
P11021	KSDIDEIVL [iTRAQ_Ni	2	335-349	8,018	626,359	2012_02_2	Nuclei_frac
P11021	KSDIDEIVL [iTRAQ_Ni	2	335-349	7,596	626,359	2012_02_2	Nuclei_frac
P11021	KSDIDEIVL [iTRAQ_Ni	2	335-349	5,719	626,36	2012_02_2	Nuclei_frac
P11021	KSQIFSTA\$ [iTRAQ_Ni	3	429-446	10,334	799,784	2012_02_2	Nuclei_frac
P11021	KSQIFSTA\$ [iTRAQ_Ni	3	429-446	5,171	600,09	2012_02_2	Nuclei_frac
P11021	KVTHAVV [iTRAQ_Ni	2	146-163	5,293	576,823	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	7,472	709,052	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	7,368	709,052	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	7,351	709,052	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	7,351	709,052	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	7,314	1063,075	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	6,993	709,052	2012_02_2	Nuclei_frac
P11021	SQIFSTASI [iTRAQ_Ni	2	430-446	6,799	709,052	2012_02_2	Nuclei_frac
P11021	TKPYIQVDI [iTRAQ_Ni	3	106-120	7,786	679,73	2012_02_2	Nuclei_frac
P11021	TKPYIQVDI [iTRAQ_Ni	3	106-120	7,756	679,728	2012_02_2	Nuclei_frac
P11021	TKPYIQVDI [iTRAQ_Ni	3	106-120	7,224	1019,091	2012_02_2	Nuclei_frac

P11021	TKPYIQVDI [iTRAQ_N1	3 106-120	4,972	510,048	2012_02_2	Nuclei_frac
P11021	TWNDPSV [iTRAQ_N1	2 84-95	7,273	859,952	2012_02_2	Nuclei_frac
P11021	VTHAVVT [iTRAQ_N1	1 147-163	5,726	678,029	2012_02_2	Nuclei_frac
P11021	VTHAVVT [iTRAQ_N1	1 147-163	5,192	678,03	2012_02_2	Nuclei_frac
P07237	DAPEEEDH [iTRAQ_N1	1 1-13	7,541	555,956	2012_02_2	Nuclei_frac
P07237	DAPEEEDH [iTRAQ_N1	2 1-14	5,573	485,269	2012_02_2	Nuclei_frac
P07237	EADDIVNW [iTRAQ_N1	2 104-113	6,909	497,607	2012_02_2	Nuclei_frac
P07237	EADDIVNW [iTRAQ_N1	2 104-113	6,584	745,909	2012_02_2	Nuclei_frac
P07237	ENLLDFIK [iTRAQ_N1	2 206-213	5,229	427,254	2012_02_2	Nuclei_frac
P07237	ENLLDFIK [iTRAQ_N1	2 206-213	4,865	640,378	2012_02_2	Nuclei_frac
P07237	FFPASADR [iTRAQ_N1	1 428-435	4,981	527,776	2012_02_2	Nuclei_frac
P07237	HNQLPLVII [iTRAQ_N1	2 214-230	5,965	751,759	2012_02_2	Nuclei_frac
P07237	HNQLPLVII [iTRAQ_N1	2 214-230	5,054	564,069	2012_02_2	Nuclei_frac
P07237	ILFIFIDSDH [iTRAQ_N1	1 269-283	9,688	660,012	2012_02_2	Nuclei_frac
P07237	LITLEEEMT [iTRAQ_N1	2 300-309	7,597	747,921	2012_02_2	Nuclei_frac
P07237	NFEDVAF [iTRAQ_N1	2 359-368	6,175	751,372	2012_02_2	Nuclei_frac
P07237	NNFEGEVT [iTRAQ_N1	3 197-213	5,487	814,784	2012_02_2	Nuclei_frac
P07237	NNFEGEVT [iTRAQ_N1	3 197-213	5,285	814,783	2012_02_2	Nuclei_frac
P07237	QLAPIWDK [iTRAQ_N1	2 385-392	5,48	629,874	2012_02_2	Nuclei_frac
P07237	RTGPAATT [iTRAQ_N1	2 115-145	4,775	845,708	2012_02_2	Nuclei_frac
P07237	TGPAATT [iTRAQ_N1	2 116-145	5,989	806,683	2012_02_2	Nuclei_frac
P07237	TGPAATT [iTRAQ_N1	2 116-145	5,38	806,683	2012_02_2	Nuclei_frac
P07237	TGPAATT [iTRAQ_N1	3 116-153	5,204	1050,545	2012_02_2	Nuclei_frac
P07237	THILLFLPK [iTRAQ_N1	2 238-246	5,519	457,298	2012_02_2	Nuclei_frac
P07237	YKPESEEL [iTRAQ_N1	2 310-321	7,954	870,459	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	6,386	929,046	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	5,968	619,701	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	5,659	619,701	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	5,577	619,701	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	5,502	619,701	2012_02_2	Nuclei_frac
P07237	YQLDKDG [iTRAQ_N1	3 179-190	5,094	619,702	2012_02_2	Nuclei_frac
	AGKPVICA [iTRAQ_N1	6 320-336	7,209	781,094	2012_02_2	Nuclei_frac
	APIIAVTR [iTRAQ_N1	1 448-455	7,022	492,82	2012_02_2	Nuclei_frac
	FGVEQDVI [iTRAQ_N1	2 231-246	7,622	674,004	2012_02_2	Nuclei_frac
	GDLGIEIPA [iTRAQ_N1	2 295-305	6,045	715,412	2012_02_2	Nuclei_frac
	GIFPVLC [iTRAQ_N1	3 468-475	5,959	611,366	2012_02_2	Nuclei_frac
	GIFPVLC [iTRAQ_N1	3 468-489	8,638	949,163	2012_02_2	Nuclei_frac
	GIFPVLC [iTRAQ_N1	3 468-489	7,714	949,164	2012_02_2	Nuclei_frac
	GIFPVLC [iTRAQ_N1	3 468-489	5,258	712,125	2012_02_2	Nuclei_frac
	GIFPVLC [iTRAQ_N1	3 468-489	5,044	712,125	2012_02_2	Nuclei_frac
	GVNLPGA [iTRAQ_N1	2 208-224	7,588	642,372	2012_02_2	Nuclei_frac
	GVNLPGA [iTRAQ_N1	2 208-224	6,058	642,372	2012_02_2	Nuclei_frac
	IYVDDGLIS [iTRAQ_N1	2 174-186	6,75	876,013	2012_02_2	Nuclei_frac
	KGDVVIVL [iTRAQ_N1	2 505-516	5,945	544,332	2012_02_2	Nuclei_frac
	KGVNLPGA [iTRAQ_N1	3 207-224	7,426	733,102	2012_02_2	Nuclei_frac
	KGVNLPGA [iTRAQ_N1	3 207-224	6,819	733,103	2012_02_2	Nuclei_frac
	LDIDSPIT [iTRAQ_N1	1 33-43	7,751	671,378	2012_02_2	Nuclei_frac
	LDIDSPIT [iTRAQ_N1	1 33-43	6,201	671,379	2012_02_2	Nuclei_frac
	LDIDSPIT [iTRAQ_N1	1 33-43	5,042	671,379	2012_02_2	Nuclei_frac
	LNFSHGTH [iTRAQ_N1	2 74-89	5,38	543,783	2012_02_2	Nuclei_frac

	NTGIICTIGF [iTRAQ_N1	2 44-56	9,648	752,408	2012_02_2	Nuclei_frac
	NTGIICTIGF [iTRAQ_N1	2 44-56	4,992	501,941	2012_02_2	Nuclei_frac
	TATESFAS [iTRAQ_N1	2 93-115	6,351	689,13	2012_02_2	Nuclei_frac
	TATESFAS [iTRAQ_N1	2 93-115	6,174	918,516	2012_02_2	Nuclei_frac
	TATESFAS [iTRAQ_N1	2 93-115	5,459	918,515	2012_02_2	Nuclei_frac
	VNFAMNV [iTRAQ_N1	3 490-498	5,931	642,356	2012_02_2	Nuclei_frac
	VNFAMNV [iTRAQ_N1	3 490-498	4,996	428,572	2012_02_2	Nuclei_frac
P06576	AIAELGIYP [iTRAQ_N1	1 341-359	5,614	1066,577	2012_02_2	Nuclei_frac
P06576	FLSQPFQV [iTRAQ_N1	3 416-433	9,575	776,406	2012_02_2	Nuclei_frac
P06576	FTQAGSEV [iTRAQ_N1	1 264-277	10,633	790,434	2012_02_2	Nuclei_frac
P06576	FTQAGSEV [iTRAQ_N1	1 264-277	10,106	790,431	2012_02_2	Nuclei_frac
P06576	FTQAGSEV [iTRAQ_N1	1 264-277	9,836	790,436	2012_02_2	Nuclei_frac
P06576	FTQAGSEV [iTRAQ_N1	1 264-277	9,255	527,29	2012_02_2	Nuclei_frac
P06576	FTQAGSEV [iTRAQ_N1	1 264-277	7,707	527,291	2012_02_2	Nuclei_frac
P06576	IGLFGGAG [iTRAQ_N1	2 155-165	6,64	632,388	2012_02_2	Nuclei_frac
P06576	IGLFGGAG [iTRAQ_N1	2 155-165	6,159	421,927	2012_02_2	Nuclei_frac
P06576	IMDPNIVGS [iTRAQ_N1	1 360-375	6,923	653,997	2012_02_2	Nuclei_frac
P06576	IMNVIGEPI [iTRAQ_N1	1 97-108	6,929	765,412	2012_02_2	Nuclei_frac
P06576	LVLEVAQ [iTRAQ_N1	1 48-62	10,397	898,018	2012_02_2	Nuclei_frac
P06576	LVLEVAQ [iTRAQ_N1	1 48-62	8,76	599,014	2012_02_2	Nuclei_frac
P06576	SLQDIIAILC [iTRAQ_N1	2 386-409	5,526	988,531	2012_02_2	Nuclei_frac
P06576	TIAMDGTE [iTRAQ_N1	1 63-74	8,21	703,876	2012_02_2	Nuclei_frac
P06576	TIAMDGTE [iTRAQ_N1	2 63-74	6,787	711,873	2012_02_2	Nuclei_frac
P06576	TVLIMELIN [iTRAQ_N1	2 166-178	6,509	873,532	2012_02_2	Nuclei_frac
P06576	TVLIMELIN [iTRAQ_N1	3 166-178	5,94	588,019	2012_02_2	Nuclei_frac
P06576	TVLIMELIN [iTRAQ_N1	2 166-178	4,906	582,688	2012_02_2	Nuclei_frac
P06576	TVLIMELIN [iTRAQ_N1	2 166-178	4,764	582,688	2012_02_2	Nuclei_frac
P06576	VALTGLTV [iTRAQ_N1	1 235-247	8,374	528,636	2012_02_2	Nuclei_frac
P06576	VALTGLTV [iTRAQ_N1	1 235-247	7,673	528,636	2012_02_2	Nuclei_frac
P06576	VALVYGQ [iTRAQ_N1	2 218-232	6,062	587,975	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	7,28	736,441	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,907	736,441	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,762	736,441	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,327	736,439	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,274	736,438	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,173	736,44	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	6,139	736,44	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	5,978	736,44	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	5,591	552,583	2012_02_2	Nuclei_frac
P06576	VLDSGAPII [iTRAQ_N1	2 78-96	4,998	552,582	2012_02_2	Nuclei_frac
P06576	VVDLLAPY [iTRAQ_N1	2 142-151	6,102	688,924	2012_02_2	Nuclei_frac
P06576	VVDLLAPY [iTRAQ_N1	2 142-151	5,136	459,619	2012_02_2	Nuclei_frac
P08238_CH	ADLINNLG [iTRAQ_N1	2 96-107	8,826	765,959	2012_02_2	Nuclei_frac
P08238_CH	ADLINNLG [iTRAQ_N1	2 96-107	8,779	765,96	2012_02_2	Nuclei_frac
P08238_CH	ADLINNLG [iTRAQ_N1	2 96-107	8,642	765,959	2012_02_2	Nuclei_frac
P08238_CH	ADLINNLG [iTRAQ_N1	2 96-107	7,488	510,975	2012_02_2	Nuclei_frac
P08238_CH	ADLINNLG [iTRAQ_N1	2 96-107	6,049	510,975	2012_02_2	Nuclei_frac
P08238_CH	ALLFIPR [iTRAQ_N1	1 331-337	5,495	487,32	2012_02_2	Nuclei_frac
P08238_CH	ELISNASD [iTRAQ_N1	2 42-53	7,683	782,428	2012_02_2	Nuclei_frac
P08238_CH	ELISNASD [iTRAQ_N1	2 42-53	7,008	521,953	2012_02_2	Nuclei_frac

P08238_CH ELISNASD\ [iTRAQ_N\	2 42-55	11,023	611,684	2012_02_2	Nuclei_frac
P08238_CH ELISNASD\ [iTRAQ_N\	2 42-55	9,971	611,683	2012_02_2	Nuclei_frac
P08238_CH ELISNASD\ [iTRAQ_N\	2 42-55	9,537	611,683	2012_02_2	Nuclei_frac
P08238_CH GVVDSIDL [iTRAQ_N\	1 379-392	8,841	829,451	2012_02_2	Nuclei_frac
P08238_CH HFSVEGQL [iTRAQ_N\	1 320-330	9,363	498,261	2012_02_2	Nuclei_frac
P08238_CH HFSVEGQL [iTRAQ_N\	1 320-330	8,014	498,261	2012_02_2	Nuclei_frac
P08238_CH HLEINPDHF [iTRAQ_N\	1 625-639	6,566	482,519	2012_02_2	Nuclei_frac
P08238_CH HSQFIGYPI [iTRAQ_N\	2 205-219	5,353	699,728	2012_02_2	Nuclei_frac
P08238_CH HSQFIGYPI [iTRAQ_N\	2 205-219	5,041	525,047	2012_02_2	Nuclei_frac
P08238_CH IDIIPNPQER [iTRAQ_N\	1 73-82	5,533	669,878	2012_02_2	Nuclei_frac
P08238_CH RAPFDLFEI [iTRAQ_N\	2 338-347	5,818	508,952	2012_02_2	Nuclei_frac
P08238_CH SIYYITGESI [iTRAQ_N\	2 482-491	6,617	724,9	2012_02_2	Nuclei_frac
P08238_CH SIYYITGESI [iTRAQ_N\	2 482-491	6,615	724,9	2012_02_2	Nuclei_frac
P08238_CH SIYYITGESI [iTRAQ_N\	2 482-491	4,758	483,603	2012_02_2	Nuclei_frac
P08238_CH SLTNDWEI [iTRAQ_N\	2 307-319	7,451	605,989	2012_02_2	Nuclei_frac
P08238_CH TLTLVDTC [iTRAQ_N\	3 83-95	5,893	551,984	2012_02_2	Nuclei_frac
P08238_CH YESLTDPSI [iTRAQ_N\	3 56-69	4,906	658,026	2012_02_2	Nuclei_frac
P08238_CH YIDQEELN\ [iTRAQ_N\	2 276-284	5,378	480,592	2012_02_2	Nuclei_frac
P08238_CH YIDQEELN\ [iTRAQ_N\	2 276-284	5,375	720,386	2012_02_2	Nuclei_frac
P02452_CH ALLLQGSN [iTRAQ_N\	1 1387-1399	8,285	800,465	2012_02_2	Nuclei_frac
P02452_CH ALLLQGSN [iTRAQ_N\	1 1387-1399	7,195	533,978	2012_02_2	Nuclei_frac
P02452_CH DRDLEVDT [iTRAQ_N\	2 1226-1236	6,915	531,628	2012_02_2	Nuclei_frac
P02452_CH DRDLEVDT [iTRAQ_N\	2 1226-1236	6,009	796,938	2012_02_2	Nuclei_frac
P02452_CH DRDLEVDT [iTRAQ_N\	2 1226-1236	5,726	531,628	2012_02_2	Nuclei_frac
P02452_CH FTYSVTVC [iTRAQ_N\	3 1406-1424	8,915	788,049	2012_02_2	Nuclei_frac
P02452_CH GEPGPVGV [iTRAQ_N\	2 449-469	5,797	754,071	2012_02_2	Nuclei_frac
P02452_CH GFPGADGV [iTRAQ_N\	2 494-505	7,964	680,876	2012_02_2	Nuclei_frac
P02452_CH GFPGADGV [iTRAQ_N\	2 494-505	6,962	680,875	2012_02_2	Nuclei_frac
P02452_CH GFPGLPGP\ [iTRAQ_N\	2 971-984	6,842	792,935	2012_02_2	Nuclei_frac
P02452_CH GFPGLPGP\ [iTRAQ_N\	2 971-984	5,523	528,96	2012_02_2	Nuclei_frac
P02452_CH GSAGPPGA [iTRAQ_N\	1 866-882	11,199	786,407	2012_02_2	Nuclei_frac
P02452_CH GVPGPPGA [iTRAQ_N\	2 599-612	7,062	724,925	2012_02_2	Nuclei_frac
P02452_CH GVPGPPGA [iTRAQ_N\	2 599-612	4,831	483,62	2012_02_2	Nuclei_frac
P02452_CH GVVGLPGC [iTRAQ_N\	1 959-967	7,072	513,812	2012_02_2	Nuclei_frac
P02452_CH GVVGLPGC [iTRAQ_N\	1 959-967	6,987	513,812	2012_02_2	Nuclei_frac
P02452_CH KALLLQGS [iTRAQ_N\	2 1386-1399	7,702	624,71	2012_02_2	Nuclei_frac
P02452_CH NSVAYMD\ [iTRAQ_N\	3 1372-1385	8,701	624,983	2012_02_2	Nuclei_frac
P02452_CH SLSQQIENI [iTRAQ_N\	1 1237-1246	8,855	666,375	2012_02_2	Nuclei_frac
P02452_CH SLSQQIENI [iTRAQ_N\	1 1237-1246	8,768	666,373	2012_02_2	Nuclei_frac
P02452_CH SLSQQIENI [iTRAQ_N\	1 1237-1246	6,308	666,368	2012_02_2	Nuclei_frac
P02452_CH SLSQQIENI [iTRAQ_N\	1 1237-1246	5,247	444,586	2012_02_2	Nuclei_frac
P02452_CH VGPPGPSG [iTRAQ_N\	2 883-903	8,775	685,04	2012_02_2	Nuclei_frac
P10809 AAVEEGIV [iTRAQ_N\	2 404-420	9,924	915,008	2012_02_2	Nuclei_frac
P10809 AAVEEGIV [iTRAQ_N\	2 404-420	7,214	610,343	2012_02_2	Nuclei_frac
P10809 ALMLQGVI [iTRAQ_N\	2 12-32	7,066	801,122	2012_02_2	Nuclei_frac
P10809 IQEIEQLD\ [iTRAQ_N\	2 345-361	6,822	776,079	2012_02_2	Nuclei_frac
P10809 IQEIEQLD\ [iTRAQ_N\	3 345-363	9,832	909,827	2012_02_2	Nuclei_frac
P10809 IQEIEQLD\ [iTRAQ_N\	3 345-363	9,406	909,829	2012_02_2	Nuclei_frac
P10809 IQEIEQLD\ [iTRAQ_N\	3 345-363	9,156	909,827	2012_02_2	Nuclei_frac
P10809 ISSIQSIVPA [iTRAQ_N\	1 225-242	8,872	1032,093	2012_02_2	Nuclei_frac

P10809	ISSIQSIVPA [iTRAQ_N1	1 225-242	7,799	688,395	2012_02_2	Nuclei_frac
P10809	KISSIQSIVF [iTRAQ_N1	2 224-242	5,156	584,6	2012_02_2	Nuclei_frac
P10809	KISSIQSIVF [iTRAQ_N1	2 224-242	4,826	584,6	2012_02_2	Nuclei_frac
P10809	LKVGLQV\ [iTRAQ_N1	3 265-275	5,602	529,366	2012_02_2	Nuclei_frac
P10809	NAGVEGSL [iTRAQ_N1	2 456-467	6,508	752,44	2012_02_2	Nuclei_frac
P10809	TALLDAAC [iTRAQ_N1	2 501-525	5,926	693,412	2012_02_2	Nuclei_frac
P10809	TALLDAAC [iTRAQ_N1	3 501-528	5,537	660,985	2012_02_2	Nuclei_frac
P10809	TALLDAAC [iTRAQ_N1	3 501-528	5,083	660,984	2012_02_2	Nuclei_frac
P10809	TLKIPAMTI [iTRAQ_N1	4 445-455	5,166	545,683	2012_02_2	Nuclei_frac
P10809	TVIIEQSWC [iTRAQ_N1	2 35-46	8,351	816,968	2012_02_2	Nuclei_frac
P10809	TVIIEQSWC [iTRAQ_N1	2 35-46	5,917	544,98	2012_02_2	Nuclei_frac
P10809	TVIIEQSWC [iTRAQ_N1	2 35-46	5,213	544,981	2012_02_2	Nuclei_frac
P10809	VGEVIVTK [iTRAQ_N1	2 319-326	5,189	566,865	2012_02_2	Nuclei_frac
P10809	VGEVIVTK [iTRAQ_N1	2 319-326	4,886	566,865	2012_02_2	Nuclei_frac
P10809	VGGTSDVE [iTRAQ_N1	2 380-391	5,646	507,939	2012_02_2	Nuclei_frac
P10809	VGLQVVA' [iTRAQ_N1	2 267-275	4,849	600,901	2012_02_2	Nuclei_frac
P04083	ALTGHLEE [iTRAQ_N1	2 98-112	8,535	947,587	2012_02_2	Nuclei_frac
P04083	ALTGHLEE [iTRAQ_N1	2 98-112	8,428	947,587	2012_02_2	Nuclei_frac
P04083	ALTGHLEE [iTRAQ_N1	2 98-112	6,475	632,06	2012_02_2	Nuclei_frac
P04083	CATSKPAF [iTRAQ_N1	4 269-280	5,616	596,995	2012_02_2	Nuclei_frac
P04083	CATSKPAF [iTRAQ_N1	4 269-280	5,178	596,996	2012_02_2	Nuclei_frac
P04083	GGPGSAVS [iTRAQ_N1	2 29-52	9,837	882,126	2012_02_2	Nuclei_frac
P04083	GGPGSAVS [iTRAQ_N1	2 29-52	8,969	882,127	2012_02_2	Nuclei_frac
P04083	GGPGSAVS [iTRAQ_N1	2 29-52	8,441	882,127	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	9,695	847,963	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	9,618	847,966	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	9,152	847,964	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	8,288	847,97	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	7,817	565,645	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	7,461	565,647	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	7,128	565,646	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	6,66	565,646	2012_02_2	Nuclei_frac
P04083	GTDVNVFM [iTRAQ_N1	1 214-227	6,032	565,647	2012_02_2	Nuclei_frac
P04083	GVDEATIIC [iTRAQ_N1	2 58-70	8,938	838,491	2012_02_2	Nuclei_frac
P04083	GVDEATIIC [iTRAQ_N1	2 58-70	5,109	559,329	2012_02_2	Nuclei_frac
P04083	GVDEATIIC [iTRAQ_N1	2 58-71	8,151	916,544	2012_02_2	Nuclei_frac
P04083	GVDEATIIC [iTRAQ_N1	2 58-71	7,462	611,365	2012_02_2	Nuclei_frac
P04083	ILVALCGGI [iTRAQ_N1	2 337-345	6,605	530,802	2012_02_2	Nuclei_frac
P04083	ILVALCGGI [iTRAQ_N1	2 337-345	5,666	530,802	2012_02_2	Nuclei_frac
P04083	ILVALCGGI [iTRAQ_N1	2 337-345	5,095	530,802	2012_02_2	Nuclei_frac
P04083	ILVALCGGI [iTRAQ_N1	2 337-345	5,071	530,803	2012_02_2	Nuclei_frac
P04083	KGTDVNVI [iTRAQ_N1	2 213-227	9,501	656,377	2012_02_2	Nuclei_frac
P04083	KGTDVNVI [iTRAQ_N1	2 213-227	9,441	656,378	2012_02_2	Nuclei_frac
P04083	KGTDVNVI [iTRAQ_N1	2 213-227	8,877	984,063	2012_02_2	Nuclei_frac
P04083	KGTDVNVI [iTRAQ_N1	2 213-227	7,292	984,068	2012_02_2	Nuclei_frac
P04083	MYGISLCQ [iTRAQ_N1	5 317-336	4,73	696,358	2012_02_2	Nuclei_frac
P04083	NALLSLAK [iTRAQ_N1	2 177-184	6,567	559,363	2012_02_2	Nuclei_frac
P04083	NALLSLAK [iTRAQ_N1	2 177-184	6,173	559,363	2012_02_2	Nuclei_frac
P04083	NALLSLAK [iTRAQ_N1	2 177-184	5,949	559,363	2012_02_2	Nuclei_frac
P04083	NALLSLAK [iTRAQ_N1	2 177-184	5,912	559,363	2012_02_2	Nuclei_frac
P04083	NALLSLAK [iTRAQ_N1	2 177-184	5,276	559,362	2012_02_2	Nuclei_frac

P04083	QAWFIENE [iTRAQ_N1	2 9-25	9,403	1215,118	2012_02_2	Nuclei_frac
P04083	QAWFIENE [iTRAQ_N1	2 9-25	8,24	810,413	2012_02_2	Nuclei_frac
P04083	QAWFIENE [iTRAQ_N1	2 9-25	8,161	810,414	2012_02_2	Nuclei_frac
P04083	QAWFIENE [iTRAQ_N1	2 9-25	7,753	810,414	2012_02_2	Nuclei_frac
P04083	SEIDMNDIK [iTRAQ_N1	2 303-311	5,293	676,852	2012_02_2	Nuclei_frac
P04083	TPAQFDAI [iTRAQ_N1	1 113-123	6,289	703,855	2012_02_2	Nuclei_frac
P22626_ISC	DYFEEYGK [iTRAQ_N1	2 130-137	5,018	669,826	2012_02_2	Nuclei_frac
P22626_ISC	GFGFVTFD [iTRAQ_N1	2 154-168	7,509	661,995	2012_02_2	Nuclei_frac
P22626_ISC	GFGFVTFD [iTRAQ_N1	2 154-168	7,335	661,995	2012_02_2	Nuclei_frac
P22626_ISC	GFGFVTFD [iTRAQ_N1	3 154-173	5,03	678,123	2012_02_2	Nuclei_frac
P22626_ISC	GGGNGFGF [iTRAQ_N1	1 214-228	9,34	761,369	2012_02_2	Nuclei_frac
P22626_ISC	GGGNGFGF [iTRAQ_N1	1 214-228	7,369	507,916	2012_02_2	Nuclei_frac
P22626_ISC	IDTIEIITDR [iTRAQ_N1	1 138-147	8,939	666,878	2012_02_2	Nuclei_frac
P22626_ISC	KLFIGGLSF [iTRAQ_N1	2 22-38	9,857	1108,12	2012_02_2	Nuclei_frac
P22626_ISC	KLFIGGLSF [iTRAQ_N1	2 22-38	8,47	739,082	2012_02_2	Nuclei_frac
P22626_ISC	KLFIGGLSF [iTRAQ_N1	2 22-38	7,138	554,561	2012_02_2	Nuclei_frac
P22626_ISC	KLFIGGLSF [iTRAQ_N1	2 22-38	5,798	554,562	2012_02_2	Nuclei_frac
P22626_ISC	KLFVGGIK [iTRAQ_N1	3 113-120	5,105	647,435	2012_02_2	Nuclei_frac
P22626_ISC	KLFVGGIK [iTRAQ_N1	3 113-120	4,865	647,435	2012_02_2	Nuclei_frac
P22626_ISC	LFIGGLSFE [iTRAQ_N1	1 23-38	9,366	648,347	2012_02_2	Nuclei_frac
P22626_ISC	LFIGGLSFE [iTRAQ_N1	1 23-38	8,633	972,014	2012_02_2	Nuclei_frac
P22626_ISC	LFVGGIKEI [iTRAQ_N1	2 114-129	8,218	723,398	2012_02_2	Nuclei_frac
P22626_ISC	LFVGGIKEI [iTRAQ_N1	2 114-129	5,95	542,799	2012_02_2	Nuclei_frac
P22626_ISC	LFVGGIKEI [iTRAQ_N1	2 114-129	5,819	542,799	2012_02_2	Nuclei_frac
P22626_ISC	LFVGGIKEI [iTRAQ_N1	2 114-129	5,72	542,799	2012_02_2	Nuclei_frac
P22626_ISC	LTDCVVM [iTRAQ_N1	4 47-59	5,536	599,316	2012_02_2	Nuclei_frac
P22626_ISC	NMGGPYGC [iTRAQ_N1	2 326-350	7,676	784,007	2012_02_2	Nuclei_frac
P22626_ISC	NYEQWGI [iTRAQ_N1	2 39-46	6,47	688,348	2012_02_2	Nuclei_frac
P22626_ISC	NYEQWGI [iTRAQ_N1	2 39-46	5,231	688,349	2012_02_2	Nuclei_frac
P22626_ISC	TLETVPLEI [iTRAQ_N1	1 4-12	6,157	601,351	2012_02_2	Nuclei_frac
P22626_ISC	TLETVPLEI [iTRAQ_N1	1 4-12	4,791	601,35	2012_02_2	Nuclei_frac
Q13748,Q6	AVCMLSN [iTRAQ_N1	3 374-390	9,063	1013,003	2012_02_2	Nuclei_frac
Q13748,Q6	AVCMLSN [iTRAQ_N1	2 374-390	7,356	670,341	2012_02_2	Nuclei_frac
Q13748,Q6	AVFVDLEF [iTRAQ_N1	1 65-79	7,488	923,51	2012_02_2	Nuclei_frac
Q13748,Q6	AVFVDLEF [iTRAQ_N1	1 65-79	5,569	616,008	2012_02_2	Nuclei_frac
Q13748,Q6	DVNAAIAT [iTRAQ_N1	2 327-336	6,99	652,395	2012_02_2	Nuclei_frac
Q13748,Q6	DVNAAIAT [iTRAQ_N1	2 327-336	6,865	652,396	2012_02_2	Nuclei_frac
Q13748,Q6	DVNAAIAT [iTRAQ_N1	2 327-336	6,722	652,393	2012_02_2	Nuclei_frac
Q13748,Q6	DVNAAIAT [iTRAQ_N1	2 327-336	5,966	435,265	2012_02_2	Nuclei_frac
Q13748,Q6	DVNAAIAT [iTRAQ_N1	2 327-336	5,337	435,266	2012_02_2	Nuclei_frac
Q13748,Q6	EIIDLVLDR [iTRAQ_N1	1 113-121	5,372	615,365	2012_02_2	Nuclei_frac
Q13748,Q6	IHFPLATY [iTRAQ_N1	2 265-280	9,449	1023,089	2012_02_2	Nuclei_frac
Q13748,Q6	IHFPLATY [iTRAQ_N1	2 265-280	9,289	1023,087	2012_02_2	Nuclei_frac
Q13748,Q6	IHFPLATY [iTRAQ_N1	2 265-280	8,234	682,394	2012_02_2	Nuclei_frac
Q13748,Q6	IHFPLATY [iTRAQ_N1	2 265-280	8,142	682,395	2012_02_2	Nuclei_frac
Q13748,Q6	IHFPLATY [iTRAQ_N1	2 265-280	5,276	512,047	2012_02_2	Nuclei_frac
Q13748,Q6	LIGQIVSSI [iTRAQ_N1	1 230-243	9,298	801,494	2012_02_2	Nuclei_frac
Q13748,Q6	LIGQIVSSI [iTRAQ_N1	1 230-243	7,98	534,662	2012_02_2	Nuclei_frac
Q13748,Q6	LIGQIVSSI [iTRAQ_N1	1 230-243	5,646	801,469	2012_02_2	Nuclei_frac
Q13748,Q6	NLDIERPTY [iTRAQ_N1	1 216-229	6,968	621,667	2012_02_2	Nuclei_frac

Q13748,Q6 NLDIERPTY [iTRAQ_N1	1 216-229	6,265	621,667	2012_02_2	Nuclei_frac
Q13748,Q6 NLDIERPTY [iTRAQ_N1	1 216-229	5,619	931,997	2012_02_2	Nuclei_frac
Q13748,Q6 NLDIERPTY [iTRAQ_N1	1 216-229	4,967	621,667	2012_02_2	Nuclei_frac
Q13748,Q6 QLFHPEQL [iTRAQ_N1	2 85-96	8,844	849,994	2012_02_2	Nuclei_frac
Q13748,Q6 QLFHPEQL [iTRAQ_N1	2 85-96	6,192	566,998	2012_02_2	Nuclei_frac
Q13748,Q6 QLFHPEQL [iTRAQ_N1	2 85-96	5,67	566,998	2012_02_2	Nuclei_frac
Q13748,Q6 TIGGGDDSI [iTRAQ_N1	2 41-60	11,646	1148,55	2012_02_2	Nuclei_frac
Q13748,Q6 TIGGGDDSI [iTRAQ_N1	2 41-60	8,351	766,039	2012_02_2	Nuclei_frac
Q13748,Q6 TIGGGDDSI [iTRAQ_N1	2 41-60	7,419	766,038	2012_02_2	Nuclei_frac
Q13748,Q6 TIGGGDDSI [iTRAQ_N1	2 41-60	6,559	766,039	2012_02_2	Nuclei_frac
Q13748,Q6 TIQFVDWC [iTRAQ_N1	3 340-352	9,346	943,991	2012_02_2	Nuclei_frac
Q13748,Q6 TIQFVDWC [iTRAQ_N1	3 340-352	8,783	943,991	2012_02_2	Nuclei_frac
Q13748,Q6 TIQFVDWC [iTRAQ_N1	3 340-352	7,041	629,665	2012_02_2	Nuclei_frac
Q13748,Q6 TIQFVDWC [iTRAQ_N1	3 340-352	6,565	629,661	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	8,943	1057,101	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	7,319	1057,103	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	7,156	1057,097	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	6,887	705,069	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	6,34	705,07	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	6,148	705,069	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	5,834	705,07	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	5,274	705,069	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	5,262	705,071	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	4,88	705,069	2012_02_2	Nuclei_frac
Q13748,Q6 VGINYQPP [iTRAQ_N1	2 353-370	4,766	529,053	2012_02_2	Nuclei_frac
AAECNIVV [iTRAQ_N1	2 435-446	9,56	751,401	2012_02_2	Nuclei_frac
AAECNIVV [iTRAQ_N1	2 435-446	9,124	751,401	2012_02_2	Nuclei_frac
DFVNYLVR [iTRAQ_N1	1 64-71	5,218	585,327	2012_02_2	Nuclei_frac
DFVNYLVR [iTRAQ_N1	1 64-71	5,025	585,327	2012_02_2	Nuclei_frac
DFVNYLVR [iTRAQ_N1	1 64-71	4,998	585,327	2012_02_2	Nuclei_frac
DINTDFLL [iTRAQ_N1	1 517-528	10,875	781,459	2012_02_2	Nuclei_frac
DINTDFLL [iTRAQ_N1	1 517-528	7,405	521,308	2012_02_2	Nuclei_frac
DVVQAYPI [iTRAQ_N1	1 529-538	5,106	660,359	2012_02_2	Nuclei_frac
GISHVIVDE [iTRAQ_N1	1 504-516	7,669	549,97	2012_02_2	Nuclei_frac
GISHVIVDE [iTRAQ_N1	1 504-516	6,27	412,73	2012_02_2	Nuclei_frac
KVFDPPVP [iTRAQ_N1	3 697-708	5,29	573,36	2012_02_2	Nuclei_frac
LAQFEPSQ [iTRAQ_N1	1 315-323	6,368	610,333	2012_02_2	Nuclei_frac
LGGIGQFL [iTRAQ_N1	2 810-819	6,188	431,271	2012_02_2	Nuclei_frac
LGGIGQFL [iTRAQ_N1	2 810-819	5,902	646,403	2012_02_2	Nuclei_frac
LQISHEAA [iTRAQ_N1	2 1090-1104	5,316	595,326	2012_02_2	Nuclei_frac
QLYHLGV [iTRAQ_N1	2 249-264	5,685	689,392	2012_02_2	Nuclei_frac
TPLHEIALS [iTRAQ_N1	2 796-806	5,084	503,98	2012_02_2	Nuclei_frac
TPLHEIALS [iTRAQ_N1	2 796-806	4,849	503,979	2012_02_2	Nuclei_frac
TTQVPQFII [iTRAQ_N1	1 418-434	5,622	732,045	2012_02_2	Nuclei_frac
YPSPPFFVF [iTRAQ_N1	2 1038-1048	5,725	803,431	2012_02_2	Nuclei_frac
YQILPLHSC [iTRAQ_N1	1 681-692	8,73	536,983	2012_02_2	Nuclei_frac
AVCMLSN [iTRAQ_N1	3 374-390	9,063	1013,003	2012_02_2	Nuclei_frac
AVCMLSN [iTRAQ_N1	2 374-390	7,356	670,341	2012_02_2	Nuclei_frac
AVFVDLEF [iTRAQ_N1	1 65-79	7,488	923,51	2012_02_2	Nuclei_frac
AVFVDLEF [iTRAQ_N1	1 65-79	5,569	616,008	2012_02_2	Nuclei_frac

DVNAAIAT [iTRAQ_N1	2 327-336	6,99	652,395	2012_02_2	Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	6,865	652,396	2012_02_2	Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	6,722	652,393	2012_02_2	Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	5,966	435,265	2012_02_2	Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	5,337	435,266	2012_02_2	Nuclei_frac
EIIDLVLDR [iTRAQ_N1	1 113-121	5,372	615,365	2012_02_2	Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	9,449	1023,089	2012_02_2	Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	9,289	1023,087	2012_02_2	Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	8,234	682,394	2012_02_2	Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	8,142	682,395	2012_02_2	Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	5,276	512,047	2012_02_2	Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1 230-243	9,344	816,497	2012_02_2	Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1 230-243	9,04	544,666	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	6,968	621,667	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	6,265	621,667	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	5,619	931,997	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	4,967	621,667	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	8,844	849,994	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	6,192	566,998	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	5,67	566,998	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	8,198	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,89	624,992	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,501	936,982	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,282	936,985	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,255	624,992	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	6,972	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	6,696	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	4,962	624,99	2012_02_2	Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	11,646	1148,55	2012_02_2	Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	8,351	766,039	2012_02_2	Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	7,419	766,038	2012_02_2	Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	6,559	766,039	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	8,943	1057,101	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,319	1057,103	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,156	1057,097	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,887	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,34	705,07	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,148	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,834	705,07	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,274	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,262	705,071	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	4,88	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	4,766	529,053	2012_02_2	Nuclei_frac

Q99715_Cf ALALGALC [iTRAQ_N1	1 2385-2395	8,061	642,4	2012_02_2	Nuclei_frac
Q99715_Cf ALALGALC [iTRAQ_N1	1 2385-2395	6,21	428,602	2012_02_2	Nuclei_frac
Q99715_Cf FTKVEDIIE [iTRAQ_N1	2 497-513	10,517	782,097	2012_02_2	Nuclei_frac
Q99715_Cf IYRPVAGG [iTRAQ_N1	1 755-766	6,938	731,419	2012_02_2	Nuclei_frac
Q99715_Cf ITWTQAPC [iTRAQ_N1	1 741-749	7,176	587,329	2012_02_2	Nuclei_frac
Q99715_Cf LQPQTTYC [iTRAQ_N1	2 1055-1070	7,658	727,752	2012_02_2	Nuclei_frac
Q99715_Cf LWSGAPC [iTRAQ_N1	2 832-840	6,035	595,842	2012_02_2	Nuclei_frac
Q99715_Cf NQPGPPGP [iTRAQ_N1	1 2863-2880	5,363	585,64	2012_02_2	Nuclei_frac

Q99715_Cf RVQIALAQ [iTRAQ_Nt	1 1235-1248	7,057	573,321	2012_02_2	Nuclei_frac
Q99715_Cf SLLQAVAN [iTRAQ_Nt	2 1261-1272	5,299	535,658	2012_02_2	Nuclei_frac
Q99715_Cf TEWQLNAl [iTRAQ_Nt	1 1249-1257	6,41	433,562	2012_02_2	Nuclei_frac
Q99715_Cf TLSFFNK [iTRAQ_Nt	2 2618-2624	4,923	572,832	2012_02_2	Nuclei_frac
Q99715_Cf VEDIIEAIN [iTRAQ_Nt	1 500-513	10,017	912,484	2012_02_2	Nuclei_frac
Q99715_Cf VLTWESGN [iTRAQ_Nt	2 2414-2423	4,798	747,92	2012_02_2	Nuclei_frac
P0C7M2_Cf DYFEQYGK [iTRAQ_Nt	2 123-130	6,695	669,334	2012_02_2	Nuclei_frac
P0C7M2_Cf EDSQRPGA [iTRAQ_Nt	2 93-105	5,06	432,249	2012_02_2	Nuclei_frac
P0C7M2_Cf GFAFVTFD [iTRAQ_Nt	2 147-161	8,295	663,326	2012_02_2	Nuclei_frac
P0C7M2_Cf GFAFVTFD [iTRAQ_Nt	3 147-166	4,855	679,121	2012_02_2	Nuclei_frac
P0C7M2_Cf GFGFVTYA [iTRAQ_Nt	1 56-75	7,401	764,709	2012_02_2	Nuclei_frac
P0C7M2_Cf GFGFVTYA [iTRAQ_Nt	3 56-78	4,926	704,36	2012_02_2	Nuclei_frac
P0C7M2_Cf GFGFVTYA [iTRAQ_Nt	3 56-78	4,743	704,36	2012_02_2	Nuclei_frac
P0C7M2_Cf IEVIEIMTDF [iTRAQ_Nt	1 131-140	7,381	681,875	2012_02_2	Nuclei_frac
P0C7M2_Cf IFVGGIKED [iTRAQ_Nt	2 107-122	8,254	723,398	2012_02_2	Nuclei_frac
P0C7M2_Cf IFVGGIKED [iTRAQ_Nt	2 107-122	5,983	542,799	2012_02_2	Nuclei_frac
P0C7M2_Cf IFVGGIKED [iTRAQ_Nt	2 107-122	5,851	542,799	2012_02_2	Nuclei_frac
P0C7M2_Cf IFVGGIKED [iTRAQ_Nt	2 107-122	5,755	542,799	2012_02_2	Nuclei_frac
P0C7M2_Cf KIFVGGIK [iTRAQ_Nt	3 106-113	5,105	647,435	2012_02_2	Nuclei_frac
P0C7M2_Cf KIFVGGIK [iTRAQ_Nt	3 106-113	4,865	647,435	2012_02_2	Nuclei_frac
P0C7M2_Cf KLFIGGLSF [iTRAQ_Nt	2 15-31	7,91	1101,109	2012_02_2	Nuclei_frac
P0C7M2_Cf KLFIGGLSF [iTRAQ_Nt	2 15-31	6,898	734,414	2012_02_2	Nuclei_frac
P0C7M2_Cf KLFIGGLSF [iTRAQ_Nt	2 15-31	6,505	551,058	2012_02_2	Nuclei_frac
P0C7M2_Cf LFIGGLSFE [iTRAQ_Nt	1 16-31	8,431	643,675	2012_02_2	Nuclei_frac
P0C7M2_Cf LFIGGLSFE [iTRAQ_Nt	1 16-31	8,299	965,01	2012_02_2	Nuclei_frac
P0C7M2_Cf SHFEQWG [iTRAQ_Nt	3 32-47	6,427	709,339	2012_02_2	Nuclei_frac
P0C7M2_Cf SHFEQWG [iTRAQ_Nt	4 32-52	5,738	707,1	2012_02_2	Nuclei_frac
P06733,P06 AAVPSGA [iTRAQ_Nt	1 32-49	9,81	975,028	2012_02_2	Nuclei_frac
P06733,P06 AAVPSGA [iTRAQ_Nt	1 32-49	5,112	650,353	2012_02_2	Nuclei_frac
P06733,P06 FGANAILG [iTRAQ_Nt	3 105-119	8,36	904,526	2012_02_2	Nuclei_frac
P06733,P06 FGANAILG [iTRAQ_Nt	3 105-119	8,023	603,352	2012_02_2	Nuclei_frac
P06733,P06 FGANAILG [iTRAQ_Nt	3 105-119	6,698	603,35	2012_02_2	Nuclei_frac
P06733,P06 FTASAGIQ [iTRAQ_Nt	2 306-325	6,807	1161,142	2012_02_2	Nuclei_frac
P06733,P06 GNPTVEVL [iTRAQ_Nt	2 15-27	10,585	847,967	2012_02_2	Nuclei_frac
P06733,P06 GNPTVEVL [iTRAQ_Nt	2 15-27	6,603	565,646	2012_02_2	Nuclei_frac
P06733,P06 GNPTVEVL [iTRAQ_Nt	2 15-27	5,635	565,645	2012_02_2	Nuclei_frac
P06733,P06 IGAEVYHN [iTRAQ_Nt	2 183-192	6,104	716,413	2012_02_2	Nuclei_frac
P06733,P06 IGAEVYHN [iTRAQ_Nt	2 183-192	5,168	477,945	2012_02_2	Nuclei_frac
P06733,P06 SFIKDYPV [iTRAQ_Nt	3 281-305	6,023	855,184	2012_02_2	Nuclei_frac
P06733,P06 SGETEDTF [iTRAQ_Nt	3 372-393	7,07	881,128	2012_02_2	Nuclei_frac
P06733,P06 TIAPALVSI [iTRAQ_Nt	2 71-79	5,559	594,383	2012_02_2	Nuclei_frac
P06733,P06 TIAPALVSI [iTRAQ_Nt	3 71-80	4,763	487,324	2012_02_2	Nuclei_frac
P06733,P06 VNQIGSVT [iTRAQ_Nt	3 343-357	12,578	961,519	2012_02_2	Nuclei_frac
P06733,P06 VNQIGSVT [iTRAQ_Nt	3 343-357	7,54	641,348	2012_02_2	Nuclei_frac
P06733,P06 VNQIGSVT [iTRAQ_Nt	3 343-357	7,352	641,347	2012_02_2	Nuclei_frac
P06733,P06 VNQIGSVT [iTRAQ_Nt	3 343-357	7,282	641,347	2012_02_2	Nuclei_frac
P06733,P06 VNQIGSVT [iTRAQ_Nt	3 343-357	6,486	641,348	2012_02_2	Nuclei_frac
P06733,P06 YISPDQLAI [iTRAQ_Nt	2 269-280	7,911	857,468	2012_02_2	Nuclei_frac
P06733,P06 YISPDQLAI [iTRAQ_Nt	2 269-280	7,433	857,469	2012_02_2	Nuclei_frac
P06733,P06 YISPDQLAI [iTRAQ_Nt	2 269-280	6,672	571,982	2012_02_2	Nuclei_frac

P06733,P06733	YISPDQLAI [iTRAQ_N1	2 269-280	6,357	571,98	2012_02_2	Nuclei_frac
P06733,P06733	YISPDQLAI [iTRAQ_N1	2 269-280	5,687	571,981	2012_02_2	Nuclei_frac
P04406	GALQNIIPA [iTRAQ_N1	2 200-214	6,431	850,501	2012_02_2	Nuclei_frac
P04406	GALQNIIPA [iTRAQ_N1	2 200-214	5,569	567,333	2012_02_2	Nuclei_frac
P04406	GALQNIIPA [iTRAQ_N1	2 200-214	5,053	567,336	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	11,11	1061,565	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	9,808	708,047	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	9,272	1061,565	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	5 145-161	7,86	708,374	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	7,834	1061,565	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	5 145-161	5,609	708,374	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	5,391	531,286	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	4 145-161	5,241	531,286	2012_02_2	Nuclei_frac
P04406	IISNASCTT [iTRAQ_N1	5 145-161	5,037	708,375	2012_02_2	Nuclei_frac
P04406	LISWYDNE [iTRAQ_N1	1 309-322	9,536	954,454	2012_02_2	Nuclei_frac
P04406	LISWYDNE [iTRAQ_N1	1 309-322	8,682	636,639	2012_02_2	Nuclei_frac
P04406	LTGMAFR [iTRAQ_N1	1 227-233	5,519	470,263	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	2 66-79	9,511	879,999	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	1 66-79	8,848	879,506	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	2 66-79	8,142	879,999	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	2 66-79	8,072	587,001	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	1 66-79	5,757	586,674	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	2 66-79	5,712	587	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	8,177	777,438	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	7,774	777,438	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	7,532	777,436	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	7,149	777,438	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	7,083	777,438	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	6,362	777,436	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	5,942	777,437	2012_02_2	Nuclei_frac
P04406	LVINGNPIT [iTRAQ_N1	3 66-83	5,036	583,331	2012_02_2	Nuclei_frac
P04406	VIHDNFGIV [iTRAQ_N1	3 162-185	9,784	967,191	2012_02_2	Nuclei_frac
P04406	VIHDNFGIV [iTRAQ_N1	3 162-185	5,451	725,646	2012_02_2	Nuclei_frac
P04406	VIHDNFGIV [iTRAQ_N1	3 162-185	4,881	725,646	2012_02_2	Nuclei_frac
P04406	VIISAPSAD [iTRAQ_N1	4 118-138	5,651	634,083	2012_02_2	Nuclei_frac
P04406	VIPELNGK [iTRAQ_N1	3 219-226	5,538	579,852	2012_02_2	Nuclei_frac
P04406	VIPELNGK [iTRAQ_N1	3 219-226	5,235	579,854	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	8,372	837,953	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	8,067	837,953	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	7,787	837,952	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	7,728	837,952	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	7,402	558,971	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	7,293	558,97	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	6,472	558,971	2012_02_2	Nuclei_frac
P04406	VPTANVS\ [iTRAQ_N1	2 234-247	5,099	558,97	2012_02_2	Nuclei_frac
P04406	VVDLMAH [iTRAQ_N1	4 323-334	5,555	550,954	2012_02_2	Nuclei_frac
P35580_CH	ADFCIIHYA [iTRAQ_N1	3 573-583	6,645	528,28	2012_02_2	Nuclei_frac
P35580_CH	AGVLAHLE [iTRAQ_N1	1 772-782	7,311	684,376	2012_02_2	Nuclei_frac
P35580_CH	AGVLAHLE [iTRAQ_N1	1 772-782	6,886	456,585	2012_02_2	Nuclei_frac
P35580_CH	ALEEALAE [iTRAQ_N1	2 1491-1504	8,851	651,346	2012_02_2	Nuclei_frac

P35580_CH EDQSILCTC [iTRAQ_N1	4 170-189	8,788	853,098	2012_02_2 Nuclei_frac
P35580_CH EDQSILCTC [iTRAQ_N1	4 170-189	5,127	640,074	2012_02_2 Nuclei_frac
P35580_CH FDQLLAEE [iTRAQ_N1	2 1453-1461	4,782	690,886	2012_02_2 Nuclei_frac
P35580_CH IVFQEFR [iTRAQ_N1	1 719-725	5,624	541,81	2012_02_2 Nuclei_frac
P35580_CH KLDAQVQI [iTRAQ_N1	3 1256-1267	5,425	453,775	2012_02_2 Nuclei_frac
P35580_CH KQEEELILF [iTRAQ_N1	2 917-930	5,736	507,531	2012_02_2 Nuclei_frac
P35580_CH LDPHLVLD [iTRAQ_N1	1 690-700	5,777	731,93	2012_02_2 Nuclei_frac
P35580_CH LDPHLVLD [iTRAQ_N1	1 690-700	5,165	488,289	2012_02_2 Nuclei_frac
P35580_CH LQQELDDL [iTRAQ_N1	1 1425-1440	11,66	694,693	2012_02_2 Nuclei_frac
P35580_CH SLEAEILQL [iTRAQ_N1	1 1684-1701	7,772	730,387	2012_02_2 Nuclei_frac
P35580_CH VVSSVLQF [iTRAQ_N1	2 349-362	6,319	605,02	2012_02_2 Nuclei_frac

AVFVDLEF [iTRAQ_N1	1 65-79	7,488	923,51	2012_02_2 Nuclei_frac
AVFVDLEF [iTRAQ_N1	1 65-79	5,569	616,008	2012_02_2 Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	6,99	652,395	2012_02_2 Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	6,865	652,396	2012_02_2 Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	6,722	652,393	2012_02_2 Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	5,966	435,265	2012_02_2 Nuclei_frac
DVNAAIAT [iTRAQ_N1	2 327-336	5,337	435,266	2012_02_2 Nuclei_frac
EIIDLVLDR [iTRAQ_N1	1 113-121	5,372	615,365	2012_02_2 Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	9,449	1023,089	2012_02_2 Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	9,289	1023,087	2012_02_2 Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	8,234	682,394	2012_02_2 Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	8,142	682,395	2012_02_2 Nuclei_frac
IHFPLATY/ [iTRAQ_N1	2 265-280	5,276	512,047	2012_02_2 Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1 230-243	9,344	816,497	2012_02_2 Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1 230-243	9,04	544,666	2012_02_2 Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	6,968	621,667	2012_02_2 Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	6,265	621,667	2012_02_2 Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	5,619	931,997	2012_02_2 Nuclei_frac
NLDIERPTY [iTRAQ_N1	1 216-229	4,967	621,667	2012_02_2 Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	8,844	849,994	2012_02_2 Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	6,192	566,998	2012_02_2 Nuclei_frac
QLFHPEQL [iTRAQ_N1	2 85-96	5,67	566,998	2012_02_2 Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	11,646	1148,55	2012_02_2 Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	8,351	766,039	2012_02_2 Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	7,419	766,038	2012_02_2 Nuclei_frac
TIGGGDDSI [iTRAQ_N1	2 41-60	6,559	766,039	2012_02_2 Nuclei_frac
TIQFVDWC [iTRAQ_N1	3 340-352	9,346	943,991	2012_02_2 Nuclei_frac
TIQFVDWC [iTRAQ_N1	3 340-352	8,783	943,991	2012_02_2 Nuclei_frac
TIQFVDWC [iTRAQ_N1	3 340-352	7,041	629,665	2012_02_2 Nuclei_frac
TIQFVDWC [iTRAQ_N1	3 340-352	6,565	629,661	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	8,943	1057,101	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,319	1057,103	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,156	1057,097	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,887	705,069	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,34	705,07	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,148	705,069	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,834	705,07	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,274	705,069	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,262	705,071	2012_02_2 Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	4,88	705,069	2012_02_2 Nuclei_frac

	VGINYQPP [iTRAQ_N1	2 353-370	4,766	529,053	2012_02_2 Nuclei_frac
Q14315	APLQVAVI [iTRAQ_N1	1 1475-1494	5,3	716,085	2012_02_2 Nuclei_frac
Q14315	DLAEDAPV [iTRAQ_N1	3 27-36	5,029	535,637	2012_02_2 Nuclei_frac
Q14315	FVPQEMGF [iTRAQ_N1	3 2245-2258	6,823	615,34	2012_02_2 Nuclei_frac
Q14315	FVPQEMGF [iTRAQ_N1	3 2245-2258	6,248	615,339	2012_02_2 Nuclei_frac
Q14315	GAGTGGLC [iTRAQ_N1	3 1089-1106	7,206	654,681	2012_02_2 Nuclei_frac
Q14315	GQHVPGSF [iTRAQ_N1	2 2261-2283	4,777	648,845	2012_02_2 Nuclei_frac
Q14315	ITESDLSQL [iTRAQ_N1	1 1936-1949	10,851	839,461	2012_02_2 Nuclei_frac
Q14315	ITESDLSQL [iTRAQ_N1	1 1936-1949	10,767	839,462	2012_02_2 Nuclei_frac
Q14315	LENVSVAL [iTRAQ_N1	1 97-109	8,96	831,968	2012_02_2 Nuclei_frac
Q14315	LGSFGSITR [iTRAQ_N1	1 2198-2206	7,204	541,312	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-80	7,95	757,993	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-80	7,897	757,99	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-80	7,872	757,993	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-80	6,792	505,665	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-80	5,857	505,664	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-81	8,016	836,043	2012_02_2 Nuclei_frac
Q14315	LIALLEVLS [iTRAQ_N1	2 70-81	6,205	557,698	2012_02_2 Nuclei_frac
Q14315	TSQLNVG1 [iTRAQ_N1	2 1921-1935	6,296	613,348	2012_02_2 Nuclei_frac
Q14315	VPQLPITNI [iTRAQ_N1	1 173-183	5,318	721,917	2012_02_2 Nuclei_frac
P19338	EVFEDAAE [iTRAQ_N1	1 410-419	5,592	661,84	2012_02_2 Nuclei_frac
P19338	GFGFVDFN [iTRAQ_N1	2 610-623	7,189	925,446	2012_02_2 Nuclei_frac
P19338	GFGFVDFN [iTRAQ_N1	2 610-623	4,967	617,3	2012_02_2 Nuclei_frac
P19338	GIAYIEFK [iTRAQ_N1	2 429-436	5,947	614,865	2012_02_2 Nuclei_frac
P19338	GIAYIEFK [iTRAQ_N1	2 429-436	5,59	614,865	2012_02_2 Nuclei_frac
P19338	GIAYIEFK [iTRAQ_N1	2 429-436	5,015	614,865	2012_02_2 Nuclei_frac
P19338	GLSEDTTE [iTRAQ_N1	2 577-596	8,309	830,086	2012_02_2 Nuclei_frac
P19338	GLSEDTTE [iTRAQ_N1	2 577-596	7,78	830,083	2012_02_2 Nuclei_frac
P19338	GYAFIEFAS [iTRAQ_N1	2 523-536	10,232	941,977	2012_02_2 Nuclei_frac
P19338	IVTDRETGS [iTRAQ_N1	2 599-609	5,93	494,28	2012_02_2 Nuclei_frac
P19338	KFGYVDFE [iTRAQ_N1	3 347-361	8,915	737,053	2012_02_2 Nuclei_frac
P19338	SISLYYTGE [iTRAQ_N1	2 457-466	6,083	483,602	2012_02_2 Nuclei_frac
P19338	SISLYYTGE [iTRAQ_N1	2 457-466	5,47	483,603	2012_02_2 Nuclei_frac
P19338	TEADAEKT [iTRAQ_N1	3 437-448	7,607	915,481	2012_02_2 Nuclei_frac
P19338	TGISDVFAI [iTRAQ_N1	2 324-332	7,756	613,357	2012_02_2 Nuclei_frac
P19338	TGISDVFAI [iTRAQ_N1	2 324-332	6,097	613,359	2012_02_2 Nuclei_frac
P19338	TGISDVFAI [iTRAQ_N1	2 324-332	5,019	409,241	2012_02_2 Nuclei_frac
P19338	TGISDVFAI [iTRAQ_N1	2 324-332	4,975	409,241	2012_02_2 Nuclei_frac
P19338	TLVLSNLS [iTRAQ_N1	2 486-507	9,135	1395,239	2012_02_2 Nuclei_frac
P19338	TLVLSNLS [iTRAQ_N1	2 486-507	8,588	930,501	2012_02_2 Nuclei_frac
P19338	TLVLSNLS [iTRAQ_N1	2 486-507	6,314	698,124	2012_02_2 Nuclei_frac
Q7Z794	FASFIDKVF [iTRAQ_N1	2 189-197	5,171	457,607	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,443	588,669	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,358	882,502	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,329	882,501	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,299	882,503	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,247	882,502	2012_02_2 Nuclei_frac
Q7Z794	FLEQQNQ\ [iTRAQ_N1	2 198-209	6,225	588,67	2012_02_2 Nuclei_frac
Q7Z794	GFSSGSASV [iTRAQ_N1	1 21-34	12,134	699,86	2012_02_2 Nuclei_frac

Q7Z794	GGGFGGGS [iTRAQ_N1	1 93-122	11,376	848,38	2012_02_2 Nuclei_frac
Q7Z794	IEISELNR [iTRAQ_N1	1 394-401	5,487	559,322	2012_02_2 Nuclei_frac
Q7Z794	NLDLDSIIA [iTRAQ_N1	2 342-353	7,613	539,983	2012_02_2 Nuclei_frac
Q7Z794	NLDLDSIIA [iTRAQ_N1	2 342-353	7,459	809,473	2012_02_2 Nuclei_frac
Q7Z794	SISISVAGG [iTRAQ_N1	1 71-92	8,486	661,678	2012_02_2 Nuclei_frac
Q7Z794	SKEEAEAL [iTRAQ_N1	3 363-374	5,026	456,754	2012_02_2 Nuclei_frac
Q7Z794	TAAENDFV [iTRAQ_N1	3 276-287	5,433	590,347	2012_02_2 Nuclei_frac
Q7Z794	VDLLNQEII [iTRAQ_N1	2 303-314	8,309	875,006	2012_02_2 Nuclei_frac
Q7Z794	VDLLNQEII [iTRAQ_N1	2 303-314	5,065	583,674	2012_02_2 Nuclei_frac
Q7Z794	YLDGLTAE [iTRAQ_N1	1 239-247	5,422	591,318	2012_02_2 Nuclei_frac
P61978,P61	DLAGSIIGK [iTRAQ_N1	2 373-381	6,048	581,359	2012_02_2 Nuclei_frac
P61978,P61	DLAGSIIGK [iTRAQ_N1	2 373-381	5,35	581,359	2012_02_2 Nuclei_frac
P61978,P61	DLAGSIIGK [iTRAQ_N1	2 373-381	5,307	581,359	2012_02_2 Nuclei_frac
P61978,P61	DLAGSIIGK [iTRAQ_N1	2 373-381	5,293	581,359	2012_02_2 Nuclei_frac
P61978,P61	DLAGSIIGK [iTRAQ_N1	2 373-381	5,068	581,358	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	8,994	1103,123	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	7,582	1103,125	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	6,401	1103,128	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	5,944	735,753	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	5,272	1103,125	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	5,132	735,752	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	4,942	735,753	2012_02_2 Nuclei_frac
P61978,P61	GSYDGLGC [iTRAQ_N1	2 354-372	4,872	735,753	2012_02_2 Nuclei_frac
P61978,P61	IILDLISESP [iTRAQ_N1	2 184-195	6,324	815,008	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	9,355	959,874	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	9,089	959,874	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	8,481	959,872	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	7,522	720,156	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	5,879	720,157	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	5,803	720,156	2012_02_2 Nuclei_frac
P61978,P61	IITITGTQDC [iTRAQ_N1	2 410-432	5,209	720,155	2012_02_2 Nuclei_frac
P61978,P61	ILLQSKNAI [iTRAQ_N1	3 47-60	5,351	615,396	2012_02_2 Nuclei_frac
P61978,P61	ILSISADIET [iTRAQ_N1	2 87-102	7,434	1002,099	2012_02_2 Nuclei_frac
P61978,P61	ILSISADIET [iTRAQ_N1	2 87-102	5,819	668,401	2012_02_2 Nuclei_frac
P61978,P61	ILSISADIET [iTRAQ_N1	3 87-103	9,535	759,133	2012_02_2 Nuclei_frac
P61978,P61	ILSISADIET [iTRAQ_N1	3 87-103	6,776	569,603	2012_02_2 Nuclei_frac
P61978,P61	ILSISADIET [iTRAQ_N1	3 87-103	6,266	569,602	2012_02_2 Nuclei_frac
P61978,P61	LFQECCPH [iTRAQ_N1	3 156-167	8,043	565,256	2012_02_2 Nuclei_frac
P61978,P61	LFQECCPH [iTRAQ_N1	3 156-167	7,811	847,382	2012_02_2 Nuclei_frac
P61978,P61	LLIHQSLAC [iTRAQ_N1	2 125-139	7,596	603,052	2012_02_2 Nuclei_frac
P61978,P61	NLPLPPPPF [iTRAQ_N1	1 282-292	6,122	669,906	2012_02_2 Nuclei_frac
P61978,P61	NLPLPPPPF [iTRAQ_N1	1 282-292	6,072	669,906	2012_02_2 Nuclei_frac
P61978,P61	NLPLPPPPF [iTRAQ_N1	1 282-292	5,241	446,939	2012_02_2 Nuclei_frac
P61978,P61	VVLIGGKPI [iTRAQ_N1	2 168-177	5,079	671,427	2012_02_2 Nuclei_frac
	AILVDLEPC [iTRAQ_N1	2 63-77	8,943	888,472	2012_02_2 Nuclei_frac
	AILVDLEPC [iTRAQ_N1	1 63-77	7,599	880,476	2012_02_2 Nuclei_frac
	EIVHIQAGC [iTRAQ_N1	3 3-19	10,288	704,381	2012_02_2 Nuclei_frac
	EIVHIQAGC [iTRAQ_N1	3 3-19	10,234	704,382	2012_02_2 Nuclei_frac
	FPGQLNAC [iTRAQ_N1	1 242-251	6,113	637,854	2012_02_2 Nuclei_frac
	FPGQLNAC [iTRAQ_N1	1 242-251	5,592	637,853	2012_02_2 Nuclei_frac

FPGQLNAC [iTRAQ_N1	1 242-251	5,557	637,854	2012_02_2	Nuclei_frac
GHYTEGAE [iTRAQ_N1	1 104-121	7,555	701,7	2012_02_2	Nuclei_frac
GHYTEGAE [iTRAQ_N1	2 104-122	8,964	792,434	2012_02_2	Nuclei_frac
GHYTEGAE [iTRAQ_N1	2 104-122	6,128	594,577	2012_02_2	Nuclei_frac
ISEQFTAMI [iTRAQ_N1	2 381-390	8,625	695,352	2012_02_2	Nuclei_frac
ISEQFTAMI [iTRAQ_N1	2 381-390	7,303	695,351	2012_02_2	Nuclei_frac
LAVNMVPI [iTRAQ_N1	2 253-262	6,896	652,37	2012_02_2	Nuclei_frac
LAVNMVPI [iTRAQ_N1	1 253-262	6,297	644,371	2012_02_2	Nuclei_frac
NSSYFVEW [iTRAQ_N1	2 337-350	8,31	993,024	2012_02_2	Nuclei_frac
NSSYFVEW [iTRAQ_N1	2 337-350	7,863	993,024	2012_02_2	Nuclei_frac
NSSYFVEW [iTRAQ_N1	2 337-350	5,527	662,353	2012_02_2	Nuclei_frac
NSSYFVEW [iTRAQ_N1	2 337-350	5,515	662,352	2012_02_2	Nuclei_frac
VAVCDIPP [iTRAQ_N1	2 351-359	5,11	585,826	2012_02_2	Nuclei_frac
YLT VATVF [iTRAQ_N1	1 310-318	8,111	607,358	2012_02_2	Nuclei_frac

P60174,P6(ELASQPDV [iTRAQ_N1	3 219-247	7,259	1154,632	2012_02_2	Nuclei_frac
P60174,P6(ELASQPDV [iTRAQ_N1	3 219-247	4,96	866,233	2012_02_2	Nuclei_frac
P60174,P6(ELASQPDV [iTRAQ_N1	3 219-247	4,885	866,232	2012_02_2	Nuclei_frac
P60174,P6(FFVGGNWI [iTRAQ_N1	2 6-13	5,41	621,847	2012_02_2	Nuclei_frac
P60174,P6(FFVGGNWI [iTRAQ_N1	2 6-13	5,148	621,847	2012_02_2	Nuclei_frac
P60174,P6(HVGESDE [iTRAQ_N1	2 100-112	5,374	582,982	2012_02_2	Nuclei_frac
P60174,P6(IAVAAQNC [iTRAQ_N1	3 59-68	6,793	713,392	2012_02_2	Nuclei_frac
P60174,P6(IAVAAQNC [iTRAQ_N1	3 59-68	5,089	475,93	2012_02_2	Nuclei_frac
P60174,P6(IYGGSVTG [iTRAQ_N1	3 206-218	9,333	807,943	2012_02_2	Nuclei_frac
P60174,P6(IYGGSVTG [iTRAQ_N1	3 206-218	8,694	538,964	2012_02_2	Nuclei_frac
P60174,P6(IYGGSVTG [iTRAQ_N1	3 206-218	8,223	538,964	2012_02_2	Nuclei_frac
P60174,P6(KFFVGGNV [iTRAQ_N1	3 5-13	7,433	505,633	2012_02_2	Nuclei_frac
P60174,P6(KQSLGELIC [iTRAQ_N1	3 18-32	8,999	659,068	2012_02_2	Nuclei_frac
P60174,P6(KQSLGELIC [iTRAQ_N1	3 18-32	8,168	659,069	2012_02_2	Nuclei_frac
P60174,P6(TATPQQA([iTRAQ_N1	2 175-187	7,816	585,648	2012_02_2	Nuclei_frac
P60174,P6(VPADTEV\ [iTRAQ_N1	2 33-52	10,392	1168,588	2012_02_2	Nuclei_frac
P60174,P6(VVLAYEPV [iTRAQ_N1	2 160-174	9,168	946,057	2012_02_2	Nuclei_frac
P60174,P6(VVLAYEPV [iTRAQ_N1	2 160-174	9,161	946,053	2012_02_2	Nuclei_frac
P60174,P6(VVLAYEPV [iTRAQ_N1	2 160-174	6,541	631,037	2012_02_2	Nuclei_frac
P60174,P6(VVLAYEPV [iTRAQ_N1	2 160-174	5,696	631,037	2012_02_2	Nuclei_frac
P60174,P6(VVLAYEPV [iTRAQ_N1	2 160-174	5,022	631,037	2012_02_2	Nuclei_frac

IQLVEEELC [iTRAQ_N1	1 92-101	7,322	463,257	2012_02_2	Nuclei_frac
IQLVEEELC [iTRAQ_N1	1 92-101	6,486	694,383	2012_02_2	Nuclei_frac
IQLVEEELC [iTRAQ_N1	1 92-105	8,6	624,67	2012_02_2	Nuclei_frac
IQLVEEELC [iTRAQ_N1	1 92-105	6,843	936,504	2012_02_2	Nuclei_frac
KLVIIEGDL [iTRAQ_N1	2 168-178	6,838	786,985	2012_02_2	Nuclei_frac
KLVIIEGDL [iTRAQ_N1	2 168-178	6,544	786,986	2012_02_2	Nuclei_frac
KLVIIEGDL [iTRAQ_N1	2 168-178	5,633	524,993	2012_02_2	Nuclei_frac
KYEEVAR [iTRAQ_N1	2 161-167	5,353	591,841	2012_02_2	Nuclei_frac
LATALQK [iTRAQ_N1	2 106-112	4,993	516,837	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,675	938,563	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	6,419	938,564	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,98	626,045	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,915	938,562	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,474	626,044	2012_02_2	Nuclei_frac
LATALQKL [iTRAQ_N1	3 106-118	5,117	626,043	2012_02_2	Nuclei_frac

	LATALQKL [iTRAQ_N1	3 106-118	5,034	626,045	2012_02_2 Nuclei_frac
	LATALQKL [iTRAQ_N1	3 106-118	4,917	626,044	2012_02_2 Nuclei_frac
	LATALQKL [iTRAQ_N1	3 106-118	4,868	626,044	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	9,383	882,949	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	9,234	882,947	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	9,216	882,948	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	8,423	441,977	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	7,313	441,977	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	7,014	441,978	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	5,942	588,967	2012_02_2 Nuclei_frac
	LEEAEKAA [iTRAQ_N1	2 113-125	5,34	588,969	2012_02_2 Nuclei_frac
	LVIIEGDLEI [iTRAQ_N1	1 169-178	6,17	650,883	2012_02_2 Nuclei_frac
	LVIIEGDLEI [iTRAQ_N1	1 169-182	6,315	606,004	2012_02_2 Nuclei_frac
	NVTNNLK [iTRAQ_N1	2 199-205	4,919	545,829	2012_02_2 Nuclei_frac
	RIQLVEEEL [iTRAQ_N1	1 91-101	9,479	772,433	2012_02_2 Nuclei_frac
	RIQLVEEEL [iTRAQ_N1	1 91-101	6,925	515,291	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	8,562	940,042	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	6,441	627,029	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	5,793	470,524	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	5,709	470,524	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	5,299	470,524	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	5,056	627,029	2012_02_2 Nuclei_frac
P08758	DLLDDLKS [iTRAQ_N1	3 63-75	4,883	470,524	2012_02_2 Nuclei_frac
P08758	ETSGNLEQ [iTRAQ_N1	2 227-241	8,606	951,564	2012_02_2 Nuclei_frac
P08758	ETSGNLEQ [iTRAQ_N1	2 227-241	4,752	476,285	2012_02_2 Nuclei_frac
P08758	FITIFGTR [iTRAQ_N1	1 193-200	7,147	549,825	2012_02_2 Nuclei_frac
P08758	GLGTDEES [iTRAQ_N1	1 29-44	8,908	617,007	2012_02_2 Nuclei_frac
P08758	GLGTDEES [iTRAQ_N1	1 29-44	7,766	925,011	2012_02_2 Nuclei_frac
P08758	GTVTDFPG [iTRAQ_N1	1 6-17	6,729	742,861	2012_02_2 Nuclei_frac
P08758	GTVTDFPG [iTRAQ_N1	1 6-17	5,123	495,576	2012_02_2 Nuclei_frac
P08758	KNFATSLY [iTRAQ_N1	4 289-300	6,248	617,684	2012_02_2 Nuclei_frac
P08758	LYDAYELK [iTRAQ_N1	2 89-96	4,722	434,911	2012_02_2 Nuclei_frac
P08758	QEISAAFK [iTRAQ_N1	2 50-57	4,997	591,343	2012_02_2 Nuclei_frac
P08758	QEISAAFK [iTRAQ_N1	2 50-57	4,813	591,343	2012_02_2 Nuclei_frac
P08758	SEIDLFNIR [iTRAQ_N1	1 276-284	5,939	625,846	2012_02_2 Nuclei_frac
P08758	SIPAYLAET [iTRAQ_N1	3 245-259	6,602	680,033	2012_02_2 Nuclei_frac
P08758	VLTEIIASR [iTRAQ_N1	1 108-116	7,456	573,355	2012_02_2 Nuclei_frac
P08758	VLTEIIASR [iTRAQ_N1	1 108-116	6,716	573,355	2012_02_2 Nuclei_frac
P08758	VLTEIIASR [iTRAQ_N1	1 108-116	5,611	573,353	2012_02_2 Nuclei_frac
P08758	VLTEIIASR [iTRAQ_N1	1 108-116	5,496	573,356	2012_02_2 Nuclei_frac
P08123_CH	EGPVGLPG [iTRAQ_N1	1 465-486	5,621	728,739	2012_02_2 Nuclei_frac
P08123_CH	GETGPSGP [iTRAQ_N1	1 979-996	6,508	569,637	2012_02_2 Nuclei_frac
P08123_CH	GIPGPVGA [iTRAQ_N1	1 328-342	8,699	698,394	2012_02_2 Nuclei_frac
P08123_CH	GIPGPVGA [iTRAQ_N1	1 328-342	8,56	465,932	2012_02_2 Nuclei_frac
P08123_CH	GLHGEFGL [iTRAQ_N1	1 574-588	6,589	535,959	2012_02_2 Nuclei_frac
P08123_CH	GLPGSPGN [iTRAQ_N1	2 451-464	5,658	503,958	2012_02_2 Nuclei_frac
P08123_CH	GLPGSPGN [iTRAQ_N1	2 451-464	5,262	503,958	2012_02_2 Nuclei_frac
P08123_CH	GPPGESGA [iTRAQ_N1	1 592-609	6,592	570,294	2012_02_2 Nuclei_frac
P08123_CH	GYPGNIGP [iTRAQ_N1	2 949-974	9,781	847,461	2012_02_2 Nuclei_frac
P08123_CH	SLNNQIETI [iTRAQ_N1	1 1141-1156	7,921	958,516	2012_02_2 Nuclei_frac

P08123_CH TGPPGPSG [iTRAQ_N1	2	795-815	8,683	690,711	2012_02_2	Nuclei_frac
P08123_CH VYCDFSTG [iTRAQ_N1	3	1193-1205	8,794	876,393	2012_02_2	Nuclei_frac
P25705 AVDSLVPIH [iTRAQ_N1	1	152-161	6,61	585,853	2012_02_2	Nuclei_frac
P25705 AVDSLVPIH [iTRAQ_N1	1	152-161	5,861	585,853	2012_02_2	Nuclei_frac
P25705 AVDSLVPIH [iTRAQ_N1	1	152-161	5,764	585,853	2012_02_2	Nuclei_frac
P25705 AVDSLVPIH [iTRAQ_N1	1	152-161	5,691	585,853	2012_02_2	Nuclei_frac
P25705 AVDSLVPIH [iTRAQ_N1	1	152-161	5,071	585,852	2012_02_2	Nuclei_frac
P25705 EAYPGDVF [iTRAQ_N1	1	292-304	6,899	566,619	2012_02_2	Nuclei_frac
P25705 FENAFLSH [iTRAQ_N1	1	464-484	9,765	837,794	2012_02_2	Nuclei_frac
P25705 FENAFLSH [iTRAQ_N1	1	464-484	6,026	628,595	2012_02_2	Nuclei_frac
P25705 GYLDKLEP [iTRAQ_N1	3	451-460	5,296	527,98	2012_02_2	Nuclei_frac
P25705 HALIYDDL [iTRAQ_N1	2	263-273	5,423	525,973	2012_02_2	Nuclei_frac
P25705 TGAIVDVP [iTRAQ_N1	1	91-106	8,375	885	2012_02_2	Nuclei_frac
P25705 TGTAEMSE [iTRAQ_N1	1	3-15	10,533	784,391	2012_02_2	Nuclei_frac
P25705 TSIAIDTIIN [iTRAQ_N1	2	176-187	7,865	802,979	2012_02_2	Nuclei_frac
P25705 TSIAIDTIIN [iTRAQ_N1	2	176-187	6,368	535,653	2012_02_2	Nuclei_frac
P25705 TSIAIDTIIN [iTRAQ_N1	2	176-187	6,094	535,655	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	7,55	572,846	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	7,317	572,846	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	6,474	572,846	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	6,002	572,847	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	5,8	572,846	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	5,432	572,846	2012_02_2	Nuclei_frac
P25705 VLSIGDGIA [iTRAQ_N1	1	31-40	5,269	572,846	2012_02_2	Nuclei_frac
P25705 VVDALGN [iTRAQ_N1	2	107-118	6,345	487,284	2012_02_2	Nuclei_frac
P30101 EATNPPVIK [iTRAQ_N1	3	459-472	7,577	671,386	2012_02_2	Nuclei_frac
P30101 EATNPPVIK [iTRAQ_N1	3	459-472	7,101	671,385	2012_02_2	Nuclei_frac
P30101 ELSDFISYL [iTRAQ_N1	1	448-458	8,908	757,903	2012_02_2	Nuclei_frac
P30101 ELSDFISYL [iTRAQ_N1	1	448-458	8,433	505,604	2012_02_2	Nuclei_frac
P30101 FISDKDASI [iTRAQ_N1	3	124-149	7,748	843,424	2012_02_2	Nuclei_frac
P30101 FLQDYFDG [iTRAQ_N1	2	328-338	6,226	549,958	2012_02_2	Nuclei_frac
P30101 FLQDYFDG [iTRAQ_N1	2	328-338	5,943	824,434	2012_02_2	Nuclei_frac
P30101 FLQDYFDG [iTRAQ_N1	2	328-339	6,72	601,993	2012_02_2	Nuclei_frac
P30101 FLQDYFDG [iTRAQ_N1	2	328-339	6,635	601,992	2012_02_2	Nuclei_frac
P30101 LAPEYEAA [iTRAQ_N1	1	39-49	8,235	668,356	2012_02_2	Nuclei_frac
P30101 LNFAVASF [iTRAQ_N1	1	273-280	5,58	511,299	2012_02_2	Nuclei_frac
P30101 LSKDPNIVI [iTRAQ_N1	3	399-409	4,896	544,014	2012_02_2	Nuclei_frac
P30101 TADGIVSH [iTRAQ_N1	2	96-105	5,348	443,598	2012_02_2	Nuclei_frac
P30101 TADGIVSH [iTRAQ_N1	2	96-105	5,108	443,598	2012_02_2	Nuclei_frac
P30101 TADGIVSH [iTRAQ_N1	3	96-106	6,354	534,33	2012_02_2	Nuclei_frac
P30101 YGVSGYPT [iTRAQ_N1	2	71-80	6,951	686,891	2012_02_2	Nuclei_frac
P30101 YGVSGYPT [iTRAQ_N1	2	71-80	6,454	686,891	2012_02_2	Nuclei_frac
P14625 DISTNYYA [iTRAQ_N1	3	651-662	7,703	617,339	2012_02_2	Nuclei_frac
P14625 ELISNASD [iTRAQ_N1	2	82-93	7,683	782,428	2012_02_2	Nuclei_frac
P14625 ELISNASD [iTRAQ_N1	2	82-93	7,008	521,953	2012_02_2	Nuclei_frac
P14625 ELISNASD [iTRAQ_N1	2	82-95	11,023	611,684	2012_02_2	Nuclei_frac
P14625 ELISNASD [iTRAQ_N1	2	82-95	9,971	611,683	2012_02_2	Nuclei_frac
P14625 ELISNASD [iTRAQ_N1	2	82-95	9,537	611,683	2012_02_2	Nuclei_frac
P14625 FAFQAEVN [iTRAQ_N1	1	55-63	5,968	613,325	2012_02_2	Nuclei_frac

P14625	FQSSHPT [iTRAQ_N1	1 491-509	8,095	802,061	2012_02_2	Nuclei_frac
P14625	IYFMAGSSI [iTRAQ_N1	2 517-525	5,845	596,302	2012_02_2	Nuclei_frac
P14625	IYFMAGSSI [iTRAQ_N1	1 517-525	5,255	588,304	2012_02_2	Nuclei_frac
P14625	LIINSLYK [iTRAQ_N1	2 67-74	5,501	626,4	2012_02_2	Nuclei_frac
P14625	NLLHVTDT [iTRAQ_N1	2 122-135	6,257	558,629	2012_02_2	Nuclei_frac
P14625	SGYLLPDT [iTRAQ_N1	2 704-712	5,575	641,368	2012_02_2	Nuclei_frac
P14625	SILFVPTSA [iTRAQ_N1	1 364-374	9,638	666,394	2012_02_2	Nuclei_frac
Q00341	ANSFTVSS [iTRAQ_N1	1 360-376	11,633	658,682	2012_02_2	Nuclei_frac
Q00341	ASVITQVF [iTRAQ_N1	1 72-86	7,728	623,685	2012_02_2	Nuclei_frac
Q00341	EALEALVP [iTRAQ_N1	1 964-984	7,644	840,799	2012_02_2	Nuclei_frac
Q00341	ELLELASR [iTRAQ_N1	1 495-502	5,907	537,817	2012_02_2	Nuclei_frac
Q00341	INIPPSVN [iTRAQ_N1	1 255-264	5,095	625,871	2012_02_2	Nuclei_frac
Q00341	IQIPRPDDP [iTRAQ_N1	2 183-196	6,031	637,029	2012_02_2	Nuclei_frac
Q00341	IQIPRPDDP [iTRAQ_N1	2 183-196	5,474	637,03	2012_02_2	Nuclei_frac
Q00341	LQTQASA [iTRAQ_N1	2 146-158	5,54	539,325	2012_02_2	Nuclei_frac
Q00341	LSVTVDPK [iTRAQ_N1	2 1054-1061	5,689	573,852	2012_02_2	Nuclei_frac
Q00341	LSVTVDPK [iTRAQ_N1	2 1054-1061	5,438	573,852	2012_02_2	Nuclei_frac
Q00341	LSVTVDPK [iTRAQ_N1	2 1054-1061	5,382	573,852	2012_02_2	Nuclei_frac
Q00341	RCDIIISGR [iTRAQ_N1	2 946-955	5,502	449,595	2012_02_2	Nuclei_frac
Q00341	TEIVFTGEK [iTRAQ_N1	2 265-282	6,023	760,095	2012_02_2	Nuclei_frac
Q00341	VIFPAAEDI [iTRAQ_N1	3 760-778	6,268	840,157	2012_02_2	Nuclei_frac
P12956	DSLIFLVD [iTRAQ_N1	2 35-45	5,658	499,292	2012_02_2	Nuclei_frac
P12956	DTGIFLDL [iTRAQ_N1	3 194-205	6,933	569,652	2012_02_2	Nuclei_frac
P12956	DTGIFLDL [iTRAQ_N1	3 194-205	6,268	569,652	2012_02_2	Nuclei_frac
P12956	IQVTPPGF [iTRAQ_N1	2 424-442	5,149	807,457	2012_02_2	Nuclei_frac
P12956	IQVTPPGF [iTRAQ_N1	2 424-443	9,487	859,491	2012_02_2	Nuclei_frac
P12956	IQVTPPGF [iTRAQ_N1	2 424-443	8,371	859,49	2012_02_2	Nuclei_frac
P12956	KQELLEAL [iTRAQ_N1	3 595-604	5,201	535,671	2012_02_2	Nuclei_frac
P12956	KQELLEAL [iTRAQ_N1	3 595-604	4,859	535,671	2012_02_2	Nuclei_frac
P12956	LGSLVDEF [iTRAQ_N1	2 517-525	6,516	648,379	2012_02_2	Nuclei_frac
P12956	LGSLVDEF [iTRAQ_N1	2 517-525	6,398	432,587	2012_02_2	Nuclei_frac
P12956	NIYVLQEL [iTRAQ_N1	2 100-113	7,817	621,354	2012_02_2	Nuclei_frac
P12956	SDSFENPV [iTRAQ_N1	1 474-487	9,182	616,645	2012_02_2	Nuclei_frac
P12956	TFNTSTGG [iTRAQ_N1	2 301-316	5,929	647,359	2012_02_2	Nuclei_frac
P12956	TFNTSTGG [iTRAQ_N1	2 301-317	10,043	699,391	2012_02_2	Nuclei_frac
P12956	TFNTSTGG [iTRAQ_N1	2 301-317	8,232	699,392	2012_02_2	Nuclei_frac
P12956	TFNTSTGG [iTRAQ_N1	2 301-317	7,278	699,392	2012_02_2	Nuclei_frac
Q7KZF4	DIQNTQCL [iTRAQ_N1	4 819-847	6,423	896,707	2012_02_2	Nuclei_frac
Q7KZF4	DYVAPTAN [iTRAQ_N1	2 327-338	6,979	811,936	2012_02_2	Nuclei_frac
Q7KZF4	DYVAPTAN [iTRAQ_N1	2 327-338	5,678	541,626	2012_02_2	Nuclei_frac
Q7KZF4	FVDGEWYF [iTRAQ_N1	1 739-746	4,993	608,299	2012_02_2	Nuclei_frac
Q7KZF4	LGTLSPAF [iTRAQ_N1	1 776-786	10,112	647,368	2012_02_2	Nuclei_frac
Q7KZF4	LGTLSPAF [iTRAQ_N1	1 776-786	6,253	431,914	2012_02_2	Nuclei_frac
Q7KZF4	NDIASHPPI [iTRAQ_N1	1 715-730	8,633	618,648	2012_02_2	Nuclei_frac
Q7KZF4	QFLPFLQR [iTRAQ_N1	1 515-522	5,825	596,852	2012_02_2	Nuclei_frac
Q7KZF4	QINLSNIR [iTRAQ_N1	1 47-54	6,769	551,329	2012_02_2	Nuclei_frac
Q7KZF4	QINLSNIR [iTRAQ_N1	1 47-54	6,606	551,329	2012_02_2	Nuclei_frac
Q7KZF4	QINLSNIR [iTRAQ_N1	1 47-54	5,86	551,328	2012_02_2	Nuclei_frac
Q7KZF4	SLLSAEEA [iTRAQ_N1	2 641-650	7,956	653,879	2012_02_2	Nuclei_frac

Q7KZF4	SLLSAEEA [iTRAQ_N1	2	641-650	5,215	436,254	2012_02_2	Nuclei_frac
Q7KZF4	TCATVTIG [iTRAQ_N1	3	438-456	7,374	736,086	2012_02_2	Nuclei_frac
Q7KZF4	VITEYLNA [iTRAQ_N1	2	873-885	6,602	585,324	2012_02_2	Nuclei_frac
Q05682	IS(EAEGAPQV [iTRAQ_N1	2	262-274	6,542	543,967	2012_02_2	Nuclei_frac
Q05682	IS(EFDPTITD/ [iTRAQ_N1	1	114-130	8,837	683,696	2012_02_2	Nuclei_frac
Q05682	IS(EFDPTITD/ [iTRAQ_N1	1	114-130	7,551	683,696	2012_02_2	Nuclei_frac
Q05682	IS(GNVFSSPT [iTRAQ_N1	2	458-472	10,808	868,465	2012_02_2	Nuclei_frac
Q05682	IS(GNVFSSPT [iTRAQ_N1	2	458-472	10,502	579,312	2012_02_2	Nuclei_frac
Q05682	IS(GNVFSSPT [iTRAQ_N1	2	458-472	6,961	579,312	2012_02_2	Nuclei_frac
Q05682	IS(KVLEEEEQ [iTRAQ_N1	2	316-324	7,035	483,272	2012_02_2	Nuclei_frac
Q05682	IS(KVLEEEEQ [iTRAQ_N1	2	316-324	5,683	483,273	2012_02_2	Nuclei_frac
Q05682	IS(LEQYTSAL [iTRAQ_N1	2	418-429	9,168	814,445	2012_02_2	Nuclei_frac
Q05682	IS(LEQYTSAL [iTRAQ_N1	2	418-429	8,442	543,299	2012_02_2	Nuclei_frac
Q05682	IS(LEQYTSAL [iTRAQ_N1	2	418-429	7,955	543,299	2012_02_2	Nuclei_frac
Q05682	IS(LEQYTSAL [iTRAQ_N1	2	418-429	6,985	543,3	2012_02_2	Nuclei_frac
Q05682	IS(QERYEIEET [iTRAQ_N1	2	151-164	7,556	681,688	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	2	297-308	7,186	844,968	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	2	297-308	6,546	844,97	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	2	297-308	4,91	563,65	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	3	297-309	8,024	654,382	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	3	297-309	7,961	654,383	2012_02_2	Nuclei_frac
Q05682	IS(QQEAAL [iTRAQ_N1	3	297-309	7,498	654,382	2012_02_2	Nuclei_frac
Q05682	IS(YEIEETETV [iTRAQ_N1	2	154-164	6,3	815,429	2012_02_2	Nuclei_frac
Q05682	IS(YEIEETETV [iTRAQ_N1	2	154-164	6,293	815,429	2012_02_2	Nuclei_frac
Q05682	IS(YEIEETETV [iTRAQ_N1	2	154-164	5,434	543,955	2012_02_2	Nuclei_frac
P53621	ISCISPLQFR [iTRAQ_N1	1	1218-1224	5,849	502,804	2012_02_2	Nuclei_frac
P53621	ISCKLDALCNII [iTRAQ_N1	3	517-529	5,672	471,765	2012_02_2	Nuclei_frac
P53621	ISCLLDHQVG [iTRAQ_N1	2	942-956	8,042	668,055	2012_02_2	Nuclei_frac
P53621	ISCLVGQSIIAY [iTRAQ_N1	2	620-631	7,198	810,999	2012_02_2	Nuclei_frac
P53621	ISCLVGQSIIAY [iTRAQ_N1	2	620-631	6,687	541,003	2012_02_2	Nuclei_frac
P53621	ISCLVGQSIIAY [iTRAQ_N1	2	620-631	5,837	541,002	2012_02_2	Nuclei_frac
P53621	ISCLVGQSIIAY [iTRAQ_N1	2	620-631	5,133	541,002	2012_02_2	Nuclei_frac
P53621	ISCSILLSVPLL [iTRAQ_N1	2	1031-1044	6,754	600,049	2012_02_2	Nuclei_frac
P53621	ISCSILLSVPLL [iTRAQ_N1	2	1031-1044	6,207	600,048	2012_02_2	Nuclei_frac
P53621	ISCTALNLFKK [iTRAQ_N1	2	1107-1114	5,215	621,382	2012_02_2	Nuclei_frac
P53621	ISCTLDLPIYV [iTRAQ_N1	1	563-572	6,757	667,896	2012_02_2	Nuclei_frac
P53621	ISCTLDLPIYV [iTRAQ_N1	1	563-572	5,631	667,896	2012_02_2	Nuclei_frac
P53621	ISCVQVPNCDI [iTRAQ_N1	2	448-467	6,651	808,424	2012_02_2	Nuclei_frac
P53621	ISCVTTVTEIGI [iTRAQ_N1	2	1203-1217	5,917	630,384	2012_02_2	Nuclei_frac
P53621	ISCVWDISGLR [iTRAQ_N1	1	161-168	6,218	545,315	2012_02_2	Nuclei_frac
P53621	ISCVAVTTGDF [iTRAQ_N1	1	551-562	6,449	482,932	2012_02_2	Nuclei_frac
Q99623	AQVSLIR [iTRAQ_N1	1	157-164	5,228	522,339	2012_02_2	Nuclei_frac
Q99623	ESVFTVEG [iTRAQ_N1	1	37-47	5,812	454,571	2012_02_2	Nuclei_frac
Q99623	FNASQLIT [iTRAQ_N1	1	147-156	7,712	661,372	2012_02_2	Nuclei_frac
Q99623	FNASQLIT [iTRAQ_N1	1	147-156	7,085	441,249	2012_02_2	Nuclei_frac
Q99623	FNASQLIT [iTRAQ_N1	1	147-156	7,057	441,25	2012_02_2	Nuclei_frac
Q99623	IGGVQQDT [iTRAQ_N1	1	54-70	10,194	666,704	2012_02_2	Nuclei_frac
Q99623	IPWFQYPII [iTRAQ_N1	1	71-83	7,742	934,518	2012_02_2	Nuclei_frac
Q99623	IPWFQYPII [iTRAQ_N1	1	71-83	7,684	934,517	2012_02_2	Nuclei_frac

Q99623	IPWFQYPII\ [iTRAQ_N1	1 71-83	6,092	623,346	2012_02_2	Nuclei_frac
Q99623	IPWFQYPII\ [iTRAQ_N1	1 71-83	5,499	623,347	2012_02_2	Nuclei_frac
Q99623	IVQAEGEA [iTRAQ_N1	2 224-235	7,49	752,418	2012_02_2	Nuclei_frac
Q99623	IVQAEGEA [iTRAQ_N1	2 224-235	7,063	501,948	2012_02_2	Nuclei_frac
Q99623	IVQAEGEA [iTRAQ_N1	2 224-235	6,526	501,947	2012_02_2	Nuclei_frac
Q99623	IYLTADNL\ [iTRAQ_N1	1 270-288	8,052	1185,127	2012_02_2	Nuclei_frac
Q99623	LGLDYEER [iTRAQ_N1	1 123-130	6,467	569,798	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	6,313	500,321	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	6,271	500,321	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	5,609	500,321	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	5,544	500,322	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	5,457	500,321	2012_02_2	Nuclei_frac
Q99623	VLPSIVNE\ [iTRAQ_N1	2 131-141	4,774	749,978	2012_02_2	Nuclei_frac
Q99623	VLSRPNAQ [iTRAQ_N1	2 107-122	5,542	683,694	2012_02_2	Nuclei_frac
P13639	DLEEDHAC [iTRAQ_N1	3 559-570	5,885	576,634	2012_02_2	Nuclei_frac
P13639	DLEEDHAC [iTRAQ_N1	4 559-571	5,149	500,777	2012_02_2	Nuclei_frac
P13639	DSVVAGFC [iTRAQ_N1	2 676-687	5,761	532,96	2012_02_2	Nuclei_frac
P13639	EGIPALDNF [iTRAQ_N1	2 845-857	7,954	866,993	2012_02_2	Nuclei_frac
P13639	EGIPALDNF [iTRAQ_N1	2 845-857	7,343	866,99	2012_02_2	Nuclei_frac
P13639	EGIPALDNF [iTRAQ_N1	2 845-857	4,805	578,329	2012_02_2	Nuclei_frac
P13639	STLTDSLVL [iTRAQ_N1	3 32-41	7,984	706,391	2012_02_2	Nuclei_frac
P13639	STLTDSLVL [iTRAQ_N1	3 32-41	6,238	471,262	2012_02_2	Nuclei_frac
P13639	STLTDSLVL [iTRAQ_N1	3 32-41	5,195	471,263	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	6,224	892,012	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	5,897	595,012	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	5,778	595,008	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	5,562	892,009	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	5,443	892,009	2012_02_2	Nuclei_frac
P13639	TFCQLILDF [iTRAQ_N1	3 287-298	5,06	595,009	2012_02_2	Nuclei_frac
P13639	VFDAIMNF [iTRAQ_N1	3 299-307	5,46	694,879	2012_02_2	Nuclei_frac
P13639	VFSGLVST [iTRAQ_N1	2 415-425	6,453	698,428	2012_02_2	Nuclei_frac
P13639	VFSGLVST [iTRAQ_N1	2 415-425	4,772	465,953	2012_02_2	Nuclei_frac
P13639	VNFTVDQI [iTRAQ_N1	1 1-9	7,227	618,348	2012_02_2	Nuclei_frac
P13639	VNFTVDQI [iTRAQ_N1	1 1-9	5,133	618,348	2012_02_2	Nuclei_frac
P13639	YLAEKYEW [iTRAQ_N1	2 633-646	6,363	677,688	2012_02_2	Nuclei_frac
P13639	YLAEKYEW [iTRAQ_N1	2 633-646	6,088	677,687	2012_02_2	Nuclei_frac
P13639	YVEPIEDVF [iTRAQ_N1	3 456-480	5,849	1016,562	2012_02_2	Nuclei_frac
P13639	YVEPIEDVF [iTRAQ_N1	3 456-480	4,831	1016,565	2012_02_2	Nuclei_frac
P26641	ALIAAQYS [iTRAQ_N1	1 17-29	7,089	497,951	2012_02_2	Nuclei_frac
P26641	EYFSWEGA [iTRAQ_N1	2 414-427	9,695	658,334	2012_02_2	Nuclei_frac
P26641	EYFSWEGA [iTRAQ_N1	2 414-427	5,225	494,003	2012_02_2	Nuclei_frac
P26641	KLDPGSEE [iTRAQ_N1	2 400-413	7,822	931,019	2012_02_2	Nuclei_frac
P26641	KLDPGSEE [iTRAQ_N1	2 400-413	7,319	621,015	2012_02_2	Nuclei_frac
P26641	LDPGSEET [iTRAQ_N1	1 401-413	6,201	794,916	2012_02_2	Nuclei_frac
P26641	QVLEPSFR [iTRAQ_N1	1 173-180	5,898	560,319	2012_02_2	Nuclei_frac
P26641	RILGLLDA\ [iTRAQ_N1	2 136-146	7,635	521,668	2012_02_2	Nuclei_frac
P26641	RILGLLDA\ [iTRAQ_N1	2 136-146	7,007	781,999	2012_02_2	Nuclei_frac
P26641	STFVLDEF [iTRAQ_N1	2 285-294	9,068	510,625	2012_02_2	Nuclei_frac
P26641	STFVLDEF [iTRAQ_N1	2 285-294	8,484	510,624	2012_02_2	Nuclei_frac
P26641	STFVLDEF [iTRAQ_N1	2 285-294	6,904	765,434	2012_02_2	Nuclei_frac

P26641	STFVLDEF [iTRAQ_N1	2 285-294	5,446	510,626	2012_02_2	Nuclei_frac
P26641	VLSAPPHF [iTRAQ_N1	1 30-44	7,629	617,996	2012_02_2	Nuclei_frac
P26641	VLSAPPHF [iTRAQ_N1	1 30-44	6,913	463,748	2012_02_2	Nuclei_frac
P26641	WFLTCINQ [iTRAQ_N1	2 189-200	8,972	585,304	2012_02_2	Nuclei_frac
P26641	WFLTCINQ [iTRAQ_N1	2 189-200	8,802	877,452	2012_02_2	Nuclei_frac
P04075	ADDGRPFP [iTRAQ_N1	2 87-98	6,244	544,31	2012_02_2	Nuclei_frac
P04075	ADDGRPFP [iTRAQ_N1	2 87-98	6,093	815,961	2012_02_2	Nuclei_frac
P04075	ADDGRPFP [iTRAQ_N1	2 87-98	5,461	544,311	2012_02_2	Nuclei_frac
P04075	ADDGRPFP [iTRAQ_N1	2 87-98	4,76	544,31	2012_02_2	Nuclei_frac
P04075	ALANSLAC [iTRAQ_N1	3 331-341	5,535	474,266	2012_02_2	Nuclei_frac
P04075	ALANSLAC [iTRAQ_N1	3 331-341	5,19	474,266	2012_02_2	Nuclei_frac
P04075	FSHEEIAM [iTRAQ_N1	2 243-257	9,125	612,654	2012_02_2	Nuclei_frac
P04075	GILAADES [iTRAQ_N1	2 28-41	9,883	810,958	2012_02_2	Nuclei_frac
P04075	GILAADES [iTRAQ_N1	2 28-42	7,867	593,008	2012_02_2	Nuclei_frac
P04075	GILAADES [iTRAQ_N1	2 28-42	7,178	593,008	2012_02_2	Nuclei_frac
P04075	IGEHTPSAI [iTRAQ_N1	2 153-172	8,272	756,406	2012_02_2	Nuclei_frac
P04075	PYQYPALT [iTRAQ_N1	2 1-12	5,316	574,98	2012_02_2	Nuclei_frac
P04075	VNPCIGGV [iTRAQ_N1	3 69-86	10,025	792,773	2012_02_2	Nuclei_frac
P04075	YTPSGQAC [iTRAQ_N1	1 342-363	7,7	791,382	2012_02_2	Nuclei_frac
P04075	YTPSGQAC [iTRAQ_N1	1 342-363	7,314	1186,569	2012_02_2	Nuclei_frac
P04075	YTPSGQAC [iTRAQ_N1	1 342-363	6,777	791,382	2012_02_2	Nuclei_frac
P11142,P11	ARFEELNA [iTRAQ_N1	1 299-310	8,104	812,934	2012_02_2	Nuclei_frac
P11142,P11	ARFEELNA [iTRAQ_N1	1 299-310	6,843	542,291	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	9,439	672,392	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	8,89	672,393	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	8,524	672,393	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	8,523	448,598	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	8,469	672,391	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	8,097	448,598	2012_02_2	Nuclei_frac
P11142,P11	DAGTIAGL [iTRAQ_N1	1 159-170	7,699	448,597	2012_02_2	Nuclei_frac
P11142,P11	EIAEAYLG [iTRAQ_N1	2 128-136	5,391	641,371	2012_02_2	Nuclei_frac
P11142,P11	LDKSQIHD [iTRAQ_N1	2 325-341	4,825	709,412	2012_02_2	Nuclei_frac
P11142,P11	LLQDFENG [iTRAQ_N1	2 348-356	6,356	685,392	2012_02_2	Nuclei_frac
P11142,P11	LLQDFENG [iTRAQ_N1	2 348-356	4,962	457,264	2012_02_2	Nuclei_frac
P11142,P11	NQVAMNP [iTRAQ_N1	3 56-70	5,751	652,004	2012_02_2	Nuclei_frac
P11142,P11	SQIHDI VLV [iTRAQ_N1	1 328-341	9,489	813,459	2012_02_2	Nuclei_frac
P11142,P11	SQIHDI VLV [iTRAQ_N1	1 328-341	8,247	813,459	2012_02_2	Nuclei_frac
P11142,P11	SQIHDI VLV [iTRAQ_N1	1 328-341	7,239	542,642	2012_02_2	Nuclei_frac
P11142,P11	TTPSYVAF [iTRAQ_N1	1 36-48	8,276	816,405	2012_02_2	Nuclei_frac
P11142,P11	TTPSYVAF [iTRAQ_N1	1 36-48	5,889	544,607	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	7,034	1063,556	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	6,128	709,375	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	6,122	709,373	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	6,008	1063,556	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	5,963	709,374	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	5,808	709,376	2012_02_2	Nuclei_frac
P11142,P11	TVTNAV V [iTRAQ_N1	1 137-154	5,622	709,374	2012_02_2	Nuclei_frac
P11142,P11	VCNPIITK [iTRAQ_N1	3 601-608	5,223	616,869	2012_02_2	Nuclei_frac
Q01995	EFTESQLQ [iTRAQ_N1	2 161-171	7,927	792,411	2012_02_2	Nuclei_frac

Q01995	GDPNWFM [iTRAQ_N1	3 146-153	5,534	649,825	2012_02_2	Nuclei_frac
Q01995	GDPNWFM [iTRAQ_N1	3 146-153	4,939	649,826	2012_02_2	Nuclei_frac
Q01995	LGFQVWLI [iTRAQ_N1	2 49-56	5,408	426,932	2012_02_2	Nuclei_frac
Q01995	LGFQVWLI [iTRAQ_N1	2 49-56	5,367	639,893	2012_02_2	Nuclei_frac
Q01995	LVEWIIVQ([iTRAQ_N1	2 29-46	6,661	1127,102	2012_02_2	Nuclei_frac
Q01995	LVEWIIVQ([iTRAQ_N1	2 29-46	6,338	751,737	2012_02_2	Nuclei_frac
Q01995	LVNSLYPD [iTRAQ_N1	2 64-74	8,02	740,918	2012_02_2	Nuclei_frac
Q01995	LVNSLYPD [iTRAQ_N1	3 64-77	7,252	650,386	2012_02_2	Nuclei_frac
Q01995	LVNSLYPD [iTRAQ_N1	3 64-77	7,196	650,385	2012_02_2	Nuclei_frac
Q01995	LVNSLYPD [iTRAQ_N1	3 64-77	6,971	975,075	2012_02_2	Nuclei_frac
Q01995	LVNSLYPD [iTRAQ_N1	3 64-77	6,042	650,386	2012_02_2	Nuclei_frac
Q01995	QMEQVAQ [iTRAQ_N1	3 89-98	5,063	509,281	2012_02_2	Nuclei_frac
Q01995	QMEQVAQ [iTRAQ_N1	3 89-98	4,931	763,417	2012_02_2	Nuclei_frac
Q01995	TDMFQTVI [iTRAQ_N1	2 108-120	8,22	909,963	2012_02_2	Nuclei_frac
Q01995	TDMFQTVI [iTRAQ_N1	2 108-120	8,163	606,978	2012_02_2	Nuclei_frac
Q01995	TLMALGSL [iTRAQ_N1	2 128-139	8,092	746,954	2012_02_2	Nuclei_frac
Q01995	TLMALGSL [iTRAQ_N1	2 128-139	7,661	498,306	2012_02_2	Nuclei_frac
Q01995	TLMALGSL [iTRAQ_N1	3 128-139	7,574	754,952	2012_02_2	Nuclei_frac
Q01995	TLMALGSL [iTRAQ_N1	3 128-139	5,269	503,636	2012_02_2	Nuclei_frac
Q01995	TLMALGSL [iTRAQ_N1	3 128-139	4,943	503,637	2012_02_2	Nuclei_frac
Q01995	VPENPPSM [iTRAQ_N1	3 78-88	6,222	774,919	2012_02_2	Nuclei_frac
Q01995	VPENPPSM [iTRAQ_N1	3 78-88	5,033	516,949	2012_02_2	Nuclei_frac
	AAELIANSI [iTRAQ_N1	1 220-239	10,909	1071,601	2012_02_2	Nuclei_frac
	AAELIANSI [iTRAQ_N1	1 220-239	10,896	714,735	2012_02_2	Nuclei_frac
	AAELIANSI [iTRAQ_N1	1 220-239	10,396	714,735	2012_02_2	Nuclei_frac
	AAELIANSI [iTRAQ_N1	1 220-239	10,04	714,736	2012_02_2	Nuclei_frac
	AAELIANSI [iTRAQ_N1	1 220-239	7,862	714,736	2012_02_2	Nuclei_frac
	AATFGLILI [iTRAQ_N1	2 158-177	9,333	803,124	2012_02_2	Nuclei_frac
	DLQNVNIT [iTRAQ_N1	1 84-93	7,097	665,386	2012_02_2	Nuclei_frac
	EFTEAVEA [iTRAQ_N1	2 178-186	5,997	656,356	2012_02_2	Nuclei_frac
	EFTEAVEA [iTRAQ_N1	2 178-186	4,813	437,907	2012_02_2	Nuclei_frac
	FDAGELIT([iTRAQ_N1	1 134-143	5,216	647,351	2012_02_2	Nuclei_frac
	FDAGELIT([iTRAQ_N1	1 134-143	5,104	647,349	2012_02_2	Nuclei_frac
	FDAGELIT([iTRAQ_N1	1 134-143	4,738	647,35	2012_02_2	Nuclei_frac
	IFTSIGEDYI [iTRAQ_N1	1 106-117	6,94	794,882	2012_02_2	Nuclei_frac
	KLEAAEDI([iTRAQ_N1	2 240-253	8,042	632,358	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	8,361	1000,074	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	8,246	667,052	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	7,567	1000,073	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	7,004	667,052	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	6,962	667,053	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	6,339	1000,076	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	5,497	1000,074	2012_02_2	Nuclei_frac
	NITYLPAG([iTRAQ_N1	1 256-272	5,394	667,053	2012_02_2	Nuclei_frac
	VLPSITTEII [iTRAQ_N1	2 118-128	6,06	751,479	2012_02_2	Nuclei_frac
	VLPSITTEII [iTRAQ_N1	2 118-128	5,919	751,481	2012_02_2	Nuclei_frac
	VLPSITTEII [iTRAQ_N1	2 118-128	5,876	751,478	2012_02_2	Nuclei_frac
	VLPSITTEII [iTRAQ_N1	2 118-128	4,935	501,322	2012_02_2	Nuclei_frac
P63244	FSPNSSNP [iTRAQ_N1	3 155-171	7,516	732,706	2012_02_2	Nuclei_frac
P63244	FSPNSSNP [iTRAQ_N1	3 155-171	7,494	732,707	2012_02_2	Nuclei_frac

P63244	FSPNSSNP [iTRAQ_Ni	3	155-171	5,988	732,706	2012_02_2	Nuclei_frac
P63244	IIVDELKQE [iTRAQ_Ni	3	264-279	8,198	1111,158	2012_02_2	Nuclei_frac
P63244	IIVDELKQE [iTRAQ_Ni	3	264-279	6,963	741,104	2012_02_2	Nuclei_frac
P63244	IIVDELKQE [iTRAQ_Ni	3	264-279	6,659	741,106	2012_02_2	Nuclei_frac
P63244	LTRDETNY [iTRAQ_Ni	1	44-56	7,346	569,637	2012_02_2	Nuclei_frac
P63244	LWDLTTG [iTRAQ_Ni	1	88-98	8,525	704,879	2012_02_2	Nuclei_frac
P63244	LWDLTTG [iTRAQ_Ni	1	88-98	7,903	704,883	2012_02_2	Nuclei_frac
P63244	LWDLTTG [iTRAQ_Ni	1	88-98	5,792	704,883	2012_02_2	Nuclei_frac
P63244	LWNTLGVI [iTRAQ_Ni	3	130-138	7,411	689,891	2012_02_2	Nuclei_frac
P63244	LWNTLGVI [iTRAQ_Ni	3	130-138	4,721	460,261	2012_02_2	Nuclei_frac
P63244	VWNLANC [iTRAQ_Ni	3	175-182	5,725	646,854	2012_02_2	Nuclei_frac
P63244	VWQVTIGI [iTRAQ_Ni	1	308-316	7,707	602,349	2012_02_2	Nuclei_frac
P63244	YTVQDESI [iTRAQ_Ni	2	139-154	7,491	709,329	2012_02_2	Nuclei_frac
P63244	YWLCAAT [iTRAQ_Ni	3	245-256	7,859	552,3	2012_02_2	Nuclei_frac
P63244	YWLCAAT [iTRAQ_Ni	3	245-256	7,159	827,947	2012_02_2	Nuclei_frac
P09382_CH	DGGAWGT [iTRAQ_Ni	1	65-74	6,703	610,792	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	9,474	815,898	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	8,102	544,267	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	6,892	544,268	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	6,738	544,267	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	6,562	544,268	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	6,437	544,27	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	6,378	544,267	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	5,541	544,266	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	4,784	408,452	2012_02_2	Nuclei_frac
P09382_CH	DSNNLCLF [iTRAQ_Ni	2	38-49	4,761	544,266	2012_02_2	Nuclei_frac
P09382_CH	EAVFPFQP [iTRAQ_Ni	3	75-100	6,937	1052,552	2012_02_2	Nuclei_frac
P09382_CH	EAVFPFQP [iTRAQ_Ni	3	75-100	6,708	1578,322	2012_02_2	Nuclei_frac
P09382_CH	EAVFPFQP [iTRAQ_Ni	3	75-100	6,307	1052,551	2012_02_2	Nuclei_frac
P09382_CH	EAVFPFQP [iTRAQ_Ni	3	75-100	6,279	1052,556	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	10,643	968,484	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	10,1	968,484	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	9,99	645,991	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	9,855	645,992	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	9,837	645,992	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	9,579	645,992	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	9,323	968,483	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	8,933	645,991	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	6,862	645,991	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	6,14	645,992	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	5,031	484,745	2012_02_2	Nuclei_frac
P09382_CH	FNAHGDAI [iTRAQ_Ni	3	50-64	4,818	484,745	2012_02_2	Nuclei_frac
P09382_CH	LNLEAINYM [iTRAQ_Ni	2	113-128	9,736	1037,031	2012_02_2	Nuclei_frac
P09382_CH	LNLEAINYM [iTRAQ_Ni	3	113-128	9,222	1045,031	2012_02_2	Nuclei_frac
P09382_CH	LNLEAINYM [iTRAQ_Ni	3	113-128	6,469	697,022	2012_02_2	Nuclei_frac
P09382_CH	LNLEAINYM [iTRAQ_Ni	2	113-128	5,728	691,691	2012_02_2	Nuclei_frac
P09382_CH	LNLEAINYM [iTRAQ_Ni	2	113-128	5,499	691,692	2012_02_2	Nuclei_frac
P09382_CH	LPDGYEFK [iTRAQ_Ni	2	101-112	5,4	443,491	2012_02_2	Nuclei_frac
P09382_CH	LPDGYEFK [iTRAQ_Ni	2	101-112	4,765	590,987	2012_02_2	Nuclei_frac
P09382_CH	SFVLNLGK [iTRAQ_Ni	2	30-37	6,81	583,365	2012_02_2	Nuclei_frac
P09382_CH	SFVLNLGK [iTRAQ_Ni	2	30-37	6,142	583,363	2012_02_2	Nuclei_frac

P09382_CH SFVLNLGK [iTRAQ_N1	2 30-37	5,613	583,363	2012_02_2 Nuclei_frac
P09382_CH SFVLNLGK [iTRAQ_N1	2 30-37	4,734	583,364	2012_02_2 Nuclei_frac
P09382_CH SFVLNLGK [iTRAQ_N1	3 30-49	6,272	659,102	2012_02_2 Nuclei_frac
P09382_CH VRGEVAPL [iTRAQ_N1	2 20-29	5,61	665,391	2012_02_2 Nuclei_frac
O60506_IS(AFSQFGK [iTRAQ_N1	2 322-328	5,662	536,803	2012_02_2 Nuclei_frac
O60506_IS(AGPIWDLR [iTRAQ_N1	1 185-192	5,504	536,308	2012_02_2 Nuclei_frac
O60506_IS(AGPIWDLR [iTRAQ_N1	1 185-192	5,065	536,308	2012_02_2 Nuclei_frac
O60506_IS(AIEALKEF [iTRAQ_N1	3 61-81	7,541	922,854	2012_02_2 Nuclei_frac
O60506_IS(EFNEDGAL [iTRAQ_N1	2 67-81	6,374	666,357	2012_02_2 Nuclei_frac
O60506_IS(HIGVCISVA [iTRAQ_N1	2 233-244	6,098	495,269	2012_02_2 Nuclei_frac
O60506_IS(LKDYAFIH [iTRAQ_N1	2 335-346	5,515	461,252	2012_02_2 Nuclei_frac
O60506_IS(TGYTLDDVT [iTRAQ_N1	1 131-142	10,237	728,383	2012_02_2 Nuclei_frac
O60506_IS(TGYTLDDVT [iTRAQ_N1	1 131-142	8,33	728,384	2012_02_2 Nuclei_frac
O60506_IS(TGYTLDDVT [iTRAQ_N1	1 131-142	8,189	728,382	2012_02_2 Nuclei_frac
O60506_IS(TKEQILEEF [iTRAQ_N1	3 255-265	6,633	595,344	2012_02_2 Nuclei_frac
O60506_IS(VADSSKGF [iTRAQ_N1	3 112-123	4,818	545,968	2012_02_2 Nuclei_frac
O60506_IS(VAEKLDEI [iTRAQ_N1	2 39-60	8,411	910,824	2012_02_2 Nuclei_frac
P78371 GATQQILD [iTRAQ_N1	1 376-387	8,313	737,885	2012_02_2 Nuclei_frac
P78371 IHPQTIIAG [iTRAQ_N1	1 120-130	6,948	479,282	2012_02_2 Nuclei_frac
P78371 IHPQTIIAG [iTRAQ_N1	1 120-130	6,437	479,282	2012_02_2 Nuclei_frac
P78371 LALVTGGE [iTRAQ_N1	2 322-341	10,017	795,784	2012_02_2 Nuclei_frac
P78371 LALVTGGE [iTRAQ_N1	2 322-341	9,763	795,78	2012_02_2 Nuclei_frac
P78371 LAVEAVLF [iTRAQ_N1	1 181-188	4,727	507,826	2012_02_2 Nuclei_frac
P78371 LKGSGNLE [iTRAQ_N1	3 189-202	5,392	642,401	2012_02_2 Nuclei_frac
P78371 LTSFIGAIA [iTRAQ_N1	2 25-39	7,662	903,553	2012_02_2 Nuclei_frac
P78371 LTSFIGAIA [iTRAQ_N1	2 25-39	7,096	602,706	2012_02_2 Nuclei_frac
P78371 LTSFIGAIA [iTRAQ_N1	2 25-39	6,09	602,705	2012_02_2 Nuclei_frac
P78371 LTSFIGAIA [iTRAQ_N1	2 25-39	5,186	602,706	2012_02_2 Nuclei_frac
P78371 QVLLSAAE [iTRAQ_N1	1 501-515	9,464	864,017	2012_02_2 Nuclei_frac
P78371 QVLLSAAE [iTRAQ_N1	1 501-515	7,973	576,345	2012_02_2 Nuclei_frac
P78371 SLHDALCV [iTRAQ_N1	3 388-401	7,973	922,024	2012_02_2 Nuclei_frac
P78371 SLHDALCV [iTRAQ_N1	3 388-401	7,331	615,02	2012_02_2 Nuclei_frac
P78371 VAEIEHAEI [iTRAQ_N1	3 263-273	5,588	572,33	2012_02_2 Nuclei_frac
Q14697,Q1 ALLDSLQL [iTRAQ_N1	2 34-56	6,198	697,655	2012_02_2 Nuclei_frac
Q14697,Q1 GLLEFEHQ [iTRAQ_N1	1 146-154	5,857	424,899	2012_02_2 Nuclei_frac
Q14697,Q1 LKVTEGGE [iTRAQ_N1	2 240-250	4,942	512,959	2012_02_2 Nuclei_frac
Q14697,Q1 LVAIVDPH [iTRAQ_N1	2 435-444	5,197	464,965	2012_02_2 Nuclei_frac
Q14697,Q1 LVAIVDPH [iTRAQ_N1	2 435-444	5,159	464,965	2012_02_2 Nuclei_frac
Q14697,Q1 NLGLYVK [iTRAQ_N1	2 457-463	4,735	547,843	2012_02_2 Nuclei_frac
Q14697,Q1 QEFLLR [iTRAQ_N1	1 830-835	5,373	475,286	2012_02_2 Nuclei_frac
Q14697,Q1 QEFLLR [iTRAQ_N1	1 830-835	4,817	475,285	2012_02_2 Nuclei_frac
Q14697,Q1 SLLSVNA [iTRAQ_N1	1 137-145	5,791	558,842	2012_02_2 Nuclei_frac
Q14697,Q1 VLLVLELQ [iTRAQ_N1	2 57-68	4,832	547,69	2012_02_2 Nuclei_frac
Q14697,Q1 VVIIGAGKF [iTRAQ_N1	3 864-880	9,909	1048,679	2012_02_2 Nuclei_frac
Q14697,Q1 VVIIGAGKF [iTRAQ_N1	3 864-880	8,845	699,457	2012_02_2 Nuclei_frac
Q14697,Q1 VVIIGAGKF [iTRAQ_N1	3 864-880	7,401	699,457	2012_02_2 Nuclei_frac
Q14697,Q1 VVIIGAGKF [iTRAQ_N1	3 864-880	4,758	524,844	2012_02_2 Nuclei_frac
Q14697,Q1 YFTWDPSF [iTRAQ_N1	1 410-422	6,048	614,313	2012_02_2 Nuclei_frac
Q14697,Q1 YRVPDVLV [iTRAQ_N1	1 85-99	7,125	609,021	2012_02_2 Nuclei_frac

Q14697,Q1 YRVPDVLV [iTRAQ_N1	1 85-99	5,119	609,021	2012_02_2 Nuclei_frac
P15144 DHSALPVI [iTRAQ_N1	1 648-657	6,88	633,357	2012_02_2 Nuclei_frac
P15144 DHSALPVI [iTRAQ_N1	1 648-657	5,87	422,574	2012_02_2 Nuclei_frac
P15144 EATDVIIH [iTRAQ_N1	2 114-124	6,961	505,299	2012_02_2 Nuclei_frac
P15144 ENSLLFDPI [iTRAQ_N1	2 363-378	6,472	671,681	2012_02_2 Nuclei_frac
P15144 EVVLQWF [iTRAQ_N1	2 955-966	7,538	589,989	2012_02_2 Nuclei_frac
P15144 GVGGSQPF [iTRAQ_N1	3 140-166	6,413	838,97	2012_02_2 Nuclei_frac
P15144 QQQDYWL [iTRAQ_N1	1 595-605	7,113	804,418	2012_02_2 Nuclei_frac
P15144 QWMENPN [iTRAQ_N1	2 777-792	8,057	712,017	2012_02_2 Nuclei_frac
P15144 SIQLPTTVF [iTRAQ_N1	1 528-536	4,96	579,852	2012_02_2 Nuclei_frac
P15144 VNYDEENV [iTRAQ_N1	1 631-639	5,789	684,817	2012_02_2 Nuclei_frac
P15144 VTLRPYLT [iTRAQ_N1	1 86-97	5,454	530,302	2012_02_2 Nuclei_frac
Q13838,Q1 CIALAQLL [iTRAQ_N1	2 299-318	9,854	807,792	2012_02_2 Nuclei_frac
Q13838,Q1 DFLLKPELI [iTRAQ_N1	2 48-57	5,586	766,479	2012_02_2 Nuclei_frac
Q13838,Q1 DFLLKPELI [iTRAQ_N1	2 48-57	4,998	766,478	2012_02_2 Nuclei_frac
Q13838,Q1 DVQEIFR [iTRAQ_N1	1 209-215	5,791	525,788	2012_02_2 Nuclei_frac
Q13838,Q1 ELAFQISK [iTRAQ_N1	2 123-130	4,96	408,579	2012_02_2 Nuclei_frac
Q13838,Q1 GLAITFVSI [iTRAQ_N1	2 384-397	6,152	589,983	2012_02_2 Nuclei_frac
Q13838,Q1 GSYVSIHS [iTRAQ_N1	1 36-47	6,401	480,917	2012_02_2 Nuclei_frac
Q13838,Q1 ILVATNLF [iTRAQ_N1	1 339-348	8,964	624,384	2012_02_2 Nuclei_frac
Q13838,Q1 ILVATNLF [iTRAQ_N1	1 339-348	7,381	416,592	2012_02_2 Nuclei_frac
Q13838,Q1 KNCPHIVV [iTRAQ_N1	3 162-174	6,024	431,499	2012_02_2 Nuclei_frac
Q13838,Q1 NCPHIVVG [iTRAQ_N1	2 163-174	5,693	484,26	2012_02_2 Nuclei_frac
Q13838,Q1 VAVFFGGL [iTRAQ_N1	2 144-154	5,341	713,439	2012_02_2 Nuclei_frac
Q13838,Q1 VAVFFGGL [iTRAQ_N1	2 144-154	5,326	475,962	2012_02_2 Nuclei_frac
P21796 KLETAVNL [iTRAQ_N1	2 200-217	6,195	745,417	2012_02_2 Nuclei_frac
P21796 LGLGLEFQ [iTRAQ_N1	1 274-282	5,221	546,314	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	2 96-108	9,928	844,941	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	2 96-108	8,872	844,942	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	2 96-108	7,694	563,631	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	3 96-109	9,22	654,364	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	3 96-109	8,521	654,363	2012_02_2 Nuclei_frac
P21796 LTFDSSFSI [iTRAQ_N1	3 96-109	8,082	654,363	2012_02_2 Nuclei_frac
P21796 LTLSALLD [iTRAQ_N1	2 256-265	7,925	659,915	2012_02_2 Nuclei_frac
P21796 LTLSALLD [iTRAQ_N1	2 256-265	7,461	659,917	2012_02_2 Nuclei_frac
P21796 LTLSALLD [iTRAQ_N1	2 256-265	5,492	440,279	2012_02_2 Nuclei_frac
P21796 LTLSALLD [iTRAQ_N1	2 256-265	4,95	440,279	2012_02_2 Nuclei_frac
P21796 VNSSLIGI [iTRAQ_N1	3 236-255	8,845	845,836	2012_02_2 Nuclei_frac
P21796 VTQSNFA [iTRAQ_N1	2 163-173	10,168	751,417	2012_02_2 Nuclei_frac
P21796 VTQSNFA [iTRAQ_N1	2 163-173	5,539	501,281	2012_02_2 Nuclei_frac
P21796 YQIDPDAC [iTRAQ_N1	3 224-235	7,25	851,921	2012_02_2 Nuclei_frac
Q92945 AINQQTGA [iTRAQ_N1	1 449-462	12,113	839,457	2012_02_2 Nuclei_frac
Q92945 GGGGPGGC [iTRAQ_N1	1 41-70	8,075	805,394	2012_02_2 Nuclei_frac
Q92945 IGGGIDVPV [iTRAQ_N1	1 321-331	7,263	612,366	2012_02_2 Nuclei_frac
Q92945 IGQQPQQP [iTRAQ_N1	2 629-646	5,427	757,069	2012_02_2 Nuclei_frac
Q92945 IINDLLQSL [iTRAQ_N1	1 385-394	7,686	664,904	2012_02_2 Nuclei_frac
Q92945 IINDLLQSL [iTRAQ_N1	1 385-394	6,642	664,905	2012_02_2 Nuclei_frac
Q92945 KIGQQPQQ [iTRAQ_N1	3 628-646	5,84	636,101	2012_02_2 Nuclei_frac

Q92945	KLASQGD\$ [iTRAQ_Nt	2 122-142	6,567	619,1	2012_02_2	Nuclei_frac
Q92945	LASQGDSI [iTRAQ_Nt	1 123-142	11,679	734,399	2012_02_2	Nuclei_frac
P36578	AAAAAAA [iTRAQ_Nt	2 353-363	7,039	622,882	2012_02_2	Nuclei_frac
P36578	APIRPDIVN [iTRAQ_Nt	1 29-44	5,034	502,291	2012_02_2	Nuclei_frac
P36578	FCIWTESA [iTRAQ_Nt	2 248-257	6,989	730,859	2012_02_2	Nuclei_frac
P36578	FCIWTESA [iTRAQ_Nt	2 248-257	6,937	730,864	2012_02_2	Nuclei_frac
P36578	IEEVPELPL [iTRAQ_Nt	3 143-161	7,783	873,159	2012_02_2	Nuclei_frac
P36578	KLDELYGT [iTRAQ_Nt	2 258-267	5,338	523,629	2012_02_2	Nuclei_frac
P36578	KLDELYGT [iTRAQ_Nt	2 258-267	5,278	523,628	2012_02_2	Nuclei_frac
P36578	NIPGITLLN [iTRAQ_Nt	2 222-233	6,863	778,986	2012_02_2	Nuclei_frac
P36578	NIPGITLLN [iTRAQ_Nt	2 222-233	6,112	519,659	2012_02_2	Nuclei_frac
P36578	NVTLPVAV [iTRAQ_Nt	2 20-28	7,205	638,898	2012_02_2	Nuclei_frac
P36578	NVTLPVAV [iTRAQ_Nt	2 20-28	6,654	426,268	2012_02_2	Nuclei_frac
P36578	QPYAVSEL [iTRAQ_Nt	1 49-70	9,072	826,072	2012_02_2	Nuclei_frac
P36578	YAICSALA [iTRAQ_Nt	4 121-139	8,617	747,748	2012_02_2	Nuclei_frac
P36578	YAICSALA [iTRAQ_Nt	4 121-139	8,5	747,746	2012_02_2	Nuclei_frac
P36578	YAICSALA [iTRAQ_Nt	4 121-139	6,357	561,063	2012_02_2	Nuclei_frac
	AAVATFLC [iTRAQ_Nt	2 785-802	6,827	741,088	2012_02_2	Nuclei_frac
	DEFEGFLK [iTRAQ_Nt	2 650-657	5,259	636,838	2012_02_2	Nuclei_frac
	KPLLESGL [iTRAQ_Nt	3 593-604	6,33	559,349	2012_02_2	Nuclei_frac
	KPLLESGL [iTRAQ_Nt	3 593-604	5,9	559,349	2012_02_2	Nuclei_frac
	LAGTQPLE [iTRAQ_Nt	1 679-693	9,402	884,511	2012_02_2	Nuclei_frac
	LAGTQPLE [iTRAQ_Nt	1 679-693	7,078	590,009	2012_02_2	Nuclei_frac
	LQTSSVLV [iTRAQ_Nt	1 70-81	6,936	702,42	2012_02_2	Nuclei_frac
	NFPNAIEH [iTRAQ_Nt	1 636-649	8,556	614,324	2012_02_2	Nuclei_frac
	SIPICTLK [iTRAQ_Nt	3 628-635	5,891	610,369	2012_02_2	Nuclei_frac
	SLVASLAE [iTRAQ_Nt	2 305-322	7,092	733,073	2012_02_2	Nuclei_frac
	YFLVGAGA [iTRAQ_Nt	3 471-485	6,622	633,695	2012_02_2	Nuclei_frac
	YFLVGAGA [iTRAQ_Nt	3 471-485	6,567	633,695	2012_02_2	Nuclei_frac
P11940,Q9	AKEFTNVY [iTRAQ_Nt	3 187-196	5,02	548,995	2012_02_2	Nuclei_frac
P11940,Q9	ALYDTFSA [iTRAQ_Nt	3 114-129	7,602	699,034	2012_02_2	Nuclei_frac
P11940,Q9	FSPAGPILS [iTRAQ_Nt	1 31-41	8,653	651,39	2012_02_2	Nuclei_frac
P11940,Q9	FSPAGPILS [iTRAQ_Nt	1 31-41	5,025	434,596	2012_02_2	Nuclei_frac
P11940,Q9	GFGFVSFE [iTRAQ_Nt	1 232-240	7,308	595,311	2012_02_2	Nuclei_frac
P11940,Q9	IVATKPLY [iTRAQ_Nt	2 357-370	6,625	916,075	2012_02_2	Nuclei_frac
P11940,Q9	IVATKPLY [iTRAQ_Nt	2 357-370	5,589	611,053	2012_02_2	Nuclei_frac
P11940,Q9	KEFSPFGTI [iTRAQ_Nt	3 312-324	9,097	615,689	2012_02_2	Nuclei_frac
P11940,Q9	KEFSPFGTI [iTRAQ_Nt	3 312-324	6,756	615,689	2012_02_2	Nuclei_frac
P11940,Q9	LFPLIQAM [iTRAQ_Nt	3 477-491	5,998	647,715	2012_02_2	Nuclei_frac
P11940,Q9	LFPLIQAM [iTRAQ_Nt	3 477-491	5,421	647,716	2012_02_2	Nuclei_frac
P11940,Q9	SGVGNIFI [iTRAQ_Nt	2 96-104	6,042	611,874	2012_02_2	Nuclei_frac
P11940,Q9	SGVGNIFI [iTRAQ_Nt	2 96-104	4,872	408,252	2012_02_2	Nuclei_frac
P11940,Q9	SKVDEAV [iTRAQ_Nt	3 516-531	5,671	709,415	2012_02_2	Nuclei_frac
P11940,Q9	SKVDEAV [iTRAQ_Nt	3 516-531	5,232	532,315	2012_02_2	Nuclei_frac
Q14240,Q1	ATQALVL [iTRAQ_Nt	1 100-110	9,918	642,892	2012_02_2	Nuclei_frac
Q14240,Q1	DQIYDIFQK [iTRAQ_Nt	2 194-202	5,596	729,402	2012_02_2	Nuclei_frac
Q14240,Q1	GFKDQIYDI [iTRAQ_Nt	3 191-202	8,381	645,365	2012_02_2	Nuclei_frac
Q14240,Q1	GFKDQIYDI [iTRAQ_Nt	3 191-202	7,874	645,364	2012_02_2	Nuclei_frac

Q14240,Q1 GYDVIAQA [iTRAQ_N1	2 69-82	8,936	841,953	2012_02_2 Nuclei_frac
Q14240,Q1 GYDVIAQA [iTRAQ_N1	2 69-82	6,367	561,637	2012_02_2 Nuclei_frac
Q14240,Q1 GYDVIAQA [iTRAQ_N1	2 69-82	6,34	561,637	2012_02_2 Nuclei_frac
Q14240,Q1 GYDVIAQA [iTRAQ_N1	2 69-82	5,6	561,638	2012_02_2 Nuclei_frac
Q14240,Q1 KEELTLEGI [iTRAQ_N1	2 238-247	5,071	492,628	2012_02_2 Nuclei_frac
Q14240,Q1 KVDWLTEI [iTRAQ_N1	3 284-291	5,416	725,937	2012_02_2 Nuclei_frac
Q14240,Q1 LQMEAPHI [iTRAQ_N1	2 147-161	6,358	593,661	2012_02_2 Nuclei_frac
Q14240,Q1 LQMEAPHI [iTRAQ_N1	1 147-161	6,033	588,324	2012_02_2 Nuclei_frac
Q14240,Q1 QFYINVERE [iTRAQ_N1	2 248-259	5,348	643,675	2012_02_2 Nuclei_frac
Q14240,Q1 VLITTDLL/ [iTRAQ_N1	1 325-334	6,906	629,898	2012_02_2 Nuclei_frac
Q14240,Q1 VLITTDLL/ [iTRAQ_N1	1 325-334	6,901	629,897	2012_02_2 Nuclei_frac
Q14240,Q1 VLITTDLL/ [iTRAQ_N1	1 325-334	6,87	629,899	2012_02_2 Nuclei_frac
Q14240,Q1 VLITTDLL/ [iTRAQ_N1	1 325-334	6,235	629,898	2012_02_2 Nuclei_frac

Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	6,264	560,778	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,984	560,779	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,489	560,78	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,253	560,779	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,222	560,781	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,208	560,78	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	5,045	560,781	2012_02_2 Nuclei_frac
Q9BYX7 AGFAGDD/ [iTRAQ_N1	1 719-728	4,84	560,78	2012_02_2 Nuclei_frac
Q9BYX7 AVFPSIVGI [iTRAQ_N1	1 729-737	8,57	545,33	2012_02_2 Nuclei_frac
Q9BYX7 AVFPSIVGI [iTRAQ_N1	1 729-737	8,103	545,331	2012_02_2 Nuclei_frac
Q9BYX7 AVFPSIVGI [iTRAQ_N1	1 729-737	8,066	545,33	2012_02_2 Nuclei_frac
Q9BYX7 AVFPSIVGI [iTRAQ_N1	1 729-737	8,028	545,33	2012_02_2 Nuclei_frac
Q9BYX7 AVFPSIVGI [iTRAQ_N1	1 729-737	7,739	545,331	2012_02_2 Nuclei_frac
Q9BYX7 EKLCYVAL [iTRAQ_N1	4 914-938	6,944	1080,543	2012_02_2 Nuclei_frac
Q9BYX7 IWHHTFYN [iTRAQ_N1	1 785-795	8,692	830,429	2012_02_2 Nuclei_frac
Q9BYX7 IWHHTFYN [iTRAQ_N1	1 785-795	7,853	553,956	2012_02_2 Nuclei_frac
Q9BYX7 IWHHTFYN [iTRAQ_N1	1 785-795	7,671	553,955	2012_02_2 Nuclei_frac
Q9BYX7 IWHHTFYN [iTRAQ_N1	1 785-795	6,661	553,954	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	9,349	1419,706	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	9,337	1419,693	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	9,087	946,799	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,717	946,803	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,704	946,798	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,695	946,8	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,464	946,798	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,4	946,793	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	8,263	946,801	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	4 916-938	8,051	1427,691	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,859	946,802	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,639	946,797	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,349	946,805	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,33	946,801	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,292	710,35	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	7,027	946,801	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	6,963	710,35	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	6,957	946,799	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	4 916-938	6,423	952,129	2012_02_2 Nuclei_frac
Q9BYX7 LCYVALDF [iTRAQ_N1	3 916-938	6,349	710,349	2012_02_2 Nuclei_frac

Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	5,86	710,348	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	5,532	710,349	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	5,511	710,349	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	5,411	710,349	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	5,22	710,347	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	4,988	710,342	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	4,948	710,346	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	4 916-938	4,842	952,13	2012_02_2 Nuclei_frac
Q9BYX7	LCYVALDF [iTRAQ_N1	3 916-938	4,812	710,352	2012_02_2 Nuclei_frac
Q9BYX7	QEYDESGP [iTRAQ_N1	1 1060-1072	9,495	554,274	2012_02_2 Nuclei_frac
Q9BYX7	QEYDESGP [iTRAQ_N1	1 1060-1072	5,931	554,276	2012_02_2 Nuclei_frac
Q9BYX7	SYELPDGQ [iTRAQ_N1	1 939-954	12,535	968,001	2012_02_2 Nuclei_frac
Q9BYX7	SYELPDGQ [iTRAQ_N1	1 939-954	11,152	968,005	2012_02_2 Nuclei_frac
Q9BYX7	SYELPDGQ [iTRAQ_N1	1 939-954	9,834	645,67	2012_02_2 Nuclei_frac
Q9BYX7	SYELPDGQ [iTRAQ_N1	1 939-954	8,819	645,67	2012_02_2 Nuclei_frac
Q9BYX7	SYELPDGQ [iTRAQ_N1	1 939-954	6,31	968,006	2012_02_2 Nuclei_frac
P04844	EETVLATV [iTRAQ_N1	1 133-156	9,703	918,494	2012_02_2 Nuclei_frac
P04844	EETVLATV [iTRAQ_N1	1 133-156	5,561	689,12	2012_02_2 Nuclei_frac
P04844	LMDHVGTF [iTRAQ_N1	3 196-207	5,634	544,297	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	9,985	1064,633	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	9,039	1064,634	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	7,818	710,092	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	7,588	710,093	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	7,145	710,092	2012_02_2 Nuclei_frac
P04844	LQVTNVL\$ [iTRAQ_N1	2 268-284	4,956	532,82	2012_02_2 Nuclei_frac
P04844	LSKEETVL [iTRAQ_N1	2 130-156	8,475	1075,931	2012_02_2 Nuclei_frac
P04844	LSKEETVL [iTRAQ_N1	2 130-156	7,013	807,199	2012_02_2 Nuclei_frac
P04844	QEIQHLFR [iTRAQ_N1	1 502-509	4,935	405,564	2012_02_2 Nuclei_frac
P04844	SIVEEIEDL' [iTRAQ_N1	1 157-168	10,721	506,282	2012_02_2 Nuclei_frac
P04844	SIVEEIEDL' [iTRAQ_N1	1 157-168	9,563	758,921	2012_02_2 Nuclei_frac
P04844	TSFTPVG D [iTRAQ_N1	2 301-318	5,256	778,411	2012_02_2 Nuclei_frac
P04844	YIANTVELI [iTRAQ_N1	1 336-344	6,883	611,85	2012_02_2 Nuclei_frac
P04844	YIANTVELI [iTRAQ_N1	1 336-344	6,239	611,849	2012_02_2 Nuclei_frac
P04844	YIANTVELI [iTRAQ_N1	1 336-344	5,063	611,852	2012_02_2 Nuclei_frac
	AVCMLSN` [iTRAQ_N1	3 374-390	9,063	1013,003	2012_02_2 Nuclei_frac
	AVCMLSN` [iTRAQ_N1	2 374-390	7,356	670,341	2012_02_2 Nuclei_frac
	IHFPLATY/ [iTRAQ_N1	2 265-280	9,449	1023,089	2012_02_2 Nuclei_frac
	IHFPLATY/ [iTRAQ_N1	2 265-280	9,289	1023,087	2012_02_2 Nuclei_frac
	IHFPLATY/ [iTRAQ_N1	2 265-280	8,234	682,394	2012_02_2 Nuclei_frac
	IHFPLATY/ [iTRAQ_N1	2 265-280	8,142	682,395	2012_02_2 Nuclei_frac
	IHFPLATY/ [iTRAQ_N1	2 265-280	5,276	512,047	2012_02_2 Nuclei_frac
	LISQIVSSIT [iTRAQ_N1	1 230-243	9,344	816,497	2012_02_2 Nuclei_frac
	LISQIVSSIT [iTRAQ_N1	1 230-243	9,04	544,666	2012_02_2 Nuclei_frac
	NLDIERPTY [iTRAQ_N1	1 216-229	6,968	621,667	2012_02_2 Nuclei_frac
	NLDIERPTY [iTRAQ_N1	1 216-229	6,265	621,667	2012_02_2 Nuclei_frac
	NLDIERPTY [iTRAQ_N1	1 216-229	5,619	931,997	2012_02_2 Nuclei_frac
	NLDIERPTY [iTRAQ_N1	1 216-229	4,967	621,667	2012_02_2 Nuclei_frac
	QLFHPEQL [iTRAQ_N1	2 85-96	8,844	849,994	2012_02_2 Nuclei_frac
	QLFHPEQL [iTRAQ_N1	2 85-96	6,192	566,998	2012_02_2 Nuclei_frac
	QLFHPEQL [iTRAQ_N1	2 85-96	5,67	566,998	2012_02_2 Nuclei_frac

SIQFVDWC [iTRAQ_N1	3 340-352	8,198	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,89	624,992	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,501	936,982	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,282	936,985	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	7,255	624,992	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	6,972	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	6,696	624,991	2012_02_2	Nuclei_frac
SIQFVDWC [iTRAQ_N1	3 340-352	4,962	624,99	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	8,943	1057,101	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,319	1057,103	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	7,156	1057,097	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,887	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,34	705,07	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	6,148	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,834	705,07	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,274	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	5,262	705,071	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	4,88	705,069	2012_02_2	Nuclei_frac
VGINYQPP [iTRAQ_N1	2 353-370	4,766	529,053	2012_02_2	Nuclei_frac

EVGDGTT [iTRAQ_N1	2 85-102	5,231	701,744	2012_02_2	Nuclei_frac
FATEAAIT [iTRAQ_N1	1 516-526	7,556	675,404	2012_02_2	Nuclei_frac
IACLDIFSLC [iTRAQ_N1	3 234-243	7,082	741,916	2012_02_2	Nuclei_frac
IACLDIFSLC [iTRAQ_N1	3 234-243	5,233	494,947	2012_02_2	Nuclei_frac
LGVQVVIT [iTRAQ_N1	2 248-264	7,992	737,772	2012_02_2	Nuclei_frac
SLHDALCV [iTRAQ_N1	3 391-400	5,7	477,273	2012_02_2	Nuclei_frac
SLLVIPNTL [iTRAQ_N1	2 444-466	5,447	881,172	2012_02_2	Nuclei_frac
SQNVMAA [iTRAQ_N1	3 19-33	7,61	607,677	2012_02_2	Nuclei_frac
TSASIILR [iTRAQ_N1	1 371-378	7,222	502,815	2012_02_2	Nuclei_frac
YPVNSVNII [iTRAQ_N1	2 190-199	6,792	717,933	2012_02_2	Nuclei_frac
YPVNSVNII [iTRAQ_N1	2 190-199	6,489	717,933	2012_02_2	Nuclei_frac

Q02878_Cf AIPQLQGYI [iTRAQ_N1	1 263-272	6,282	651,888	2012_02_2	Nuclei_frac
Q02878_Cf AIPQLQGYI [iTRAQ_N1	1 263-272	6,058	434,927	2012_02_2	Nuclei_frac
Q02878_Cf ASITPGTIL [iTRAQ_N1	1 142-156	8,702	835,52	2012_02_2	Nuclei_frac
Q02878_Cf ASITPGTIL [iTRAQ_N1	1 142-156	8,631	835,523	2012_02_2	Nuclei_frac
Q02878_Cf ASITPGTIL [iTRAQ_N1	1 142-156	6,953	557,352	2012_02_2	Nuclei_frac
Q02878_Cf ASITPGTIL [iTRAQ_N1	1 142-156	6,542	557,352	2012_02_2	Nuclei_frac
Q02878_Cf AVDSQILPI [iTRAQ_N1	2 252-260	5,856	629,883	2012_02_2	Nuclei_frac
Q02878_Cf AVDSQILPI [iTRAQ_N1	2 252-260	5,622	629,886	2012_02_2	Nuclei_frac
Q02878_Cf HLTDAYFK [iTRAQ_N1	2 211-218	6,123	641,856	2012_02_2	Nuclei_frac
Q02878_Cf HLTDAYFK [iTRAQ_N1	2 211-218	5,373	428,239	2012_02_2	Nuclei_frac
Q02878_Cf IDISNVK [iTRAQ_N1	2 201-207	4,97	538,832	2012_02_2	Nuclei_frac
Q02878_Cf IDISNVK [iTRAQ_N1	2 201-207	4,955	538,833	2012_02_2	Nuclei_frac
Q02878_Cf IDISNVK [iTRAQ_N1	2 201-207	4,832	538,831	2012_02_2	Nuclei_frac
Q02878_Cf QLASGLLL [iTRAQ_N1	1 167-183	9,625	954,591	2012_02_2	Nuclei_frac
Q02878_Cf QLASGLLL [iTRAQ_N1	1 167-183	6,882	636,727	2012_02_2	Nuclei_frac
Q02878_Cf QLASGLLL [iTRAQ_N1	1 167-183	6,185	636,73	2012_02_2	Nuclei_frac
Q02878_Cf VLATVTKF [iTRAQ_N1	3 88-100	5,035	573,024	2012_02_2	Nuclei_frac
Q02878_Cf YYPTEDVP [iTRAQ_N1	1 115-123	7,647	642,323	2012_02_2	Nuclei_frac
Q02878_Cf YYPTEDVP [iTRAQ_N1	1 115-123	6,94	642,323	2012_02_2	Nuclei_frac
Q02878_Cf YYPTEDVP [iTRAQ_N1	2 115-124	6,173	519,285	2012_02_2	Nuclei_frac

Q14152	DLYNWLEI [iTRAQ_N1	2 388-401	8,984	690,039	2012_02_2	Nuclei_frac
Q14152	ILQEHEQIK [iTRAQ_N1	2 623-631	5,43	475,95	2012_02_2	Nuclei_frac
Q14152	LATLLGLQ [iTRAQ_N1	1 354-366	9,041	747,961	2012_02_2	Nuclei_frac
Q14152	LATLLGLQ [iTRAQ_N1	1 354-366	8,415	498,977	2012_02_2	Nuclei_frac
Q14152	LESLNIQR [iTRAQ_N1	1 581-588	5,253	558,83	2012_02_2	Nuclei_frac
Q14152	LLLTPWVK [iTRAQ_N1	2 143-150	4,759	629,413	2012_02_2	Nuclei_frac
Q14152	LLQQVSQI [iTRAQ_N1	1 438-453	7,204	695,049	2012_02_2	Nuclei_frac
Q14152	LTSLVPFV [iTRAQ_N1	1 454-468	5,459	627,023	2012_02_2	Nuclei_frac
Q14152	LYHDIAQQ [iTRAQ_N1	2 172-182	6,018	541,303	2012_02_2	Nuclei_frac
Q14152	VLLATLSIF [iTRAQ_N1	1 321-334	7,155	834,015	2012_02_2	Nuclei_frac
	GLAAFLK [iTRAQ_N1	2 742-748	4,736	504,329	2012_02_2	Nuclei_frac
	ICFELLELL [iTRAQ_N1	3 1058-1067	5,631	783,465	2012_02_2	Nuclei_frac
	IWDPTPSH [iTRAQ_N1	1 253-270	6,502	659,347	2012_02_2	Nuclei_frac
	IYNSIYGSC [iTRAQ_N1	1 1268-1286	10,89	780,084	2012_02_2	Nuclei_frac
	IYNSIYGSC [iTRAQ_N1	1 1268-1286	10,626	780,086	2012_02_2	Nuclei_frac
	KLSSWDQ [iTRAQ_N1	2 214-231	5,345	575,308	2012_02_2	Nuclei_frac
	RWDQTAD [iTRAQ_N1	2 199-213	12,05	654,01	2012_02_2	Nuclei_frac
	VKPYLPQK [iTRAQ_N1	3 925-939	6,948	706,741	2012_02_2	Nuclei_frac
	VLPPPAGY [iTRAQ_N1	1 414-425	7,107	474,959	2012_02_2	Nuclei_frac
	VLPPPAGY [iTRAQ_N1	1 414-425	4,891	711,934	2012_02_2	Nuclei_frac
P13010_CH	ANPQVGV [iTRAQ_N1	2 401-413	7,447	555,994	2012_02_2	Nuclei_frac
P13010_CH	HIEIFTDLS [iTRAQ_N1	1 131-141	8,737	487,933	2012_02_2	Nuclei_frac
P13010_CH	HIEIFTDLS [iTRAQ_N1	1 131-141	6	731,396	2012_02_2	Nuclei_frac
P13010_CH	IQPGSQQA [iTRAQ_N1	2 98-125	4,748	836,195	2012_02_2	Nuclei_frac
P13010_CH	LFQCLLHR [iTRAQ_N1	2 490-497	5,334	410,902	2012_02_2	Nuclei_frac
P13010_CH	LGGHGPSF [iTRAQ_N1	2 185-195	5,597	466,609	2012_02_2	Nuclei_frac
P13010_CH	LTIGSNLSII [iTRAQ_N1	1 251-260	7,563	609,37	2012_02_2	Nuclei_frac
P13010_CH	SQLDIIHSL [iTRAQ_N1	2 145-155	6,84	518,987	2012_02_2	Nuclei_frac
P13010_CH	SQLDIIHSL [iTRAQ_N1	2 145-155	5,937	518,986	2012_02_2	Nuclei_frac
P13010_CH	TLFPLIEAK [iTRAQ_N1	2 535-543	6,497	660,414	2012_02_2	Nuclei_frac
P13010_CH	TLFPLIEAK [iTRAQ_N1	2 535-543	5,645	440,612	2012_02_2	Nuclei_frac
P13010_CH	TLFPLIEAK [iTRAQ_N1	2 535-543	5,303	440,611	2012_02_2	Nuclei_frac
P13010_CH	TWTVVDA [iTRAQ_N1	2 275-282	5,456	604,352	2012_02_2	Nuclei_frac
P23396	AELNEFLT [iTRAQ_N1	1 18-26	8,788	618,84	2012_02_2	Nuclei_frac
P23396	DEILPTTPI [iTRAQ_N1	2 214-226	7,244	879,99	2012_02_2	Nuclei_frac
P23396	DEILPTTPI [iTRAQ_N1	2 214-226	7,179	879,99	2012_02_2	Nuclei_frac
P23396	DEILPTTPI [iTRAQ_N1	2 214-226	7,109	586,996	2012_02_2	Nuclei_frac
P23396	DEILPTTPI [iTRAQ_N1	2 214-226	6,82	879,99	2012_02_2	Nuclei_frac
P23396	ELTAVVQK [iTRAQ_N1	2 67-74	4,918	588,366	2012_02_2	Nuclei_frac
P23396	FGFPEGSV [iTRAQ_N1	2 76-89	6,466	620,992	2012_02_2	Nuclei_frac
P23396	GGKPEPPA [iTRAQ_N1	3 227-242	4,81	939,508	2012_02_2	Nuclei_frac
P23396	GLCAIAQA [iTRAQ_N1	2 94-105	7,097	716,889	2012_02_2	Nuclei_frac
P23396	GLCAIAQA [iTRAQ_N1	2 94-105	6,967	716,889	2012_02_2	Nuclei_frac
P23396	GLCAIAQA [iTRAQ_N1	2 94-105	5,124	478,262	2012_02_2	Nuclei_frac
P23396	IMLPWDPT [iTRAQ_N1	3 187-196	5,6	731,408	2012_02_2	Nuclei_frac
P23396	KFVADGIFI [iTRAQ_N1	3 9-17	5,653	486,302	2012_02_2	Nuclei_frac
P23396	KFVADGIFI [iTRAQ_N1	3 9-17	5,424	486,3	2012_02_2	Nuclei_frac
P23396	TEIILATR [iTRAQ_N1	1 45-53	6,915	587,37	2012_02_2	Nuclei_frac

P23396	TEIILATR [iTRAQ_N1	1 45-53	6,135	587,371	2012_02_2 Nuclei_frac
P46940	DHINDIHK [iTRAQ_N1	2 833-840	5,655	419,247	2012_02_2 Nuclei_frac
P46940	GVLLEIEDL [iTRAQ_N1	2 1571-1585	5,777	678,393	2012_02_2 Nuclei_frac
P46940	IIGNLLYYR [iTRAQ_N1	1 1185-1193	8,064	634,878	2012_02_2 Nuclei_frac
P46940	ILAIGLINEA [iTRAQ_N1	2 538-555	8,418	724,412	2012_02_2 Nuclei_frac
P46940	ITLQDVVS [iTRAQ_N1	2 924-934	8,438	505,631	2012_02_2 Nuclei_frac
P46940	ITLQDVVS [iTRAQ_N1	2 924-934	7,36	505,631	2012_02_2 Nuclei_frac
P46940	LAVALIN [iTRAQ_N1	2 388-400	6,965	792,509	2012_02_2 Nuclei_frac
P46940	LAVALIN [iTRAQ_N1	2 388-400	6,001	528,676	2012_02_2 Nuclei_frac
P46940	LEGVLAEV [iTRAQ_N1	1 567-584	7,914	733,736	2012_02_2 Nuclei_frac
P46940	LGNFFSPK [iTRAQ_N1	2 80-87	5,545	599,347	2012_02_2 Nuclei_frac
O00571,O1	DLLDLLVE [iTRAQ_N1	2 554-563	7,212	708,931	2012_02_2 Nuclei_frac
O00571,O1	DLLDLLVE [iTRAQ_N1	2 554-563	5,664	472,957	2012_02_2 Nuclei_frac
O00571,O1	GLDISNVK [iTRAQ_N1	2 503-510	5,661	567,343	2012_02_2 Nuclei_frac
O00571,O1	QYPISLVL [iTRAQ_N1	1 264-275	8,256	751,447	2012_02_2 Nuclei_frac
O00571,O1	SFLDLLN [iTRAQ_N1	2 428-439	7,389	790,471	2012_02_2 Nuclei_frac
O00571,O1	SFLDLLN [iTRAQ_N1	2 428-439	6,301	527,316	2012_02_2 Nuclei_frac
O00571,O1	TAAFLLPIL [iTRAQ_N1	1 230-251	5,64	826,126	2012_02_2 Nuclei_frac
O00571,O1	VGNLGLAT [iTRAQ_N1	1 534-547	11,945	834,948	2012_02_2 Nuclei_frac
O00571,O1	VGNLGLAT [iTRAQ_N1	1 534-547	9,01	556,968	2012_02_2 Nuclei_frac
O00571,O1	VRPCVVYC [iTRAQ_N1	2 294-310	9,98	678,036	2012_02_2 Nuclei_frac
P62805	DAVITYTEF [iTRAQ_N1	2 68-77	7,848	474,923	2012_02_2 Nuclei_frac
P62805	DAVITYTEF [iTRAQ_N1	2 68-77	6,057	474,922	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	7,774	538,659	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	7,388	807,484	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	6,963	538,659	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	6,572	538,658	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	5,907	538,658	2012_02_2 Nuclei_frac
P62805	DNIQGITKF [iTRAQ_N1	2 24-35	4,834	404,246	2012_02_2 Nuclei_frac
P62805	GVLKVFLE [iTRAQ_N1	2 56-67	5,471	559,022	2012_02_2 Nuclei_frac
P62805	ISGLIYEETF [iTRAQ_N1	1 46-55	8,288	662,867	2012_02_2 Nuclei_frac
P62805	ISGLIYEETF [iTRAQ_N1	1 46-55	7,473	442,247	2012_02_2 Nuclei_frac
P62805	RISGLIYEET [iTRAQ_N1	1 45-55	8,227	740,917	2012_02_2 Nuclei_frac
P62805	RISGLIYEET [iTRAQ_N1	1 45-55	7,127	494,281	2012_02_2 Nuclei_frac
P62805	TLYGFEGG [iTRAQ_N1	1 96-102	5,177	429,728	2012_02_2 Nuclei_frac
P62805	TLYGFEGG [iTRAQ_N1	1 96-102	5,153	429,729	2012_02_2 Nuclei_frac
P62805	TVTAMDV [iTRAQ_N1	3 80-92	6,355	591,006	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	6,804	567,345	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	6,787	567,344	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5,904	567,345	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5,73	567,344	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5,725	567,344	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5,479	567,343	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5,425	567,345	2012_02_2 Nuclei_frac
P62805	VFLENVIR [iTRAQ_N1	1 60-67	5	567,345	2012_02_2 Nuclei_frac
P20700	ALYETELA [iTRAQ_N1	1 79-89	7,936	698,367	2012_02_2 Nuclei_frac
P20700	ALYETELA [iTRAQ_N1	1 79-90	6,289	517,947	2012_02_2 Nuclei_frac
P20700	DAALATAI [iTRAQ_N1	3 145-156	8,281	535,992	2012_02_2 Nuclei_frac

P20700	DAALATAI [iTRAQ_N1	3 145-156	8,266	535,992	2012_02_2	Nuclei_frac
P20700	DAALATAI [iTRAQ_N1	3 145-156	7,892	535,992	2012_02_2	Nuclei_frac
P20700	DAALATAI [iTRAQ_N1	3 145-156	7,84	535,992	2012_02_2	Nuclei_frac
P20700	IESLSSQLS [iTRAQ_N1	2 299-311	10,478	867,997	2012_02_2	Nuclei_frac
P20700	IESLSSQLS [iTRAQ_N1	2 299-311	7,979	579	2012_02_2	Nuclei_frac
P20700	IQELEDLLA [iTRAQ_N1	2 320-329	5,465	730,436	2012_02_2	Nuclei_frac
P20700	IQELEDLLA [iTRAQ_N1	2 320-329	5,449	730,436	2012_02_2	Nuclei_frac
P20700	IQELEDLLA [iTRAQ_N1	2 320-329	5,225	730,436	2012_02_2	Nuclei_frac
P20700	IQELEDLLA [iTRAQ_N1	2 320-329	4,948	487,293	2012_02_2	Nuclei_frac
P20700	LAVYIDK [iTRAQ_N1	2 42-48	4,818	555,344	2012_02_2	Nuclei_frac
P20700	LAVYIDKV [iTRAQ_N1	2 42-50	5,171	455,623	2012_02_2	Nuclei_frac
P20700	LYKEELEQ [iTRAQ_N1	3 258-270	7,418	695,387	2012_02_2	Nuclei_frac
P55072	ETVVEVPC [iTRAQ_N1	2 465-486	9,258	929,502	2012_02_2	Nuclei_frac
P55072	ETVVEVPC [iTRAQ_N1	2 465-486	6,36	697,376	2012_02_2	Nuclei_frac
P55072	GILLYGPPC [iTRAQ_N1	2 239-250	7,813	730,94	2012_02_2	Nuclei_frac
P55072	GILLYGPPC [iTRAQ_N1	2 239-250	5,676	487,629	2012_02_2	Nuclei_frac
P55072	KGDIFLVR [iTRAQ_N1	2 147-154	4,866	412,595	2012_02_2	Nuclei_frac
P55072	LDQLIYPLI [iTRAQ_N1	2 638-650	6,391	923,034	2012_02_2	Nuclei_frac
P55072	LGDVISIQP [iTRAQ_N1	3 95-108	6,494	915,009	2012_02_2	Nuclei_frac
P55072	NAPAIIFIDE [iTRAQ_N1	2 295-311	9,357	1050,104	2012_02_2	Nuclei_frac
P55072	NAPAIIFIDE [iTRAQ_N1	2 295-311	6,895	700,405	2012_02_2	Nuclei_frac
P55072	QAAPCVLF [iTRAQ_N1	3 567-583	11,636	1106,579	2012_02_2	Nuclei_frac
P55072	QAAPCVLF [iTRAQ_N1	3 567-583	6,983	738,057	2012_02_2	Nuclei_frac
P50990	AIADTGAN [iTRAQ_N1	2 281-295	11,077	830,977	2012_02_2	Nuclei_frac
P50990	AIADTGAN [iTRAQ_N1	2 281-295	6,963	554,322	2012_02_2	Nuclei_frac
P50990	AIADTGAN [iTRAQ_N1	2 281-295	6,238	554,321	2012_02_2	Nuclei_frac
P50990	AVDDGVN [iTRAQ_N1	2 390-399	7,516	677,368	2012_02_2	Nuclei_frac
P50990	LATNAAV [iTRAQ_N1	1 509-519	11,368	636,891	2012_02_2	Nuclei_frac
P50990	LFVTNDA [iTRAQ_N1	1 62-73	7,741	739,43	2012_02_2	Nuclei_frac
P50990	LFVTNDA [iTRAQ_N1	1 62-73	7,735	739,43	2012_02_2	Nuclei_frac
P50990	LFVTNDA [iTRAQ_N1	1 62-73	7,261	739,428	2012_02_2	Nuclei_frac
P50990	LIAQACVS [iTRAQ_N1	2 181-202	10,072	873,117	2012_02_2	Nuclei_frac
P50990	LVPGGGA [iTRAQ_N1	2 407-420	7,865	821,987	2012_02_2	Nuclei_frac
Q9NQC3_1S	AYLESEVA [iTRAQ_N1	2 256-271	9,728	1048,577	2012_02_2	Nuclei_frac
Q9NQC3_1S	GPLPAAPP [iTRAQ_N1	1 92-104	9,542	708,411	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	11,365	841,459	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	11,11	841,461	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	10,845	841,454	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	10,03	841,457	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	7,003	561,306	2012_02_2	Nuclei_frac
Q9NQC3_1S	GSSGSVV [iTRAQ_N1	1 180-193	6,843	561,306	2012_02_2	Nuclei_frac
Q9NQC3_1S	HQAQIDHY [iTRAQ_N1	2 339-352	6,272	632,682	2012_02_2	Nuclei_frac
Q9NQC3_1S	HQAQIDHY [iTRAQ_N1	2 339-352	5,244	474,764	2012_02_2	Nuclei_frac
Q9NQC3_1S	RGSSGSVV [iTRAQ_N1	1 179-193	8,448	613,344	2012_02_2	Nuclei_frac
Q9NQC3_1S	RGSSGSVV [iTRAQ_N1	2 179-193	7,901	639,999	2012_02_2	Nuclei_frac
Q9NQC3_1S	YSNSALGH [iTRAQ_N1	3 272-285	10,022	617,992	2012_02_2	Nuclei_frac
P08865	AIVAIENPA [iTRAQ_N1	1 63-79	9,474	943,03	2012_02_2	Nuclei_frac
P08865	AIVAIENPA [iTRAQ_N1	1 63-79	4,745	629,024	2012_02_2	Nuclei_frac

P08865	FAAATGA ⁺ [iTRAQ_N1	1 89-101	8,986	449,921	2012_02_2	Nuclei_frac
P08865	FTPGTFTN [iTRAQ_N1	1 102-116	11,122	921,987	2012_02_2	Nuclei_frac
P08865	KSDGIYIINL [iTRAQ_N1	3 41-51	5,353	848,523	2012_02_2	Nuclei_frac
P08865	KSDGIYIINL [iTRAQ_N1	3 41-51	5,078	566,017	2012_02_2	Nuclei_frac
P08865	KSDGIYIINL [iTRAQ_N1	3 41-51	4,884	566,017	2012_02_2	Nuclei_frac
P08865	LLVVTDPR [iTRAQ_N1	1 120-127	7,42	528,832	2012_02_2	Nuclei_frac
P08865	LLVVTDPR [iTRAQ_N1	1 120-127	7,15	528,831	2012_02_2	Nuclei_frac
P08865	LLVVTDPR [iTRAQ_N1	1 120-127	5,344	528,831	2012_02_2	Nuclei_frac
P08865	SDGIYIINLK [iTRAQ_N1	2 42-51	5,63	712,426	2012_02_2	Nuclei_frac
P08865	YVDIAIPCN [iTRAQ_N1	3 155-165	7,146	797,93	2012_02_2	Nuclei_frac
	ASVGFGGS [iTRAQ_N1	3 268-279	6,922	511,597	2012_02_2	Nuclei_frac
	AVQALCA' [iTRAQ_N1	2 191-205	8,655	648,342	2012_02_2	Nuclei_frac
	DVLNLVYL [iTRAQ_N1	2 280-298	9,567	782,428	2012_02_2	Nuclei_frac
	INAWNSPT [iTRAQ_N1	2 42-58	6,475	734,411	2012_02_2	Nuclei_frac
	RIPYAPSGE [iTRAQ_N1	2 470-481	6,633	539,323	2012_02_2	Nuclei_frac
	RIPYAPSGE [iTRAQ_N1	2 470-481	5,961	539,319	2012_02_2	Nuclei_frac
	VLDGLHNE [iTRAQ_N1	2 444-464	6,727	871,825	2012_02_2	Nuclei_frac
	VLIGGDETI [iTRAQ_N1	1 178-190	9,563	757,9	2012_02_2	Nuclei_frac
	VLIGGDETI [iTRAQ_N1	1 178-190	6,302	757,9	2012_02_2	Nuclei_frac
P05556_ISC	DKLPQPVC [iTRAQ_N1	4 657-672	10,052	759,751	2012_02_2	Nuclei_frac
P05556_ISC	DKLPQPVC [iTRAQ_N1	4 657-672	9,486	759,75	2012_02_2	Nuclei_frac
P05556_ISC	DKLPQPVC [iTRAQ_N1	4 657-672	7,141	570,065	2012_02_2	Nuclei_frac
P05556_ISC	DKLPQPVC [iTRAQ_N1	4 657-672	6,993	570,065	2012_02_2	Nuclei_frac
P05556_ISC	IGFGSFVEK [iTRAQ_N1	2 162-170	5,413	636,366	2012_02_2	Nuclei_frac
P05556_ISC	LKPEDITQI [iTRAQ_N1	2 86-102	7,196	769,791	2012_02_2	Nuclei_frac
P05556_ISC	LKPEDITQI [iTRAQ_N1	2 86-102	7,142	769,792	2012_02_2	Nuclei_frac
P05556_ISC	LLVFSTDA [iTRAQ_N1	2 253-269	8,568	690,703	2012_02_2	Nuclei_frac
P05556_ISC	LLVFSTDA [iTRAQ_N1	2 253-269	4,912	518,273	2012_02_2	Nuclei_frac
P05556_ISC	LSEGVTSIY [iTRAQ_N1	2 369-378	8,667	692,901	2012_02_2	Nuclei_frac
P05556_ISC	LSEGVTSIY [iTRAQ_N1	2 369-378	8,114	692,9	2012_02_2	Nuclei_frac
P05556_ISC	LSEGVTSIY [iTRAQ_N1	2 369-378	7,793	692,9	2012_02_2	Nuclei_frac
P05556_ISC	LSENNIQTI [iTRAQ_N1	2 306-326	6,736	920,16	2012_02_2	Nuclei_frac
P05556_ISC	NVLSLTNK [iTRAQ_N1	3 201-218	7,776	798,464	2012_02_2	Nuclei_frac
Q5VTE0,Q0	EHALLAYT [iTRAQ_N1	2 135-146	6,207	534,987	2012_02_2	Nuclei_frac
Q5VTE0,Q0	IGGIGTVPV [iTRAQ_N1	1 256-266	6,989	585,36	2012_02_2	Nuclei_frac
Q5VTE0,Q0	LPLQDVYK [iTRAQ_N1	2 248-255	5,534	632,382	2012_02_2	Nuclei_frac
Q5VTE0,Q0	LPLQDVYK [iTRAQ_N1	2 248-255	5,502	632,384	2012_02_2	Nuclei_frac
Q5VTE0,Q0	LPLQDVYK [iTRAQ_N1	2 248-255	5,308	632,382	2012_02_2	Nuclei_frac
Q5VTE0,Q0	LPLQDVYK [iTRAQ_N1	2 248-255	5,082	632,382	2012_02_2	Nuclei_frac
Q5VTE0,Q0	NMITGTSQ [iTRAQ_N1	3 101-129	5,374	800,168	2012_02_2	Nuclei_frac
Q5VTE0,Q0	QTVAVGV [iTRAQ_N1	2 431-439	6,512	601,89	2012_02_2	Nuclei_frac
Q5VTE0,Q0	QTVAVGV [iTRAQ_N1	2 431-439	4,912	401,597	2012_02_2	Nuclei_frac
Q5VTE0,Q0	THINIVVIGI [iTRAQ_N1	2 6-20	8,079	626,365	2012_02_2	Nuclei_frac
Q5VTE0,Q0	THINIVVIGI [iTRAQ_N1	2 6-20	6,523	470,026	2012_02_2	Nuclei_frac
Q5VTE0,Q0	THINIVVIGI [iTRAQ_N1	2 6-20	6,422	470,027	2012_02_2	Nuclei_frac
Q5VTE0,Q0	THINIVVIGI [iTRAQ_N1	2 6-20	5,758	470,027	2012_02_2	Nuclei_frac
Q5VTE0,Q0	VETGVLKF [iTRAQ_N1	4 267-290	8,683	988,571	2012_02_2	Nuclei_frac
Q5VTE0,Q0	VETGVLKF [iTRAQ_N1	3 267-290	8,068	983,239	2012_02_2	Nuclei_frac
Q5VTE0,Q0	VETGVLKF [iTRAQ_N1	4 267-290	8,057	988,57	2012_02_2	Nuclei_frac

Q5VTE0,Q0 VETGVLKF [iTRAQ_N1	3	267-290	7,413	983,237	2012_02_2	Nuclei_frac
Q5VTE0,Q0 VETGVLKF [iTRAQ_N1	4	267-290	7,25	988,572	2012_02_2	Nuclei_frac
Q5VTE0,Q0 VETGVLKF [iTRAQ_N1	3	267-290	4,984	737,678	2012_02_2	Nuclei_frac
Q5VTE0,Q0 VETGVLKF [iTRAQ_N1	4	267-290	4,792	741,679	2012_02_2	Nuclei_frac
Q5VTE0,Q0 YYVTIIDAP [iTRAQ_N1	1	85-96	6,87	774,92	2012_02_2	Nuclei_frac
Q5VTE0,Q0 YYVTIIDAP [iTRAQ_N1	1	85-96	6,709	516,949	2012_02_2	Nuclei_frac
Q5VTE0,Q0 YYVTIIDAP [iTRAQ_N1	1	85-96	6,437	516,949	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	2	97-109	10,113	858,96	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	2	97-109	9,525	572,974	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	2	97-109	7,811	572,974	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	2	97-109	7,183	572,975	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	2	97-109	6,5	572,974	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	3	97-110	9,86	663,707	2012_02_2	Nuclei_frac
P45880_CH LTFDITFS [iTRAQ_N1	3	97-110	8,678	663,707	2012_02_2	Nuclei_frac
P45880_CH LTLALVD [iTRAQ_N1	2	257-266	8,277	652,907	2012_02_2	Nuclei_frac
P45880_CH LTLALVD [iTRAQ_N1	2	257-266	7,721	652,907	2012_02_2	Nuclei_frac
P45880_CH LTLALVD [iTRAQ_N1	2	257-266	4,943	435,607	2012_02_2	Nuclei_frac
P45880_CH NNFAVGIF [iTRAQ_N1	1	167-174	7,511	542,788	2012_02_2	Nuclei_frac
P45880_CH NNFAVGIF [iTRAQ_N1	1	167-174	7,471	542,787	2012_02_2	Nuclei_frac
P45880_CH SCSEVIFS [iTRAQ_N1	3	35-53	8,485	732,67	2012_02_2	Nuclei_frac
P45880_CH YQLDPTAS [iTRAQ_N1	2	225-236	9,143	791,442	2012_02_2	Nuclei_frac
P45880_CH YQLDPTAS [iTRAQ_N1	2	225-236	8,6	791,444	2012_02_2	Nuclei_frac
P45880_CH YQLDPTAS [iTRAQ_N1	2	225-236	8,298	791,445	2012_02_2	Nuclei_frac
P45880_CH YQLDPTAS [iTRAQ_N1	2	225-236	6,168	527,964	2012_02_2	Nuclei_frac
P45880_CH YQLDPTAS [iTRAQ_N1	2	225-236	5,826	527,963	2012_02_2	Nuclei_frac
P51991 EDSVKPGA [iTRAQ_N1	3	92-104	6,676	605,024	2012_02_2	Nuclei_frac
P51991 IETIEVMED [iTRAQ_N1	1	130-139	6,882	689,871	2012_02_2	Nuclei_frac
P51991 IFVGGIKED [iTRAQ_N1	2	106-121	5,582	724,391	2012_02_2	Nuclei_frac
P51991 KIFVGGIK [iTRAQ_N1	3	105-112	5,105	647,435	2012_02_2	Nuclei_frac
P51991 KIFVGGIK [iTRAQ_N1	3	105-112	4,865	647,435	2012_02_2	Nuclei_frac
P51991 KLFIGGLSF [iTRAQ_N1	2	14-30	9,068	729,737	2012_02_2	Nuclei_frac
P51991 KLFIGGLSF [iTRAQ_N1	3	14-30	7,769	1101,109	2012_02_2	Nuclei_frac
P51991 LFIGGLSFE [iTRAQ_N1	2	15-35	6,485	683,109	2012_02_2	Nuclei_frac
P51991 LFIGGLSFE [iTRAQ_N1	2	15-35	5,019	683,109	2012_02_2	Nuclei_frac
P51991 SSGSPYGG [iTRAQ_N1	1	333-354	13,261	1027,951	2012_02_2	Nuclei_frac
P51991 SSGSPYGG [iTRAQ_N1	1	333-354	8,746	685,637	2012_02_2	Nuclei_frac
AVCMLSN [iTRAQ_N1	3	374-390	9,063	1013,003	2012_02_2	Nuclei_frac
AVCMLSN [iTRAQ_N1	2	374-390	7,356	670,341	2012_02_2	Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1	230-243	9,344	816,497	2012_02_2	Nuclei_frac
LISQIVSSIT [iTRAQ_N1	1	230-243	9,04	544,666	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1	216-229	6,968	621,667	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1	216-229	6,265	621,667	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1	216-229	5,619	931,997	2012_02_2	Nuclei_frac
NLDIERPTY [iTRAQ_N1	1	216-229	4,967	621,667	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2	85-96	8,844	849,994	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2	85-96	6,192	566,998	2012_02_2	Nuclei_frac
QLFHPEQL [iTRAQ_N1	2	85-96	5,67	566,998	2012_02_2	Nuclei_frac
TIQFVDWC [iTRAQ_N1	3	340-352	9,346	943,991	2012_02_2	Nuclei_frac
TIQFVDWC [iTRAQ_N1	3	340-352	8,783	943,991	2012_02_2	Nuclei_frac

	TIQFVDWC [iTRAQ_N1	3 340-352	7,041	629,665	2012_02_2	Nuclei_frac
	TIQFVDWC [iTRAQ_N1	3 340-352	6,565	629,661	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	8,943	1057,101	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	7,319	1057,103	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	7,156	1057,097	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	6,887	705,069	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	6,34	705,07	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	6,148	705,069	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	5,834	705,07	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	5,274	705,069	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	5,262	705,071	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	4,88	705,069	2012_02_2	Nuclei_frac
	VGINYQPP [iTRAQ_N1	2 353-370	4,766	529,053	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	8,858	796,967	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	8,066	796,967	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	8,059	531,646	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	6,886	531,646	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	6,798	531,647	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	6,678	531,647	2012_02_2	Nuclei_frac
	Q8WWI1_1: AFENLLGQ [iTRAQ_N1	2 195-206	5,963	531,648	2012_02_2	Nuclei_frac
	Q8WWI1_1: ALEDSSFL [iTRAQ_N1	2 207-216	6,575	485,28	2012_02_2	Nuclei_frac
	Q8WWI1_1: ALEDSSFL [iTRAQ_N1	2 207-216	5,563	485,28	2012_02_2	Nuclei_frac
	Q8WWI1_1: AQETGHLV [iTRAQ_N1	1 777-788	5,921	500,598	2012_02_2	Nuclei_frac
	Q8WWI1_1: ISINQTPGK [iTRAQ_N1	2 709-717	6,75	623,375	2012_02_2	Nuclei_frac
	Q8WWI1_1: KAQSNPY [iTRAQ_N1	3 179-194	5,018	569,821	2012_02_2	Nuclei_frac
	Q8WWI1_1: KSYTSDLQ [iTRAQ_N1	3 416-424	6,713	501,292	2012_02_2	Nuclei_frac
	Q8WWI1_1: KSYTSDLQ [iTRAQ_N1	3 416-424	5,455	501,293	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	6,917	1002,095	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	6,187	668,398	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	5,789	668,398	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	5,601	668,399	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	5,056	668,399	2012_02_2	Nuclei_frac
	Q8WWI1_1: LSTPIAGL [iTRAQ_N1	2 115-130	4,798	668,4	2012_02_2	Nuclei_frac
	Q8WWI1_1: SLDFGFTIK [iTRAQ_N1	2 718-726	5,652	658,381	2012_02_2	Nuclei_frac
	Q8WWI1_1: SLDFGFTIK [iTRAQ_N1	2 718-726	5,039	439,255	2012_02_2	Nuclei_frac
	Q8WWI1_1: SLDFGFTIK [iTRAQ_N1	2 718-726	5,007	658,382	2012_02_2	Nuclei_frac
P13489	DLCGIVAS [iTRAQ_N1	3 217-225	5,847	625,854	2012_02_2	Nuclei_frac
P13489	ELCQGLGC [iTRAQ_N1	2 359-372	8,58	829,445	2012_02_2	Nuclei_frac
P13489	ELCQGLGC [iTRAQ_N1	2 359-372	8,137	829,445	2012_02_2	Nuclei_frac
P13489	LGDVGMAI [iTRAQ_N1	3 238-256	8,814	723,707	2012_02_2	Nuclei_frac
P13489	LQLEYCSL [iTRAQ_N1	3 146-166	8,282	837,763	2012_02_2	Nuclei_frac
P13489	LSLQNCCL [iTRAQ_N1	4 89-109	8,268	804,405	2012_02_2	Nuclei_frac
P13489	SNELGDVC [iTRAQ_N1	4 64-85	4,961	672,346	2012_02_2	Nuclei_frac
P13489	VNPALAE [iTRAQ_N1	1 53-63	7,261	677,407	2012_02_2	Nuclei_frac
P15880	AFVAIGDY [iTRAQ_N1	2 125-141	7,565	669,042	2012_02_2	Nuclei_frac
P15880	ATFDAISK [iTRAQ_N1	2 238-245	5,057	570,828	2012_02_2	Nuclei_frac
P15880	ATFDAISK [iTRAQ_N1	2 238-245	4,959	570,829	2012_02_2	Nuclei_frac
P15880	ATFDAISK [iTRAQ_N1	2 238-245	4,831	570,829	2012_02_2	Nuclei_frac
P15880	ESEIIDFFLC [iTRAQ_N1	3 89-107	7,332	862,49	2012_02_2	Nuclei_frac

P15880	ESEIIDFFLC [iTRAQ_N1	3 89-107	4,817	647,116	2012_02_2	Nuclei_frac
P15880	GCTATLGN [iTRAQ_N1	3 227-237	7,409	714,382	2012_02_2	Nuclei_frac
P15880	GCTATLGN [iTRAQ_N1	3 227-237	5,562	476,59	2012_02_2	Nuclei_frac
P15880	GTGIVSAP' [iTRAQ_N1	2 200-210	6,852	657,406	2012_02_2	Nuclei_frac
P15880	GTGIVSAP' [iTRAQ_N1	2 200-210	4,725	438,606	2012_02_2	Nuclei_frac
P15880	SPYQEFTD [iTRAQ_N1	2 263-274	8,513	584,646	2012_02_2	Nuclei_frac
P15880	SPYQEFTD [iTRAQ_N1	2 263-274	7,485	584,646	2012_02_2	Nuclei_frac
P15880	TYSYLTPD [iTRAQ_N1	2 246-256	9,162	837,953	2012_02_2	Nuclei_frac
P15880	TYSYLTPD [iTRAQ_N1	2 246-256	8,586	837,953	2012_02_2	Nuclei_frac
P15880	TYSYLTPD [iTRAQ_N1	2 246-256	6,391	558,971	2012_02_2	Nuclei_frac
O00159_1S	GVSFYEVP [iTRAQ_N1	1 71-90	7,158	804,427	2012_02_2	Nuclei_frac
O00159_1S	HLGYKPEE [iTRAQ_N1	3 665-674	5,595	424,743	2012_02_2	Nuclei_frac
O00159_1S	KYEAFLQR [iTRAQ_N1	2 632-639	7,519	448,263	2012_02_2	Nuclei_frac
O00159_1S	LLSVEGST [iTRAQ_N1	1 306-315	7,459	609,864	2012_02_2	Nuclei_frac
O00159_1S	LLSVEGST [iTRAQ_N1	1 306-315	5,041	609,85	2012_02_2	Nuclei_frac
O00159_1S	MSLLQLVE [iTRAQ_N1	3 571-583	5,064	602,696	2012_02_2	Nuclei_frac
O00159_1S	TFTWLVGf [iTRAQ_N1	2 354-361	5,102	620,373	2012_02_2	Nuclei_frac
O00159_1S	TSFLLNLR [iTRAQ_N1	1 779-786	7,299	554,336	2012_02_2	Nuclei_frac
O00159_1S	YLGLLENLI [iTRAQ_N1	1 613-621	6,542	617,869	2012_02_2	Nuclei_frac
O00159_1S	YLGLLENLI [iTRAQ_N1	1 613-621	5,868	617,869	2012_02_2	Nuclei_frac
Q12906_1S	AYAALAAI [iTRAQ_N1	2 578-587	5,945	654,893	2012_02_2	Nuclei_frac
Q12906_1S	EDITQSAQ [iTRAQ_N1	1 312-323	9,457	756,901	2012_02_2	Nuclei_frac
Q12906_1S	EDITQSAQ [iTRAQ_N1	1 312-323	7,478	504,936	2012_02_2	Nuclei_frac
Q12906_1S	EKPTTALL [iTRAQ_N1	3 118-127	5,014	516,651	2012_02_2	Nuclei_frac
Q12906_1S	EKPTTALL [iTRAQ_N1	3 118-127	4,923	516,651	2012_02_2	Nuclei_frac
Q12906_1S	EPPLSLTIH [iTRAQ_N1	1 162-177	6,601	635,045	2012_02_2	Nuclei_frac
Q12906_1S	LAAFGQLf [iTRAQ_N1	2 324-332	4,91	424,928	2012_02_2	Nuclei_frac
Q12906_1S	LFPDTPLA [iTRAQ_N1	2 588-600	8,421	851,986	2012_02_2	Nuclei_frac
Q12906_1S	LFPDTPLA [iTRAQ_N1	3 588-601	5,614	659,059	2012_02_2	Nuclei_frac
Q12906_1S	VPTWGPLf [iTRAQ_N1	1 240-247	5,575	535,317	2012_02_2	Nuclei_frac
P19367_1S	ATDCVGHl [iTRAQ_N1	2 613-626	6,658	567,306	2012_02_2	Nuclei_frac
P19367_1S	DFNPTATV [iTRAQ_N1	2 42-50	7,028	640,863	2012_02_2	Nuclei_frac
P19367_1S	GAALITAV [iTRAQ_N1	1 888-898	7,809	586,369	2012_02_2	Nuclei_frac
P19367_1S	GAAMVTA [iTRAQ_N1	2 440-450	9,02	635,342	2012_02_2	Nuclei_frac
P19367_1S	ITPELLTR [iTRAQ_N1	1 312-319	5,449	543,837	2012_02_2	Nuclei_frac
P19367_1S	ITPELLTR [iTRAQ_N1	1 312-319	5,17	543,836	2012_02_2	Nuclei_frac
P19367_1S	NILIDFTK [iTRAQ_N1	2 744-751	6,279	626,383	2012_02_2	Nuclei_frac
P19367_1S	SANLVAA ⁺ [iTRAQ_N1	1 370-384	9,204	814,485	2012_02_2	Nuclei_frac
P19367_1S	SANLVAA ⁺ [iTRAQ_N1	1 370-384	8,084	543,325	2012_02_2	Nuclei_frac
	AIFLADGN' [iTRAQ_N1	1 224-239	10,827	930,493	2012_02_2	Nuclei_frac
	NADPILISL [iTRAQ_N1	2 382-391	5,392	686,427	2012_02_2	Nuclei_frac
	NILDSKPT/ [iTRAQ_N1	3 408-418	6,217	544,994	2012_02_2	Nuclei_frac
	QLALWNPI [iTRAQ_N1	2 244-251	6,791	629,382	2012_02_2	Nuclei_frac
	QLALWNPI [iTRAQ_N1	2 244-251	6,065	629,382	2012_02_2	Nuclei_frac
	QLALWNPI [iTRAQ_N1	2 244-251	5,725	629,38	2012_02_2	Nuclei_frac
	QLALWNPI [iTRAQ_N1	2 244-251	5,338	419,924	2012_02_2	Nuclei_frac
	SIKDTICNQ [iTRAQ_N1	3 450-461	6,249	589,639	2012_02_2	Nuclei_frac
	SIKDTICNQ [iTRAQ_N1	3 450-461	5,577	589,642	2012_02_2	Nuclei_frac

	VGIVAWHF [iTRAQ_N1	1 133-143	5,977	450,931	2012_02_2 Nuclei_frac
	VTWDSSF [iTRAQ_N1	2 32-44	9,582	841,906	2012_02_2 Nuclei_frac
	VTWDSSF [iTRAQ_N1	2 32-44	5,412	561,608	2012_02_2 Nuclei_frac
	APILIATDV [iTRAQ_N1	1 392-403	7,964	685,912	2012_02_2 Nuclei_frac
	APILIATDV [iTRAQ_N1	1 392-403	7,162	685,911	2012_02_2 Nuclei_frac
	APILIATDV [iTRAQ_N1	1 392-403	6,767	685,913	2012_02_2 Nuclei_frac
	DGWPAMG [iTRAQ_N1	3 364-375	6,359	529,934	2012_02_2 Nuclei_frac
	DWVLNEF [iTRAQ_N1	2 381-388	4,75	669,869	2012_02_2 Nuclei_frac
	GVEICIATP [iTRAQ_N1	2 217-227	6,765	658,861	2012_02_2 Nuclei_frac
	GVEICIATP [iTRAQ_N1	2 217-227	4,859	658,853	2012_02_2 Nuclei_frac
	LIDFLECGK [iTRAQ_N1	3 228-236	5,112	691,887	2012_02_2 Nuclei_frac
	LLQLVEDR [iTRAQ_N1	1 471-478	5,849	565,341	2012_02_2 Nuclei_frac
	NFYQEHDP [iTRAQ_N1	1 57-67	6,479	511,925	2012_02_2 Nuclei_frac
	QVSDLISV [iTRAQ_N1	1 452-461	7,533	637,383	2012_02_2 Nuclei_frac
	QVSDLISV [iTRAQ_N1	1 452-461	6,818	637,384	2012_02_2 Nuclei_frac
	QVSDLISV [iTRAQ_N1	1 452-461	6,815	637,384	2012_02_2 Nuclei_frac
P48643	AVTIFIR [iTRAQ_N1	1 381-387	6,885	482,309	2012_02_2 Nuclei_frac
P48643	DVDFELIK [iTRAQ_N1	3 202-213	6,246	608,688	2012_02_2 Nuclei_frac
P48643	EMNPALGI [iTRAQ_N1	4 483-495	7,365	601,314	2012_02_2 Nuclei_frac
P48643	IAILTCPFEI [iTRAQ_N1	4 247-260	6,649	681,742	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	9,285	978,558	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	9,254	978,557	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	8,363	652,707	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	7,787	652,707	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	7,42	652,708	2012_02_2 Nuclei_frac
P48643	LGFAGLVC [iTRAQ_N1	2 352-367	7,394	652,708	2012_02_2 Nuclei_frac
P48643	QQHVIETL [iTRAQ_N1	2 502-512	5,876	518,648	2012_02_2 Nuclei_frac
P48643	QQHVIETL [iTRAQ_N1	2 502-512	4,851	518,648	2012_02_2 Nuclei_frac
P48643	SLHDALCV [iTRAQ_N1	2 400-409	7,409	443,248	2012_02_2 Nuclei_frac
P48643	SLHDALCV [iTRAQ_N1	2 400-409	7,083	443,247	2012_02_2 Nuclei_frac
Q01518,Q0	AGAAPYVC [iTRAQ_N1	2 37-59	6,522	880,481	2012_02_2 Nuclei_frac
Q01518,Q0	ALLVTASC [iTRAQ_N1	3 84-99	11,519	682,702	2012_02_2 Nuclei_frac
Q01518,Q0	ALLVTASC [iTRAQ_N1	3 84-99	10,665	682,702	2012_02_2 Nuclei_frac
Q01518,Q0	ALLVTASC [iTRAQ_N1	3 84-99	10,194	682,702	2012_02_2 Nuclei_frac
Q01518,Q0	ALLVTASC [iTRAQ_N1	3 84-99	10,187	682,703	2012_02_2 Nuclei_frac
Q01518,Q0	INSITVDNC [iTRAQ_N1	3 366-375	6,994	484,598	2012_02_2 Nuclei_frac
Q01518,Q0	KEPAVLEL [iTRAQ_N1	3 316-326	5,875	549,001	2012_02_2 Nuclei_frac
Q01518,Q0	KEPAVLEL [iTRAQ_N1	3 316-326	4,726	549,001	2012_02_2 Nuclei_frac
Q01518,Q0	LGLVFDDV [iTRAQ_N1	2 377-394	6,673	740,103	2012_02_2 Nuclei_frac
Q01518,Q0	LSDLLAPIS [iTRAQ_N1	2 100-112	5,936	572,344	2012_02_2 Nuclei_frac
Q01518,Q0	VPTISINK [iTRAQ_N1	2 404-411	6,134	580,368	2012_02_2 Nuclei_frac
Q01518,Q0	VPTISINK [iTRAQ_N1	2 404-411	5,837	580,369	2012_02_2 Nuclei_frac
	KVPVSVNI [iTRAQ_N1	3 178-188	7,335	539,354	2012_02_2 Nuclei_frac
	KVPVSVNI [iTRAQ_N1	3 178-188	5,808	539,355	2012_02_2 Nuclei_frac
	LLPSLIGR [iTRAQ_N1	1 164-171	6,448	506,837	2012_02_2 Nuclei_frac
	LLSSDFFL [iTRAQ_N1	1 148-160	10,914	838,445	2012_02_2 Nuclei_frac
	SAALPIFS [iTRAQ_N1	2 258-277	9,167	838,778	2012_02_2 Nuclei_frac
	TVSQIISLQ [iTRAQ_N1	2 125-136	6,369	540,338	2012_02_2 Nuclei_frac

	TVSQIISLQ [iTRAQ_N1	3 125-137	9,106	631,072	2012_02_2	Nuclei_frac
	TVSQIISLQ [iTRAQ_N1	3 125-137	8,03	631,073	2012_02_2	Nuclei_frac
P15311	APDFVFYA [iTRAQ_N1	1 263-272	7,147	663,853	2012_02_2	Nuclei_frac
P15311	APDFVFYA [iTRAQ_N1	1 263-272	6,392	663,854	2012_02_2	Nuclei_frac
P15311	AQEEAERL [iTRAQ_N1	1 381-392	8,496	780,892	2012_02_2	Nuclei_frac
P15311	AQEEAERL [iTRAQ_N1	1 381-392	5,73	520,93	2012_02_2	Nuclei_frac
P15311	EVWYFGLF [iTRAQ_N1	2 40-52	6,989	653,339	2012_02_2	Nuclei_frac
P15311	IALLEEAR [iTRAQ_N1	1 427-434	5,506	529,821	2012_02_2	Nuclei_frac
P15311	IGFPWSEIR [iTRAQ_N1	1 237-245	6,595	624,848	2012_02_2	Nuclei_frac
P15311	IGFPWSEIR [iTRAQ_N1	1 237-245	6,171	624,848	2012_02_2	Nuclei_frac
P15311	IGFPWSEIR [iTRAQ_N1	1 237-245	6,021	624,847	2012_02_2	Nuclei_frac
P15311	IGFPWSEIR [iTRAQ_N1	1 237-245	5,605	624,845	2012_02_2	Nuclei_frac
P15311	KAPDFVFY [iTRAQ_N1	2 262-272	4,995	533,636	2012_02_2	Nuclei_frac
P15311	QLLTLSSEI [iTRAQ_N1	1 529-541	9,577	795,454	2012_02_2	Nuclei_frac
	EIVHIQAGC [iTRAQ_N1	3 3-19	8,759	714,385	2012_02_2	Nuclei_frac
	FPGQLNAC [iTRAQ_N1	1 242-251	6,113	637,854	2012_02_2	Nuclei_frac
	FPGQLNAC [iTRAQ_N1	1 242-251	5,592	637,853	2012_02_2	Nuclei_frac
	FPGQLNAC [iTRAQ_N1	1 242-251	5,557	637,854	2012_02_2	Nuclei_frac
	LAVNMVPI [iTRAQ_N1	2 253-262	6,896	652,37	2012_02_2	Nuclei_frac
	LAVNMVPI [iTRAQ_N1	1 253-262	6,297	644,371	2012_02_2	Nuclei_frac
	LHFFMPGF [iTRAQ_N1	2 263-276	5,964	594,316	2012_02_2	Nuclei_frac
	NSSYFVEV [iTRAQ_N1	2 337-350	8,31	993,024	2012_02_2	Nuclei_frac
	NSSYFVEV [iTRAQ_N1	2 337-350	7,863	993,024	2012_02_2	Nuclei_frac
	NSSYFVEV [iTRAQ_N1	2 337-350	5,527	662,353	2012_02_2	Nuclei_frac
	NSSYFVEV [iTRAQ_N1	2 337-350	5,515	662,352	2012_02_2	Nuclei_frac
	VAVCDIPP [iTRAQ_N1	2 351-359	5,11	585,826	2012_02_2	Nuclei_frac
	YLT VATVF [iTRAQ_N1	1 310-318	8,111	607,358	2012_02_2	Nuclei_frac
	AGNFYVPA [iTRAQ_N1	2 78-88	7,296	740,908	2012_02_2	Nuclei_frac
	EANNFLWI [iTRAQ_N1	2 203-212	6,082	777,423	2012_02_2	Nuclei_frac
	EANNFLWI [iTRAQ_N1	2 203-212	5,948	777,427	2012_02_2	Nuclei_frac
	FKEANNFL [iTRAQ_N1	3 201-212	5,69	658,371	2012_02_2	Nuclei_frac
	IALTDNAL [iTRAQ_N1	1 167-177	9,558	657,899	2012_02_2	Nuclei_frac
	IALTDNAL [iTRAQ_N1	1 167-177	9,038	657,897	2012_02_2	Nuclei_frac
	IALTDNAL [iTRAQ_N1	1 167-177	5,829	657,898	2012_02_2	Nuclei_frac
	KAGNFYVF [iTRAQ_N1	3 77-88	6,338	585,006	2012_02_2	Nuclei_frac
	KAGNFYVF [iTRAQ_N1	3 77-88	5,973	585,006	2012_02_2	Nuclei_frac
	LAFVIR [iTRAQ_N1	1 89-94	5,421	431,785	2012_02_2	Nuclei_frac
	RIALTDNAL [iTRAQ_N1	1 166-177	8,604	490,968	2012_02_2	Nuclei_frac
P23284	DFMIQGGD [iTRAQ_N1	2 66-76	7,363	723,844	2012_02_2	Nuclei_frac
P23284	DFMIQGGD [iTRAQ_N1	1 66-76	6,352	715,845	2012_02_2	Nuclei_frac
P23284	HYGPGWV [iTRAQ_N1	3 99-112	6,721	593,636	2012_02_2	Nuclei_frac
P23284	SIYGERFPD [iTRAQ_N1	2 84-96	6,8	630,66	2012_02_2	Nuclei_frac
P23284	SIYGERFPD [iTRAQ_N1	2 84-96	6,697	630,66	2012_02_2	Nuclei_frac
P23284	SIYGERFPD [iTRAQ_N1	2 84-96	6,387	630,66	2012_02_2	Nuclei_frac
P23284	TVDNFVAI [iTRAQ_N1	2 39-51	9,479	826,959	2012_02_2	Nuclei_frac
P23284	TVDNFVAI [iTRAQ_N1	2 39-51	6,9	551,641	2012_02_2	Nuclei_frac
P23284	TVDNFVAI [iTRAQ_N1	2 39-51	5,677	551,642	2012_02_2	Nuclei_frac
P23284	VIFGLFGK [iTRAQ_N1	2 27-34	5,844	584,87	2012_02_2	Nuclei_frac

P23284	VIFGLFGK [iTRAQ_N1	2 27-34	5,384	584,87	2012_02_2	Nuclei_frac
P23284	VIKDFMIQC [iTRAQ_N1	2 63-76	7,243	639,015	2012_02_2	Nuclei_frac
P23284	VIKDFMIQC [iTRAQ_N1	3 63-76	5,905	644,347	2012_02_2	Nuclei_frac
P23284	VLEGMEV\ [iTRAQ_N1	1 139-147	5,152	588,335	2012_02_2	Nuclei_frac
Q9NR30	GAVEALA\ [iTRAQ_N1	1 538-559	12,318	1126,614	2012_02_2	Nuclei_frac
Q9NR30	GAVEALA\ [iTRAQ_N1	1 538-559	9,801	751,415	2012_02_2	Nuclei_frac
Q9NR30	GAVEALA\ [iTRAQ_N1	1 538-559	4,861	563,811	2012_02_2	Nuclei_frac
Q9NR30	LLDSVPPT [iTRAQ_N1	2 514-527	8,856	605,023	2012_02_2	Nuclei_frac
Q9NR30	QDAQSLHC [iTRAQ_N1	2 394-406	6,623	575,646	2012_02_2	Nuclei_frac
Q9NR30	QDAQSLHC [iTRAQ_N1	2 394-406	6,537	575,646	2012_02_2	Nuclei_frac
Q9NR30	RWQLSVA\ [iTRAQ_N1	1 634-650	9,201	714,049	2012_02_2	Nuclei_frac
Q9NR30	TAITVEHL\ [iTRAQ_N1	2 339-349	5,223	495,31	2012_02_2	Nuclei_frac
Q9NR30	TFSFAIPLIE [iTRAQ_N1	2 169-179	6,366	777,469	2012_02_2	Nuclei_frac
Q9NR30	TFSFAIPLIE [iTRAQ_N1	2 169-179	4,763	518,647	2012_02_2	Nuclei_frac
	ACAELHQM [iTRAQ_N1	3 285-296	5,898	557,634	2012_02_2	Nuclei_frac
	ACAELHQM [iTRAQ_N1	3 285-296	5,569	557,633	2012_02_2	Nuclei_frac
	AQLAAITL [iTRAQ_N1	1 623-637	7,254	881,03	2012_02_2	Nuclei_frac
	ILVGTNLVI [iTRAQ_N1	1 218-226	5,453	564,864	2012_02_2	Nuclei_frac
	ILVGTNLVI [iTRAQ_N1	1 218-226	5,415	564,864	2012_02_2	Nuclei_frac
	ILVGTNLVI [iTRAQ_N1	1 218-226	5,017	564,865	2012_02_2	Nuclei_frac
	IPVDTYNNI [iTRAQ_N1	2 404-417	4,951	631,043	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	10,982	998,555	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	10,753	998,555	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	10,582	666,038	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	9,864	666,04	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	9,476	998,556	2012_02_2	Nuclei_frac
	LFDIFSQQ\ [iTRAQ_N1	1 324-339	7,853	666,04	2012_02_2	Nuclei_frac
	LNLEHIAT\ [iTRAQ_N1	2 383-396	6,374	586,671	2012_02_2	Nuclei_frac
	QIVLTGILE [iTRAQ_N1	2 240-254	7,605	629,359	2012_02_2	Nuclei_frac
O60814_Cf	AMGIMNSF [iTRAQ_N1	2 59-73	7,656	952,463	2012_02_2	Nuclei_frac
O60814_Cf	AMGIMNSF [iTRAQ_N1	3 59-73	7,066	960,456	2012_02_2	Nuclei_frac
O60814_Cf	AMGIMNSF [iTRAQ_N1	2 59-73	5,875	635,312	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVR [iTRAQ_N1	1 94-100	6,58	480,785	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVR [iTRAQ_N1	1 94-100	6,341	480,784	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVR [iTRAQ_N1	1 94-100	5,811	480,785	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVR [iTRAQ_N1	1 94-100	5,504	480,785	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVR [iTRAQ_N1	1 94-100	4,736	480,785	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVRLI [iTRAQ_N1	2 94-109	7,523	680,423	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVRLI [iTRAQ_N1	2 94-109	6,557	680,424	2012_02_2	Nuclei_frac
O60814_Cf	EIQTAVRLI [iTRAQ_N1	2 94-109	6,034	680,424	2012_02_2	Nuclei_frac
O60814_Cf	ESYSVYVY [iTRAQ_N1	2 36-44	7,338	713,38	2012_02_2	Nuclei_frac
O60814_Cf	ESYSVYVY [iTRAQ_N1	2 36-44	7,31	713,381	2012_02_2	Nuclei_frac
O60814_Cf	ESYSVYVY [iTRAQ_N1	2 36-44	6,508	713,378	2012_02_2	Nuclei_frac
O60814_Cf	KESYSVYV [iTRAQ_N1	3 35-44	5,958	566,654	2012_02_2	Nuclei_frac
O60814_Cf	KESYSVYV [iTRAQ_N1	3 35-44	5,575	566,653	2012_02_2	Nuclei_frac
O60814_Cf	LLLPGELAI [iTRAQ_N1	2 101-109	5,141	414,608	2012_02_2	Nuclei_frac
O60814_Cf	QVHPDTGI [iTRAQ_N1	2 48-58	8,04	486,273	2012_02_2	Nuclei_frac
O60814_Cf	QVHPDTGI [iTRAQ_N1	2 48-58	7,228	486,273	2012_02_2	Nuclei_frac
O60814_Cf	QVHPDTGI [iTRAQ_N1	2 48-58	6,686	486,272	2012_02_2	Nuclei_frac

O60814_Cf QVHPDTGI [iTRAQ_N1	2 48-58	5,83	486,272	2012_02_2 Nuclei_frac
O60814_Cf QVHPDTGI [iTRAQ_N1	2 48-58	5,215	486,271	2012_02_2 Nuclei_frac
O60814_Cf QVHPDTGI [iTRAQ_N1	2 48-58	4,736	728,906	2012_02_2 Nuclei_frac
P23527_CH AMGIMNSF [iTRAQ_N1	2 58-72	7,656	952,463	2012_02_2 Nuclei_frac
P23527_CH AMGIMNSF [iTRAQ_N1	3 58-72	7,066	960,456	2012_02_2 Nuclei_frac
P23527_CH AMGIMNSF [iTRAQ_N1	2 58-72	5,875	635,312	2012_02_2 Nuclei_frac
P23527_CH EIQTAVR [iTRAQ_N1	1 93-99	6,58	480,785	2012_02_2 Nuclei_frac
P23527_CH EIQTAVR [iTRAQ_N1	1 93-99	6,341	480,784	2012_02_2 Nuclei_frac
P23527_CH EIQTAVR [iTRAQ_N1	1 93-99	5,811	480,785	2012_02_2 Nuclei_frac
P23527_CH EIQTAVR [iTRAQ_N1	1 93-99	5,504	480,785	2012_02_2 Nuclei_frac
P23527_CH EIQTAVR [iTRAQ_N1	1 93-99	4,736	480,785	2012_02_2 Nuclei_frac
P23527_CH EIQTAVRLI [iTRAQ_N1	2 93-108	7,523	680,423	2012_02_2 Nuclei_frac
P23527_CH EIQTAVRLI [iTRAQ_N1	2 93-108	6,557	680,424	2012_02_2 Nuclei_frac
P23527_CH EIQTAVRLI [iTRAQ_N1	2 93-108	6,034	680,424	2012_02_2 Nuclei_frac
P23527_CH ESYSIYVYK [iTRAQ_N1	2 35-43	6,854	720,388	2012_02_2 Nuclei_frac
P23527_CH KESYSIYVY [iTRAQ_N1	3 34-43	6,371	571,325	2012_02_2 Nuclei_frac
P23527_CH KESYSIYVY [iTRAQ_N1	3 34-43	5,132	571,326	2012_02_2 Nuclei_frac
P23527_CH LLLPGELAI [iTRAQ_N1	2 100-108	5,141	414,608	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	8,04	486,273	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	7,228	486,273	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	6,686	486,272	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	5,83	486,272	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	5,215	486,271	2012_02_2 Nuclei_frac
P23527_CH QVHPDTGI [iTRAQ_N1	2 47-57	4,736	728,906	2012_02_2 Nuclei_frac
O75643_IS(AIFEIVLNR [iTRAQ_N1	1 1094-1102	7,896	609,873	2012_02_2 Nuclei_frac
O75643_IS(AIFEIVLNR [iTRAQ_N1	1 1094-1102	6,552	609,872	2012_02_2 Nuclei_frac
O75643_IS(DILCGAAD [iTRAQ_N1	3 130-144	6,931	625,689	2012_02_2 Nuclei_frac
O75643_IS(ETYEVLLSI [iTRAQ_N1	1 111-129	8,204	765,41	2012_02_2 Nuclei_frac
O75643_IS(ILYIAPMR [iTRAQ_N1	2 538-545	5,91	568,839	2012_02_2 Nuclei_frac
O75643_IS(LELSVHLQ [iTRAQ_N1	1 1184-1195	5,758	517,312	2012_02_2 Nuclei_frac
O75643_IS(LTAIDILTT [iTRAQ_N1	2 1571-1586	7,985	640,352	2012_02_2 Nuclei_frac
O75643_IS(TYTQLVR [iTRAQ_N1	1 604-610	5,456	512,799	2012_02_2 Nuclei_frac
P40926 ANTFFVAEL [iTRAQ_N1	2 153-161	6,683	640,875	2012_02_2 Nuclei_frac
P40926 IFGVTTLDI [iTRAQ_N1	1 142-152	7,983	689,416	2012_02_2 Nuclei_frac
P40926 IFGVTTLDI [iTRAQ_N1	1 142-152	7,764	689,417	2012_02_2 Nuclei_frac
P40926 IFGVTTLDI [iTRAQ_N1	1 142-152	7,32	689,414	2012_02_2 Nuclei_frac
P40926 IFGVTTLDI [iTRAQ_N1	1 142-152	5,681	459,946	2012_02_2 Nuclei_frac
P40926 LTLYDIAH ⁺ [iTRAQ_N1	2 29-50	7,814	885,158	2012_02_2 Nuclei_frac
P40926 LTLYDIAH ⁺ [iTRAQ_N1	2 29-50	6,635	664,118	2012_02_2 Nuclei_frac
P40926 LTLYDIAH ⁺ [iTRAQ_N1	2 29-50	5,992	664,118	2012_02_2 Nuclei_frac
P40926 TIIP LISQCT [iTRAQ_N1	3 180-191	10,332	829,99	2012_02_2 Nuclei_frac
P40926 TIIP LISQCT [iTRAQ_N1	3 180-191	6,274	553,664	2012_02_2 Nuclei_frac
P40926 VAVLGAS([iTRAQ_N1	2 3-21	9,3	694,437	2012_02_2 Nuclei_frac
P40926 VAVLGAS([iTRAQ_N1	2 3-21	9,068	1041,149	2012_02_2 Nuclei_frac
P40926 VAVLGAS([iTRAQ_N1	2 3-21	8,806	694,435	2012_02_2 Nuclei_frac
P40926 VNVPVIGG [iTRAQ_N1	2 168-179	6,026	479,292	2012_02_2 Nuclei_frac
Q9BQG0_IS AQHQQAL [iTRAQ_N1	1 1077-1094	7,607	737,75	2012_02_2 Nuclei_frac
Q9BQG0_IS KLPAIALDI [iTRAQ_N1	2 263-273	5,681	504,338	2012_02_2 Nuclei_frac

Q9BQG0_1S	LITGLGVGI [iTRAQ_N1	1	77-85	4,805	515,331	2012_02_2	Nuclei_frac
Q9BQG0_1S	LLEYLR [iTRAQ_N1	1	57-62	5,768	475,795	2012_02_2	Nuclei_frac
Q9BQG0_1S	LLGAALPL [iTRAQ_N1	2	308-318	6,691	699,472	2012_02_2	Nuclei_frac
Q9BQG0_1S	LLQALAQY [iTRAQ_N1	1	162-178	9,164	732,068	2012_02_2	Nuclei_frac
Q9BQG0_1S	VYSTALSS [iTRAQ_N1	2	977-988	8,375	802,964	2012_02_2	Nuclei_frac
	AGTQIENIE [iTRAQ_N1	1	55-67	7,829	833,414	2012_02_2	Nuclei_frac
	AGTQIENIE [iTRAQ_N1	2	55-71	5,032	741,39	2012_02_2	Nuclei_frac
	CQLEINFN [iTRAQ_N1	3	339-351	7,515	633,01	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2	141-154	7,428	609,332	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2	141-154	7,153	913,495	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1	384-394	7,607	783,408	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1	384-394	7,41	783,407	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1	384-394	6,589	783,406	2012_02_2	Nuclei_frac
	GYEEWLLN [iTRAQ_N1	1	384-394	5,258	522,608	2012_02_2	Nuclei_frac
	ISNRPAFMI [iTRAQ_N1	3	354-366	5,036	579,979	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2	72-83	7,637	511,634	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	1	72-83	7,344	758,951	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2	72-83	7,344	766,947	2012_02_2	Nuclei_frac
P12236	AAYFGVYI [iTRAQ_N1	2	188-198	6,501	747,399	2012_02_2	Nuclei_frac
P12236	DFLAGGIA [iTRAQ_N1	2	10-22	8,023	761,445	2012_02_2	Nuclei_frac
P12236	DFLAGGIA [iTRAQ_N1	2	10-22	7,86	761,439	2012_02_2	Nuclei_frac
P12236	DFLAGGIA [iTRAQ_N1	2	10-22	7,581	761,45	2012_02_2	Nuclei_frac
P12236	GAWSNVL [iTRAQ_N1	1	272-279	5,688	523,797	2012_02_2	Nuclei_frac
P12236	GMGGAFVI [iTRAQ_N1	3	280-294	5,524	639,358	2012_02_2	Nuclei_frac
P12236	KGADIMYT [iTRAQ_N1	4	244-258	7,5	693,009	2012_02_2	Nuclei_frac
P12236	LLLQVQH/ [iTRAQ_N1	2	33-42	6,599	475,633	2012_02_2	Nuclei_frac
P12236	LLLQVQH/ [iTRAQ_N1	2	33-42	5,547	475,634	2012_02_2	Nuclei_frac
P12236	LLLQVQH/ [iTRAQ_N1	2	33-42	5,039	712,947	2012_02_2	Nuclei_frac
P12236	YFPTQALN [iTRAQ_N1	2	80-91	8,222	867,976	2012_02_2	Nuclei_frac
P12236	YFPTQALN [iTRAQ_N1	2	80-91	6,07	578,987	2012_02_2	Nuclei_frac
	ALEIIPR [iTRAQ_N1	1	441-447	6,121	478,307	2012_02_2	Nuclei_frac
	ALEIIPR [iTRAQ_N1	1	441-447	5,131	478,306	2012_02_2	Nuclei_frac
	ATISNDGA [iTRAQ_N1	2	56-67	8,12	746,436	2012_02_2	Nuclei_frac
	IALLNVELE [iTRAQ_N1	2	237-247	5,32	514,996	2012_02_2	Nuclei_frac
	INALTAAS [iTRAQ_N1	3	500-521	5,996	859,807	2012_02_2	Nuclei_frac
	INALTAAS [iTRAQ_N1	3	500-524	9,263	982,207	2012_02_2	Nuclei_frac
	INALTAAS [iTRAQ_N1	3	500-524	6,119	736,909	2012_02_2	Nuclei_frac
	SLHDAIMIV [iTRAQ_N1	2	388-397	6,773	438,916	2012_02_2	Nuclei_frac
	YNFFTGCP [iTRAQ_N1	3	358-366	6,098	711,36	2012_02_2	Nuclei_frac
	DICNDVLSI [iTRAQ_N1	3	92-103	7,703	569,646	2012_02_2	Nuclei_frac
	DICNDVLSI [iTRAQ_N1	3	92-103	7,167	853,965	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	2	213-222	7,509	675,381	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	1	213-222	7,419	667,386	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	2	213-222	7,187	675,384	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	2	213-222	6,717	675,383	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	2	213-222	6,697	675,385	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	2	213-222	6,558	675,381	2012_02_2	Nuclei_frac
	DSTLIMQLI [iTRAQ_N1	1	213-222	6,536	667,389	2012_02_2	Nuclei_frac

DSTLMQLI [iTRAQ_N1	1 213-222	6,27	667,387	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	6,266	675,383	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,92	450,592	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,891	450,592	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,792	675,385	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,475	450,592	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,303	450,591	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	5,105	675,384	2012_02_2	Nuclei_frac
DSTLMQLI [iTRAQ_N1	2 213-222	4,863	450,592	2012_02_2	Nuclei_frac
EMQPTHPII [iTRAQ_N1	2 159-167	4,76	423,557	2012_02_2	Nuclei_frac
FLIPNASQV [iTRAQ_N1	2 104-115	5,735	796,949	2012_02_2	Nuclei_frac
GIVDQSQQ [iTRAQ_N1	3 140-158	9,517	867,804	2012_02_2	Nuclei_frac
GIVDQSQQ [iTRAQ_N1	3 140-158	5,927	651,105	2012_02_2	Nuclei_frac
NLLSVAYK [iTRAQ_N1	2 42-49	5,612	598,368	2012_02_2	Nuclei_frac
YLAEVAAK [iTRAQ_N1	3 128-139	6,228	571,326	2012_02_2	Nuclei_frac
YLAEVAAK [iTRAQ_N1	3 128-139	5,759	571,324	2012_02_2	Nuclei_frac
Q9BSJ8_ISC ALTLGALT [iTRAQ_N1	1 551-563	7,778	727,468	2012_02_2	Nuclei_frac
Q9BSJ8_ISC ALTLGALT [iTRAQ_N1	1 551-563	6,945	485,313	2012_02_2	Nuclei_frac
Q9BSJ8_ISC IHVLEAQD [iTRAQ_N1	2 651-662	6,276	546,667	2012_02_2	Nuclei_frac
Q9BSJ8_ISC LLAETVAF [iTRAQ_N1	1 160-170	7,756	642,395	2012_02_2	Nuclei_frac
Q9BSJ8_ISC LLVPLVPD [iTRAQ_N1	1 308-323	6,721	967,085	2012_02_2	Nuclei_frac
Q9BSJ8_ISC LLVPLVPD [iTRAQ_N1	1 308-323	5,617	645,058	2012_02_2	Nuclei_frac
Q9BSJ8_ISC VLQASVLI [iTRAQ_N1	1 423-445	9,6	903,155	2012_02_2	Nuclei_frac
Q9BSJ8_ISC WFTLSSGC [iTRAQ_N1	1 894-907	8,743	868,499	2012_02_2	Nuclei_frac
AQLGGPEA [iTRAQ_N1	3 189-205	6,256	692,721	2012_02_2	Nuclei_frac
KYTLPPGV [iTRAQ_N1	4 141-171	5,893	919,498	2012_02_2	Nuclei_frac
LATQSNEI [iTRAQ_N1	1 172-188	9,715	1025,554	2012_02_2	Nuclei_frac
LATQSNEI [iTRAQ_N1	1 172-188	7,056	684,038	2012_02_2	Nuclei_frac
LFDQAFGL [iTRAQ_N1	1 28-37	6,254	654,366	2012_02_2	Nuclei_frac
LFDQAFGL [iTRAQ_N1	1 28-37	5,935	654,366	2012_02_2	Nuclei_frac
LFDQAFGL [iTRAQ_N1	1 28-37	5,654	654,365	2012_02_2	Nuclei_frac
TKDGVVEI [iTRAQ_N1	3 113-123	8,68	526,987	2012_02_2	Nuclei_frac
TKDGVVEI [iTRAQ_N1	3 113-123	8,128	789,978	2012_02_2	Nuclei_frac
TKDGVVEI [iTRAQ_N1	3 113-123	7,288	526,987	2012_02_2	Nuclei_frac
TKDGVVEI [iTRAQ_N1	3 113-123	6,573	526,987	2012_02_2	Nuclei_frac
VSLDVNHF [iTRAQ_N1	2 97-112	10,017	691,382	2012_02_2	Nuclei_frac
VSLDVNHF [iTRAQ_N1	2 97-112	8,994	691,382	2012_02_2	Nuclei_frac
Q8NHW5 AFLADPSA [iTRAQ_N1	2 267-297	7,351	1014,232	2012_02_2	Nuclei_frac
Q8NHW5 AFLADPSA [iTRAQ_N1	2 267-297	6,985	1014,231	2012_02_2	Nuclei_frac
Q8NHW5 AFLADPSA [iTRAQ_N1	2 267-297	5,219	760,926	2012_02_2	Nuclei_frac
Q8NHW5 AGAIAPCE [iTRAQ_N1	3 113-134	8,256	823,441	2012_02_2	Nuclei_frac
Q8NHW5 AGAIAPCE [iTRAQ_N1	3 113-134	5,07	823,434	2012_02_2	Nuclei_frac
Q8NHW5 DMLLANK [iTRAQ_N1	3 100-112	4,998	558,658	2012_02_2	Nuclei_frac
Q8NHW5 GTIEILSDV [iTRAQ_N1	2 150-162	5,937	859,016	2012_02_2	Nuclei_frac
Q8NHW5 GTIEILSDV [iTRAQ_N1	2 150-162	4,932	573,017	2012_02_2	Nuclei_frac
Q8NHW5 TSFFQALG [iTRAQ_N1	2 135-146	9,043	801,459	2012_02_2	Nuclei_frac
Q8NHW5 VLALSVET [iTRAQ_N1	2 248-264	11,211	1092,605	2012_02_2	Nuclei_frac
Q8NHW5 VLALSVET [iTRAQ_N1	2 248-264	7,265	728,74	2012_02_2	Nuclei_frac

Q9UBF2	AIVDCIISIE [iTRAQ_Ni	3 416-432	7,967	736,728	2012_02_2 Nuclei_frac
Q9UBF2	EMSCIAED' [iTRAQ_Ni	3 94-111	7,602	762,072	2012_02_2 Nuclei_frac
Q9UBF2	EMSCIAED' [iTRAQ_Ni	3 94-111	6,074	762,074	2012_02_2 Nuclei_frac
Q9UBF2	GLGPLFK [iTRAQ_Ni	2 625-631	4,962	510,328	2012_02_2 Nuclei_frac
Q9UBF2	ILHLLGQEC [iTRAQ_Ni	2 455-465	7,797	498,308	2012_02_2 Nuclei_frac
Q9UBF2	ILHLLGQEC [iTRAQ_Ni	2 455-465	7,166	498,309	2012_02_2 Nuclei_frac
Q9UBF2	SIATLAITT [iTRAQ_Ni	2 339-350	7,185	766,999	2012_02_2 Nuclei_frac
Q9UBF2	VFNETPINF [iTRAQ_Ni	1 33-42	5,352	665,866	2012_02_2 Nuclei_frac
Q9UBF2	VVVVQAIS [iTRAQ_Ni	3 377-389	5,927	568,344	2012_02_2 Nuclei_frac
P61019,Q8'	EHGLIFMEI [iTRAQ_Ni	3 139-150	4,84	556,297	2012_02_2 Nuclei_frac
P61019,Q8'	FQPVHDLT [iTRAQ_Ni	1 30-45	8,067	644,016	2012_02_2 Nuclei_frac
P61019,Q8'	GAAGALL\ [iTRAQ_Ni	1 77-89	6,599	732,428	2012_02_2 Nuclei_frac
P61019,Q8'	GAAGALL\ [iTRAQ_Ni	1 77-89	6,21	732,422	2012_02_2 Nuclei_frac
P61019,Q8'	GAAGALL\ [iTRAQ_Ni	1 77-90	6,871	540,651	2012_02_2 Nuclei_frac
P61019,Q8'	LQIWDTAC [iTRAQ_Ni	1 56-68	9,691	847,935	2012_02_2 Nuclei_frac
P61019,Q8'	SCLLLQFTI [iTRAQ_Ni	3 19-29	5,419	556,984	2012_02_2 Nuclei_frac
P61019,Q8'	SCLLLQFTI [iTRAQ_Ni	3 19-29	4,768	556,983	2012_02_2 Nuclei_frac
P61019,Q8'	YIIIGDTGV\ [iTRAQ_Ni	2 8-18	5,277	712,425	2012_02_2 Nuclei_frac
P06396_CH	AGKEPGLC [iTRAQ_Ni	2 11-21	7,347	514,971	2012_02_2 Nuclei_frac
P06396_CH	AGKEPGLC [iTRAQ_Ni	2 11-21	6,111	514,971	2012_02_2 Nuclei_frac
P06396_CH	AQPVQVA [iTRAQ_Ni	2 576-597	7,378	854,101	2012_02_2 Nuclei_frac
P06396_CH	DSQEEKT [iTRAQ_Ni	3 663-677	6,897	700,033	2012_02_2 Nuclei_frac
P06396_CH	HVVPNEV\ [iTRAQ_Ni	1 127-137	7,377	473,944	2012_02_2 Nuclei_frac
P06396_CH	NWRDPDQ [iTRAQ_Ni	1 344-368	4,797	747,624	2012_02_2 Nuclei_frac
P06396_CH	QTQVSVLf [iTRAQ_Ni	2 323-339	7,433	706,729	2012_02_2 Nuclei_frac
P06396_CH	QTQVSVLf [iTRAQ_Ni	2 323-339	6,73	706,728	2012_02_2 Nuclei_frac
P06396_CH	TASDFITK [iTRAQ_Ni	2 310-317	5,13	585,834	2012_02_2 Nuclei_frac
P37802	DGTVLCEL [iTRAQ_Ni	3 57-77	7,369	859,128	2012_02_2 Nuclei_frac
P37802	DGTVLCEL [iTRAQ_Ni	3 57-77	5,148	644,596	2012_02_2 Nuclei_frac
P37802	DGTVLCEL [iTRAQ_Ni	4 57-78	9,018	949,869	2012_02_2 Nuclei_frac
P37802	DGTVLCEL [iTRAQ_Ni	4 57-78	6,992	712,648	2012_02_2 Nuclei_frac
P37802	DGTVLCEL [iTRAQ_Ni	4 57-78	6,707	712,647	2012_02_2 Nuclei_frac
P37802	ENFQNWLI [iTRAQ_Ni	2 49-56	5,482	683,872	2012_02_2 Nuclei_frac
P37802	ENFQNWLI [iTRAQ_Ni	2 49-56	5,001	456,25	2012_02_2 Nuclei_frac
P37802	KIQASTMA [iTRAQ_Ni	4 78-87	5,88	524,975	2012_02_2 Nuclei_frac
P37802	TLMNLGGL [iTRAQ_Ni	2 127-138	8,687	688,396	2012_02_2 Nuclei_frac
P37802	TLMNLGGL [iTRAQ_Ni	2 127-138	6,455	459,268	2012_02_2 Nuclei_frac
P37802	YGINTTDIF [iTRAQ_Ni	2 102-119	9,847	1194,623	2012_02_2 Nuclei_frac
P37802	YGINTTDIF [iTRAQ_Ni	2 102-119	8,036	796,75	2012_02_2 Nuclei_frac
P37802	YGINTTDIF [iTRAQ_Ni	2 102-119	7,062	796,749	2012_02_2 Nuclei_frac
P38646	AQFEGIVTI [iTRAQ_Ni	1 303-314	8,863	753,431	2012_02_2 Nuclei_frac
P38646	AQFEGIVTI [iTRAQ_Ni	1 303-314	5,982	502,62	2012_02_2 Nuclei_frac
P38646	DAGQISGL [iTRAQ_Ni	1 161-172	9,156	693,895	2012_02_2 Nuclei_frac
P38646	DAGQISGL [iTRAQ_Ni	1 161-172	8,478	693,897	2012_02_2 Nuclei_frac
P38646	DAGQISGL [iTRAQ_Ni	1 161-172	7,963	693,896	2012_02_2 Nuclei_frac
P38646	DAGQISGL [iTRAQ_Ni	1 161-172	7,097	462,934	2012_02_2 Nuclei_frac
P38646	DAGQISGL [iTRAQ_Ni	1 161-172	6,405	462,932	2012_02_2 Nuclei_frac
P38646	ETAENYLG [iTRAQ_Ni	2 130-141	8,442	541,287	2012_02_2 Nuclei_frac

P38646	LLGQFTLIC [iTRAQ_N1	1 453-467	8,805	869,033	2012_02_2	Nuclei_frac
P38646	LLGQFTLIC [iTRAQ_N1	1 453-467	7,111	869,036	2012_02_2	Nuclei_frac
P38646	LLGQFTLIC [iTRAQ_N1	1 453-467	7,073	579,691	2012_02_2	Nuclei_frac
P38646	VQQTVD [iTRAQ_N1	1 349-359	10,984	717,896	2012_02_2	Nuclei_frac
P38646	VQQTVD [iTRAQ_N1	1 349-359	9,029	717,897	2012_02_2	Nuclei_frac
P38646	VQQTVD [iTRAQ_N1	1 349-359	8,144	717,896	2012_02_2	Nuclei_frac
Q9UHB6	ELSVEEQIK [iTRAQ_N1	2 579-587	5,418	681,892	2012_02_2	Nuclei_frac
Q9UHB6	ELSVEEQIK [iTRAQ_N1	2 579-588	6,89	506,965	2012_02_2	Nuclei_frac
Q9UHB6	ELSVEEQIK [iTRAQ_N1	2 579-588	6,509	759,943	2012_02_2	Nuclei_frac
Q9UHB6	ELSVEEQIK [iTRAQ_N1	2 579-588	6,307	506,964	2012_02_2	Nuclei_frac
Q9UHB6	ETPHSPGV [iTRAQ_N1	3 326-340	5,555	639,321	2012_02_2	Nuclei_frac
Q9UHB6	IYCKPHFNC [iTRAQ_N1	4 276-287	5,72	676,38	2012_02_2	Nuclei_frac
Q9UHB6	KGWSMSEI [iTRAQ_N1	3 454-469	6,271	686,67	2012_02_2	Nuclei_frac
Q9UHB6	SEVQQPVI [iTRAQ_N1	2 190-206	5,053	548,055	2012_02_2	Nuclei_frac
Q9UHB6	SLNWSSFV [iTRAQ_N1	2 544-565	5,816	721,101	2012_02_2	Nuclei_frac
Q9UHB6	SLNWSSFV [iTRAQ_N1	2 544-565	5,635	721,101	2012_02_2	Nuclei_frac
Q9UHB6	SLNWSSFV [iTRAQ_N1	2 544-565	5,471	721,103	2012_02_2	Nuclei_frac
Q9UHB6	YNVPLNR [iTRAQ_N1	1 30-36	5,41	510,293	2012_02_2	Nuclei_frac
Q7L7L0_CH AGLQFPVC [iTRAQ_N1	1 21-29	8,317	544,82	2012_02_2	Nuclei_frac	
Q7L7L0_CH AGLQFPVC [iTRAQ_N1	1 21-29	8,193	544,82	2012_02_2	Nuclei_frac	
Q7L7L0_CH AGLQFPVC [iTRAQ_N1	1 21-29	5,536	544,819	2012_02_2	Nuclei_frac	
Q7L7L0_CH AGLQFPVC [iTRAQ_N1	1 21-29	5,077	544,821	2012_02_2	Nuclei_frac	
Q7L7L0_CH HLQLAIR [iTRAQ_N1	1 82-88	8,921	497,818	2012_02_2	Nuclei_frac	
Q7L7L0_CH LLGRVTIA [iTRAQ_N1	2 96-118	7,904	886,885	2012_02_2	Nuclei_frac	
Q7L7L0_CH NDEELNK [iTRAQ_N1	2 89-95	4,796	575,303	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	9,875	1110,199	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	8,605	740,464	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	8,547	740,464	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	8,156	1110,189	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	8,121	740,464	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,974	1110,191	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,506	740,465	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,352	740,464	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,315	740,465	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,172	740,468	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,083	740,464	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	7,013	740,465	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,666	740,462	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,631	740,461	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,458	740,461	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,266	740,462	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,17	1110,191	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	6,153	740,467	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,79	740,47	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,775	740,466	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,542	740,463	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,503	555,599	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,38	555,599	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,347	740,469	2012_02_2	Nuclei_frac	
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	5,053	555,599	2012_02_2	Nuclei_frac	

Q7L7L0_CH VTIAQGGV [iTRAQ_N1	2 100-118	4,891	555,599	2012_02_2	Nuclei_frac
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	3 100-119	6,095	623,656	2012_02_2	Nuclei_frac
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	3 100-119	5,753	623,657	2012_02_2	Nuclei_frac
Q7L7L0_CH VTIAQGGV [iTRAQ_N1	3 100-119	5,702	623,657	2012_02_2	Nuclei_frac
AITIAGVPC [iTRAQ_N1	3 145-160	7,866	654,372	2012_02_2	Nuclei_frac
AITIAGVPC [iTRAQ_N1	3 145-160	7,305	654,373	2012_02_2	Nuclei_frac
AITIAGVPC [iTRAQ_N1	3 145-160	5,939	654,374	2012_02_2	Nuclei_frac
EVGSIIK [iTRAQ_N1	2 24-31	5,709	545,84	2012_02_2	Nuclei_frac
EVGSIIK [iTRAQ_N1	2 24-31	5,624	545,84	2012_02_2	Nuclei_frac
IITLTGPTN [iTRAQ_N1	2 58-70	7,155	839,016	2012_02_2	Nuclei_frac
IITLTGPTN [iTRAQ_N1	2 58-70	6,48	559,678	2012_02_2	Nuclei_frac
IITLTGPTN [iTRAQ_N1	2 58-70	5,287	559,678	2012_02_2	Nuclei_frac
IITLTGPTN [iTRAQ_N1	2 58-70	4,855	559,679	2012_02_2	Nuclei_frac
INISEGNCP [iTRAQ_N1	2 47-57	6,071	716,853	2012_02_2	Nuclei_frac
LVVPATQC [iTRAQ_N1	3 102-115	8,875	866,008	2012_02_2	Nuclei_frac
LVVPATQC [iTRAQ_N1	3 102-115	7,896	577,674	2012_02_2	Nuclei_frac
LVVPATQC [iTRAQ_N1	3 102-115	7,558	577,674	2012_02_2	Nuclei_frac
QVTITGSA [iTRAQ_N1	1 326-346	10,154	774,44	2012_02_2	Nuclei_frac
ENVFQEH [iTRAQ_N1	2 60-70	5,791	554,307	2012_02_2	Nuclei_frac
LRENVFQE [iTRAQ_N1	2 58-70	5,65	483,276	2012_02_2	Nuclei_frac
LRENVFQE [iTRAQ_N1	2 58-70	5,323	483,277	2012_02_2	Nuclei_frac
QDSAAVGI [iTRAQ_N1	2 280-290	4,881	744,892	2012_02_2	Nuclei_frac
TVPVEAV [iTRAQ_N1	2 337-346	7,832	659,898	2012_02_2	Nuclei_frac
TVQGSQGH [iTRAQ_N1	2 43-57	5,091	494,022	2012_02_2	Nuclei_frac
YGLFPANY [iTRAQ_N1	1 538-549	8,846	793,43	2012_02_2	Nuclei_frac
YGLFPANY [iTRAQ_N1	1 538-550	7,74	857,458	2012_02_2	Nuclei_frac
AHLVAVFI [iTRAQ_N1	1 389-400	8,986	530,955	2012_02_2	Nuclei_frac
AHLVAVFI [iTRAQ_N1	1 389-400	8,66	795,929	2012_02_2	Nuclei_frac
GVGTDEAC [iTRAQ_N1	2 287-302	9,69	924,489	2012_02_2	Nuclei_frac
LLISLSQGM [iTRAQ_N1	1 337-346	8,113	622,879	2012_02_2	Nuclei_frac
NTPAFFAE [iTRAQ_N1	1 431-439	6,156	598,813	2012_02_2	Nuclei_frac
SETDLLDIF [iTRAQ_N1	1 462-470	5,825	603,327	2012_02_2	Nuclei_frac
TPVLFDIYE [iTRAQ_N1	2 272-282	6,788	813,475	2012_02_2	Nuclei_frac
TPVLFDIYE [iTRAQ_N1	2 272-282	6,002	542,651	2012_02_2	Nuclei_frac
TPVLFDIYE [iTRAQ_N1	2 272-282	4,968	542,652	2012_02_2	Nuclei_frac
P29692,P29 ATAPQTQ [iTRAQ_N1	2 123-135	7,401	528,609	2012_02_2	Nuclei_frac
P29692,P29 GVVQELQ [iTRAQ_N1	2 95-106	7,845	794,471	2012_02_2	Nuclei_frac
P29692,P29 GVVQELQ [iTRAQ_N1	2 95-106	7,671	794,477	2012_02_2	Nuclei_frac
P29692,P29 GVVQELQ [iTRAQ_N1	2 95-106	7,333	529,983	2012_02_2	Nuclei_frac
P29692,P29 GVVQELQ [iTRAQ_N1	2 95-106	5,702	529,984	2012_02_2	Nuclei_frac
P29692,P29 IASLEVEN [iTRAQ_N1	1 83-94	7,668	751,922	2012_02_2	Nuclei_frac
P29692,P29 IASLEVEN [iTRAQ_N1	1 83-94	7,15	501,617	2012_02_2	Nuclei_frac
P29692,P29 SIQLDGLV [iTRAQ_N1	2 219-231	9,965	831,483	2012_02_2	Nuclei_frac
P29692,P29 SIQLDGLV [iTRAQ_N1	2 219-231	9,732	831,482	2012_02_2	Nuclei_frac
P29692,P29 SIQLDGLV [iTRAQ_N1	2 219-231	4,831	554,655	2012_02_2	Nuclei_frac
P29692,P29 SLAGSSGP [iTRAQ_N1	1 59-82	12,464	777,057	2012_02_2	Nuclei_frac
P29692,P29 SLAGSSGP [iTRAQ_N1	1 59-82	11,858	777,056	2012_02_2	Nuclei_frac
P29692,P29 SLAGSSGP [iTRAQ_N1	1 59-82	11,568	777,057	2012_02_2	Nuclei_frac

P29692,P29692 SLAGSSGP [iTRAQ_N1	1 59-82	11,271	777,057	2012_02_2 Nuclei_frac
P60660,P60660 ALGQNPTM [iTRAQ_N1	2 37-49	9,739	548,318	2012_02_2 Nuclei_frac
P60660,P60660 ALGQNPTM [iTRAQ_N1	2 37-49	8,624	821,972	2012_02_2 Nuclei_frac
P60660,P60660 ALGQNPTM [iTRAQ_N1	2 37-49	7,99	821,973	2012_02_2 Nuclei_frac
P60660,P60660 ALGQNPTM [iTRAQ_N1	2 37-49	7,693	821,973	2012_02_2 Nuclei_frac
P60660,P60660 EAFQLFDR [iTRAQ_N1	1 13-20	5,64	585,308	2012_02_2 Nuclei_frac
P60660,P60660 HVLVTLGE [iTRAQ_N1	2 110-118	6,465	642,401	2012_02_2 Nuclei_frac
P60660,P60660 HVLVTLGE [iTRAQ_N1	2 110-118	4,968	428,603	2012_02_2 Nuclei_frac
P60660,P60660 ILYSQCGD\ [iTRAQ_N1	3 26-36	6,398	751,368	2012_02_2 Nuclei_frac
P60660,P60660 ILYSQCGD\ [iTRAQ_N1	3 26-36	6,067	501,248	2012_02_2 Nuclei_frac
P60660,P60660 ILYSQCGD\ [iTRAQ_N1	3 26-36	6,049	751,371	2012_02_2 Nuclei_frac
P60660,P60660 ILYSQCGD\ [iTRAQ_N1	3 26-36	5,985	751,368	2012_02_2 Nuclei_frac
P60660,P60660 NKDQGTYE [iTRAQ_N1	2 79-93	9,893	1038,02	2012_02_2 Nuclei_frac
P60660,P60660 NKDQGTYE [iTRAQ_N1	2 79-93	9,751	1038,018	2012_02_2 Nuclei_frac
P60660,P60660 NKDQGTYE [iTRAQ_N1	2 79-93	9,553	692,349	2012_02_2 Nuclei_frac
P60660,P60660 NKDQGTYE [iTRAQ_N1	2 79-93	8,531	692,347	2012_02_2 Nuclei_frac
P60660,P60660 NKDQGTYE [iTRAQ_N1	2 79-93	8,027	692,347	2012_02_2 Nuclei_frac
P60660,P60660 VLDFEHFL [iTRAQ_N1	3 63-78	7,206	731,409	2012_02_2 Nuclei_frac
P60660,P60660 VLDFEHFL [iTRAQ_N1	3 63-78	7,04	731,408	2012_02_2 Nuclei_frac
O75083,O75083 FGAVFLWI [iTRAQ_N1	2 126-146	11,287	832,764	2012_02_2 Nuclei_frac
O75083,O75083 LYSILGTTL [iTRAQ_N1	3 470-483	6,407	657,39	2012_02_2 Nuclei_frac
O75083,O75083 LYSILGTTL [iTRAQ_N1	3 470-483	6,15	657,39	2012_02_2 Nuclei_frac
O75083,O75083 NIDNPALA [iTRAQ_N1	2 43-64	5,526	677,367	2012_02_2 Nuclei_frac
O75083,O75083 SIQCLTVHI [iTRAQ_N1	3 321-329	5,782	458,599	2012_02_2 Nuclei_frac
O75083,O75083 VFASLPQV [iTRAQ_N1	1 7-16	5,666	645,372	2012_02_2 Nuclei_frac
O75083,O75083 VINSVDIK [iTRAQ_N1	2 147-154	4,851	588,367	2012_02_2 Nuclei_frac
O75083,O75083 YTSLMLR [iTRAQ_N1	2 389-395	5,577	522,287	2012_02_2 Nuclei_frac
Q8NBS9 ALAPTWEI [iTRAQ_N1	2 190-209	11,157	827,793	2012_02_2 Nuclei_frac
Q8NBS9 ALAPTWEI [iTRAQ_N1	2 190-209	10,403	827,796	2012_02_2 Nuclei_frac
Q8NBS9 ALAPTWEI [iTRAQ_N1	2 190-209	10,046	827,793	2012_02_2 Nuclei_frac
Q8NBS9 EFPGLAGV [iTRAQ_N1	2 335-343	5,318	603,36	2012_02_2 Nuclei_frac
Q8NBS9 EFPGLAGV [iTRAQ_N1	2 335-343	4,847	603,361	2012_02_2 Nuclei_frac
Q8NBS9 FVLSQAKI [iTRAQ_N1	2 391-400	4,752	479,945	2012_02_2 Nuclei_frac
Q8NBS9 IGKVDCTQ [iTRAQ_N1	4 210-228	7,359	638,821	2012_02_2 Nuclei_frac
Q8NBS9 VDCTAHSI [iTRAQ_N1	3 87-102	9,563	953,44	2012_02_2 Nuclei_frac
Q8NBS9 VDCTAHSI [iTRAQ_N1	3 87-102	7,525	635,962	2012_02_2 Nuclei_frac
Q8NBS9 VDCTAHSI [iTRAQ_N1	3 87-102	7,352	635,962	2012_02_2 Nuclei_frac
Q8NBS9 VDCTQHYE [iTRAQ_N1	3 213-228	6,815	703,992	2012_02_2 Nuclei_frac
P00338,P00338 DLADELAL [iTRAQ_N1	3 42-58	5,407	583,59	2012_02_2 Nuclei_frac
P00338,P00338 KSADTLWI [iTRAQ_N1	3 317-327	5,542	560,333	2012_02_2 Nuclei_frac
P00338,P00338 LLIVSNPVI [iTRAQ_N1	2 132-148	6,227	744,783	2012_02_2 Nuclei_frac
P00338,P00338 LVIITAGAR [iTRAQ_N1	1 90-98	5,232	529,346	2012_02_2 Nuclei_frac
P00338,P00338 QVVESAYE [iTRAQ_N1	2 232-242	5,583	518,3	2012_02_2 Nuclei_frac
P00338,P00338 SADTLWGI [iTRAQ_N1	2 318-327	6,674	703,898	2012_02_2 Nuclei_frac
P00338,P00338 SADTLWGI [iTRAQ_N1	2 318-327	5,158	469,601	2012_02_2 Nuclei_frac
P00338,P00338 VIGSGCNLI [iTRAQ_N1	2 157-168	10,114	696,856	2012_02_2 Nuclei_frac
P00338,P00338 VIGSGCNLI [iTRAQ_N1	2 157-168	9,184	696,856	2012_02_2 Nuclei_frac
P00338,P00338 VIGSGCNLI [iTRAQ_N1	2 157-168	7,849	696,855	2012_02_2 Nuclei_frac

P00338,P00338	VIGSGCNLI [iTRAQ_N1	2	157-168	7,487	464,906	2012_02_2	Nuclei_frac
P26038	AKFYPEDV [iTRAQ_N1	2	81-99	5,712	857,122	2012_02_2	Nuclei_frac
P26038	ALTSELAN [iTRAQ_N1	1	523-532	7,574	595,338	2012_02_2	Nuclei_frac
P26038	ALTSELAN [iTRAQ_N1	1	523-532	7,122	595,337	2012_02_2	Nuclei_frac
P26038	APDFVFYA [iTRAQ_N1	1	263-272	7,147	663,853	2012_02_2	Nuclei_frac
P26038	APDFVFYA [iTRAQ_N1	1	263-272	6,392	663,854	2012_02_2	Nuclei_frac
P26038	AQMVQED [iTRAQ_N1	2	448-457	6,972	739,893	2012_02_2	Nuclei_frac
P26038	ESEAVEWC [iTRAQ_N1	2	438-447	5,639	507,932	2012_02_2	Nuclei_frac
P26038	IGFPWSEIR [iTRAQ_N1	1	237-245	6,595	624,848	2012_02_2	Nuclei_frac
P26038	IGFPWSEIR [iTRAQ_N1	1	237-245	6,171	624,848	2012_02_2	Nuclei_frac
P26038	IGFPWSEIR [iTRAQ_N1	1	237-245	6,021	624,847	2012_02_2	Nuclei_frac
P26038	IGFPWSEIR [iTRAQ_N1	1	237-245	5,605	624,845	2012_02_2	Nuclei_frac
P26038	KAPDFVFY [iTRAQ_N1	2	262-272	4,995	533,636	2012_02_2	Nuclei_frac
P00387_ISC	DILLRPELE [iTRAQ_N1	1	189-200	7,911	547,321	2012_02_2	Nuclei_frac
P00387_ISC	GFVDLVIK [iTRAQ_N1	2	78-85	5,226	589,874	2012_02_2	Nuclei_frac
P00387_ISC	GPSGLLVY [iTRAQ_N1	2	118-128	9,094	703,917	2012_02_2	Nuclei_frac
P00387_ISC	LIDREIISHD [iTRAQ_N1	1	21-32	5,78	403,729	2012_02_2	Nuclei_frac
P00387_ISC	STPAITLES [iTRAQ_N1	2	4-20	7,424	730,422	2012_02_2	Nuclei_frac
P00387_ISC	SVGMIAGG [iTRAQ_N1	3	148-166	9,068	693,047	2012_02_2	Nuclei_frac
P62701,P22701	ECLPLIIFLR [iTRAQ_N1	2	39-48	8,117	709,423	2012_02_2	Nuclei_frac
P62701,P22701	ECLPLIIFLR [iTRAQ_N1	2	39-48	7,902	709,428	2012_02_2	Nuclei_frac
P62701,P22701	ECLPLIIFLR [iTRAQ_N1	2	39-48	7,732	709,42	2012_02_2	Nuclei_frac
P62701,P22701	ECLPLIIFLR [iTRAQ_N1	2	39-48	6,898	709,419	2012_02_2	Nuclei_frac
P62701,P22701	ECLPLIIFLR [iTRAQ_N1	2	39-48	4,821	473,284	2012_02_2	Nuclei_frac
P62701,P22701	FDTGNLCM [iTRAQ_N1	3	174-190	5,992	648,31	2012_02_2	Nuclei_frac
P62701,P22701	GIPHLVTHI [iTRAQ_N1	1	134-144	9,1	680,386	2012_02_2	Nuclei_frac
P62701,P22701	GIPHLVTHI [iTRAQ_N1	1	134-144	5,606	453,926	2012_02_2	Nuclei_frac
P62701,P22701	LSNIFVIGK [iTRAQ_N1	2	221-229	7,611	426,938	2012_02_2	Nuclei_frac
P62701,P22701	LSNIFVIGK [iTRAQ_N1	2	221-229	7,511	639,904	2012_02_2	Nuclei_frac
P62701,P22701	LTGVFAPR [iTRAQ_N1	1	22-29	8,535	502,805	2012_02_2	Nuclei_frac
P62701,P22701	LTGVFAPR [iTRAQ_N1	1	22-29	6,142	502,804	2012_02_2	Nuclei_frac
P62701,P22701	YALTGDEV [iTRAQ_N1	3	53-62	4,916	519,307	2012_02_2	Nuclei_frac
O00148	DFLKPELI [iTRAQ_N1	2	47-56	5,586	766,479	2012_02_2	Nuclei_frac
O00148	DFLKPELI [iTRAQ_N1	2	47-56	4,998	766,478	2012_02_2	Nuclei_frac
O00148	DVQEIFR [iTRAQ_N1	1	208-214	5,791	525,788	2012_02_2	Nuclei_frac
O00148	ELAFQISK [iTRAQ_N1	2	122-129	4,96	408,579	2012_02_2	Nuclei_frac
O00148	GLAIFVSI [iTRAQ_N1	2	383-396	6,152	589,983	2012_02_2	Nuclei_frac
O00148	GSYVSIHS [iTRAQ_N1	1	35-46	6,401	480,917	2012_02_2	Nuclei_frac
O00148	ILVATNLFC [iTRAQ_N1	1	338-347	8,964	624,384	2012_02_2	Nuclei_frac
O00148	ILVATNLFC [iTRAQ_N1	1	338-347	7,381	416,592	2012_02_2	Nuclei_frac
O00148	VSVFFGGL [iTRAQ_N1	2	143-153	6,231	721,438	2012_02_2	Nuclei_frac
O00148	VSVFFGGL [iTRAQ_N1	2	143-153	5,725	481,295	2012_02_2	Nuclei_frac
P23246_ISC	FAQHGTFE [iTRAQ_N1	1	480-493	8,2	636,301	2012_02_2	Nuclei_frac
P23246_ISC	FATHAAAI [iTRAQ_N1	1	366-376	5,771	429,915	2012_02_2	Nuclei_frac
P23246_ISC	FGQGAGF [iTRAQ_N1	1	667-681	9,006	743,388	2012_02_2	Nuclei_frac
P23246_ISC	FGQGAGF [iTRAQ_N1	1	667-681	7,5	495,927	2012_02_2	Nuclei_frac
P23246_ISC	GIVEFASKF [iTRAQ_N1	2	414-425	8,284	511,971	2012_02_2	Nuclei_frac

P23246_ISC LFGVNLPA [iTRAQ_N1	2 299-314	5,6	699,376	2012_02_2 Nuclei_frac
P23246_ISC LFGVNLPA [iTRAQ_N1	2 299-315	7,079	751,411	2012_02_2 Nuclei_frac
ATILDLSCN [iTRAQ_N1	3 41-50	7,451	474,936	2012_02_2 Nuclei_frac
ATILDLSCN [iTRAQ_N1	3 41-50	6,98	711,899	2012_02_2 Nuclei_frac
ATILDLSCN [iTRAQ_N1	3 41-50	5,819	474,935	2012_02_2 Nuclei_frac
ATILDLSCN [iTRAQ_N1	3 41-50	5,221	711,881	2012_02_2 Nuclei_frac
ATILDLSCN [iTRAQ_N1	3 41-50	5,178	474,934	2012_02_2 Nuclei_frac
DNPLDPVL [iTRAQ_N1	2 117-126	5,786	685,4	2012_02_2 Nuclei_frac
DNPLDPVL [iTRAQ_N1	2 117-126	5,517	457,269	2012_02_2 Nuclei_frac
LQQLPADF [iTRAQ_N1	1 74-83	6,915	644,861	2012_02_2 Nuclei_frac
LQQLPADF [iTRAQ_N1	1 74-83	5,525	644,862	2012_02_2 Nuclei_frac
LTTLPSDF [iTRAQ_N1	3 51-66	9,302	1045,584	2012_02_2 Nuclei_frac
LTTLPSDF [iTRAQ_N1	3 51-66	8,483	697,391	2012_02_2 Nuclei_frac
LVNLQHLC [iTRAQ_N1	2 84-96	8,4	911,546	2012_02_2 Nuclei_frac
LVNLQHLC [iTRAQ_N1	2 84-96	7,788	608,031	2012_02_2 Nuclei_frac
LVNLQHLC [iTRAQ_N1	2 84-96	7,416	608,033	2012_02_2 Nuclei_frac
LVTLPVSF [iTRAQ_N1	2 97-108	5,91	802,506	2012_02_2 Nuclei_frac
LVTLPVSF [iTRAQ_N1	2 97-108	5,609	535,34	2012_02_2 Nuclei_frac
LVTLPVSF [iTRAQ_N1	2 97-108	4,887	535,341	2012_02_2 Nuclei_frac
AAAQCYID [iTRAQ_N1	3 280-291	8,496	833,979	2012_02_2 Nuclei_frac
AAAQCYID [iTRAQ_N1	3 280-291	4,92	556,32	2012_02_2 Nuclei_frac
DLQHPNEF [iTRAQ_N1	1 108-117	5,309	471,585	2012_02_2 Nuclei_frac
TLQLALDL [iTRAQ_N1	1 340-351	8,459	487,293	2012_02_2 Nuclei_frac
TLQLALDL [iTRAQ_N1	1 340-351	8,069	730,434	2012_02_2 Nuclei_frac
TLQLALDL [iTRAQ_N1	1 340-351	7,254	730,434	2012_02_2 Nuclei_frac
TLQLALDL [iTRAQ_N1	1 340-351	7,098	730,438	2012_02_2 Nuclei_frac
VLQDLVMI [iTRAQ_N1	2 317-327	7,651	737,926	2012_02_2 Nuclei_frac
VLSTPDLE [iTRAQ_N1	1 328-337	5,914	636,866	2012_02_2 Nuclei_frac
YEAAGTLV [iTRAQ_N1	2 262-279	7,842	694,395	2012_02_2 Nuclei_frac
YEAAGTLV [iTRAQ_N1	2 262-279	6,398	694,4	2012_02_2 Nuclei_frac
P25398 DVIEEYFK [iTRAQ_N1	2 121-128	5,226	665,859	2012_02_2 Nuclei_frac
P25398 KLGEWVGI [iTRAQ_N1	4 83-92	5,611	541,32	2012_02_2 Nuclei_frac
P25398 KVVGCSCV [iTRAQ_N1	5 101-111	6,464	556,328	2012_02_2 Nuclei_frac
P25398 KVVGCSCV [iTRAQ_N1	5 101-111	6,413	833,991	2012_02_2 Nuclei_frac
P25398 LGEWVGLC [iTRAQ_N1	3 84-92	6,14	675,379	2012_02_2 Nuclei_frac
P25398 LGEWVGLC [iTRAQ_N1	3 84-92	5,974	675,379	2012_02_2 Nuclei_frac
P25398 LVEALCAE [iTRAQ_N1	3 63-77	6,741	680,392	2012_02_2 Nuclei_frac
P25398 TALIHDGL [iTRAQ_N1	1 23-32	6,919	404,239	2012_02_2 Nuclei_frac
P25398 TALIHDGL [iTRAQ_N1	1 23-32	6,083	605,856	2012_02_2 Nuclei_frac
P25398 TALIHDGL [iTRAQ_N1	1 23-32	5,314	404,24	2012_02_2 Nuclei_frac
P25398 VVGCSCV [iTRAQ_N1	4 102-111	6,405	697,891	2012_02_2 Nuclei_frac
O43852,O4 EEIVDKYDI [iTRAQ_N1	2 269-292	7,887	997,184	2012_02_2 Nuclei_frac
O43852,O4 EEIVDKYDI [iTRAQ_N1	2 269-292	5,054	748,139	2012_02_2 Nuclei_frac
O43852,O4 HLVYESDC [iTRAQ_N1	3 253-265	5,694	492,017	2012_02_2 Nuclei_frac
O43852,O4 IDGDKDGF [iTRAQ_N1	3 61-75	7,133	695,047	2012_02_2 Nuclei_frac
O43852,O4 IDGDKDGF [iTRAQ_N1	3 61-75	6,55	695,048	2012_02_2 Nuclei_frac
O43852,O4 TFDQLTPE [iTRAQ_N1	2 41-51	9,51	791,916	2012_02_2 Nuclei_frac
O43852,O4 TFDQLTPE [iTRAQ_N1	2 41-53	8,189	934,487	2012_02_2 Nuclei_frac

O43852,O4 TFDQLTPE [iTRAQ_N1	2 41-53	8	623,327	2012_02_2	Nuclei_frac
O43852,O4 TFDQLTPE [iTRAQ_N1	2 41-53	6,101	467,746	2012_02_2	Nuclei_frac
O43852,O4 WIYEDVER [iTRAQ_N1	1 85-92	5,072	627,316	2012_02_2	Nuclei_frac
P52272_CH AFITNIPFD [iTRAQ_N1	2 73-83	6,421	776,953	2012_02_2	Nuclei_frac
P52272_CH AFITNIPFD [iTRAQ_N1	2 73-83	5,954	776,954	2012_02_2	Nuclei_frac
P52272_CH GCAVVEFK [iTRAQ_N1	3 113-120	5,003	599,333	2012_02_2	Nuclei_frac
P52272_CH GNFGGSFA [iTRAQ_N1	1 589-611	11,862	727,022	2012_02_2	Nuclei_frac
P52272_CH INEILSNAL [iTRAQ_N1	2 333-342	7,057	701,931	2012_02_2	Nuclei_frac
P52272_CH INEILSNAL [iTRAQ_N1	2 333-342	6,959	468,29	2012_02_2	Nuclei_frac
P52272_CH INEILSNAL [iTRAQ_N1	2 333-342	5,746	701,935	2012_02_2	Nuclei_frac
P52272_CH INEILSNAL [iTRAQ_N1	2 333-342	5,133	468,29	2012_02_2	Nuclei_frac
P52272_CH LGSTVFVA [iTRAQ_N1	2 163-175	6,709	572,326	2012_02_2	Nuclei_frac
P52272_CH NLPDFTW [iTRAQ_N1	2 620-628	6,213	728,398	2012_02_2	Nuclei_frac
P52272_CH NLPDFTW [iTRAQ_N1	2 620-628	5,396	485,935	2012_02_2	Nuclei_frac
P21291 GFGFGQGA [iTRAQ_N1	1 178-192	9,652	526,6	2012_02_2	Nuclei_frac
P21291 GFGFGQGA [iTRAQ_N1	1 178-192	8,836	789,397	2012_02_2	Nuclei_frac
P21291 GLESTTLA [iTRAQ_N1	4 151-167	8,873	778,073	2012_02_2	Nuclei_frac
P21291 GLESTTLA [iTRAQ_N1	4 151-167	5,231	583,807	2012_02_2	Nuclei_frac
P21291 KNLDSTTV [iTRAQ_N1	4 41-58	6,802	624,834	2012_02_2	Nuclei_frac
P21291 KNLDSTTV [iTRAQ_N1	4 41-58	5,293	624,835	2012_02_2	Nuclei_frac
P21291 NLDSTTV [iTRAQ_N1	3 42-58	9,197	742,044	2012_02_2	Nuclei_frac
P21291 TVYFAEEV [iTRAQ_N1	3 15-31	8,526	778,373	2012_02_2	Nuclei_frac
P21291 TVYFAEEV [iTRAQ_N1	3 15-31	5,213	584,035	2012_02_2	Nuclei_frac
P13674,P13 ATISNPITG [iTRAQ_N1	1 346-362	7,12	677,693	2012_02_2	Nuclei_frac
P13674,P13 DPEGFVGH [iTRAQ_N1	2 56-69	6,994	601,321	2012_02_2	Nuclei_frac
P13674,P13 DPEGFVGH [iTRAQ_N1	2 56-69	6,764	601,321	2012_02_2	Nuclei_frac
P13674,P13 LLELDPEH [iTRAQ_N1	1 214-223	5,103	465,256	2012_02_2	Nuclei_frac
P13674,P13 LNTEWSEL [iTRAQ_N1	2 74-87	7,574	659,369	2012_02_2	Nuclei_frac
P13674,P13 LTSTATKC [iTRAQ_N1	3 49-69	5,334	662,866	2012_02_2	Nuclei_frac
P13674,P13 LTSTATKC [iTRAQ_N1	3 49-69	5,021	662,866	2012_02_2	Nuclei_frac
P13674,P13 SAWLSGYE [iTRAQ_N1	1 366-379	10,513	854,943	2012_02_2	Nuclei_frac
P13674,P13 SAWLSGYE [iTRAQ_N1	1 366-379	5,189	570,293	2012_02_2	Nuclei_frac
P16403,P16 ALAAAGYI [iTRAQ_N1	2 64-74	6,41	698,392	2012_02_2	Nuclei_frac
P16403,P16 ALAAAGYI [iTRAQ_N1	2 64-78	7,344	623,003	2012_02_2	Nuclei_frac
P16403,P16 ALAAAGYI [iTRAQ_N1	2 64-78	7,338	623,002	2012_02_2	Nuclei_frac
P16403,P16 ASGPPVSE [iTRAQ_N1	2 34-45	5,577	743,943	2012_02_2	Nuclei_frac
P16403,P16 KALAAAG [iTRAQ_N1	3 63-74	6,71	556,662	2012_02_2	Nuclei_frac
P16403,P16 KASGPPVS [iTRAQ_N1	3 33-45	5,298	587,027	2012_02_2	Nuclei_frac
P16403,P16 KASGPPVS [iTRAQ_N1	3 33-45	5,251	587,03	2012_02_2	Nuclei_frac
P16403,P16 SGVSLAAL [iTRAQ_N1	3 54-63	5,659	469,309	2012_02_2	Nuclei_frac
P16403,P16 SGVSLAAL [iTRAQ_N1	3 54-63	5,287	703,46	2012_02_2	Nuclei_frac
P16403,P16 SLVSKGTL [iTRAQ_N1	3 85-96	5,608	565,025	2012_02_2	Nuclei_frac
P16403,P16 SLVSKGTL [iTRAQ_N1	3 85-96	4,919	565,025	2012_02_2	Nuclei_frac
P62820_CH EFADSLGIF [iTRAQ_N1	2 138-153	9,214	1007,045	2012_02_2	Nuclei_frac
P62820_CH EFADSLGIF [iTRAQ_N1	2 138-153	9,202	1007,044	2012_02_2	Nuclei_frac
P62820_CH EFADSLGIF [iTRAQ_N1	2 138-153	7,748	1007,046	2012_02_2	Nuclei_frac
P62820_CH EFADSLGIF [iTRAQ_N1	2 138-153	6,958	671,699	2012_02_2	Nuclei_frac

P62820_CH LLLIGDSG\ [iTRAQ_N1	2 11-21	6,471	680,428	2012_02_2	Nuclei_frac
P62820_CH LLLIGDSG\ [iTRAQ_N1	2 11-21	5,985	680,427	2012_02_2	Nuclei_frac
P62820_CH LLLIGDSG\ [iTRAQ_N1	2 11-21	5,355	453,953	2012_02_2	Nuclei_frac
P62820_CH LQIWDTAG [iTRAQ_N1	1 59-69	7,713	730,884	2012_02_2	Nuclei_frac
P62820_CH QWLQEIDR [iTRAQ_N1	1 101-108	7,138	616,333	2012_02_2	Nuclei_frac
P62820_CH SCLLLR [iTRAQ_N1	2 22-27	5,095	453,272	2012_02_2	Nuclei_frac
P62820_CH TITSSYYR [iTRAQ_N1	1 72-79	6,974	567,8	2012_02_2	Nuclei_frac
Q86VP6,Q8 ALTLIAGSF [iTRAQ_N1	2 630-640	6,804	457,966	2012_02_2	Nuclei_frac
Q86VP6,Q8 ALTLIAGSF [iTRAQ_N1	2 630-640	5,449	686,445	2012_02_2	Nuclei_frac
Q86VP6,Q8 IDLRPVLGE [iTRAQ_N1	1 641-659	6,928	737,113	2012_02_2	Nuclei_frac
Q86VP6,Q8 ISGSILNELI [iTRAQ_N1	1 729-742	7,349	814,499	2012_02_2	Nuclei_frac
Q86VP6,Q8 ISGSILNELI [iTRAQ_N1	1 729-742	7,223	814,499	2012_02_2	Nuclei_frac
Q86VP6,Q8 ITSEALLV1 [iTRAQ_N1	2 534-547	6,631	611,044	2012_02_2	Nuclei_frac
Q86VP6,Q8 LGTLSALD [iTRAQ_N1	2 667-678	6,196	772,999	2012_02_2	Nuclei_frac
Q86VP6,Q8 TYIQCIAAI\ [iTRAQ_N1	2 232-242	8,238	720,394	2012_02_2	Nuclei_frac
CIESLIAVF\ [iTRAQ_N1	3 13-23	7,891	798,462	2012_02_2	Nuclei_frac
CIESLIAVF\ [iTRAQ_N1	3 13-23	6,874	798,462	2012_02_2	Nuclei_frac
CIESLIAVF\ [iTRAQ_N1	3 13-23	6,375	532,645	2012_02_2	Nuclei_frac
CIESLIAVF\ [iTRAQ_N1	3 13-23	6,365	532,642	2012_02_2	Nuclei_frac
DGYNYTLS [iTRAQ_N1	2 28-36	8,188	674,853	2012_02_2	Nuclei_frac
DGYNYTLS [iTRAQ_N1	2 28-36	7,914	674,855	2012_02_2	Nuclei_frac
DGYNYTLS [iTRAQ_N1	2 28-36	7,806	674,854	2012_02_2	Nuclei_frac
DGYNYTLS [iTRAQ_N1	2 28-36	5,368	450,238	2012_02_2	Nuclei_frac
ISSPTETER [iTRAQ_N1	1 4-12	5,296	582,303	2012_02_2	Nuclei_frac
ISSPTETER [iTRAQ_N1	1 4-12	5,213	582,306	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	2 37-52	11,452	1069,558	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	3 37-52	10,403	1077,556	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	2 37-52	8,999	713,375	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	2 37-52	7,06	535,283	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	3 37-52	6,388	718,709	2012_02_2	Nuclei_frac
TEFLSFMN [iTRAQ_N1	3 37-52	5,946	718,71	2012_02_2	Nuclei_frac
YAGKDGYN [iTRAQ_N1	3 24-36	9,292	638,011	2012_02_2	Nuclei_frac
P31943,P5\ ATENDIYN\ [iTRAQ_N1	1 299-315	7,53	714,365	2012_02_2	Nuclei_frac
P31943,P5\ ATENDIYN\ [iTRAQ_N1	1 299-315	6,867	1071,042	2012_02_2	Nuclei_frac
P31943,P5\ DLNYCFSG [iTRAQ_N1	3 262-274	6,229	587,92	2012_02_2	Nuclei_frac
P31943,P5\ STGEAFVC [iTRAQ_N1	2 150-166	10,39	1065,549	2012_02_2	Nuclei_frac
P31943,P5\ STGEAFVC [iTRAQ_N1	2 150-166	8,43	710,704	2012_02_2	Nuclei_frac
P31943,P5\ STGEAFVC [iTRAQ_N1	2 150-166	7,639	710,705	2012_02_2	Nuclei_frac
P31943,P5\ VHIEIGPDG [iTRAQ_N1	1 316-325	7,215	412,899	2012_02_2	Nuclei_frac
P31943,P5\ VHIEIGPDG [iTRAQ_N1	1 316-325	5,478	618,846	2012_02_2	Nuclei_frac
P31943,P5\ YVELFLNS [iTRAQ_N1	1 355-374	10,392	762,715	2012_02_2	Nuclei_frac
GSIFVVFD\ [iTRAQ_N1	2 152-165	6,59	893,999	2012_02_2	Nuclei_frac
GSIFVVFD\ [iTRAQ_N1	2 152-165	6,413	596,333	2012_02_2	Nuclei_frac
GSIFVVFD\ [iTRAQ_N1	3 152-166	7,232	687,068	2012_02_2	Nuclei_frac
ICHQIEYYF\ [iTRAQ_N1	2 17-32	8,932	739,36	2012_02_2	Nuclei_frac
IIEDQQESL [iTRAQ_N1	2 318-328	7,014	802,94	2012_02_2	Nuclei_frac
KIIEDQQES [iTRAQ_N1	3 317-328	5,714	626,361	2012_02_2	Nuclei_frac
LTTDFNVI\ [iTRAQ_N1	2 61-74	5,991	613,355	2012_02_2	Nuclei_frac

Q32P28,Q3 AVGFSSGT [iTRAQ_N1	2	626-640	8,01	592,316	2012_02_2	Nuclei_frac
Q32P28,Q3 AVGFSSGT [iTRAQ_N1	2	626-640	7,436	592,315	2012_02_2	Nuclei_frac
Q32P28,Q3 DLSFFGGL [iTRAQ_N1	1	84-93	9,068	634,859	2012_02_2	Nuclei_frac
Q32P28,Q3 DLSFFGGL [iTRAQ_N1	1	84-93	8,638	634,86	2012_02_2	Nuclei_frac
Q32P28,Q3 DLSFFGGL [iTRAQ_N1	1	84-93	8,455	634,858	2012_02_2	Nuclei_frac
Q32P28,Q3 FYGVTVFK [iTRAQ_N1	2	491-498	5,184	624,865	2012_02_2	Nuclei_frac
Q32P28,Q3 LTNVAAT\$ [iTRAQ_N1	1	467-479	10,379	734,881	2012_02_2	Nuclei_frac
Q32P28,Q3 LTNVAAT\$ [iTRAQ_N1	1	467-479	5,166	490,256	2012_02_2	Nuclei_frac
Q32P28,Q3 QNCVTELA [iTRAQ_N1	2	258-270	8,749	548,273	2012_02_2	Nuclei_frac
ATIGADFL [iTRAQ_N1	2	39-48	8,141	662,89	2012_02_2	Nuclei_frac
ATIGADFL [iTRAQ_N1	2	39-48	5,491	442,261	2012_02_2	Nuclei_frac
EAINVEQA [iTRAQ_N1	1	158-171	9,237	867,473	2012_02_2	Nuclei_frac
EAINVEQA [iTRAQ_N1	1	158-171	8,58	578,649	2012_02_2	Nuclei_frac
FQSLGVAF [iTRAQ_N1	1	70-79	7,256	666,366	2012_02_2	Nuclei_frac
FQSLGVAF [iTRAQ_N1	1	70-79	7,201	444,58	2012_02_2	Nuclei_frac
TLDSWRDI [iTRAQ_N1	1	98-113	8,676	693,366	2012_02_2	Nuclei_frac
VILGDSGV [iTRAQ_N1	2	11-21	8,03	673,417	2012_02_2	Nuclei_frac
DIPGLTDT [iTRAQ_N1	1	120-131	8,61	714,896	2012_02_2	Nuclei_frac
GCIVDANL [iTRAQ_N1	3	99-115	5,466	705,752	2012_02_2	Nuclei_frac
GCIVDANL [iTRAQ_N1	3	99-115	5,365	705,755	2012_02_2	Nuclei_frac
GCIVDANL [iTRAQ_N1	3	99-115	5,029	705,755	2012_02_2	Nuclei_frac
KLNISFPA1 [iTRAQ_N1	4	2-14	8,917	632,698	2012_02_2	Nuclei_frac
KLNISFPA1 [iTRAQ_N1	4	2-14	8,628	632,698	2012_02_2	Nuclei_frac
KLNISFPA1 [iTRAQ_N1	4	2-14	7,567	474,775	2012_02_2	Nuclei_frac
LNISFPATC [iTRAQ_N1	3	3-14	10,35	541,964	2012_02_2	Nuclei_frac
LNISFPATC [iTRAQ_N1	3	3-14	8,081	812,443	2012_02_2	Nuclei_frac
MKLNISFPA [iTRAQ_N1	5	1-14	7,979	681,709	2012_02_2	Nuclei_frac
P05141 DFLAGGV\$ [iTRAQ_N1	2	10-22	8,393	754,439	2012_02_2	Nuclei_frac
P05141 DFLAGGV\$ [iTRAQ_N1	2	10-22	7,452	754,442	2012_02_2	Nuclei_frac
P05141 DFLAGGV\$ [iTRAQ_N1	2	10-22	5,824	503,297	2012_02_2	Nuclei_frac
P05141 GAWSNVL [iTRAQ_N1	1	272-279	5,688	523,797	2012_02_2	Nuclei_frac
P05141 GMGGAFVI [iTRAQ_N1	3	280-294	5,524	639,358	2012_02_2	Nuclei_frac
P05141 LLLQVQH\$ [iTRAQ_N1	2	33-42	6,599	475,633	2012_02_2	Nuclei_frac
P05141 LLLQVQH\$ [iTRAQ_N1	2	33-42	5,547	475,634	2012_02_2	Nuclei_frac
P05141 LLLQVQH\$ [iTRAQ_N1	2	33-42	5,039	712,947	2012_02_2	Nuclei_frac
P05141 QIFLGGVDI [iTRAQ_N1	2	96-105	6,534	474,289	2012_02_2	Nuclei_frac
P05141 QIFLGGVDI [iTRAQ_N1	2	96-105	6,281	474,29	2012_02_2	Nuclei_frac
P05141 YFPTQALN [iTRAQ_N1	2	80-91	8,222	867,976	2012_02_2	Nuclei_frac
P05141 YFPTQALN [iTRAQ_N1	2	80-91	6,07	578,987	2012_02_2	Nuclei_frac
O60716_IS(ALSAIADLI [iTRAQ_N1	1	382-396	11,16	599,66	2012_02_2	Nuclei_frac
O60716_IS(EVHLGACC [iTRAQ_N1	3	100-110	5,249	481,605	2012_02_2	Nuclei_frac
O60716_IS(GIPVLVGLI [iTRAQ_N1	2	86-98	7,631	549,347	2012_02_2	Nuclei_frac
O60716_IS(HIEWESVL [iTRAQ_N1	2	197-212	8,668	677,349	2012_02_2	Nuclei_frac
O60716_IS(TPAILEAS\$ [iTRAQ_N1	2	348-366	8,123	686,371	2012_02_2	Nuclei_frac
AGTQIENIE [iTRAQ_N1	1	62-74	7,829	833,414	2012_02_2	Nuclei_frac
AGTQIENIE [iTRAQ_N1	2	62-78	5,032	741,39	2012_02_2	Nuclei_frac

	ALDFIASK [iTRAQ_N1	2 110-117	5,307	576,847	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 110-117	5,273	576,848	2012_02_2	Nuclei_frac
	ALDFIASK [iTRAQ_N1	2 110-117	4,847	576,847	2012_02_2	Nuclei_frac
	CQLEINFN [iTRAQ_N1	3 346-358	7,515	633,01	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 148-161	7,428	609,332	2012_02_2	Nuclei_frac
	FAIQDISVE [iTRAQ_N1	2 148-161	7,153	913,495	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2 79-90	7,637	511,634	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	1 79-90	7,344	758,951	2012_02_2	Nuclei_frac
	LMLLLEVIS [iTRAQ_N1	2 79-90	7,344	766,947	2012_02_2	Nuclei_frac
	LEGHGLPA [iTRAQ_N1	1 517-528	5,178	473,275	2012_02_2	Nuclei_frac
	LFELEEQDI [iTRAQ_N1	1 270-280	6,293	791,915	2012_02_2	Nuclei_frac
	LLPLEEHYF [iTRAQ_N1	1 33-41	6,181	438,583	2012_02_2	Nuclei_frac
	LNPFGNTF [iTRAQ_N1	1 125-135	7,308	718,893	2012_02_2	Nuclei_frac
	TSFIQYLLE [iTRAQ_N1	1 72-87	9,052	1006,029	2012_02_2	Nuclei_frac
	TSFIQYLLE [iTRAQ_N1	1 72-87	5,859	671,026	2012_02_2	Nuclei_frac
	VVGTPEVL [iTRAQ_N1	1 243-251	6,673	557,342	2012_02_2	Nuclei_frac
	VVGTPEVL [iTRAQ_N1	1 243-251	6,039	557,341	2012_02_2	Nuclei_frac
P27797	FYALSASF [iTRAQ_N1	2 57-70	10,238	948,494	2012_02_2	Nuclei_frac
P27797	FYALSASF [iTRAQ_N1	2 57-70	7,975	632,665	2012_02_2	Nuclei_frac
P27797	GQTLVVQI [iTRAQ_N1	2 71-81	9,492	754,458	2012_02_2	Nuclei_frac
P27797	GQTLVVQI [iTRAQ_N1	2 71-81	6,06	503,308	2012_02_2	Nuclei_frac
P27797	IDNSQVES [iTRAQ_N1	3 169-190	9,924	984,507	2012_02_2	Nuclei_frac
P27797	IDNSQVES [iTRAQ_N1	3 169-190	6,571	738,632	2012_02_2	Nuclei_frac
P27797	IDNSQVES [iTRAQ_N1	3 169-190	6,127	738,631	2012_02_2	Nuclei_frac
P27797	KVHVIFNYI [iTRAQ_N1	3 126-134	4,838	527,328	2012_02_2	Nuclei_frac
P27797	VHVIFNYK [iTRAQ_N1	2 127-134	6,166	436,595	2012_02_2	Nuclei_frac
P26599_ISC	GQPIYIQFS [iTRAQ_N1	2 123-134	7,091	573,985	2012_02_2	Nuclei_frac
P26599_ISC	IAIPGLAGA [iTRAQ_N1	1 326-348	8,54	1210,196	2012_02_2	Nuclei_frac
P26599_ISC	IAIPGLAGA [iTRAQ_N1	1 326-348	7,922	807,133	2012_02_2	Nuclei_frac
P26599_ISC	IAIPGLAGA [iTRAQ_N1	1 326-348	7,787	807,133	2012_02_2	Nuclei_frac
P26599_ISC	IAIPGLAGA [iTRAQ_N1	1 326-348	7,695	807,134	2012_02_2	Nuclei_frac
P26599_ISC	IAIPGLAGA [iTRAQ_N1	1 326-348	7,503	807,133	2012_02_2	Nuclei_frac
P26599_ISC	KLPIDVTEC [iTRAQ_N1	3 65-84	6,555	848,839	2012_02_2	Nuclei_frac
P26599_ISC	LSLDGQNI [iTRAQ_N1	3 239-254	6,912	681,332	2012_02_2	Nuclei_frac
P26599_ISC	LTSLNVK [iTRAQ_N1	2 260-266	5,476	531,842	2012_02_2	Nuclei_frac
P26599_ISC	VTNLLMLK [iTRAQ_N1	2 85-92	6,042	610,388	2012_02_2	Nuclei_frac
P26599_ISC	VTNLLMLK [iTRAQ_N1	3 85-92	5,935	618,386	2012_02_2	Nuclei_frac
P26599_ISC	VTNLLMLK [iTRAQ_N1	3 85-92	4,962	618,387	2012_02_2	Nuclei_frac
O75947_Cf	AGLVDDFE [iTRAQ_N1	2 64-72	5,576	641,354	2012_02_2	Nuclei_frac
O75947_Cf	AGLVDDFE [iTRAQ_N1	3 64-73	5,452	518,638	2012_02_2	Nuclei_frac
O75947_Cf	KYPYWPHC [iTRAQ_N1	2 125-137	6,743	658,357	2012_02_2	Nuclei_frac
O75947_Cf	KYPYWPHC [iTRAQ_N1	2 125-137	6,729	658,357	2012_02_2	Nuclei_frac
O75947_Cf	KYPYWPHC [iTRAQ_N1	2 125-137	5,686	658,357	2012_02_2	Nuclei_frac
O75947_Cf	KYPYWPHC [iTRAQ_N1	2 125-137	5,336	658,359	2012_02_2	Nuclei_frac
O75947_Cf	SCAEWVSI [iTRAQ_N1	3 76-85	7,583	727,884	2012_02_2	Nuclei_frac
O75947_Cf	SWNETLT [iTRAQ_N1	1 33-41	8,681	619,32	2012_02_2	Nuclei_frac
O75947_Cf	TIDWVAFA [iTRAQ_N1	2 10-25	6,258	721,065	2012_02_2	Nuclei_frac

P62277	GLAPDLPE [iTRAQ_N1	2 78-92	7,32	661,379	2012_02_2 Nuclei_frac
P62277	GLSQSALP [iTRAQ_N1	1 9-18	7,361	618,345	2012_02_2 Nuclei_frac
P62277	GLTPSQIG\ [iTRAQ_N1	1 43-54	7,839	699,434	2012_02_2 Nuclei_frac
P62277	GLTPSQIG\ [iTRAQ_N1	1 43-54	5,23	466,625	2012_02_2 Nuclei_frac
P62277	KGLTPSQIK [iTRAQ_N1	2 42-54	7,81	557,356	2012_02_2 Nuclei_frac
P62277	KGLTPSQIK [iTRAQ_N1	2 42-54	7,756	557,357	2012_02_2 Nuclei_frac
P62277	KGLTPSQIK [iTRAQ_N1	2 42-54	6,832	557,356	2012_02_2 Nuclei_frac
P62277	LTSDDVKE [iTRAQ_N1	3 27-38	5,1	624,354	2012_02_2 Nuclei_frac
P62277	SVPTWLK [iTRAQ_N1	2 20-26	4,737	559,844	2012_02_2 Nuclei_frac
P12235	AAYFGVYI [iTRAQ_N1	2 188-198	6,501	747,399	2012_02_2 Nuclei_frac
P12235	GAWSNVL [iTRAQ_N1	1 272-279	5,688	523,797	2012_02_2 Nuclei_frac
P12235	GMGGAFVI [iTRAQ_N1	3 280-294	5,524	639,358	2012_02_2 Nuclei_frac
P12235	KGADIMYT [iTRAQ_N1	4 244-258	7,5	693,009	2012_02_2 Nuclei_frac
P12235	LLLQVQH\ [iTRAQ_N1	2 33-42	6,599	475,633	2012_02_2 Nuclei_frac
P12235	LLLQVQH\ [iTRAQ_N1	2 33-42	5,547	475,634	2012_02_2 Nuclei_frac
P12235	LLLQVQH\ [iTRAQ_N1	2 33-42	5,039	712,947	2012_02_2 Nuclei_frac
P12235	YFPTQALN [iTRAQ_N1	2 80-91	8,222	867,976	2012_02_2 Nuclei_frac
P12235	YFPTQALN [iTRAQ_N1	2 80-91	6,07	578,987	2012_02_2 Nuclei_frac
O15143	ASSEGGTA [iTRAQ_N1	2 308-325	11,628	639,67	2012_02_2 Nuclei_frac
O15143	ASSEGGTA [iTRAQ_N1	2 308-325	10,185	639,67	2012_02_2 Nuclei_frac
O15143	ASSEGGTA [iTRAQ_N1	2 308-325	9,513	639,67	2012_02_2 Nuclei_frac
O15143	EVEERPAP [iTRAQ_N1	2 174-187	5,46	624,339	2012_02_2 Nuclei_frac
O15143	NSVSQISV [iTRAQ_N1	2 326-338	5,861	521,97	2012_02_2 Nuclei_frac
O15143	NSVSQISV [iTRAQ_N1	2 326-338	5,636	521,97	2012_02_2 Nuclei_frac
O15143	STVLSLDV [iTRAQ_N1	3 142-164	7,224	944,831	2012_02_2 Nuclei_frac
O15143	TWKPTLVI [iTRAQ_N1	2 84-93	4,857	505,661	2012_02_2 Nuclei_frac
O15143	VAWVSHD [iTRAQ_N1	4 216-233	4,766	609,327	2012_02_2 Nuclei_frac
Q9BTV4	FFLSSGLID [iTRAQ_N1	3 189-203	6,612	721,416	2012_02_2 Nuclei_frac
Q9BTV4	FFLSSGLID [iTRAQ_N1	3 189-203	5,531	541,312	2012_02_2 Nuclei_frac
Q9BTV4	LLSDPNYG [iTRAQ_N1	2 99-113	7,282	637,704	2012_02_2 Nuclei_frac
Q9BTV4	LLSDPNYG [iTRAQ_N1	2 99-113	5,622	637,703	2012_02_2 Nuclei_frac
Q9BTV4	LVHIIGALR [iTRAQ_N1	1 87-95	6,269	568,376	2012_02_2 Nuclei_frac
Q9BTV4	SGDTLLLL [iTRAQ_N1	1 278-298	5,252	505,66	2012_02_2 Nuclei_frac
Q9BTV4	VSFSYAGL [iTRAQ_N1	1 240-265	8,753	929,824	2012_02_2 Nuclei_frac
Q9BTV4	YSYNTEWF [iTRAQ_N1	1 144-151	5,607	631,8	2012_02_2 Nuclei_frac
P35606	AAESLADF [iTRAQ_N1	2 783-801	4,81	785,078	2012_02_2 Nuclei_frac
P35606	ETHADLWI [iTRAQ_N1	2 812-821	5,657	485,934	2012_02_2 Nuclei_frac
P35606	LNYYVGGE [iTRAQ_N1	1 542-558	8,608	693,046	2012_02_2 Nuclei_frac
P35606	TYLPSQVS [iTRAQ_N1	1 759-767	6,951	597,835	2012_02_2 Nuclei_frac
P35606	VLPTIPK [iTRAQ_N1	2 608-614	5,086	528,358	2012_02_2 Nuclei_frac
P35606	VWQLGSS [iTRAQ_N1	2 168-185	8,521	768,734	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	10,605	957,023	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	9,522	638,352	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	8,71	638,353	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	8,523	638,352	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	6,344	638,353	2012_02_2 Nuclei_frac
P00558_CH	ACANPAA [iTRAQ_N1	2 107-123	6,305	638,351	2012_02_2 Nuclei_frac

P00558_CH AEPKIEAI [iTRAQ_N1	2 142-151	4,76	473,945	2012_02_2 Nuclei_frac
P00558_CH AHSSMVG\ [iTRAQ_N1	3 172-184	7,586	557,974	2012_02_2 Nuclei_frac
P00558_CH ALESPERPI [iTRAQ_N1	2 200-216	6,858	686,407	2012_02_2 Nuclei_frac
P00558_CH ALESPERPI [iTRAQ_N1	2 200-216	6,264	686,406	2012_02_2 Nuclei_frac
P00558_CH ALESPERPI [iTRAQ_N1	2 200-216	6,142	686,406	2012_02_2 Nuclei_frac
P00558_CH ALESPERPI [iTRAQ_N1	2 200-216	5,937	686,406	2012_02_2 Nuclei_frac
P00558_CH ALESPERPI [iTRAQ_N1	2 200-216	5,422	686,407	2012_02_2 Nuclei_frac
P00558_CH GCITIIGGGI [iTRAQ_N1	5 366-382	9,426	681,669	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	6,264	560,778	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,984	560,779	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,489	560,78	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,253	560,779	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,222	560,781	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,208	560,78	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	5,045	560,781	2012_02_2 Nuclei_frac
AGFAGDD\ [iTRAQ_N1	1 719-728	4,84	560,78	2012_02_2 Nuclei_frac
AVFPSIVGI [iTRAQ_N1	1 729-737	8,57	545,33	2012_02_2 Nuclei_frac
AVFPSIVGI [iTRAQ_N1	1 729-737	8,103	545,331	2012_02_2 Nuclei_frac
AVFPSIVGI [iTRAQ_N1	1 729-737	8,066	545,33	2012_02_2 Nuclei_frac
AVFPSIVGI [iTRAQ_N1	1 729-737	8,028	545,33	2012_02_2 Nuclei_frac
AVFPSIVGI [iTRAQ_N1	1 729-737	7,739	545,331	2012_02_2 Nuclei_frac
IWHHTFYNI [iTRAQ_N1	1 785-795	8,692	830,429	2012_02_2 Nuclei_frac
IWHHTFYNI [iTRAQ_N1	1 785-795	7,853	553,956	2012_02_2 Nuclei_frac
IWHHTFYNI [iTRAQ_N1	1 785-795	7,671	553,955	2012_02_2 Nuclei_frac
IWHHTFYNI [iTRAQ_N1	1 785-795	6,661	553,954	2012_02_2 Nuclei_frac
LCYVALDF [iTRAQ_N1	3 916-938	5,562	956,795	2012_02_2 Nuclei_frac
QEYDESGP [iTRAQ_N1	1 1060-1072	9,495	554,274	2012_02_2 Nuclei_frac
QEYDESGP [iTRAQ_N1	1 1060-1072	5,931	554,276	2012_02_2 Nuclei_frac
AVAQALE\ [iTRAQ_N1	1 439-449	7,84	655,901	2012_02_2 Nuclei_frac
AVAQALE\ [iTRAQ_N1	1 439-449	7,598	655,902	2012_02_2 Nuclei_frac
EILSEVER [iTRAQ_N1	1 382-389	4,975	559,812	2012_02_2 Nuclei_frac
ELGIWEPL\ [iTRAQ_N1	2 492-502	7,032	771,964	2012_02_2 Nuclei_frac
ELGIWEPL\ [iTRAQ_N1	2 492-502	5,005	514,977	2012_02_2 Nuclei_frac
IDDIVSGHK [iTRAQ_N1	2 519-527	6,395	424,579	2012_02_2 Nuclei_frac
IVLLDSSLE [iTRAQ_N1	2 238-248	5,437	523,312	2012_02_2 Nuclei_frac
TAVETAVI [iTRAQ_N1	1 508-518	6,618	665,415	2012_02_2 Nuclei_frac
TAVETAVI [iTRAQ_N1	1 508-518	6,236	665,416	2012_02_2 Nuclei_frac
TAVETAVI [iTRAQ_N1	1 508-518	6,205	665,416	2012_02_2 Nuclei_frac
DLTTAGA\ [iTRAQ_N1	2 99-111	12,242	800,401	2012_02_2 Nuclei_frac
DLTTAGA\ [iTRAQ_N1	2 99-111	11,178	800,4	2012_02_2 Nuclei_frac
DLTTAGA\ [iTRAQ_N1	2 99-111	11,011	800,401	2012_02_2 Nuclei_frac
DLTTAGA\ [iTRAQ_N1	2 99-111	8,83	800,402	2012_02_2 Nuclei_frac
DLTTAGA\ [iTRAQ_N1	2 99-111	6,224	533,935	2012_02_2 Nuclei_frac
FWYFVSQI [iTRAQ_N1	2 44-52	6,943	753,424	2012_02_2 Nuclei_frac
FWYFVSQI [iTRAQ_N1	2 44-52	5,583	502,62	2012_02_2 Nuclei_frac
IFAPNHVV\ [iTRAQ_N1	2 32-41	5,203	692,422	2012_02_2 Nuclei_frac
NFGIWLR [iTRAQ_N1	1 77-83	7,156	525,304	2012_02_2 Nuclei_frac
NFGIWLR [iTRAQ_N1	1 77-83	6,912	525,304	2012_02_2 Nuclei_frac
RPNTFF [iTRAQ_N1	1 171-176	6,632	463,254	2012_02_2 Nuclei_frac

Q15084,Q1 ALDLFSDN [iTRAQ_N1	2 246-270	6,771	1027,898	2012_02_2	Nuclei_frac
Q15084,Q1 GSTAPVGC [iTRAQ_N1	1 374-396	5,58	834,096	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	11,403	836,482	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	10,068	836,482	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	9,994	836,48	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	9,673	836,484	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	9,044	557,99	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	8,857	557,99	2012_02_2	Nuclei_frac
Q15084,Q1 LAAVDAT' [iTRAQ_N1	1 198-212	6,878	557,991	2012_02_2	Nuclei_frac
Q15084,Q1 NLEPEWA/ [iTRAQ_N1	2 176-189	5,001	601,656	2012_02_2	Nuclei_frac
Q15084,Q1 TGEAIVDA [iTRAQ_N1	1 100-113	9,334	510,958	2012_02_2	Nuclei_frac
Q15084,Q1 TGEAIVDA [iTRAQ_N1	1 100-113	8,239	765,934	2012_02_2	Nuclei_frac
P62834_CH INVNEIFYD [iTRAQ_N1	1 152-163	7,767	546,972	2012_02_2	Nuclei_frac
P62834_CH LVVLGSGC [iTRAQ_N1	2 6-16	6,361	637,407	2012_02_2	Nuclei_frac
P62834_CH SALTQFV [iTRAQ_N1	2 17-31	8,411	652,049	2012_02_2	Nuclei_frac
P62834_CH SALTQFV [iTRAQ_N1	2 17-31	8,109	652,048	2012_02_2	Nuclei_frac
P62834_CH SALTQFV [iTRAQ_N1	2 17-31	6,469	652,05	2012_02_2	Nuclei_frac
P62834_CH SKINVNEIF [iTRAQ_N1	2 150-163	8,177	666,715	2012_02_2	Nuclei_frac
P62834_CH YDPTIEDSY [iTRAQ_N1	2 32-42	7,137	558,96	2012_02_2	Nuclei_frac
P62834_CH YDPTIEDSY [iTRAQ_N1	2 32-42	6,138	558,959	2012_02_2	Nuclei_frac
P13929_ISC AAVPSGA' [iTRAQ_N1	1 33-50	9,81	975,028	2012_02_2	Nuclei_frac
P13929_ISC AAVPSGA' [iTRAQ_N1	1 33-50	5,112	650,353	2012_02_2	Nuclei_frac
P13929_ISC FGANAILG' [iTRAQ_N1	3 63-77	8,36	904,526	2012_02_2	Nuclei_frac
P13929_ISC FGANAILG' [iTRAQ_N1	3 63-77	8,023	603,352	2012_02_2	Nuclei_frac
P13929_ISC FGANAILG' [iTRAQ_N1	3 63-77	6,698	603,35	2012_02_2	Nuclei_frac
P13929_ISC SGETEDTF [iTRAQ_N1	3 330-351	7,07	881,128	2012_02_2	Nuclei_frac
P13929_ISC VNQIGSVT [iTRAQ_N1	3 301-315	12,578	961,519	2012_02_2	Nuclei_frac
P13929_ISC VNQIGSVT [iTRAQ_N1	3 301-315	7,487	641,348	2012_02_2	Nuclei_frac
P13929_ISC VNQIGSVT [iTRAQ_N1	3 301-315	7,354	641,347	2012_02_2	Nuclei_frac
P13929_ISC VNQIGSVT [iTRAQ_N1	3 301-315	7,226	641,347	2012_02_2	Nuclei_frac
P13929_ISC VNQIGSVT [iTRAQ_N1	3 301-315	6,431	641,348	2012_02_2	Nuclei_frac
Q9NVA2,Q' AAAQLLQ' [iTRAQ_N1	2 399-417	12,687	749,076	2012_02_2	Nuclei_frac
Q9NVA2,Q' AAAQLLQ' [iTRAQ_N1	3 399-418	5,265	630,11	2012_02_2	Nuclei_frac
Q9NVA2,Q' KAAAQLLQ' [iTRAQ_N1	3 398-417	6,432	630,109	2012_02_2	Nuclei_frac
Q9NVA2,Q' NLSLSGHV [iTRAQ_N1	2 14-33	7,575	810,11	2012_02_2	Nuclei_frac
Q9NVA2,Q' VNIPIIAK [iTRAQ_N1	2 175-183	5,73	634,93	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	2 137-149	9,483	817,474	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	2 137-149	7,012	545,318	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	2 137-149	6,981	545,318	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	2 137-149	6,884	545,319	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	2 137-149	6,091	545,316	2012_02_2	Nuclei_frac
P62424 AGVNTVT [iTRAQ_N1	3 137-150	8,32	636,05	2012_02_2	Nuclei_frac
P62424 LKVPPAINC [iTRAQ_N1	2 73-88	6,818	700,412	2012_02_2	Nuclei_frac
P62424 LKVPPAINC [iTRAQ_N1	2 73-88	6,514	700,414	2012_02_2	Nuclei_frac
P62424 LKVPPAINC [iTRAQ_N1	2 73-88	6,456	700,413	2012_02_2	Nuclei_frac
P62424 LKVPPAINC [iTRAQ_N1	2 73-88	5,681	700,414	2012_02_2	Nuclei_frac
P62424 LKVPPAINC [iTRAQ_N1	2 73-88	5,05	525,562	2012_02_2	Nuclei_frac

P62424	NFGIGQDIC [iTRAQ_N1	2 37-47	7,77	752,923	2012_02_2 Nuclei_frac
P62424	NFGIGQDIC [iTRAQ_N1	2 37-47	7,098	502,283	2012_02_2 Nuclei_frac
P62424	NFGIGQDIC [iTRAQ_N1	2 37-47	5,034	502,284	2012_02_2 Nuclei_frac
P62424	VVNPLFEK [iTRAQ_N1	2 26-33	5,29	617,377	2012_02_2 Nuclei_frac
P46781	ELLTLDEK [iTRAQ_N1	2 58-68	5,125	539,641	2012_02_2 Nuclei_frac
P46781	KQVVNIPS [iTRAQ_N1	2 138-149	5,549	563,353	2012_02_2 Nuclei_frac
P46781	KQVVNIPS [iTRAQ_N1	2 138-149	5,404	563,353	2012_02_2 Nuclei_frac
P46781	LDYILGLK [iTRAQ_N1	2 93-100	5,496	408,261	2012_02_2 Nuclei_frac
P46781	LQTQVFK [iTRAQ_N1	2 109-115	6,167	576,355	2012_02_2 Nuclei_frac
P46781	QVVNIPSF [iTRAQ_N1	1 139-149	5,983	472,621	2012_02_2 Nuclei_frac
P46781	RLFEGNAL [iTRAQ_N1	1 69-78	9,277	444,934	2012_02_2 Nuclei_frac
	ALAGCDFL [iTRAQ_N1	3 246-258	9,341	840,965	2012_02_2 Nuclei_frac
	ALAGCDFL [iTRAQ_N1	3 246-258	5,979	560,98	2012_02_2 Nuclei_frac
	ALAGCDFL [iTRAQ_N1	3 246-258	5,02	560,979	2012_02_2 Nuclei_frac
	ILDWHVAN [iTRAQ_N1	3 193-204	6,762	624,694	2012_02_2 Nuclei_frac
	LFVLFGAE [iTRAQ_N1	2 87-97	5,326	513,326	2012_02_2 Nuclei_frac
	LFVLFGAE [iTRAQ_N1	2 87-97	5,164	769,483	2012_02_2 Nuclei_frac
	LSFDKDAM [iTRAQ_N1	3 111-121	4,79	519,616	2012_02_2 Nuclei_frac
	LSSTWEGH [iTRAQ_N1	2 143-154	5,085	522,29	2012_02_2 Nuclei_frac
	RLIELYK [iTRAQ_N1	2 124-130	6,23	408,263	2012_02_2 Nuclei_frac
Q14764	DITPLQVV [iTRAQ_N1	2 107-123	7,936	720,771	2012_02_2 Nuclei_frac
Q14764	IEEGSVLC [iTRAQ_N1	2 734-744	6,83	709,911	2012_02_2 Nuclei_frac
Q14764	IEEGSVLC [iTRAQ_N1	2 734-744	5,642	473,609	2012_02_2 Nuclei_frac
Q14764	KEVEVVEI [iTRAQ_N1	2 154-168	8,807	676,748	2012_02_2 Nuclei_frac
Q14764	LAQDPFPL [iTRAQ_N1	2 91-106	6,364	702,056	2012_02_2 Nuclei_frac
Q14764	LKAQALAI [iTRAQ_N1	2 745-760	7,047	691,406	2012_02_2 Nuclei_frac
P39023	IGQGYLIK [iTRAQ_N1	2 286-293	4,882	590,37	2012_02_2 Nuclei_frac
P39023	KSLLVQTK [iTRAQ_N1	3 348-355	5,653	450,302	2012_02_2 Nuclei_frac
P39023	SINPLGGFV [iTRAQ_N1	3 312-333	7,494	914,476	2012_02_2 Nuclei_frac
P39023	SINPLGGFV [iTRAQ_N1	3 312-333	6,589	914,477	2012_02_2 Nuclei_frac
P39023	SINPLGGFV [iTRAQ_N1	3 312-333	4,88	686,113	2012_02_2 Nuclei_frac
P39023	SINPLGGFV [iTRAQ_N1	3 312-333	4,836	686,113	2012_02_2 Nuclei_frac
P39023	TVFAEHIS [iTRAQ_N1	3 103-114	5,813	575,29	2012_02_2 Nuclei_frac
P39023	TVFAEHIS [iTRAQ_N1	3 103-115	4,735	470,745	2012_02_2 Nuclei_frac
P39023	VACIGAWF [iTRAQ_N1	2 250-260	8,396	461,248	2012_02_2 Nuclei_frac
P62258	AASDIAMT [iTRAQ_N1	2 132-148	5,513	660,685	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	7,509	675,381	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	1 194-203	7,419	667,386	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	7,187	675,384	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	6,717	675,383	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	6,697	675,385	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	6,558	675,381	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	1 194-203	6,536	667,389	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	1 194-203	6,27	667,387	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	6,266	675,383	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	5,92	450,592	2012_02_2 Nuclei_frac
P62258	DSTLIMQL [iTRAQ_N1	2 194-203	5,891	450,592	2012_02_2 Nuclei_frac

P62258	DSTLIMQLI [iTRAQ_N1	2 194-203	5,792	675,385	2012_02_2	Nuclei_frac
P62258	DSTLIMQLI [iTRAQ_N1	2 194-203	5,475	450,592	2012_02_2	Nuclei_frac
P62258	DSTLIMQLI [iTRAQ_N1	2 194-203	5,303	450,591	2012_02_2	Nuclei_frac
P62258	DSTLIMQLI [iTRAQ_N1	2 194-203	5,105	675,384	2012_02_2	Nuclei_frac
P62258	DSTLIMQLI [iTRAQ_N1	2 194-203	4,863	450,592	2012_02_2	Nuclei_frac
P62258	IISIEQK [iTRAQ_N1	2 40-47	5,502	402,583	2012_02_2	Nuclei_frac
P62258	IISIEQK [iTRAQ_N1	2 40-47	5,476	603,372	2012_02_2	Nuclei_frac
P62258	IISIEQK [iTRAQ_N1	2 40-47	5,346	603,372	2012_02_2	Nuclei_frac
P62258	IISIEQK [iTRAQ_N1	2 40-47	5,32	603,373	2012_02_2	Nuclei_frac
P62258	LICCDILDV [iTRAQ_N1	4 73-84	7,16	882,977	2012_02_2	Nuclei_frac
P62258	LICCDILDV [iTRAQ_N1	4 73-84	6,81	588,988	2012_02_2	Nuclei_frac
P62258	NLLSVAYK [iTRAQ_N1	2 21-28	5,612	598,368	2012_02_2	Nuclei_frac
P62258	YLAEFATG [iTRAQ_N1	2 109-120	5,413	558,301	2012_02_2	Nuclei_frac
Q7Z406,Q7	EDQSILCT [iTRAQ_N1	4 189-208	8,788	853,098	2012_02_2	Nuclei_frac
Q7Z406,Q7	EDQSILCT [iTRAQ_N1	4 189-208	5,127	640,074	2012_02_2	Nuclei_frac
Q7Z406,Q7	EQADFALE [iTRAQ_N1	2 433-444	6,982	531,962	2012_02_2	Nuclei_frac
Q7Z406,Q7	EQADFALE [iTRAQ_N1	2 433-444	6,74	797,439	2012_02_2	Nuclei_frac
Q7Z406,Q7	EQADFALE [iTRAQ_N1	2 433-444	6,585	797,438	2012_02_2	Nuclei_frac
Q7Z406,Q7	EQADFALE [iTRAQ_N1	2 433-444	6,514	797,439	2012_02_2	Nuclei_frac
Q7Z406,Q7	EQADFALE [iTRAQ_N1	2 433-444	5,318	531,961	2012_02_2	Nuclei_frac
Q7Z406,Q7	FDQLLAE [iTRAQ_N1	2 1469-1477	4,782	690,886	2012_02_2	Nuclei_frac
Q7Z406,Q7	KEEELQAA [iTRAQ_N1	2 1104-1114	7,342	773,446	2012_02_2	Nuclei_frac
Q7Z406,Q7	KEEELQAA [iTRAQ_N1	2 1104-1114	5,45	515,967	2012_02_2	Nuclei_frac
Q7Z406,Q7	QLLQANPII [iTRAQ_N1	2 236-251	8,519	1008,083	2012_02_2	Nuclei_frac
Q7Z406,Q7	QLLQANPII [iTRAQ_N1	2 236-251	8,427	1008,084	2012_02_2	Nuclei_frac
Q7Z406,Q7	QLLQANPII [iTRAQ_N1	2 236-251	6,921	672,39	2012_02_2	Nuclei_frac
Q7Z406,Q7	QLLQANPII [iTRAQ_N1	2 236-251	6,644	672,39	2012_02_2	Nuclei_frac
Q7Z406,Q7	QLLQANPII [iTRAQ_N1	2 236-251	5,777	672,389	2012_02_2	Nuclei_frac
P21964	AIYKGPGE [iTRAQ_N1	2 210-221	6,272	717,895	2012_02_2	Nuclei_frac
P21964	GTVLLADN [iTRAQ_N1	2 163-184	8,74	827,113	2012_02_2	Nuclei_frac
P21964	KGTVLLAE [iTRAQ_N1	3 162-184	6,685	688,635	2012_02_2	Nuclei_frac
P21964	KGTVLLAE [iTRAQ_N1	3 162-184	6,154	688,635	2012_02_2	Nuclei_frac
P21964	LITIEINPDC [iTRAQ_N1	2 86-101	6,918	986,541	2012_02_2	Nuclei_frac
P21964	YLPDTLLLI [iTRAQ_N1	2 147-161	7,75	975,033	2012_02_2	Nuclei_frac
P21964	YLPDTLLLI [iTRAQ_N1	2 147-161	5,65	650,358	2012_02_2	Nuclei_frac
	AAVENLPT [iTRAQ_N1	1 28-42	7,985	902,014	2012_02_2	Nuclei_frac
	AAVENLPT [iTRAQ_N1	1 28-42	7,161	601,675	2012_02_2	Nuclei_frac
	GALQYLVF [iTRAQ_N1	2 317-332	7,276	1024,123	2012_02_2	Nuclei_frac
	LAATNALI [iTRAQ_N1	2 192-206	9,226	632,036	2012_02_2	Nuclei_frac
	LAATNALI [iTRAQ_N1	2 192-206	8,539	632,036	2012_02_2	Nuclei_frac
	LQQVLQMI [iTRAQ_N1	2 558-574	5,263	720,701	2012_02_2	Nuclei_frac
	TVSPDRLE [iTRAQ_N1	2 10-23	6,57	615,684	2012_02_2	Nuclei_frac
Q14103_IS	DLKDYFSK [iTRAQ_N1	3 93-100	4,943	724,414	2012_02_2	Nuclei_frac
Q14103_IS	FGEVVDCT [iTRAQ_N1	3 101-110	5,803	728,395	2012_02_2	Nuclei_frac
Q14103_IS	FGEVVDCT [iTRAQ_N1	3 101-110	5,542	728,392	2012_02_2	Nuclei_frac
Q14103_IS	FGEVVDCT [iTRAQ_N1	3 101-110	4,891	485,93	2012_02_2	Nuclei_frac
Q14103_IS	GFCFITFK [iTRAQ_N1	3 205-212	5,714	654,357	2012_02_2	Nuclei_frac
Q14103_IS	GFGFVLFK [iTRAQ_N1	2 120-127	5,171	601,863	2012_02_2	Nuclei_frac

Q14103_ISIFVGGLSPC	[iTRAQ_N1	2	165-178	8,278	888,986	2012_02_2	Nuclei_frac	
Q14103_ISIFVGGLSPC	[iTRAQ_N1	2	165-178	6,902	592,992	2012_02_2	Nuclei_frac	
Q14103_ISIFVGGLSPC	[iTRAQ_N1	2	165-178	5,841	592,992	2012_02_2	Nuclei_frac	
Q14103_ISMFIGGLSW	[iTRAQ_N1	4	80-92	6,314	644,694	2012_02_2	Nuclei_frac	
Q16629_ISAFSYYGPL	[iTRAQ_N1	1	30-38	5,824	609,327	2012_02_2	Nuclei_frac	
Q16629_ISNPPGFAFV	[iTRAQ_N1	1	45-58	5,902	883,436	2012_02_2	Nuclei_frac	
Q16629_ISNPPGFAFV	[iTRAQ_N1	1	45-58	5,255	589,295	2012_02_2	Nuclei_frac	
Q16629_ISVRVELSTG	[iTRAQ_N1	2	77-87	8,079	468,931	2012_02_2	Nuclei_frac	
Q16629_ISVYVGNLG1	[iTRAQ_N1	2	13-24	7,762	712,413	2012_02_2	Nuclei_frac	
Q16629_ISVYVGNLG1	[iTRAQ_N1	2	13-24	5,141	475,278	2012_02_2	Nuclei_frac	
Q16629_ISVYVGNLG1	[iTRAQ_N1	2	13-29	8,345	670,043	2012_02_2	Nuclei_frac	
Q16629_ISVYVGNLG1	[iTRAQ_N1	2	13-29	5,878	670,043	2012_02_2	Nuclei_frac	
POCG47_C1ESTLHLVL	[iTRAQ_N1	1	64-72	7,738	606,366	2012_02_2	Nuclei_frac	
POCG47_C1ESTLHLVL	[iTRAQ_N1	1	64-72	6,156	404,579	2012_02_2	Nuclei_frac	
POCG47_C1TITLEVEPS	[iTRAQ_N1	2	12-27	9,049	1038,57	2012_02_2	Nuclei_frac	
POCG47_C1TITLEVEPS	[iTRAQ_N1	2	12-27	7,047	692,716	2012_02_2	Nuclei_frac	
POCG47_C1TITLEVEPS	[iTRAQ_N1	2	12-27	5,864	692,715	2012_02_2	Nuclei_frac	
POCG47_C1TITLEVEPS	[iTRAQ_N1	3	12-29	5,744	807,129	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-63	6,933	685,383	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-63	6,903	685,386	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-63	6,869	685,385	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-63	6,336	685,383	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-72	6,381	605,347	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-72	5,899	605,346	2012_02_2	Nuclei_frac	
POCG47_C1TSLSDYNIQ1	[iTRAQ_N1	2	55-72	5,653	605,346	2012_02_2	Nuclei_frac	
Q02809	EQINITLDH	[iTRAQ_N1	2	176-187	4,849	566,978	2012_02_2	Nuclei_frac
Q02809	FLGSGGFIC	[iTRAQ_N1	2	133-148	10,26	958,531	2012_02_2	Nuclei_frac
Q02809	FLGSGGFIC	[iTRAQ_N1	2	133-148	8,503	639,355	2012_02_2	Nuclei_frac
Q02809	IFQNLDGAI	[iTRAQ_N1	2	188-202	7,311	654,709	2012_02_2	Nuclei_frac
Q02809	LQLNYLGN	[iTRAQ_N1	1	230-241	8,105	804,457	2012_02_2	Nuclei_frac
Q02809	LQLNYLGN	[iTRAQ_N1	1	230-241	7,733	536,639	2012_02_2	Nuclei_frac
Q02809	LTHYHEGL	[iTRAQ_N1	1	686-697	5,068	523,615	2012_02_2	Nuclei_frac
	AGVMALA	[iTRAQ_N1	2	132-145	8,335	829,481	2012_02_2	Nuclei_frac
	AGVMALA	[iTRAQ_N1	2	132-145	6,987	553,326	2012_02_2	Nuclei_frac
	EGLPVALD	[iTRAQ_N1	2	177-185	4,858	615,37	2012_02_2	Nuclei_frac
	HILGFDTG1	[iTRAQ_N1	1	186-205	7,128	766,421	2012_02_2	Nuclei_frac
	NFIVWLED	[iTRAQ_N1	2	27-36	5,808	790,441	2012_02_2	Nuclei_frac
	NFIVWLED	[iTRAQ_N1	2	27-36	5,546	527,298	2012_02_2	Nuclei_frac
	QEAIWLL	[iTRAQ_N1	1	77-89	9,453	814,47	2012_02_2	Nuclei_frac
	QEAIWLL	[iTRAQ_N1	1	77-89	7,378	543,314	2012_02_2	Nuclei_frac
P21980_CH	ALLVEPV11	[iTRAQ_N1	1	565-580	7,122	972,57	2012_02_2	Nuclei_frac
P21980_CH	ALLVEPV11	[iTRAQ_N1	1	565-580	6,949	648,716	2012_02_2	Nuclei_frac
P21980_CH	DLYLENPE1	[iTRAQ_N1	2	581-590	4,803	761,422	2012_02_2	Nuclei_frac
P21980_CH	SVPLCILYE	[iTRAQ_N1	3	541-550	6,849	755,433	2012_02_2	Nuclei_frac
P21980_CH	SVPLCILYE	[iTRAQ_N1	3	541-550	5,613	755,434	2012_02_2	Nuclei_frac
P21980_CH	VVTNYS1	[iTRAQ_N1	1	297-317	9,513	881,112	2012_02_2	Nuclei_frac
P21980_CH	YLLNLNLE1	[iTRAQ_N1	2	528-540	7,023	623,353	2012_02_2	Nuclei_frac

P21980_CH YLLNLNLEI [iTRAQ_N1	2	528-540	6,783	934,531	2012_02_2	Nuclei_frac
Q9NVI7_CF GLLLFVDE [iTRAQ_N1	1	405-418	9,786	861,982	2012_02_2	Nuclei_frac
Q9NVI7_CF GLLLFVDE [iTRAQ_N1	1	405-418	7,722	574,989	2012_02_2	Nuclei_frac
Q9NVI7_CF ITVLEALR [iTRAQ_N1	1	291-298	5,637	529,84	2012_02_2	Nuclei_frac
Q9NVI7_CF ITVLEALR [iTRAQ_N1	1	291-298	5,474	529,839	2012_02_2	Nuclei_frac
Q9NVI7_CF LFDWANT [iTRAQ_N1	1	395-403	5,723	627,325	2012_02_2	Nuclei_frac
Q9NVI7_CF LLSRPQDA [iTRAQ_N1	1	307-327	6,618	798,786	2012_02_2	Nuclei_frac
Q9NVI7_CF QQQLLNEE [iTRAQ_N1	1	147-157	7,538	764,917	2012_02_2	Nuclei_frac
P67809,P16 EDVVFVHQ [iTRAQ_N1	2	81-91	6,968	525,631	2012_02_2	Nuclei_frac
P67809,P16 EDVVFVHQ [iTRAQ_N1	2	81-91	6,754	787,944	2012_02_2	Nuclei_frac
P67809,P16 GAEAAANV [iTRAQ_N1	2	118-136	11,277	992,544	2012_02_2	Nuclei_frac
P67809,P16 GAEAAANV [iTRAQ_N1	2	118-136	11,026	662,031	2012_02_2	Nuclei_frac
P67809,P16 GAEAAANV [iTRAQ_N1	2	118-136	10,2	662,03	2012_02_2	Nuclei_frac
P67809,P16 GAEAAANV [iTRAQ_N1	2	118-136	8,033	662,031	2012_02_2	Nuclei_frac
P67809,P16 NDTKEDVF [iTRAQ_N1	3	77-91	9,459	726,404	2012_02_2	Nuclei_frac
P67809,P16 NDTKEDVF [iTRAQ_N1	3	77-91	4,915	545,054	2012_02_2	Nuclei_frac
P67809,P16 NYQQNYQI [iTRAQ_N1	2	156-184	7,538	1182,538	2012_02_2	Nuclei_frac
P67809,P16 NYQQNYQI [iTRAQ_N1	2	156-184	6,306	887,156	2012_02_2	Nuclei_frac
P67809,P16 NYQQNYQI [iTRAQ_N1	3	156-184	6,063	907,149	2012_02_2	Nuclei_frac
P67809,P16 NYQQNYQI [iTRAQ_N1	2	156-184	5,166	709,927	2012_02_2	Nuclei_frac
Q15155_CF EGYVLTAV [iTRAQ_N1	2	825-840	8,777	663,028	2012_02_2	Nuclei_frac
Q15155_CF EQQLAEIE [iTRAQ_N1	1	677-686	6,94	665,858	2012_02_2	Nuclei_frac
Q15155_CF FLLFSSLV [iTRAQ_N1	2	204-213	5,64	721,948	2012_02_2	Nuclei_frac
Q15155_CF ITITGYR [iTRAQ_N1	1	921-927	6,004	484,289	2012_02_2	Nuclei_frac
Q15155_CF VLPGDYEIL [iTRAQ_N1	2	145-162	7,858	771,437	2012_02_2	Nuclei_frac
AIIFVVPVC [iTRAQ_N1	2	59-70	7,135	813,534	2012_02_2	Nuclei_frac
AIIFVVPVC [iTRAQ_N1	2	59-70	6,74	813,535	2012_02_2	Nuclei_frac
ELNITAAK [iTRAQ_N1	2	42-49	5,592	574,351	2012_02_2	Nuclei_frac
ELNITAAK [iTRAQ_N1	2	42-49	4,822	574,351	2012_02_2	Nuclei_frac
KAIIFVVPV [iTRAQ_N1	3	58-70	7,205	633,423	2012_02_2	Nuclei_frac
TLTAVHDA [iTRAQ_N1	2	121-142	7,139	885,836	2012_02_2	Nuclei_frac
VETFSGVY [iTRAQ_N1	2	170-178	8,091	659,374	2012_02_2	Nuclei_frac
VETFSGVY [iTRAQ_N1	2	170-178	7,691	659,371	2012_02_2	Nuclei_frac
VETFSGVY [iTRAQ_N1	2	170-178	7,421	659,372	2012_02_2	Nuclei_frac
P07910_ISC GFAFVQYV [iTRAQ_N1	1	51-61	5,911	737,385	2012_02_2	Nuclei_frac
P07910_ISC KSDVEAIF [iTRAQ_N1	3	30-39	7,033	519,308	2012_02_2	Nuclei_frac
P07910_ISC KSDVEAIF [iTRAQ_N1	3	30-39	5,717	519,307	2012_02_2	Nuclei_frac
P07910_ISC QKVDSLLE [iTRAQ_N1	3	149-160	6,821	616,701	2012_02_2	Nuclei_frac
P07910_ISC QKVDSLLE [iTRAQ_N1	3	149-160	6,757	616,701	2012_02_2	Nuclei_frac
P07910_ISC QKVDSLLE [iTRAQ_N1	3	149-160	6,19	616,701	2012_02_2	Nuclei_frac
P07910_ISC VFIGNLNTI [iTRAQ_N1	2	18-29	7,131	803,003	2012_02_2	Nuclei_frac
P07910_ISC VFIGNLNTI [iTRAQ_N1	2	18-29	7,079	803,004	2012_02_2	Nuclei_frac
P07910_ISC VFIGNLNTI [iTRAQ_N1	2	18-29	6,178	535,672	2012_02_2	Nuclei_frac
P07910_ISC VFIGNLNTI [iTRAQ_N1	3	18-30	8,203	626,405	2012_02_2	Nuclei_frac
EDQSILCTC [iTRAQ_N1	4	170-189	8,788	853,098	2012_02_2	Nuclei_frac
EDQSILCTC [iTRAQ_N1	4	170-189	5,127	640,074	2012_02_2	Nuclei_frac

	FDQLLAEE [iTRAQ_N1	2 1453-1461	4,782	690,886	2012_02_2 Nuclei_frac
	IVFQEFR [iTRAQ_N1	1 719-725	5,624	541,81	2012_02_2 Nuclei_frac
	KEEELQAA [iTRAQ_N1	2 1088-1098	7,342	773,446	2012_02_2 Nuclei_frac
	KEEELQAA [iTRAQ_N1	2 1088-1098	5,45	515,967	2012_02_2 Nuclei_frac
	QLLQANPII [iTRAQ_N1	2 217-232	8,519	1008,083	2012_02_2 Nuclei_frac
	QLLQANPII [iTRAQ_N1	2 217-232	8,427	1008,084	2012_02_2 Nuclei_frac
	QLLQANPII [iTRAQ_N1	2 217-232	6,921	672,39	2012_02_2 Nuclei_frac
	QLLQANPII [iTRAQ_N1	2 217-232	6,644	672,39	2012_02_2 Nuclei_frac
	QLLQANPII [iTRAQ_N1	2 217-232	5,777	672,389	2012_02_2 Nuclei_frac
P22695	AVAFQNP([iTRAQ_N1	1 149-169	10,64	832,11	2012_02_2 Nuclei_frac
P22695	AVAFQNP([iTRAQ_N1	1 149-169	4,951	624,334	2012_02_2 Nuclei_frac
P22695	RWEVADLI [iTRAQ_N1	2 134-145	5,702	591,01	2012_02_2 Nuclei_frac
P22695	TIAQGNLSI [iTRAQ_N1	2 346-361	10	640,355	2012_02_2 Nuclei_frac
P22695	TIAQGNLSI [iTRAQ_N1	2 346-361	9,937	960,029	2012_02_2 Nuclei_frac
P22695	YEDFSNLG [iTRAQ_N1	1 57-70	8,557	603,98	2012_02_2 Nuclei_frac
P61586_CH	HFCPNVP([iTRAQ_N1	3 105-118	5,118	632,698	2012_02_2 Nuclei_frac
P61586_CH	HFCPNVP([iTRAQ_N1	4 105-119	8,422	723,43	2012_02_2 Nuclei_frac
P61586_CH	HFCPNVP([iTRAQ_N1	4 105-119	8,246	723,43	2012_02_2 Nuclei_frac
P61586_CH	KLIVVGDG [iTRAQ_N1	4 7-18	7,104	550,33	2012_02_2 Nuclei_frac
P61586_CH	LVIVGDGA [iTRAQ_N1	3 8-18	7,877	688,895	2012_02_2 Nuclei_frac
P61586_CH	TCLLIVFSK [iTRAQ_N1	3 19-27	6,359	456,944	2012_02_2 Nuclei_frac
P61586_CH	TCLLIVFSK [iTRAQ_N1	3 19-27	6,082	684,913	2012_02_2 Nuclei_frac
Q16643,Q1	LAASGEGC [iTRAQ_N1	2 42-61	11,12	787,413	2012_02_2 Nuclei_frac
Q16643,Q1	LAASGEGC [iTRAQ_N1	2 42-61	5,692	590,81	2012_02_2 Nuclei_frac
Q16643,Q1	SESEVEEA [iTRAQ_N1	1 271-290	8,853	776,062	2012_02_2 Nuclei_frac
Q16643,Q1	SPSDSSTA [iTRAQ_N1	1 336-353	6,148	669,335	2012_02_2 Nuclei_frac
Q16643,Q1	YVLINWVC [iTRAQ_N1	1 79-93	8,682	945,501	2012_02_2 Nuclei_frac
Q16643,Q1	YVLINWVC [iTRAQ_N1	1 79-93	5,59	630,668	2012_02_2 Nuclei_frac
P08107,P48	AQIHDLVL [iTRAQ_N1	1 328-341	5,884	537,312	2012_02_2 Nuclei_frac
P08107,P48	ARFEELCSI [iTRAQ_N1	2 299-310	6,733	562,953	2012_02_2 Nuclei_frac
P08107,P48	DAGVIAGL [iTRAQ_N1	1 159-170	8,494	671,403	2012_02_2 Nuclei_frac
P08107,P48	DAGVIAGL [iTRAQ_N1	1 159-170	8,417	671,404	2012_02_2 Nuclei_frac
P08107,P48	DAGVIAGL [iTRAQ_N1	1 159-170	7,92	671,404	2012_02_2 Nuclei_frac
P08107,P48	DAGVIAGL [iTRAQ_N1	1 159-170	7,73	671,404	2012_02_2 Nuclei_frac
P08107,P48	ELEQVCNP [iTRAQ_N1	3 597-627	5,35	836,674	2012_02_2 Nuclei_frac
P08107,P48	TTPSYVAF [iTRAQ_N1	1 36-48	8,276	816,405	2012_02_2 Nuclei_frac
P08107,P48	TTPSYVAF [iTRAQ_N1	1 36-48	5,889	544,607	2012_02_2 Nuclei_frac
P39019	ALAAFLK [iTRAQ_N1	2 16-22	6,107	511,336	2012_02_2 Nuclei_frac
P39019	ALAAFLKK [iTRAQ_N1	3 16-23	4,976	647,434	2012_02_2 Nuclei_frac
P39019	ALAAFLKK [iTRAQ_N1	3 16-23	4,963	431,958	2012_02_2 Nuclei_frac
P39019	ELAPYDEN [iTRAQ_N1	1 43-55	6,729	924,438	2012_02_2 Nuclei_frac
P39019	LKVPEWVI [iTRAQ_N1	3 27-37	4,965	582,691	2012_02_2 Nuclei_frac
P39019	RVLQALEC [iTRAQ_N1	2 101-110	6,078	707,954	2012_02_2 Nuclei_frac
P39019	VLQALEGL [iTRAQ_N1	2 102-110	5,874	629,904	2012_02_2 Nuclei_frac
P39019	VLQALEGL [iTRAQ_N1	2 102-110	5,666	629,903	2012_02_2 Nuclei_frac
P39019	VLQALEGL [iTRAQ_N1	2 102-110	5,634	629,904	2012_02_2 Nuclei_frac
P39019	VLQALEGL [iTRAQ_N1	2 102-110	4,989	629,903	2012_02_2 Nuclei_frac

Q96D15	AGDGDGW [iTRAQ_N1	1 70-83	8,189	795,407	2012_02_2	Nuclei_frac
Q96D15	AGDGDGW [iTRAQ_N1	1 70-83	7,796	795,407	2012_02_2	Nuclei_frac
Q96D15	DIVIAETLE [iTRAQ_N1	2 182-196	10,233	678,044	2012_02_2	Nuclei_frac
Q96D15	DIVIAETLE [iTRAQ_N1	2 182-196	9,533	678,044	2012_02_2	Nuclei_frac
Q96D15	DIVIAETLE [iTRAQ_N1	2 182-196	9,424	678,045	2012_02_2	Nuclei_frac
Q96D15	DIVIAETLE [iTRAQ_N1	2 182-196	6,267	508,784	2012_02_2	Nuclei_frac
Q96D15	EELTAFLH [iTRAQ_N1	1 166-181	6,542	532,517	2012_02_2	Nuclei_frac
Q96D15	EELTAFLH [iTRAQ_N1	2 166-181	5,729	536,515	2012_02_2	Nuclei_frac
Q96D15	EVAKEFDC [iTRAQ_N1	2 43-59	9,595	755,726	2012_02_2	Nuclei_frac
Q96D15	EVAKEFDC [iTRAQ_N1	2 43-59	9,215	755,725	2012_02_2	Nuclei_frac
	ALASILLQI [iTRAQ_N1	1 45-56	8,941	747,451	2012_02_2	Nuclei_frac
	ALASILLQI [iTRAQ_N1	1 45-56	8,422	498,635	2012_02_2	Nuclei_frac
	DLDVVVV [iTRAQ_N1	1 57-70	7,895	795,954	2012_02_2	Nuclei_frac
	DLDVVVV [iTRAQ_N1	1 57-70	6,466	795,953	2012_02_2	Nuclei_frac
	GLLEYFK [iTRAQ_N1	2 320-326	4,961	579,348	2012_02_2	Nuclei_frac
	IYQGEDLP [iTRAQ_N1	2 331-341	5,531	528,958	2012_02_2	Nuclei_frac
	IYQGEDLP [iTRAQ_N1	2 331-341	4,843	528,959	2012_02_2	Nuclei_frac
	IYQGEDLP [iTRAQ_N1	2 331-341	4,835	792,927	2012_02_2	Nuclei_frac
	SFILDFMLF [iTRAQ_N1	2 74-82	7,174	651,355	2012_02_2	Nuclei_frac
	ENVNLAQI [iTRAQ_N1	1 123-131	6,28	600,845	2012_02_2	Nuclei_frac
	LFTAESLIC [iTRAQ_N1	2 337-347	6,537	740,458	2012_02_2	Nuclei_frac
	NSNILEDLE [iTRAQ_N1	1 73-84	8,687	780,922	2012_02_2	Nuclei_frac
	TRIEGLLA [iTRAQ_N1	2 27-38	5,249	535,332	2012_02_2	Nuclei_frac
	VLLAAAV [iTRAQ_N1	3 2-11	7,707	667,41	2012_02_2	Nuclei_frac
	GIFEALRPL [iTRAQ_N1	1 2805-2823	7,75	756,45	2012_02_2	Nuclei_frac
	LALESICLL [iTRAQ_N1	3 3319-3336	6,288	779,761	2012_02_2	Nuclei_frac
	LLNTFLER [iTRAQ_N1	1 4264-4271	4,916	575,342	2012_02_2	Nuclei_frac
	LSLSNAIST [iTRAQ_N1	1 4575-4591	9,378	971,581	2012_02_2	Nuclei_frac
	LSLSNAIST [iTRAQ_N1	1 4575-4591	6,418	648,053	2012_02_2	Nuclei_frac
	TPVSITEHF [iTRAQ_N1	2 1688-1697	6,105	466,275	2012_02_2	Nuclei_frac
P28331	ILQDIASGS [iTRAQ_N1	2 428-444	7,76	710,074	2012_02_2	Nuclei_frac
P28331	LVNQQLL [iTRAQ_N1	2 651-669	4,928	796,823	2012_02_2	Nuclei_frac
P28331	NDGAAILA [iTRAQ_N1	2 461-476	6,919	606,352	2012_02_2	Nuclei_frac
P28331	VAVTPPGL [iTRAQ_N1	1 585-594	5,78	562,85	2012_02_2	Nuclei_frac
P28331	VLFLLGAD [iTRAQ_N1	2 521-534	8,844	818,457	2012_02_2	Nuclei_frac
P28331	VLFLLGAD [iTRAQ_N1	2 521-534	7,963	545,973	2012_02_2	Nuclei_frac
P62937	IIPGFMCG [iTRAQ_N1	2 55-68	8,086	871,927	2012_02_2	Nuclei_frac
P62937	IIPGFMCG [iTRAQ_N1	3 55-68	6,566	586,953	2012_02_2	Nuclei_frac
P62937	IIPGFMCG [iTRAQ_N1	3 55-68	6,062	879,925	2012_02_2	Nuclei_frac
P62937	KITIADCGC [iTRAQ_N1	3 154-164	6,383	768,422	2012_02_2	Nuclei_frac
P62937	SIYGEKFED [iTRAQ_N1	3 76-90	5,567	755,412	2012_02_2	Nuclei_frac
P62937	SIYGEKFED [iTRAQ_N1	3 76-90	5,476	1132,614	2012_02_2	Nuclei_frac
P62937	VNPTVFFC [iTRAQ_N1	1 1-18	7,03	1045,556	2012_02_2	Nuclei_frac
P62937	VNPTVFFC [iTRAQ_N1	1 1-18	6,297	697,371	2012_02_2	Nuclei_frac
P62937	VSFELFAD [iTRAQ_N1	3 19-30	6,945	604,695	2012_02_2	Nuclei_frac
P62937	VSFELFAD [iTRAQ_N1	3 19-30	6,907	906,54	2012_02_2	Nuclei_frac

P62937	VSFELFAD [iTRAQ_N1	3 19-30	6,904	604,694	2012_02_2	Nuclei_frac
P62937	VSFELFAD [iTRAQ_N1	3 19-30	6,747	906,539	2012_02_2	Nuclei_frac
P62937	VSFELFAD [iTRAQ_N1	3 19-30	5,221	453,772	2012_02_2	Nuclei_frac
Q99729	IS(FGEVVDCI [iTRAQ_N1	3 93-102	5,803	728,395	2012_02_2	Nuclei_frac
Q99729	IS(FGEVVDCI [iTRAQ_N1	3 93-102	5,542	728,392	2012_02_2	Nuclei_frac
Q99729	IS(FGEVVDCI [iTRAQ_N1	3 93-102	4,907	485,93	2012_02_2	Nuclei_frac
Q99729	IS(GFGFILFK [iTRAQ_N1	2 112-119	6,33	406,25	2012_02_2	Nuclei_frac
Q99729	IS(GFGFILFK [iTRAQ_N1	2 112-119	5,763	608,871	2012_02_2	Nuclei_frac
Q99729	IS(GFVFITFK [iTRAQ_N1	2 196-203	6,55	623,876	2012_02_2	Nuclei_frac
Q99729	IS(GFVFITFK [iTRAQ_N1	2 196-203	4,903	416,252	2012_02_2	Nuclei_frac
Q99729	IS(IFVGGLNPF [iTRAQ_N1	2 156-169	8,769	896,492	2012_02_2	Nuclei_frac
Q99729	IS(IFVGGLNPF [iTRAQ_N1	2 156-169	8,329	896,493	2012_02_2	Nuclei_frac
Q99729	IS(IFVGGLNPF [iTRAQ_N1	2 156-169	7,523	597,996	2012_02_2	Nuclei_frac
Q99729	IS(IFVGGLNPF [iTRAQ_N1	2 156-169	6,749	597,997	2012_02_2	Nuclei_frac
Q99729	IS(IFVGGLNPF [iTRAQ_N1	2 156-169	5,534	597,996	2012_02_2	Nuclei_frac
Q99729	IS(MFVGGLSV [iTRAQ_N1	4 72-84	6,391	635,35	2012_02_2	Nuclei_frac
	AELATEEF [iTRAQ_N1	1 880-901	7,138	867,83	2012_02_2	Nuclei_frac
	AELATEEF [iTRAQ_N1	1 880-901	5,415	1301,243	2012_02_2	Nuclei_frac
	LNILDTLSK [iTRAQ_N1	2 704-712	6,055	652,908	2012_02_2	Nuclei_frac
	LVGSQEEL [iTRAQ_N1	1 144-160	9,082	702,026	2012_02_2	Nuclei_frac
	SSTTSMTS [iTRAQ_N1	4 84-97	6,122	638,034	2012_02_2	Nuclei_frac
	VQREPLLT [iTRAQ_N1	2 179-189	5,439	528,675	2012_02_2	Nuclei_frac
O43390	AGPIWDLR [iTRAQ_N1	1 187-194	5,504	536,308	2012_02_2	Nuclei_frac
O43390	AGPIWDLR [iTRAQ_N1	1 187-194	5,065	536,308	2012_02_2	Nuclei_frac
O43390	EFNEEGAL [iTRAQ_N1	2 69-83	6,37	676,361	2012_02_2	Nuclei_frac
O43390	HLGVCISV [iTRAQ_N1	2 235-246	6,081	495,269	2012_02_2	Nuclei_frac
O43390	NLATTVTE [iTRAQ_N1	2 346-358	5,626	583,667	2012_02_2	Nuclei_frac
O43390	TGYTLDDVT [iTRAQ_N1	1 133-144	10,237	728,383	2012_02_2	Nuclei_frac
O43390	TGYTLDDVT [iTRAQ_N1	1 133-144	8,33	728,384	2012_02_2	Nuclei_frac
O43390	TGYTLDDVT [iTRAQ_N1	1 133-144	8,189	728,382	2012_02_2	Nuclei_frac
	AFLTLAED [iTRAQ_N1	1 162-172	7,86	703,414	2012_02_2	Nuclei_frac
	AFLTLAED [iTRAQ_N1	1 162-172	7,807	469,278	2012_02_2	Nuclei_frac
	AFLTLAED [iTRAQ_N1	2 162-173	6,413	560,013	2012_02_2	Nuclei_frac
	KTYDLLFK [iTRAQ_N1	3 4-11	5,264	487,301	2012_02_2	Nuclei_frac
	LLLIGDSG\ [iTRAQ_N1	2 12-22	6,471	680,428	2012_02_2	Nuclei_frac
	LLLIGDSG\ [iTRAQ_N1	2 12-22	5,985	680,427	2012_02_2	Nuclei_frac
	LLLIGDSG\ [iTRAQ_N1	2 12-22	5,355	453,953	2012_02_2	Nuclei_frac
	LQIWDTAG [iTRAQ_N1	1 60-70	7,713	730,884	2012_02_2	Nuclei_frac
P10606	ASGGGVPI [iTRAQ_N1	1 1-18	9,995	959,467	2012_02_2	Nuclei_frac
P10606	ASGGGVPI [iTRAQ_N1	1 1-18	9,496	959,467	2012_02_2	Nuclei_frac
P10606	ASGGGVPI [iTRAQ_N1	1 1-18	7,168	639,981	2012_02_2	Nuclei_frac
P10606	EDPNLVPS [iTRAQ_N1	2 44-56	5,592	586,334	2012_02_2	Nuclei_frac
P10606	EDPNLVPS [iTRAQ_N1	2 44-56	5,525	586,331	2012_02_2	Nuclei_frac
P10606	EDPNLVPS [iTRAQ_N1	2 44-56	5,119	586,331	2012_02_2	Nuclei_frac
P10606	GLDPYNVL [iTRAQ_N1	2 27-37	5,56	492,29	2012_02_2	Nuclei_frac
P10606	GLDPYNVL [iTRAQ_N1	2 27-37	5,077	492,29	2012_02_2	Nuclei_frac
P10606	KGLDPYNV [iTRAQ_N1	3 26-37	6,508	874,03	2012_02_2	Nuclei_frac

P10606	LVPQQLAF [iTRAQ_N1	1 91-98	5,974	525,316	2012_02_2 Nuclei_frac
Q96AY3	GGTYDTYV [iTRAQ_N1	2 172-186	6,438	635,671	2012_02_2 Nuclei_frac
Q96AY3	IIIPPFLAYG [iTRAQ_N1	2 203-214	5,41	825,002	2012_02_2 Nuclei_frac
Q96AY3	IIIPPFLAYG [iTRAQ_N1	2 203-214	5,34	825,001	2012_02_2 Nuclei_frac
Q96AY3	KIIIPPFLAY [iTRAQ_N1	3 202-214	7,765	641,067	2012_02_2 Nuclei_frac
Q96AY3	NTLVAIVV [iTRAQ_N1	1 60-71	6,625	447,95	2012_02_2 Nuclei_frac
Q96AY3	NTLVAIVV [iTRAQ_N1	1 60-71	6,401	671,422	2012_02_2 Nuclei_frac
Q96AY3	QLIVPPHLA [iTRAQ_N1	1 427-442	7,385	609,344	2012_02_2 Nuclei_frac
Q07020	GCGTVLLS [iTRAQ_N1	2 132-142	9,752	630,847	2012_02_2 Nuclei_frac
Q07020	ILTFDQLAI [iTRAQ_N1	2 119-131	9,334	875,007	2012_02_2 Nuclei_frac
Q07020	ILTFDQLAI [iTRAQ_N1	2 119-131	8,511	875,005	2012_02_2 Nuclei_frac
Q07020	ILTFDQLAI [iTRAQ_N1	2 119-131	7,439	583,673	2012_02_2 Nuclei_frac
Q07020	ILTFDQLAI [iTRAQ_N1	2 119-131	6,37	583,674	2012_02_2 Nuclei_frac
Q07020	TAVVVGTI [iTRAQ_N1	1 78-90	9,701	745,419	2012_02_2 Nuclei_frac
Q07020	TAVVVGTI [iTRAQ_N1	1 78-90	5,129	497,283	2012_02_2 Nuclei_frac
Q07020	TNSTFNQV [iTRAQ_N1	2 38-48	4,826	513,631	2012_02_2 Nuclei_frac
Q07020	TNSTFNQV [iTRAQ_N1	2 38-48	4,776	513,631	2012_02_2 Nuclei_frac
P62873	ELAGHTGY [iTRAQ_N1	3 137-149	6,485	556,596	2012_02_2 Nuclei_frac
P62873	KACADATI [iTRAQ_N1	3 22-41	10,499	811,433	2012_02_2 Nuclei_frac
P62873	LFVSGACE [iTRAQ_N1	3 197-208	7,702	757,399	2012_02_2 Nuclei_frac
P62873	LFVSGACE [iTRAQ_N1	3 197-208	5,918	505,269	2012_02_2 Nuclei_frac
P62873	LIIWDSYTT [iTRAQ_N1	2 78-88	8,873	821,46	2012_02_2 Nuclei_frac
P62873	LIIWDSYTT [iTRAQ_N1	2 78-88	8,237	821,459	2012_02_2 Nuclei_frac
P62873	LIIWDSYTT [iTRAQ_N1	2 78-88	7,933	547,974	2012_02_2 Nuclei_frac
P62873	LIIWDSYTT [iTRAQ_N1	2 78-88	7,799	821,458	2012_02_2 Nuclei_frac
P62873	LIIWDSYTT [iTRAQ_N1	2 78-88	7,314	547,974	2012_02_2 Nuclei_frac
P08195_ISC	GLVLGPIH [iTRAQ_N1	2 157-165	5,028	407,937	2012_02_2 Nuclei_frac
P08195_ISC	GRLDYLSS [iTRAQ_N1	2 145-154	4,986	480,62	2012_02_2 Nuclei_frac
P08195_ISC	IGDLQAFQ [iTRAQ_N1	2 126-144	9,778	719,067	2012_02_2 Nuclei_frac
P08195_ISC	IGDLQAFQ [iTRAQ_N1	2 126-144	8,356	719,067	2012_02_2 Nuclei_frac
P08195_ISC	LLTSFLPA [iTRAQ_N1	1 339-350	6,22	758,473	2012_02_2 Nuclei_frac
P08195_ISC	LLTSFLPA [iTRAQ_N1	1 339-350	5,334	758,472	2012_02_2 Nuclei_frac
P08195_ISC	VILDLTNP [iTRAQ_N1	1 203-212	7,519	674,396	2012_02_2 Nuclei_frac
P08195_ISC	VILDLTNP [iTRAQ_N1	1 203-212	6,744	674,392	2012_02_2 Nuclei_frac
P54886	ILHLLTQE [iTRAQ_N1	2 513-528	8,168	687,422	2012_02_2 Nuclei_frac
P54886	LASIVEQV [iTRAQ_N1	1 95-110	11,001	629,027	2012_02_2 Nuclei_frac
P54886	LNSLAIGLF [iTRAQ_N1	1 431-439	6,493	550,849	2012_02_2 Nuclei_frac
P54886	YLHENLPIF [iTRAQ_N1	1 780-790	7,765	508,619	2012_02_2 Nuclei_frac
Q86UP2	AQIQQFHS [iTRAQ_N1	2 583-607	5,131	756,663	2012_02_2 Nuclei_frac
Q86UP2	DAVSNTT [iTRAQ_N1	2 431-443	7,082	565,633	2012_02_2 Nuclei_frac
Q86UP2	SVLAETEG [iTRAQ_N1	2 1112-1123	7,939	525,981	2012_02_2 Nuclei_frac
Q86UP2	TVEELLET [iTRAQ_N1	2 746-769	5,702	747,421	2012_02_2 Nuclei_frac
Q86UP2	VSVPSNLS [iTRAQ_N1	2 1054-1071	7,479	779,746	2012_02_2 Nuclei_frac
Q92841_ISC	APILIATDV [iTRAQ_N1	1 390-401	7,964	685,912	2012_02_2 Nuclei_frac
Q92841_ISC	APILIATDV [iTRAQ_N1	1 390-401	7,162	685,911	2012_02_2 Nuclei_frac

Q92841_ISC APILIATDV [iTRAQ_N1	1 390-401	6,767	685,913	2012_02_2 Nuclei_frac
Q92841_ISC ELIKVLEEA [iTRAQ_N1	3 453-468	5,088	561,093	2012_02_2 Nuclei_frac
Q92841_ISC ELIKVLEEA [iTRAQ_N1	3 453-468	4,94	747,79	2012_02_2 Nuclei_frac
Q92841_ISC GVEICIATP [iTRAQ_N1	2 215-225	6,765	658,861	2012_02_2 Nuclei_frac
Q92841_ISC GVEICIATP [iTRAQ_N1	2 215-225	4,859	658,853	2012_02_2 Nuclei_frac
Q92841_ISC LTPYEVDE [iTRAQ_N1	1 65-75	6,693	512,285	2012_02_2 Nuclei_frac
Q92841_ISC NFYVEHPE [iTRAQ_N1	1 54-64	6,504	502,261	2012_02_2 Nuclei_frac
AQGWAPL [iTRAQ_N1	3 515-529	6,257	665,071	2012_02_2 Nuclei_frac
AQGWAPL [iTRAQ_N1	3 515-529	5,672	665,072	2012_02_2 Nuclei_frac
EALAQTVL [iTRAQ_N1	1 495-514	4,841	793,773	2012_02_2 Nuclei_frac
LYGPTNFA [iTRAQ_N1	1 385-400	8,211	643,028	2012_02_2 Nuclei_frac
SDPFLEFF [iTRAQ_N1	1 158-166	7,18	651,336	2012_02_2 Nuclei_frac
TLQLEYR [iTRAQ_N1	1 61-67	6,524	533,805	2012_02_2 Nuclei_frac
P30050_ISC CTGGEVGA [iTRAQ_N1	3 17-31	5,261	569,64	2012_02_2 Nuclei_frac
P30050_ISC CTGGEVGA [iTRAQ_N1	3 17-31	5,162	569,638	2012_02_2 Nuclei_frac
P30050_ISC EILGTAQS [iTRAQ_N1	2 131-146	11,98	607,308	2012_02_2 Nuclei_frac
P30050_ISC EILGTAQS [iTRAQ_N1	2 131-146	11,066	910,459	2012_02_2 Nuclei_frac
P30050_ISC HSGNITFDI [iTRAQ_N1	1 100-114	8,989	610,66	2012_02_2 Nuclei_frac
P30050_ISC HSGNITFDI [iTRAQ_N1	1 100-114	8,625	915,487	2012_02_2 Nuclei_frac
P30050_ISC HSGNITFDI [iTRAQ_N1	1 100-114	8,235	610,66	2012_02_2 Nuclei_frac
P30050_ISC QAQIEVVP [iTRAQ_N1	2 68-83	6,683	978,097	2012_02_2 Nuclei_frac
P30050_ISC QAQIEVVP [iTRAQ_N1	2 68-83	5,919	652,4	2012_02_2 Nuclei_frac
P30050_ISC QAQIEVVP [iTRAQ_N1	2 68-83	4,901	652,402	2012_02_2 Nuclei_frac
P63241_CH EDLRLPEGI [iTRAQ_N1	2 110-121	7,28	543,974	2012_02_2 Nuclei_frac
P63241_CH EDLRLPEGI [iTRAQ_N1	2 110-121	6,453	543,974	2012_02_2 Nuclei_frac
P63241_CH KYEDICPST [iTRAQ_N1	5 68-85	7,125	653,084	2012_02_2 Nuclei_frac
P63241_CH KYEDICPST [iTRAQ_N1	5 68-85	6,313	653,083	2012_02_2 Nuclei_frac
P63241_CH KYEDICPST [iTRAQ_N1	4 68-85	5,647	649,084	2012_02_2 Nuclei_frac
P63241_CH RNDFQLIGI [iTRAQ_N1	1 86-109	7,629	960,841	2012_02_2 Nuclei_frac
P63241_CH RNDFQLIGI [iTRAQ_N1	1 86-109	5,628	720,883	2012_02_2 Nuclei_frac
P63241_CH VHLVGIDIF [iTRAQ_N1	2 56-67	10,876	529,656	2012_02_2 Nuclei_frac
P63241_CH VHLVGIDIF [iTRAQ_N1	2 56-67	9,026	793,98	2012_02_2 Nuclei_frac
Q02978 AVVVNAA [iTRAQ_N1	2 190-205	8,748	642,029	2012_02_2 Nuclei_frac
Q02978 GIYTGLSA [iTRAQ_N1	1 78-89	10,095	682,906	2012_02_2 Nuclei_frac
Q02978 GIYTGLSA [iTRAQ_N1	1 78-89	8,355	455,606	2012_02_2 Nuclei_frac
Q02978 LGIYTVLFE [iTRAQ_N1	1 98-107	6,552	677,899	2012_02_2 Nuclei_frac
Q02978 NVFNALIR [iTRAQ_N1	1 162-169	7,363	545,83	2012_02_2 Nuclei_frac
Q02978 NVFNALIR [iTRAQ_N1	1 162-169	6,454	545,83	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLDTIFVF [iTRAQ_N1	2 97-109	9,27	854,002	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLDTIFVF [iTRAQ_N1	2 97-109	6,031	569,668	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLDTIFVF [iTRAQ_N1	3 97-110	7,699	660,403	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLSALIDC [iTRAQ_N1	2 257-266	7,925	659,915	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLSALIDC [iTRAQ_N1	2 257-266	7,461	659,917	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLSALIDC [iTRAQ_N1	2 257-266	5,422	440,279	2012_02_2 Nuclei_frac
Q9Y277_ISC LTLSALIDC [iTRAQ_N1	2 257-266	4,892	440,279	2012_02_2 Nuclei_frac
Q9Y277_ISC SCSGVEFS [iTRAQ_N1	3 35-53	7,828	760,356	2012_02_2 Nuclei_frac

	ILITTVPPN [iTRAQ_N1	1 175-185	5,11	690,94	2012_02_2	Nuclei_frac
	ILPTLEAV/ [iTRAQ_N1	2 128-141	6,942	849,526	2012_02_2	Nuclei_frac
	ILPTLEAV/ [iTRAQ_N1	2 128-141	5,59	566,685	2012_02_2	Nuclei_frac
	INNVIDNLI' [iTRAQ_N1	1 81-103	7,659	909,504	2012_02_2	Nuclei_frac
	QPLALNV/ [iTRAQ_N1	1 260-269	6,351	644,884	2012_02_2	Nuclei_frac
	VLQSALA/ [iTRAQ_N1	1 197-206	6,592	593,377	2012_02_2	Nuclei_frac
Q14980	LGHELQQA [iTRAQ_N1	2 1641-1651	5,211	494,628	2012_02_2	Nuclei_frac
Q14980	LTAQVASI [iTRAQ_N1	2 496-525	7,223	869,23	2012_02_2	Nuclei_frac
Q14980	SLEAQVA/ [iTRAQ_N1	1 1668-1681	7,127	570,641	2012_02_2	Nuclei_frac
Q14980	SLEAQVA/ [iTRAQ_N1	1 1668-1681	6,823	570,641	2012_02_2	Nuclei_frac
Q14980	VAGIESHSI [iTRAQ_N1	1 856-869	4,789	557,305	2012_02_2	Nuclei_frac
Q14980	VEFATLQE [iTRAQ_N1	2 1043-1059	8,096	720,405	2012_02_2	Nuclei_frac
P57721_ISC	AITIAGIPQ/ [iTRAQ_N1	3 145-160	5,88	667,728	2012_02_2	Nuclei_frac
P57721_ISC	AITIAGIPQ/ [iTRAQ_N1	3 145-160	5,501	1001,088	2012_02_2	Nuclei_frac
P57721_ISC	AITIAGIPQ/ [iTRAQ_N1	3 145-160	5,428	667,727	2012_02_2	Nuclei_frac
P57721_ISC	EVGSIIK [iTRAQ_N1	2 24-31	5,709	545,84	2012_02_2	Nuclei_frac
P57721_ISC	EVGSIIK [iTRAQ_N1	2 24-31	5,624	545,84	2012_02_2	Nuclei_frac
P57721_ISC	IITLAGPTN [iTRAQ_N1	2 58-70	6,064	824,009	2012_02_2	Nuclei_frac
P57721_ISC	IITLAGPTN [iTRAQ_N1	2 58-70	4,723	549,676	2012_02_2	Nuclei_frac
P57721_ISC	INISEGNCP [iTRAQ_N1	2 47-57	6,071	716,853	2012_02_2	Nuclei_frac
P57721_ISC	LVVPASQC [iTRAQ_N1	3 102-115	8,644	859,001	2012_02_2	Nuclei_frac
	IIALDGDTK [iTRAQ_N1	2 335-343	5,39	617,366	2012_02_2	Nuclei_frac
	KISSDLDG/ [iTRAQ_N1	3 102-114	5,469	457,019	2012_02_2	Nuclei_frac
	LDNLVAILI [iTRAQ_N1	1 175-186	6,882	756,947	2012_02_2	Nuclei_frac
	LGQSDPAF [iTRAQ_N1	3 187-204	7,724	791,742	2012_02_2	Nuclei_frac
	NMAEQIIQE [iTRAQ_N1	3 265-281	6,826	776,415	2012_02_2	Nuclei_frac
P02786	AVLGTSNF [iTRAQ_N1	2 387-395	6,934	612,862	2012_02_2	Nuclei_frac
P02786	GFVEPDHY [iTRAQ_N1	1 295-309	4,779	606,322	2012_02_2	Nuclei_frac
P02786	ILNIFGVIK [iTRAQ_N1	2 286-294	5,472	435,624	2012_02_2	Nuclei_frac
P02786	LTVSNVLK [iTRAQ_N1	2 275-282	6,077	581,377	2012_02_2	Nuclei_frac
P02786	SSGLPNIPV [iTRAQ_N1	1 226-239	8,947	806,961	2012_02_2	Nuclei_frac
P02786	SSGLPNIPV [iTRAQ_N1	1 226-239	5,824	538,31	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	8,798	687,707	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	8,738	687,708	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	8,652	1031,059	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	8,258	687,708	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	7,858	687,707	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	5,988	516,033	2012_02_2	Nuclei_frac
	ILDSVGIEA [iTRAQ_N1	2 26-41	4,849	516,033	2012_02_2	Nuclei_frac
	LASVPAGC [iTRAQ_N1	2 62-94	7,642	1021,555	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	7,444	772,949	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	7,431	772,949	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	7,19	772,949	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	7,145	515,635	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	6,436	772,948	2012_02_2	Nuclei_frac
	NIEDVIAQC [iTRAQ_N1	2 50-61	6,331	515,635	2012_02_2	Nuclei_frac
	YVASYLEA [iTRAQ_N1	2 3-21	8,105	719,731	2012_02_2	Nuclei_frac

YVASYLLA [iTRAQ_N1	2 3-21	6,164	1079,092	2012_02_2	Nuclei_frac
YVASYLLA [iTRAQ_N1	2 3-21	5,97	719,729	2012_02_2	Nuclei_frac
O14979_IS(DLTEYLSR [iTRAQ_N1	1 44-51	7,128	570,805	2012_02_2	Nuclei_frac
O14979_IS(FGEVVDCT [iTRAQ_N1	3 52-61	5,803	728,395	2012_02_2	Nuclei_frac
O14979_IS(FGEVVDCT [iTRAQ_N1	3 52-61	5,542	728,392	2012_02_2	Nuclei_frac
O14979_IS(FGEVVDCT [iTRAQ_N1	3 52-61	4,907	485,93	2012_02_2	Nuclei_frac
O14979_IS(GFCFITYTC [iTRAQ_N1	4 156-170	4,911	567,301	2012_02_2	Nuclei_frac
O14979_IS(GGFGVLFK [iTRAQ_N1	2 71-78	5,171	601,863	2012_02_2	Nuclei_frac
O14979_IS(MFIGGLSW [iTRAQ_N1	4 31-43	8,89	640,021	2012_02_2	Nuclei_frac
O14979_IS(MFIGGLSW [iTRAQ_N1	3 31-43	5,229	634,684	2012_02_2	Nuclei_frac
P62158_CH DTDSEEEIF [iTRAQ_N1	1 79-91	6,166	580,943	2012_02_2	Nuclei_frac
P62158_CH EAFSLFDK [iTRAQ_N1	3 15-31	10,177	1139,104	2012_02_2	Nuclei_frac
P62158_CH EAFSLFDK [iTRAQ_N1	3 15-31	8,616	759,738	2012_02_2	Nuclei_frac
P62158_CH EAFSLFDK [iTRAQ_N1	3 15-31	8,596	1139,105	2012_02_2	Nuclei_frac
P62158_CH EAFSLFDK [iTRAQ_N1	3 15-31	6,12	570,056	2012_02_2	Nuclei_frac
P62158_CH EAFSLFDK [iTRAQ_N1	3 15-31	5,762	570,055	2012_02_2	Nuclei_frac
P62158_CH ELGTVMR [iTRAQ_N1	2 32-38	5,25	483,265	2012_02_2	Nuclei_frac
P62158_CH VFDDKGN [iTRAQ_N1	2 92-107	10,27	681,698	2012_02_2	Nuclei_frac
P62158_CH VFDDKGN [iTRAQ_N1	2 92-107	9,073	681,698	2012_02_2	Nuclei_frac
Q96QV6,P1 AGLQFPVC [iTRAQ_N1	1 21-29	8,317	544,82	2012_02_2	Nuclei_frac
Q96QV6,P1 AGLQFPVC [iTRAQ_N1	1 21-29	8,193	544,82	2012_02_2	Nuclei_frac
Q96QV6,P1 AGLQFPVC [iTRAQ_N1	1 21-29	5,536	544,819	2012_02_2	Nuclei_frac
Q96QV6,P1 AGLQFPVC [iTRAQ_N1	1 21-29	5,077	544,821	2012_02_2	Nuclei_frac
Q96QV6,P1 HLQLAIR [iTRAQ_N1	1 82-88	8,921	497,818	2012_02_2	Nuclei_frac
Q96QV6,P1 LLGGVTIA [iTRAQ_N1	2 96-118	9,767	1280,29	2012_02_2	Nuclei_frac
Q96QV6,P1 LLGGVTIA [iTRAQ_N1	2 96-118	8,374	853,87	2012_02_2	Nuclei_frac
Q96QV6,P1 NDEELNK [iTRAQ_N1	2 89-95	4,796	575,303	2012_02_2	Nuclei_frac
Q6NZI2_ISC IIGAVDQIQ [iTRAQ_N1	1 61-78	10,48	1085,105	2012_02_2	Nuclei_frac
Q6NZI2_ISC IIGAVDQIQ [iTRAQ_N1	1 61-78	7,72	723,738	2012_02_2	Nuclei_frac
Q6NZI2_ISC KLEVNEAE [iTRAQ_N1	2 137-147	6,787	534,654	2012_02_2	Nuclei_frac
Q6NZI2_ISC KLEVNEAE [iTRAQ_N1	2 137-147	6,13	534,655	2012_02_2	Nuclei_frac
Q6NZI2_ISC KLEVNEAE [iTRAQ_N1	2 137-147	5,679	534,654	2012_02_2	Nuclei_frac
Q6NZI2_ISC QAEMEGA [iTRAQ_N1	2 79-95	9,429	698,365	2012_02_2	Nuclei_frac
Q6NZI2_ISC VMIYQDEV [iTRAQ_N1	4 153-165	5,034	661,386	2012_02_2	Nuclei_frac
Q15942 FGPVVAPK [iTRAQ_N1	3 25-34	5,179	491,318	2012_02_2	Nuclei_frac
Q15942 QNVAVNEI [iTRAQ_N1	2 375-385	8,211	702,363	2012_02_2	Nuclei_frac
Q15942 SPGAPGPL [iTRAQ_N1	2 343-353	5,933	663,405	2012_02_2	Nuclei_frac
Q15942 SSTKPAAG [iTRAQ_N1	3 184-200	6,194	700,074	2012_02_2	Nuclei_frac
Q15942 VNPFRPGD [iTRAQ_N1	1 35-53	6,196	711,706	2012_02_2	Nuclei_frac
Q07954 AALSGAN [iTRAQ_N1	2 2342-2355	6,825	844,515	2012_02_2	Nuclei_frac
Q07954 AALSGAN [iTRAQ_N1	2 2342-2355	5,749	563,345	2012_02_2	Nuclei_frac
Q07954 ILWIDAR [iTRAQ_N1	1 1429-1435	4,96	515,812	2012_02_2	Nuclei_frac
Q07954 IVFPHGITL [iTRAQ_N1	1 347-360	7,006	571,006	2012_02_2	Nuclei_frac
Q07954 LSVIGSIR [iTRAQ_N1	1 4047-4054	5,883	494,818	2012_02_2	Nuclei_frac
Q07954 LSVIGSIR [iTRAQ_N1	1 4047-4054	5,084	494,806	2012_02_2	Nuclei_frac
Q07954 SCEGVTHV [iTRAQ_N1	4 1077-1090	7,036	621,639	2012_02_2	Nuclei_frac

Q07955_Cf DGTGVVEF	[iTRAQ_Nt	1 155-164	8,135	611,832	2012_02_2	Nuclei_frac
Q07955_Cf DIEDVFYK	[iTRAQ_Nt	2 31-38	5,448	658,853	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	6,471	700,906	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	6,177	700,908	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	5,995	700,908	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	5,86	700,91	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	5,47	700,907	2012_02_2	Nuclei_frac
Q07955_Cf IYVGNLPPI	[iTRAQ_Nt	1 18-28	5,416	467,605	2012_02_2	Nuclei_frac
Q07955_Cf TKDIEDVF	[iTRAQ_Nt	3 29-38	5,906	563,988	2012_02_2	Nuclei_frac
Q07955_Cf VVVSGLPF	[iTRAQ_Nt	2 123-138	5,608	653,041	2012_02_2	Nuclei_frac
Q07955_Cf VVVSGLPF	[iTRAQ_Nt	2 123-138	5,424	653,04	2012_02_2	Nuclei_frac
Q07955_Cf VVVSGLPF	[iTRAQ_Nt	2 123-138	4,807	653,04	2012_02_2	Nuclei_frac
P39656	GFELTFK	[iTRAQ_Nt	2 29-35	5,737	565,33	2012_02_2 Nuclei_frac
P39656	GFELTFK	[iTRAQ_Nt	2 29-35	5,18	565,328	2012_02_2 Nuclei_frac
P39656	NTLLIAGLC	[iTRAQ_Nt	1 198-208	7,734	657,405	2012_02_2 Nuclei_frac
P39656	NTLLIAGLC	[iTRAQ_Nt	1 198-208	6,01	438,609	2012_02_2 Nuclei_frac
P39656	SSLNPILFR	[iTRAQ_Nt	1 148-156	6,275	595,854	2012_02_2 Nuclei_frac
P39656	TADDPSLS	[iTRAQ_Nt	2 36-46	5,592	724,417	2012_02_2 Nuclei_frac
P39656	TLVLLDNL	[iTRAQ_Nt	1 5-15	6,137	707,434	2012_02_2 Nuclei_frac
P39656	TLVLLDNL	[iTRAQ_Nt	1 5-15	5,561	707,433	2012_02_2 Nuclei_frac
P39656	TLVLLDNL	[iTRAQ_Nt	1 5-15	5,46	471,957	2012_02_2 Nuclei_frac
P39656	TLVLLDNL	[iTRAQ_Nt	1 5-15	5,348	471,957	2012_02_2 Nuclei_frac
Q9NZN3	EHQJSPGDI	[iTRAQ_Nt	1 345-357	5,129	542,951	2012_02_2 Nuclei_frac
Q9NZN3	LADVDDKI	[iTRAQ_Nt	3 487-509	5,961	747,408	2012_02_2 Nuclei_frac
Q9NZN3	LLPLEEHYF	[iTRAQ_Nt	1 33-41	6,181	438,583	2012_02_2 Nuclei_frac
Q9NZN3	LNAFGNAF	[iTRAQ_Nt	1 125-135	8,519	690,88	2012_02_2 Nuclei_frac
Q9NZN3	SKLPNTVL	[iTRAQ_Nt	3 474-483	5,646	496,988	2012_02_2 Nuclei_frac
P55209_CH	GIPEFWLT	[iTRAQ_Nt	2 166-176	9,183	812,975	2012_02_2 Nuclei_frac
P55209_CH	GIPEFWLT	[iTRAQ_Nt	2 166-176	8,692	812,975	2012_02_2 Nuclei_frac
P55209_CH	GIPEFWLT	[iTRAQ_Nt	2 166-176	5,373	542,318	2012_02_2 Nuclei_frac
P55209_CH	KYAVLYQF	[iTRAQ_Nt	3 105-116	6,718	639,713	2012_02_2 Nuclei_frac
P55209_CH	LDGLVETP	[iTRAQ_Nt	1 56-72	9,891	1002,544	2012_02_2 Nuclei_frac
P55209_CH	LDGLVETP	[iTRAQ_Nt	1 56-72	9,868	668,698	2012_02_2 Nuclei_frac
P55209_CH	YAVLYQPL	[iTRAQ_Nt	2 106-117	5,558	601,015	2012_02_2 Nuclei_frac
P55209_CH	YAVLYQPL	[iTRAQ_Nt	2 106-117	4,983	601,015	2012_02_2 Nuclei_frac
P62241	IIDVVYNAS	[iTRAQ_Nt	1 77-91	8,835	932,005	2012_02_2 Nuclei_frac
P62241	IIDVVYNAS	[iTRAQ_Nt	1 77-91	8,612	932,012	2012_02_2 Nuclei_frac
P62241	IIDVVYNAS	[iTRAQ_Nt	1 77-91	6,949	621,674	2012_02_2 Nuclei_frac
P62241	IIDVVYNAS	[iTRAQ_Nt	1 77-91	5,383	621,674	2012_02_2 Nuclei_frac
P62241	ISSLLEEQF	[iTRAQ_Nt	2 157-169	7,531	599,001	2012_02_2 Nuclei_frac
P62241	ISSLLEEQF	[iTRAQ_Nt	2 157-169	7,327	897,996	2012_02_2 Nuclei_frac
P62241	ISSLLEEQF	[iTRAQ_Nt	2 157-169	7,321	897,997	2012_02_2 Nuclei_frac
P62241	ISSLLEEQF	[iTRAQ_Nt	2 157-169	6,626	599,001	2012_02_2 Nuclei_frac
P62241	LTPEEEIIL	[iTRAQ_Nt	2 128-138	6,929	801,945	2012_02_2 Nuclei_frac
P62241	LTPEEEIIL	[iTRAQ_Nt	2 128-138	5,109	534,965	2012_02_2 Nuclei_frac
P62241	NCIVLIDST	[iTRAQ_Nt	2 98-109	8,022	797,923	2012_02_2 Nuclei_frac
P62241	NCIVLIDST	[iTRAQ_Nt	2 98-109	7,066	797,923	2012_02_2 Nuclei_frac

P62241	NCIVLIDST [iTRAQ_N1	2 98-109	6,938	797,926	2012_02_2 Nuclei_frac
P27695_CH	ICSWNVDC [iTRAQ_N1	2 33-42	6,826	682,352	2012_02_2 Nuclei_frac
P27695_CH	KPLVLCGD [iTRAQ_N1	3 172-190	6,201	620,596	2012_02_2 Nuclei_frac
P27695_CH	LDYFLLSH [iTRAQ_N1	3 251-268	9,978	794,1	2012_02_2 Nuclei_frac
P27695_CH	LDYFLLSH [iTRAQ_N1	3 251-268	5,574	595,828	2012_02_2 Nuclei_frac
P27695_CH	QGFGELLQ [iTRAQ_N1	1 207-223	8,244	996,539	2012_02_2 Nuclei_frac
P21589	AKGPLASC [iTRAQ_N1	3 120-136	6,337	746,781	2012_02_2 Nuclei_frac
P21589	ETPFLSNP [iTRAQ_N1	3 154-182	5,469	919,998	2012_02_2 Nuclei_frac
P21589	FPILSANIK [iTRAQ_N1	2 111-119	5,843	645,904	2012_02_2 Nuclei_frac
P21589	FPILSANIK [iTRAQ_N1	2 111-119	5,842	645,905	2012_02_2 Nuclei_frac
P21589	FPILSANIK [iTRAQ_N1	2 111-119	5,716	645,904	2012_02_2 Nuclei_frac
P21589	FPILSANIK [iTRAQ_N1	2 111-119	4,814	430,941	2012_02_2 Nuclei_frac
P21589	GPLASQISC [iTRAQ_N1	2 122-136	8,168	632,365	2012_02_2 Nuclei_frac
P21589	VIYPAVEGI [iTRAQ_N1	1 511-519	5,428	574,333	2012_02_2 Nuclei_frac
	AVPSWFVI [iTRAQ_N1	1 411-418	6,197	553,321	2012_02_2 Nuclei_frac
	FVDILTNI [iTRAQ_N1	1 726-736	5,972	785,431	2012_02_2 Nuclei_frac
	LYLINSPI [iTRAQ_N1	1 625-634	5,103	659,405	2012_02_2 Nuclei_frac
	LYTVVPR [iTRAQ_N1	1 716-722	6,361	496,308	2012_02_2 Nuclei_frac
	SVVTSIFG [iTRAQ_N1	2 1116-1125	7,576	662,909	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	7,509	675,381	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	1 213-222	7,419	667,386	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	7,187	675,384	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	6,717	675,383	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	6,697	675,385	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	6,558	675,381	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	1 213-222	6,536	667,389	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	1 213-222	6,27	667,387	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	6,266	675,383	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,92	450,592	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,891	450,592	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,792	675,385	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,475	450,592	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,303	450,591	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	5,105	675,384	2012_02_2 Nuclei_frac
P31946_ISC	DSTLIMQL [iTRAQ_N1	2 213-222	4,863	450,592	2012_02_2 Nuclei_frac
P31946_ISC	EMQPTHPI [iTRAQ_N1	2 159-167	4,76	423,557	2012_02_2 Nuclei_frac
P31946_ISC	NLLSVAYK [iTRAQ_N1	2 42-49	5,612	598,368	2012_02_2 Nuclei_frac
P31946_ISC	SICCTVLEI [iTRAQ_N1	3 92-103	7,169	840,483	2012_02_2 Nuclei_frac
P31946_ISC	SICCTVLEI [iTRAQ_N1	3 92-103	5,242	560,655	2012_02_2 Nuclei_frac
P31946_ISC	VISSIEQK [iTRAQ_N1	2 61-68	6,093	596,363	2012_02_2 Nuclei_frac
P31946_ISC	VISSIEQK [iTRAQ_N1	2 61-68	6,059	596,363	2012_02_2 Nuclei_frac
Q58FF8	ADLINNLG [iTRAQ_N1	2 95-106	8,826	765,959	2012_02_2 Nuclei_frac
Q58FF8	ADLINNLG [iTRAQ_N1	2 95-106	8,779	765,96	2012_02_2 Nuclei_frac
Q58FF8	ADLINNLG [iTRAQ_N1	2 95-106	8,642	765,959	2012_02_2 Nuclei_frac
Q58FF8	ADLINNLG [iTRAQ_N1	2 95-106	7,488	510,975	2012_02_2 Nuclei_frac
Q58FF8	ADLINNLG [iTRAQ_N1	2 95-106	6,049	510,975	2012_02_2 Nuclei_frac
Q58FF8	HSQFLGYP [iTRAQ_N1	2 126-140	5,302	699,728	2012_02_2 Nuclei_frac

Q58FF8	HSQFLGYP [iTRAQ_N1	2 126-140	4,965	525,047	2012_02_2	Nuclei_frac
Q58FF8	SIYYITGESI [iTRAQ_N1	2 257-266	6,617	724,9	2012_02_2	Nuclei_frac
Q58FF8	SIYYITGESI [iTRAQ_N1	2 257-266	6,615	724,9	2012_02_2	Nuclei_frac
Q58FF8	SIYYITGESI [iTRAQ_N1	2 257-266	4,758	483,603	2012_02_2	Nuclei_frac
Q58FF8	YESLTDPSI [iTRAQ_N1	3 55-68	4,906	658,026	2012_02_2	Nuclei_frac
Q58FF8	YIDQEELN1 [iTRAQ_N1	2 197-205	5,378	480,592	2012_02_2	Nuclei_frac
Q58FF8	YIDQEELN1 [iTRAQ_N1	2 197-205	5,375	720,386	2012_02_2	Nuclei_frac
Q02218,Q9	KPLIIFTPK [iTRAQ_N1	3 812-820	5,408	497,002	2012_02_2	Nuclei_frac
Q02218,Q9	LNVLANVI [iTRAQ_N1	1 275-283	5,041	578,371	2012_02_2	Nuclei_frac
Q02218,Q9	LVEDHLAV [iTRAQ_N1	1 83-95	6,792	546,322	2012_02_2	Nuclei_frac
Q02218,Q9	SWDIFFR [iTRAQ_N1	1 35-41	5,56	557,794	2012_02_2	Nuclei_frac
Q02218,Q9	VFHLPTTT [iTRAQ_N1	1 145-164	8,088	776,77	2012_02_2	Nuclei_frac
P61106	IYQNIQDGE [iTRAQ_N1	2 171-200	6,82	860,448	2012_02_2	Nuclei_frac
P61106	LQIWDTAG [iTRAQ_N1	1 61-71	7,713	730,884	2012_02_2	Nuclei_frac
P61106	NLTNPNTV [iTRAQ_N1	2 110-124	9,222	956,579	2012_02_2	Nuclei_frac
P61106	NLTNPNTV [iTRAQ_N1	2 110-124	5,897	638,055	2012_02_2	Nuclei_frac
P61106	STYNHLSS [iTRAQ_N1	1 96-109	7,065	598,966	2012_02_2	Nuclei_frac
P61313_CH	FFEVLIDPF [iTRAQ_N1	2 129-140	8,637	598,347	2012_02_2	Nuclei_frac
P61313_CH	FFEVLIDPF [iTRAQ_N1	2 129-140	8,325	598,346	2012_02_2	Nuclei_frac
P61313_CH	FFEVLIDPF [iTRAQ_N1	2 129-140	8,15	598,348	2012_02_2	Nuclei_frac
P61313_CH	FFEVLIDPF [iTRAQ_N1	2 129-140	8,051	897,019	2012_02_2	Nuclei_frac
P61313_CH	GATYGKPV [iTRAQ_N1	3 78-93	5,997	713,415	2012_02_2	Nuclei_frac
P61313_CH	QGYVIYR [iTRAQ_N1	1 57-63	5,806	521,794	2012_02_2	Nuclei_frac
P61313_CH	VLNSYWV1 [iTRAQ_N1	2 115-128	10,034	975,001	2012_02_2	Nuclei_frac
P07195	GLTSVINQ1 [iTRAQ_N1	2 299-307	7,411	624,382	2012_02_2	Nuclei_frac
P07195	ITVVGVGQ [iTRAQ_N1	4 23-42	7,526	759,77	2012_02_2	Nuclei_frac
P07195	ITVVGVGQ [iTRAQ_N1	4 23-42	5,189	759,769	2012_02_2	Nuclei_frac
P07195	IVVVTAGV [iTRAQ_N1	1 91-99	5,35	529,346	2012_02_2	Nuclei_frac
P07195	VIGSGCNLI [iTRAQ_N1	2 158-169	10,114	696,856	2012_02_2	Nuclei_frac
P07195	VIGSGCNLI [iTRAQ_N1	2 158-169	9,184	696,856	2012_02_2	Nuclei_frac
P07195	VIGSGCNLI [iTRAQ_N1	2 158-169	7,849	696,855	2012_02_2	Nuclei_frac
P07195	VIGSGCNLI [iTRAQ_N1	2 158-169	7,487	464,906	2012_02_2	Nuclei_frac
	ANVVGNV [iTRAQ_N1	1 789-797	7,37	579,828	2012_02_2	Nuclei_frac
	GFLWDEGF [iTRAQ_N1	1 447-461	7,38	659,017	2012_02_2	Nuclei_frac
	LAGSLLTQ [iTRAQ_N1	1 352-369	9,525	682,037	2012_02_2	Nuclei_frac
	VDPALFPP [iTRAQ_N1	1 424-441	6,039	689,734	2012_02_2	Nuclei_frac
	VDPALFPP [iTRAQ_N1	1 424-441	5,501	1034,106	2012_02_2	Nuclei_frac
	VDPALFPP [iTRAQ_N1	1 424-441	4,949	689,733	2012_02_2	Nuclei_frac
	VDPALFPP [iTRAQ_N1	1 424-441	4,881	689,734	2012_02_2	Nuclei_frac
P30044_ISC	GVLFVPG [iTRAQ_N1	3 35-50	6,58	628,009	2012_02_2	Nuclei_frac
P30044_ISC	KGVLFGVF [iTRAQ_N1	4 34-50	9,605	718,742	2012_02_2	Nuclei_frac
P30044_ISC	LLADPTGA [iTRAQ_N1	2 97-107	7,637	689,403	2012_02_2	Nuclei_frac
P30044_ISC	LLADPTGA [iTRAQ_N1	2 97-107	7,12	689,402	2012_02_2	Nuclei_frac
P30044_ISC	LLADPTGA [iTRAQ_N1	2 97-107	6,413	689,404	2012_02_2	Nuclei_frac
P30044_ISC	LLADPTGA [iTRAQ_N1	2 97-107	5,585	459,938	2012_02_2	Nuclei_frac
P30044_ISC	VNLAELFK [iTRAQ_N1	2 24-31	6,321	611,364	2012_02_2	Nuclei_frac

P30044_ISC VNLAELFK [iTRAQ_N1	2 24-31	6,252	611,37	2012_02_2 Nuclei_frac
P30044_ISC VNLAELFK [iTRAQ_N1	2 24-31	5,921	611,365	2012_02_2 Nuclei_frac
AINCATSG [iTRAQ_N1	3 1445-1461	7,516	650,014	2012_02_2 Nuclei_frac
ALGLGVEC [iTRAQ_N1	2 902-927	6,931	769,206	2012_02_2 Nuclei_frac
EGGFLLH [iTRAQ_N1	1 1338-1349	5,407	504,973	2012_02_2 Nuclei_frac
TLLEGSGLI [iTRAQ_N1	1 2483-2505	10,289	856,147	2012_02_2 Nuclei_frac
P62906 FPSLLTHN [iTRAQ_N1	3 133-146	7,034	635,677	2012_02_2 Nuclei_frac
P62906 FSVCVLGC [iTRAQ_N1	4 62-77	8,189	727,683	2012_02_2 Nuclei_frac
P62906 KYDAFLAS [iTRAQ_N1	3 105-117	7,489	639,709	2012_02_2 Nuclei_frac
P62906 KYDAFLAS [iTRAQ_N1	3 105-117	6,729	639,708	2012_02_2 Nuclei_frac
P62906 KYDAFLAS [iTRAQ_N1	3 105-117	5,85	639,709	2012_02_2 Nuclei_frac
P62906 VLCLAVA [iTRAQ_N1	3 161-172	7,174	518,654	2012_02_2 Nuclei_frac
O94925_C1 CVQSNIVL [iTRAQ_N1	2 203-216	8,475	598,332	2012_02_2 Nuclei_frac
O94925_C1 GSTHPQPG [iTRAQ_N1	2 86-106	7,174	737,07	2012_02_2 Nuclei_frac
O94925_C1 QGLLPSEI [iTRAQ_N1	2 133-153	8,382	884,821	2012_02_2 Nuclei_frac
O94925_C1 VADYIPQL [iTRAQ_N1	2 246-255	5,723	703,419	2012_02_2 Nuclei_frac
P41091,Q2' AGGEAGV [iTRAQ_N1	1 1-16	8,246	565,308	2012_02_2 Nuclei_frac
P41091,Q2' IVSLFAEH [iTRAQ_N1	2 317-341	5,982	953,532	2012_02_2 Nuclei_frac
P41091,Q2' LIGWGQIR [iTRAQ_N1	1 452-459	4,992	543,831	2012_02_2 Nuclei_frac
P41091,Q2' QATINIGTI [iTRAQ_N1	2 38-53	5,099	477,029	2012_02_2 Nuclei_frac
P41091,Q2' VGQEIEVRI [iTRAQ_N1	2 289-302	5,425	600,362	2012_02_2 Nuclei_frac
P41091,Q2' VGQEIEVRI [iTRAQ_N1	2 289-302	5,39	600,361	2012_02_2 Nuclei_frac
P41091,Q2' VGQEIEVRI [iTRAQ_N1	2 289-302	4,994	600,36	2012_02_2 Nuclei_frac
FICTTSAIQ [iTRAQ_N1	2 18-28	6,513	727,884	2012_02_2 Nuclei_frac
GVTIIGPAT [iTRAQ_N1	4 617-635	7,234	768,788	2012_02_2 Nuclei_frac
LGLVGVNI [iTRAQ_N1	2 69-82	7,489	843,528	2012_02_2 Nuclei_frac
LGLVGVNI [iTRAQ_N1	2 69-82	5,931	562,684	2012_02_2 Nuclei_frac
TIAIIAEGIP [iTRAQ_N1	1 593-607	8,291	856,51	2012_02_2 Nuclei_frac
TIAIIAEGIP [iTRAQ_N1	1 593-607	6,971	571,342	2012_02_2 Nuclei_frac
O95782 ALQVGCLI [iTRAQ_N1	2 914-922	6,141	587,348	2012_02_2 Nuclei_frac
O95782 ATIQGVLR [iTRAQ_N1	1 557-564	6,149	501,315	2012_02_2 Nuclei_frac
O95782 DFLTPLL [iTRAQ_N1	1 811-821	5,431	701,416	2012_02_2 Nuclei_frac
O95782 GLAVFISDI [iTRAQ_N1	1 12-21	6,674	617,867	2012_02_2 Nuclei_frac
O95782 VLQIVTNR [iTRAQ_N1	1 465-472	4,959	543,842	2012_02_2 Nuclei_frac
Q16891_IS1 EVAGAKP [iTRAQ_N1	3 284-298	5,703	637,706	2012_02_2 Nuclei_frac
Q16891_IS1 QHITLALH [iTRAQ_N1	2 396-404	6,315	447,609	2012_02_2 Nuclei_frac
Q16891_IS1 QTASVTLC [iTRAQ_N1	2 198-225	5,523	780,942	2012_02_2 Nuclei_frac
Q16891_IS1 TSSAETPT [iTRAQ_N1	2 550-568	5,156	720,743	2012_02_2 Nuclei_frac
Q16891_IS1 VVSQYHEL [iTRAQ_N1	1 322-334	6,651	557,982	2012_02_2 Nuclei_frac
Q15019_IS1 ASIPFSVV [iTRAQ_N1	2 233-249	6,208	683,394	2012_02_2 Nuclei_frac
Q15019_IS1 STLINSLFL [iTRAQ_N1	1 51-66	10,091	1013,553	2012_02_2 Nuclei_frac
Q15019_IS1 STLINSLFL [iTRAQ_N1	1 51-66	6,278	676,04	2012_02_2 Nuclei_frac
Q15019_IS1 TIISYIDEQF [iTRAQ_N1	1 117-128	7,875	829,431	2012_02_2 Nuclei_frac
Q15019_IS1 VNIVPVIA [iTRAQ_N1	2 175-183	5,149	620,916	2012_02_2 Nuclei_frac

P07737	STGGAPTF [iTRAQ_N1	2 91-104	9,945	834,465	2012_02_2	Nuclei_frac
P07737	STGGAPTF [iTRAQ_N1	2 91-104	9,613	834,464	2012_02_2	Nuclei_frac
P07737	STGGAPTF [iTRAQ_N1	2 91-104	9,174	556,645	2012_02_2	Nuclei_frac
P07737	STGGAPTF [iTRAQ_N1	2 91-104	8,004	556,645	2012_02_2	Nuclei_frac
P07737	STGGAPTF [iTRAQ_N1	2 91-104	7,521	556,645	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	7,77	966,575	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	6,799	966,578	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	6,777	966,577	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	6,615	966,577	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	6,011	966,58	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-53	4,734	644,72	2012_02_2	Nuclei_frac
P07737	TFVNITPAI [iTRAQ_N1	2 38-55	6,251	735,098	2012_02_2	Nuclei_frac
P07737	TLVLLMGK [iTRAQ_N1	3 108-115	5,308	589,875	2012_02_2	Nuclei_frac
P07737	TLVLLMGK [iTRAQ_N1	2 108-115	4,971	581,877	2012_02_2	Nuclei_frac
	AKELLGQC [iTRAQ_N1	2 642-653	6,186	533,678	2012_02_2	Nuclei_frac
	AKELLGQC [iTRAQ_N1	2 642-653	5,569	533,679	2012_02_2	Nuclei_frac
	DAHNALLI [iTRAQ_N1	1 628-641	6,766	547,622	2012_02_2	Nuclei_frac
	ELLGQGLL [iTRAQ_N1	1 644-653	5,505	628,397	2012_02_2	Nuclei_frac
	KLNEILQAI [iTRAQ_N1	2 332-340	5,108	458,283	2012_02_2	Nuclei_frac
	VWDLFPE/ [iTRAQ_N1	2 765-776	5,68	588,331	2012_02_2	Nuclei_frac
	IQSGLGAL! [iTRAQ_N1	1 60-69	9,825	573,342	2012_02_2	Nuclei_frac
	LASMLETI [iTRAQ_N1	1 32-40	6,742	589,341	2012_02_2	Nuclei_frac
	LASMLETI [iTRAQ_N1	2 32-40	4,976	597,338	2012_02_2	Nuclei_frac
	LASMLETI [iTRAQ_N1	2 32-40	4,958	597,339	2012_02_2	Nuclei_frac
	LEANHGLL [iTRAQ_N1	1 109-119	6,058	446,266	2012_02_2	Nuclei_frac
	SHDTTSNT [iTRAQ_N1	2 70-84	6,604	630,018	2012_02_2	Nuclei_frac
	SHDTTSNT [iTRAQ_N1	2 70-84	6,571	630,017	2012_02_2	Nuclei_frac
P16188,P01	AQSQTDR\ [iTRAQ_N1	1 69-82	5,982	568,644	2012_02_2	Nuclei_frac
P16188,P01	AYLEGTCV [iTRAQ_N1	2 158-169	8,312	820,914	2012_02_2	Nuclei_frac
P16188,P01	FIAVGYVD [iTRAQ_N1	1 22-35	9,324	887,469	2012_02_2	Nuclei_frac
P16188,P01	FIAVGYVD [iTRAQ_N1	1 22-35	8,367	591,981	2012_02_2	Nuclei_frac
P16188,P01	YFSTSVSR [iTRAQ_N1	1 7-21	5,491	590,968	2012_02_2	Nuclei_frac
P16188,P01	YFSTSVSR [iTRAQ_N1	1 7-21	4,933	590,968	2012_02_2	Nuclei_frac
P52597	ATENDIYN [iTRAQ_N1	1 299-315	7,53	714,365	2012_02_2	Nuclei_frac
P52597	ATENDIYN [iTRAQ_N1	1 299-315	6,867	1071,042	2012_02_2	Nuclei_frac
P52597	GLPFGCTK [iTRAQ_N1	3 116-123	5,089	584,327	2012_02_2	Nuclei_frac
P52597	ITGEAFVQI [iTRAQ_N1	2 150-166	9,227	719,389	2012_02_2	Nuclei_frac
P52597	ITGEAFVQI [iTRAQ_N1	2 150-166	8,694	719,388	2012_02_2	Nuclei_frac
P52597	ITGEAFVQI [iTRAQ_N1	2 150-166	7,887	719,388	2012_02_2	Nuclei_frac
P52597	VHIEIGPDG [iTRAQ_N1	1 316-325	7,215	412,899	2012_02_2	Nuclei_frac
P52597	VHIEIGPDG [iTRAQ_N1	1 316-325	5,478	618,846	2012_02_2	Nuclei_frac
P27824	APVPTGEV [iTRAQ_N1	1 42-57	9,132	957,971	2012_02_2	Nuclei_frac
P27824	IVDDWANI [iTRAQ_N1	3 426-439	8,306	683,711	2012_02_2	Nuclei_frac
P27824	KIPNPDFFE [iTRAQ_N1	2 381-395	6,154	718,05	2012_02_2	Nuclei_frac
P27824	KIPNPDFFE [iTRAQ_N1	2 381-395	5,007	718,053	2012_02_2	Nuclei_frac
P27824	LHFIFR [iTRAQ_N1	1 180-185	5,456	488,796	2012_02_2	Nuclei_frac

	DISLSDYK [iTRAQ_N1	2 28-35	7,273	614,838	2012_02_2	Nuclei_frac
	LVQAFQFT [iTRAQ_N1	2 159-168	7,304	742,922	2012_02_2	Nuclei_frac
	QITVNDLP [iTRAQ_N1	1 141-151	7,565	678,393	2012_02_2	Nuclei_frac
	QITVNDLP [iTRAQ_N1	1 141-151	6,881	678,394	2012_02_2	Nuclei_frac
	TIAQDYGV [iTRAQ_N1	2 111-120	6,89	698,408	2012_02_2	Nuclei_frac
	TIAQDYGV [iTRAQ_N1	2 111-120	6,328	698,407	2012_02_2	Nuclei_frac
P55769	AYPLADAF [iTRAQ_N1	2 9-19	5,465	496,62	2012_02_2	Nuclei_frac
P55769	KLLDLVQC [iTRAQ_N1	4 20-32	8,575	681,056	2012_02_2	Nuclei_frac
P55769	KLLDLVQC [iTRAQ_N1	4 20-32	8,373	681,055	2012_02_2	Nuclei_frac
P55769	KLLDLVQC [iTRAQ_N1	4 20-32	4,786	511,044	2012_02_2	Nuclei_frac
P55769	LLDLVQQS [iTRAQ_N1	3 21-32	7,066	590,323	2012_02_2	Nuclei_frac
P55769	QQIQSIQQ [iTRAQ_N1	1 113-124	7,896	801,442	2012_02_2	Nuclei_frac
P04899,P04	EIYTHFTCA [iTRAQ_N1	3 318-330	7,057	625,645	2012_02_2	Nuclei_frac
P04899,P04	IAQSDYIPT [iTRAQ_N1	1 162-176	7,726	946,007	2012_02_2	Nuclei_frac
P04899,P04	LLLLGAGE [iTRAQ_N1	2 35-45	7,65	673,416	2012_02_2	Nuclei_frac
P04899,P04	LLLLGAGE [iTRAQ_N1	2 35-45	7,138	673,418	2012_02_2	Nuclei_frac
P04899,P04	LLLLGAGE [iTRAQ_N1	2 35-45	4,964	449,281	2012_02_2	Nuclei_frac
P04899,P04	TTGIVETHI [iTRAQ_N1	2 181-192	6,565	556,978	2012_02_2	Nuclei_frac
P04899,P04	TTGIVETHI [iTRAQ_N1	2 181-192	6,498	556,977	2012_02_2	Nuclei_frac
Q15907_C1	AITSAYYR [iTRAQ_N1	1 74-81	7,315	544,797	2012_02_2	Nuclei_frac
Q15907_C1	GAVGALL [iTRAQ_N1	2 82-94	6,98	789,481	2012_02_2	Nuclei_frac
Q15907_C1	GAVGALL [iTRAQ_N1	2 82-94	5,333	526,655	2012_02_2	Nuclei_frac
Q15907_C1	STIGVEFA [iTRAQ_N1	1 41-50	6,993	612,84	2012_02_2	Nuclei_frac
Q15907_C1	VVLIGDSG [iTRAQ_N1	2 13-23	7,644	666,41	2012_02_2	Nuclei_frac
P62280	AYQKQPTI [iTRAQ_N1	3 8-19	5,192	633,363	2012_02_2	Nuclei_frac
P62280	CPFTGNVS [iTRAQ_N1	2 59-68	5,264	647,839	2012_02_2	Nuclei_frac
P62280	EAIEGTYID [iTRAQ_N1	3 48-58	8,263	566,993	2012_02_2	Nuclei_frac
P62280	EAIEGTYID [iTRAQ_N1	3 48-58	7,617	566,994	2012_02_2	Nuclei_frac
P62280	EAIEGTYID [iTRAQ_N1	3 48-58	6,516	566,993	2012_02_2	Nuclei_frac
P62280	EAIEGTYID [iTRAQ_N1	3 48-58	6,401	566,994	2012_02_2	Nuclei_frac
P62280	EAIEGTYID [iTRAQ_N1	3 48-58	4,955	425,497	2012_02_2	Nuclei_frac
P62280	ILSGVVTK [iTRAQ_N1	2 71-78	4,813	552,866	2012_02_2	Nuclei_frac
P62280	OPTIFQNK [iTRAQ_N1	2 12-19	5,29	632,369	2012_02_2	Nuclei_frac
Q99714,Q9	DLAPIGIR [iTRAQ_N1	1 184-191	5,053	499,811	2012_02_2	Nuclei_frac
Q99714,Q9	GLVAVITG [iTRAQ_N1	1 9-28	8,79	979,068	2012_02_2	Nuclei_frac
Q99714,Q9	GLVAVITG [iTRAQ_N1	1 9-28	8,573	653,046	2012_02_2	Nuclei_frac
Q99714,Q9	VCNFLASC [iTRAQ_N1	2 212-225	9,329	883,463	2012_02_2	Nuclei_frac
Q99714,Q9	VCNFLASC [iTRAQ_N1	2 212-225	6,447	589,312	2012_02_2	Nuclei_frac
Q99714,Q9	VMTIAPGL [iTRAQ_N1	3 192-211	5,601	797,129	2012_02_2	Nuclei_frac
	ILQVSFK [iTRAQ_N1	2 314-320	5,631	561,859	2012_02_2	Nuclei_frac
	RSEAEAAI [iTRAQ_N1	2 157-171	5,175	655,338	2012_02_2	Nuclei_frac
	SLFSSIGEV [iTRAQ_N1	2 38-50	8,227	547,97	2012_02_2	Nuclei_frac
	VLVDQTT [iTRAQ_N1	1 137-147	9,737	666,885	2012_02_2	Nuclei_frac
	VLVDQTT [iTRAQ_N1	1 137-147	7,414	666,885	2012_02_2	Nuclei_frac

O15460_IS	APQLLIAPF [iTRAQ_N1	2	298-319	5,145	720,396	2012_02_2	Nuclei_frac
O15460_IS	LLSLDPSH [iTRAQ_N1	1	212-221	6,137	437,578	2012_02_2	Nuclei_frac
O15460_IS	SAADAEG [iTRAQ_N1	2	51-67	8,196	689,026	2012_02_2	Nuclei_frac
O15460_IS	SAADAEG [iTRAQ_N1	2	51-67	5,213	517,021	2012_02_2	Nuclei_frac
O15460_IS	TGVLTVAS [iTRAQ_N1	1	350-359	9,01	605,849	2012_02_2	Nuclei_frac
	AATAAAD [iTRAQ_N1	2	74-84	8,602	663,37	2012_02_2	Nuclei_frac
	AATAAAD [iTRAQ_N1	2	74-84	6,123	442,583	2012_02_2	Nuclei_frac
	LWDHATM [iTRAQ_N1	3	168-178	5,026	545,621	2012_02_2	Nuclei_frac
	LWQTVVG [iTRAQ_N1	2	291-298	5,562	609,877	2012_02_2	Nuclei_frac
	QGDTGDW [iTRAQ_N1	2	45-59	9,29	640,668	2012_02_2	Nuclei_frac
P04216	HVLFGTVG [iTRAQ_N1	1	42-56	9,217	619,336	2012_02_2	Nuclei_frac
P04216	VLYLSAFT [iTRAQ_N1	2	69-78	7,888	708,92	2012_02_2	Nuclei_frac
P04216	VLYLSAFT [iTRAQ_N1	2	69-78	6,736	472,949	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	11,21	853,966	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	10,691	853,965	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	9,848	853,966	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	9,15	569,647	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	7,259	569,647	2012_02_2	Nuclei_frac
P04216	VTSLTACL [iTRAQ_N1	2	3-16	7,226	569,647	2012_02_2	Nuclei_frac
	AGGAADV [iTRAQ_N1	2	78-92	9,108	590	2012_02_2	Nuclei_frac
	DVACGAN [iTRAQ_N1	3	334-350	6,094	543,792	2012_02_2	Nuclei_frac
	LFDFPGR [iTRAQ_N1	1	378-384	5,115	498,275	2012_02_2	Nuclei_frac
	VFSWGFGR [iTRAQ_N1	1	351-361	7,551	688,847	2012_02_2	Nuclei_frac
	AITGASLA [iTRAQ_N1	3	81-93	7,259	522,633	2012_02_2	Nuclei_frac
	AITGASLA [iTRAQ_N1	2	81-93	5,26	517,302	2012_02_2	Nuclei_frac
	KGQSEEIQ [iTRAQ_N1	3	61-69	6,701	493,623	2012_02_2	Nuclei_frac
	QINWTVLY [iTRAQ_N1	1	48-56	8,403	668,879	2012_02_2	Nuclei_frac
	VFQFLNAK [iTRAQ_N1	2	28-35	5,494	627,878	2012_02_2	Nuclei_frac
	VFQFLNAK [iTRAQ_N1	2	28-35	5,216	418,92	2012_02_2	Nuclei_frac
Q92616	KLLSSLGG [iTRAQ_N1	3	589-598	5,491	494,651	2012_02_2	Nuclei_frac
Q92616	LTSADALR [iTRAQ_N1	1	2292-2311	6,157	737,438	2012_02_2	Nuclei_frac
Q92616	VLAFLSSV [iTRAQ_N1	1	2092-2106	9,976	832,479	2012_02_2	Nuclei_frac
Q92616	VLPQLISTI [iTRAQ_N1	1	737-755	6,211	722,431	2012_02_2	Nuclei_frac
P00505	FVTVQTIS [iTRAQ_N1	1	97-110	11,699	797,46	2012_02_2	Nuclei_frac
P00505	FVTVQTIS [iTRAQ_N1	1	97-110	6,815	531,973	2012_02_2	Nuclei_frac
P00505	IAAAILNTF [iTRAQ_N1	1	297-308	8,277	706,426	2012_02_2	Nuclei_frac
P00505	ISVAGVTS [iTRAQ_N1	2	379-401	7,664	660,875	2012_02_2	Nuclei_frac
P49756_IS	EKEELEIR [iTRAQ_N1	2	539-547	5,693	488,273	2012_02_2	Nuclei_frac
P49756_IS	EYSSELNA [iTRAQ_N1	1	217-234	9,059	726,337	2012_02_2	Nuclei_frac
P49756_IS	LLAEGHPD [iTRAQ_N1	1	550-564	5,247	602,316	2012_02_2	Nuclei_frac
P49756_IS	RFPVAPLIF [iTRAQ_N1	2	247-261	7,471	1007,132	2012_02_2	Nuclei_frac
P49756_IS	RFPVAPLIF [iTRAQ_N1	2	247-261	6,502	671,756	2012_02_2	Nuclei_frac
Q16658	FLIVAHDD [iTRAQ_N1	1	90-99	5,504	429,573	2012_02_2	Nuclei_frac
Q16658	FLIVAHDD [iTRAQ_N1	1	90-99	5,476	429,572	2012_02_2	Nuclei_frac

Q16658	YLAADKDC [iTRAQ_N1	3 68-81	6,542	633,988	2012_02_2 Nuclei_frac
Q16658	YLAPSGPS [iTRAQ_N1	2 229-240	6,127	739,927	2012_02_2 Nuclei_frac
Q16658	YWTLTATC [iTRAQ_N1	2 313-329	9,279	682,697	2012_02_2 Nuclei_frac
Q16658	YWTLTATC [iTRAQ_N1	2 313-329	8,39	682,698	2012_02_2 Nuclei_frac
O75396	IMVANIEEV [iTRAQ_N1	1 147-158	7,334	779,943	2012_02_2 Nuclei_frac
O75396	IMVANIEEV [iTRAQ_N1	2 147-158	6,109	787,94	2012_02_2 Nuclei_frac
O75396	IMVANIEEV [iTRAQ_N1	2 147-158	5,755	525,628	2012_02_2 Nuclei_frac
O75396	NLGSINTEL [iTRAQ_N1	1 133-146	11,166	865,962	2012_02_2 Nuclei_frac
O75396	VLLTMIAR [iTRAQ_N1	1 1-8	8,89	530,837	2012_02_2 Nuclei_frac
O75396	VLLTMIAR [iTRAQ_N1	2 1-8	5,978	538,835	2012_02_2 Nuclei_frac
Q5XKE5,O9	FASFIDKVF [iTRAQ_N1	2 179-187	5,171	457,607	2012_02_2 Nuclei_frac
Q5XKE5,O9	ISISTSGGS [iTRAQ_N1	1 74-84	9,324	628,344	2012_02_2 Nuclei_frac
Q5XKE5,O9	NLDLDSIIA [iTRAQ_N1	2 332-343	7,613	539,983	2012_02_2 Nuclei_frac
Q5XKE5,O9	NLDLDSIIA [iTRAQ_N1	2 332-343	7,459	809,473	2012_02_2 Nuclei_frac
Q5XKE5,O9	SLYNLGGG [iTRAQ_N1	2 64-73	5,21	461,607	2012_02_2 Nuclei_frac
P59998	AENFFILR [iTRAQ_N1	1 97-104	7,436	577,329	2012_02_2 Nuclei_frac
P59998	AENFFILR [iTRAQ_N1	1 97-104	6,973	577,331	2012_02_2 Nuclei_frac
P59998	ATLQAALC [iTRAQ_N1	2 13-31	7,26	760,732	2012_02_2 Nuclei_frac
P59998	ELLLQPVT [iTRAQ_N1	1 44-54	6,225	706,934	2012_02_2 Nuclei_frac
P59998	ELLLQPVT [iTRAQ_N1	1 44-54	5,144	706,935	2012_02_2 Nuclei_frac
P59998	ELLLQPVT [iTRAQ_N1	1 44-54	5,014	471,626	2012_02_2 Nuclei_frac
P59998	ELLLQPVT [iTRAQ_N1	1 44-54	4,938	706,937	2012_02_2 Nuclei_frac
P59998	VLIEGSINS [iTRAQ_N1	1 60-70	6,391	665,893	2012_02_2 Nuclei_frac
	EAQTSFLH [iTRAQ_N1	1 721-738	8,878	760,076	2012_02_2 Nuclei_frac
	ELLIIGGVA [iTRAQ_N1	1 320-330	5,816	628,397	2012_02_2 Nuclei_frac
	ELLIIGGVA [iTRAQ_N1	1 320-330	5,461	628,4	2012_02_2 Nuclei_frac
	LQVIVCSA [iTRAQ_N1	3 401-416	7,145	702,393	2012_02_2 Nuclei_frac
	TGAFSIPVI [iTRAQ_N1	2 53-69	5,402	723,095	2012_02_2 Nuclei_frac
P62269	IAFAITAIK [iTRAQ_N1	2 25-33	5,214	618,402	2012_02_2 Nuclei_frac
P62269	IAFAITAIK [iTRAQ_N1	2 25-33	5,082	412,605	2012_02_2 Nuclei_frac
P62269	IPDWFLNR [iTRAQ_N1	1 78-85	5,189	602,834	2012_02_2 Nuclei_frac
P62269	IPDWFLNR [iTRAQ_N1	1 78-85	4,963	602,835	2012_02_2 Nuclei_frac
P62269	KIAFAITAIK [iTRAQ_N1	3 24-33	4,747	503,336	2012_02_2 Nuclei_frac
P62269	VITIMQNPF [iTRAQ_N1	2 66-74	6,79	616,353	2012_02_2 Nuclei_frac
P62269	VITIMQNPF [iTRAQ_N1	2 66-74	5,634	411,237	2012_02_2 Nuclei_frac
P62269	VLNTNIDG [iTRAQ_N1	1 14-22	5,274	573,325	2012_02_2 Nuclei_frac
O75367_C1	AGVIFPVG [iTRAQ_N1	1 19-27	6,328	530,326	2012_02_2 Nuclei_frac
O75367_C1	EFVEAVLE [iTRAQ_N1	1 237-246	5,782	674,885	2012_02_2 Nuclei_frac
O75367_C1	GVTIASGG [iTRAQ_N1	2 97-116	9,09	758,787	2012_02_2 Nuclei_frac
O75367_C1	GVTIASGG [iTRAQ_N1	2 97-116	8,512	758,786	2012_02_2 Nuclei_frac
O75367_C1	SLFLGQK [iTRAQ_N1	2 190-196	5,867	540,839	2012_02_2 Nuclei_frac
P61247	ACQSIYPL [iTRAQ_N1	2 199-212	9,887	924,983	2012_02_2 Nuclei_frac
P61247	ACQSIYPL [iTRAQ_N1	2 199-212	8,698	616,989	2012_02_2 Nuclei_frac
P61247	LITEDVQGI [iTRAQ_N1	2 85-93	5,601	645,88	2012_02_2 Nuclei_frac
P61247	NCLTNFHC [iTRAQ_N1	3 94-106	6,022	580,276	2012_02_2 Nuclei_frac

P61247	TTDGYLLR [iTRAQ_N1	1 128-135	5,384	541,802	2012_02_2 Nuclei_frac
P22392_ISC	DRPFFAGL [iTRAQ_N1	2 56-65	5,1	479,953	2012_02_2 Nuclei_frac
P22392_ISC	GDFCIQVG [iTRAQ_N1	2 105-113	7,249	598,306	2012_02_2 Nuclei_frac
P22392_ISC	GDFCIQVG [iTRAQ_N1	2 105-113	6,91	598,306	2012_02_2 Nuclei_frac
P22392_ISC	GDFCIQVG [iTRAQ_N1	2 105-113	5,773	598,304	2012_02_2 Nuclei_frac
P22392_ISC	TFIAIKPDG [iTRAQ_N1	2 6-17	7,426	816,988	2012_02_2 Nuclei_frac
P22392_ISC	VMLGETNF [iTRAQ_N1	3 88-104	7,103	697,377	2012_02_2 Nuclei_frac
P22392_ISC	VMLGETNF [iTRAQ_N1	3 88-104	5,581	697,378	2012_02_2 Nuclei_frac
Q00839_C1	DLPEHAVL [iTRAQ_N1	2 608-616	5,488	655,391	2012_02_2 Nuclei_frac
Q00839_C1	DLPEHAVL [iTRAQ_N1	2 608-616	5,38	437,263	2012_02_2 Nuclei_frac
Q00839_C1	EKPYFPIPE [iTRAQ_N1	2 444-465	6,644	1004,858	2012_02_2 Nuclei_frac
Q00839_C1	EKPYFPIPE [iTRAQ_N1	2 444-465	6,022	1004,859	2012_02_2 Nuclei_frac
Q00839_C1	EKPYFPIPE [iTRAQ_N1	2 444-465	5,236	753,896	2012_02_2 Nuclei_frac
Q00839_C1	EKPYFPIPE [iTRAQ_N1	2 444-465	4,765	753,897	2012_02_2 Nuclei_frac
Q00839_C1	LNTLLQR [iTRAQ_N1	1 533-539	5,413	501,314	2012_02_2 Nuclei_frac
Q00839_C1	NFILDQTN' [iTRAQ_N1	1 557-571	9,082	896,482	2012_02_2 Nuclei_frac
Q00839_C1	NFILDQTN' [iTRAQ_N1	1 557-571	8,99	896,486	2012_02_2 Nuclei_frac
Q00839_C1	NFILDQTN' [iTRAQ_N1	1 557-571	8,74	896,48	2012_02_2 Nuclei_frac
Q00839_C1	NFILDQTN' [iTRAQ_N1	1 557-571	7,107	597,989	2012_02_2 Nuclei_frac
Q00839_C1	NFILDQTN' [iTRAQ_N1	1 557-571	5,432	597,988	2012_02_2 Nuclei_frac
Q13310	AKEFTNVY [iTRAQ_N1	3 187-196	5,02	548,995	2012_02_2 Nuclei_frac
Q13310	ALYDTFSA [iTRAQ_N1	3 114-129	7,602	699,034	2012_02_2 Nuclei_frac
Q13310	FSPAGPVL [iTRAQ_N1	1 31-41	8,231	644,383	2012_02_2 Nuclei_frac
Q13310	IVGSKPLYN [iTRAQ_N1	2 357-370	5,683	601,708	2012_02_2 Nuclei_frac
	AINQGGLT [iTRAQ_N1	1 31-43	11,897	715,416	2012_02_2 Nuclei_frac
	AINQGGLT [iTRAQ_N1	1 31-43	8,118	477,281	2012_02_2 Nuclei_frac
	HITIFSPEGI [iTRAQ_N1	1 12-21	8,09	434,242	2012_02_2 Nuclei_frac
	LLDSSTVT [iTRAQ_N1	2 60-71	6,547	550,323	2012_02_2 Nuclei_frac
P30504,Q21	AYLEGTCV [iTRAQ_N1	2 158-169	8,312	820,914	2012_02_2 Nuclei_frac
P30504,Q21	FIAVGYVD [iTRAQ_N1	1 22-35	9,324	887,469	2012_02_2 Nuclei_frac
P30504,Q21	FIAVGYVD [iTRAQ_N1	1 22-35	8,367	591,981	2012_02_2 Nuclei_frac
P30504,Q21	YFSTSVSW [iTRAQ_N1	1 7-17	8,845	715,863	2012_02_2 Nuclei_frac
P32119	ATAVVDG [iTRAQ_N1	2 16-25	7,111	633,869	2012_02_2 Nuclei_frac
P32119	ATAVVDG [iTRAQ_N1	2 16-25	5,688	422,915	2012_02_2 Nuclei_frac
P32119	KEGGLGPL [iTRAQ_N1	2 91-108	6,639	717,764	2012_02_2 Nuclei_frac
P32119	KEGGLGPL [iTRAQ_N1	2 91-108	6,485	717,763	2012_02_2 Nuclei_frac
P32119	LSEDYGVN [iTRAQ_N1	2 110-118	5,119	656,372	2012_02_2 Nuclei_frac
P32119	QITVNDLP [iTRAQ_N1	1 139-149	7,565	678,393	2012_02_2 Nuclei_frac
P32119	QITVNDLP [iTRAQ_N1	1 139-149	6,881	678,394	2012_02_2 Nuclei_frac
P61619_CH	AFSPTTVN [iTRAQ_N1	1 75-85	6,69	647,848	2012_02_2 Nuclei_frac
P61619_CH	ETSMVHEL [iTRAQ_N1	1 286-295	4,954	453,9	2012_02_2 Nuclei_frac
P61619_CH	FSGNLLVS [iTRAQ_N1	1 192-214	8,801	822,766	2012_02_2 Nuclei_frac
P61619_CH	FSGNLLVS [iTRAQ_N1	1 192-214	8,659	822,762	2012_02_2 Nuclei_frac
P61619_CH	FSGNLLVS [iTRAQ_N1	1 192-214	8,338	822,764	2012_02_2 Nuclei_frac
P61619_CH	GQYNTYPII [iTRAQ_N1	2 154-162	5,749	686,38	2012_02_2 Nuclei_frac

Q9Y262	IDESIHLQL [iTRAQ_N1	1 381-390	5,083	456,598	2012_02_2	Nuclei_frac
Q9Y262	LAGFLDLT [iTRAQ_N1	1 474-486	8,158	841,95	2012_02_2	Nuclei_frac
Q9Y262	LHSLLGDY [iTRAQ_N1	2 279-291	5,748	603,675	2012_02_2	Nuclei_frac
Q9Y262	RYGDFFIR [iTRAQ_N1	1 537-544	7,128	406,557	2012_02_2	Nuclei_frac
	AALQELLS [iTRAQ_N1	2 86-94	7,307	630,893	2012_02_2	Nuclei_frac
	AALQELLS [iTRAQ_N1	2 86-94	6,914	630,894	2012_02_2	Nuclei_frac
	AALQELLS [iTRAQ_N1	2 86-94	6,378	630,893	2012_02_2	Nuclei_frac
	AALQELLS [iTRAQ_N1	2 86-94	6,181	630,894	2012_02_2	Nuclei_frac
	DKLNNLVL [iTRAQ_N1	3 42-52	4,939	584,354	2012_02_2	Nuclei_frac
	LITPAVVSI [iTRAQ_N1	1 67-76	7,868	614,875	2012_02_2	Nuclei_frac
	LITPAVVSI [iTRAQ_N1	1 67-76	6,727	614,874	2012_02_2	Nuclei_frac
	LNNLVLFD [iTRAQ_N1	2 44-52	5,829	682,415	2012_02_2	Nuclei_frac
	LNNLVLFD [iTRAQ_N1	2 44-52	4,853	682,414	2012_02_2	Nuclei_frac
P43243	GAPPSSNIE [iTRAQ_N1	2 270-286	7,177	689,709	2012_02_2	Nuclei_frac
P43243	GAPPSSNIE [iTRAQ_N1	2 270-286	6,88	689,71	2012_02_2	Nuclei_frac
P43243	IGPYQPNVI [iTRAQ_N1	2 780-797	6,02	1129,149	2012_02_2	Nuclei_frac
P43243	IGPYQPNVI [iTRAQ_N1	2 780-797	5,181	753,102	2012_02_2	Nuclei_frac
P43243	IGPYQPNVI [iTRAQ_N1	2 780-797	5,089	753,101	2012_02_2	Nuclei_frac
P43243	ITPENLPQII [iTRAQ_N1	2 132-145	6,849	636,731	2012_02_2	Nuclei_frac
P43243	ITPENLPQII [iTRAQ_N1	2 132-145	6,556	954,596	2012_02_2	Nuclei_frac
P43243	ITPENLPQII [iTRAQ_N1	2 132-145	6,253	636,733	2012_02_2	Nuclei_frac
P43243	ITPENLPQII [iTRAQ_N1	2 132-145	5,718	636,733	2012_02_2	Nuclei_frac
P43243	VVHIMDFQ [iTRAQ_N1	2 398-406	5,813	435,568	2012_02_2	Nuclei_frac
Q9UBV2,Q9LVANHVA [iTRAQ_N1		1 299-318	10,85	723,069	2012_02_2	Nuclei_frac
Q9UBV2,Q9TTLTSDES [iTRAQ_N1		2 16-32	7,043	527,529	2012_02_2	Nuclei_frac
Q9UBV2,Q9TTLTSDES [iTRAQ_N1		2 16-32	6,407	527,529	2012_02_2	Nuclei_frac
Q9UBV2,Q9VSYALLFG [iTRAQ_N1		1 204-222	7,887	761,749	2012_02_2	Nuclei_frac
Q14651	AYFHLLNQ [iTRAQ_N1	2 301-312	6,525	568,335	2012_02_2	Nuclei_frac
Q14651	AYFHLLNQ [iTRAQ_N1	2 301-312	5,826	568,334	2012_02_2	Nuclei_frac
Q14651	LNLAFFVAN [iTRAQ_N1	2 365-376	7,733	826,493	2012_02_2	Nuclei_frac
Q14651	LNLAFFVAN [iTRAQ_N1	2 365-376	6,062	551,33	2012_02_2	Nuclei_frac
Q14651	QFVTPAD\ [iTRAQ_N1	2 351-364	4,851	582,992	2012_02_2	Nuclei_frac
Q14651	TISSSLAV\ [iTRAQ_N1	3 548-573	6,631	1031,568	2012_02_2	Nuclei_frac
Q9UHD8_1S DITSSIHFE [iTRAQ_N1		1 531-542	7,015	528,271	2012_02_2	Nuclei_frac
Q9UHD8_1S QVENAGAI [iTRAQ_N1		1 99-110	4,783	448,247	2012_02_2	Nuclei_frac
Q9UHD8_1S STLINTLFK [iTRAQ_N1		2 293-301	7,198	662,908	2012_02_2	Nuclei_frac
Q9UHD8_1S VVNIVPVIA [iTRAQ_N1		2 417-426	6,686	670,448	2012_02_2	Nuclei_frac
P63010_1SC LAPPLVTL [iTRAQ_N1		1 284-304	7,031	803,805	2012_02_2	Nuclei_frac
P63010_1SC LASQANIA [iTRAQ_N1		2 345-359	7,244	929,061	2012_02_2	Nuclei_frac
P63010_1SC LASQANIA [iTRAQ_N1		2 345-359	5,693	619,708	2012_02_2	Nuclei_frac
P63010_1SC LASQANIA [iTRAQ_N1		2 345-359	4,834	619,708	2012_02_2	Nuclei_frac
P63010_1SC LLSTDPVT [iTRAQ_N1		2 529-538	5,651	666,903	2012_02_2	Nuclei_frac
P63010_1SC QVFLATWI [iTRAQ_N1		2 835-842	5,64	640,884	2012_02_2	Nuclei_frac
P06744	ILLANFLAC [iTRAQ_N1	2 423-437	8,776	622,024	2012_02_2	Nuclei_frac

P06744	VFEGNRPT [iTRAQ_N1	2 466-480	5,905	666,374	2012_02_2	Nuclei_frac
P06744	VWYVSNI [iTRAQ_N1	2 180-193	10,714	631,015	2012_02_2	Nuclei_frac
P06744	VWYVSNI [iTRAQ_N1	2 180-193	9,84	631,016	2012_02_2	Nuclei_frac
P06744	VWYVSNI [iTRAQ_N1	2 180-193	8,328	631,015	2012_02_2	Nuclei_frac
P07602_ISC	EIVDSYLP\ [iTRAQ_N1	2 108-122	7,311	1009,61	2012_02_2	Nuclei_frac
P07602_ISC	EIVDSYLP\ [iTRAQ_N1	2 108-122	5,723	673,407	2012_02_2	Nuclei_frac
P07602_ISC	LPGMADI [iTRAQ_N1	4 233-242	6,559	683,358	2012_02_2	Nuclei_frac
P07602_ISC	LVGYLDR [iTRAQ_N1	1 415-421	5,681	490,289	2012_02_2	Nuclei_frac
P07602_ISC	LVGYLDR [iTRAQ_N1	1 415-421	5,351	490,292	2012_02_2	Nuclei_frac
P07602_ISC	LVGYLDR [iTRAQ_N1	1 415-421	5,106	490,291	2012_02_2	Nuclei_frac
P07602_ISC	SDVYCEVC [iTRAQ_N1	4 311-323	5,823	645,986	2012_02_2	Nuclei_frac
	HRLDLGED [iTRAQ_N1	2 5-17	6,916	592,318	2012_02_2	Nuclei_frac
	IRVESLLVT [iTRAQ_N1	2 451-463	5,562	573,034	2012_02_2	Nuclei_frac
	LQLPVWE\ [iTRAQ_N1	2 135-143	6,047	732,429	2012_02_2	Nuclei_frac
	SNLGSVVL [iTRAQ_N1	2 505-515	6,788	482,636	2012_02_2	Nuclei_frac
P20073	DLLSSVSR [iTRAQ_N1	1 368-375	7,09	510,795	2012_02_2	Nuclei_frac
P20073	DLLSSVSR [iTRAQ_N1	1 368-375	5,997	510,794	2012_02_2	Nuclei_frac
P20073	RLLLAIVG\ [iTRAQ_N1	1 458-466	5,897	563,874	2012_02_2	Nuclei_frac
P20073	TILQCALNI [iTRAQ_N1	2 387-402	4,97	684,369	2012_02_2	Nuclei_frac
P20073	VLIEILCTR [iTRAQ_N1	2 257-265	7,324	630,878	2012_02_2	Nuclei_frac
P20073	VLIEILCTR [iTRAQ_N1	2 257-265	6,136	630,878	2012_02_2	Nuclei_frac
P20073	VLIEILCTR [iTRAQ_N1	2 257-265	6,007	630,879	2012_02_2	Nuclei_frac
	DFSSIIQTC [iTRAQ_N1	2 21-35	8,273	623,982	2012_02_2	Nuclei_frac
	DFSSIIQTC [iTRAQ_N1	2 21-35	7,669	623,981	2012_02_2	Nuclei_frac
	LQENLQQI [iTRAQ_N1	2 59-75	9,321	761,089	2012_02_2	Nuclei_frac
	LQENLQQI [iTRAQ_N1	2 59-75	4,8	571,068	2012_02_2	Nuclei_frac
	QLEADILD\ [iTRAQ_N1	2 190-203	7,565	645,369	2012_02_2	Nuclei_frac
Q9UKM9	LEQIAAEQ\ [iTRAQ_N1	2 192-200	6,988	439,927	2012_02_2	Nuclei_frac
Q9UKM9	LEQIAAEQ\ [iTRAQ_N1	2 192-200	5,125	659,387	2012_02_2	Nuclei_frac
Q9UKM9	LSPVPVPR [iTRAQ_N1	1 118-125	6,064	504,819	2012_02_2	Nuclei_frac
Q9UKM9	SNIDALLSF [iTRAQ_N1	1 183-191	4,859	566,829	2012_02_2	Nuclei_frac
Q9UKM9	VFIGNLNT\ [iTRAQ_N1	2 23-34	7,246	788,986	2012_02_2	Nuclei_frac
Q9UKM9	VFIGNLNT\ [iTRAQ_N1	2 23-34	6,41	526,327	2012_02_2	Nuclei_frac
	DAGVIAGL [iTRAQ_N1	1 162-173	8,494	671,403	2012_02_2	Nuclei_frac
	DAGVIAGL [iTRAQ_N1	1 162-173	8,417	671,404	2012_02_2	Nuclei_frac
	DAGVIAGL [iTRAQ_N1	1 162-173	7,92	671,404	2012_02_2	Nuclei_frac
	DAGVIAGL [iTRAQ_N1	1 162-173	7,73	671,404	2012_02_2	Nuclei_frac
	NQVAMNP [iTRAQ_N1	3 59-73	8,336	991,009	2012_02_2	Nuclei_frac
	NQVAMNP [iTRAQ_N1	3 59-73	6,615	661,008	2012_02_2	Nuclei_frac
	NQVAMNP [iTRAQ_N1	3 59-73	6,351	661,008	2012_02_2	Nuclei_frac
	TTPSYVAF [iTRAQ_N1	1 39-51	8,276	816,405	2012_02_2	Nuclei_frac
	TTPSYVAF [iTRAQ_N1	1 39-51	5,889	544,607	2012_02_2	Nuclei_frac
P62136,P3\	EIFLSQPILL [iTRAQ_N1	2 43-59	7,008	1121,173	2012_02_2	Nuclei_frac
P62136,P3\	EIFLSQPILL [iTRAQ_N1	2 43-59	6,75	747,783	2012_02_2	Nuclei_frac
P62136,P3\	EIFLSQPILL [iTRAQ_N1	2 43-59	5,553	561,092	2012_02_2	Nuclei_frac

P62136,P3€ IKYPENFFL [iTRAQ_N1	2 111-121	5,968	576,674	2012_02_2 Nuclei_frac
P62136,P3€ LNLDSIIGR [iTRAQ_N1	1 6-14	5,674	572,845	2012_02_2 Nuclei_frac
P62136,P3€ TFTDCFNC [iTRAQ_N1	4 150-167	6,268	801,402	2012_02_2 Nuclei_frac
P62136,P3€ TFTDCFNC [iTRAQ_N1	4 150-167	4,793	801,403	2012_02_2 Nuclei_frac
Q8NC51_IS EETQPPVA [iTRAQ_N1	3 93-103	5,027	558,007	2012_02_2 Nuclei_frac
Q8NC51_IS PGHLQEGF [iTRAQ_N1	2 2-16	8,382	605,643	2012_02_2 Nuclei_frac
Q8NC51_IS SAAQAAA [iTRAQ_N1	2 53-68	6,695	583,644	2012_02_2 Nuclei_frac
Q8NC51_IS SKSEEHAH [iTRAQ_N1	3 307-324	4,732	604,789	2012_02_2 Nuclei_frac
P11279 ALQATVGI [iTRAQ_N1	2 299-309	8,567	720,411	2012_02_2 Nuclei_frac
P11279 FFLQGIQLM [iTRAQ_N1	1 271-286	10,374	995,569	2012_02_2 Nuclei_frac
P11279 FFLQGIQLM [iTRAQ_N1	1 271-286	9,838	664,048	2012_02_2 Nuclei_frac
P11279 FFLQGIQLM [iTRAQ_N1	1 271-286	7,928	664,048	2012_02_2 Nuclei_frac
P11279 FFLQGIQLM [iTRAQ_N1	1 271-286	6,365	664,049	2012_02_2 Nuclei_frac
P11279 TVESITDIR [iTRAQ_N1	1 110-118	5,754	589,33	2012_02_2 Nuclei_frac
O00469,O0 GFALLNFV [iTRAQ_N1	2 620-629	5,018	698,437	2012_02_2 Nuclei_frac
O00469,O0 IIAPLVTR [iTRAQ_N1	1 388-395	5,713	513,843	2012_02_2 Nuclei_frac
O00469,O0 LLVITVATI [iTRAQ_N1	2 14-22	5,418	623,422	2012_02_2 Nuclei_frac
O00469,O0 VVFAADGI [iTRAQ_N1	2 111-124	8,54	625,696	2012_02_2 Nuclei_frac
O00469,O0 VVFAADGI [iTRAQ_N1	2 111-124	7,845	625,697	2012_02_2 Nuclei_frac
P40939 DSIFSNLTG [iTRAQ_N1	2 387-404	7,59	784,068	2012_02_2 Nuclei_frac
P40939 KTVLGTPE [iTRAQ_N1	2 130-151	7,624	808,482	2012_02_2 Nuclei_frac
P40939 KTVLGTPE [iTRAQ_N1	2 130-151	6,548	808,482	2012_02_2 Nuclei_frac
P40939 TVLGTPEV [iTRAQ_N1	1 131-151	9,383	1076,118	2012_02_2 Nuclei_frac
P40939 TVLGTPEV [iTRAQ_N1	1 131-151	7,493	717,749	2012_02_2 Nuclei_frac
P40939 TVLGTPEV [iTRAQ_N1	1 131-151	5,488	717,748	2012_02_2 Nuclei_frac
P16401 ALAAGGYI [iTRAQ_N1	2 67-77	6,889	691,384	2012_02_2 Nuclei_frac
P16401 ALAAGGYI [iTRAQ_N1	2 67-81	6,492	618,331	2012_02_2 Nuclei_frac
P16401 ATGPPVSE [iTRAQ_N1	2 37-48	5,539	750,947	2012_02_2 Nuclei_frac
P16401 SLVSKGTL [iTRAQ_N1	3 88-99	5,608	565,025	2012_02_2 Nuclei_frac
P16401 SLVSKGTL [iTRAQ_N1	3 88-99	4,919	565,025	2012_02_2 Nuclei_frac
P62140,P3€ EIFLSQPILL [iTRAQ_N1	2 42-58	7,008	1121,173	2012_02_2 Nuclei_frac
P62140,P3€ EIFLSQPILL [iTRAQ_N1	2 42-58	6,75	747,783	2012_02_2 Nuclei_frac
P62140,P3€ EIFLSQPILL [iTRAQ_N1	2 42-58	5,553	561,092	2012_02_2 Nuclei_frac
P62140,P3€ ICGDIHGQY [iTRAQ_N1	2 59-72	5,28	602,309	2012_02_2 Nuclei_frac
P62140,P3€ IKYPENFFL [iTRAQ_N1	2 110-120	5,968	576,674	2012_02_2 Nuclei_frac
P62140,P3€ TFTDCFNC [iTRAQ_N1	4 149-166	6,268	801,402	2012_02_2 Nuclei_frac
P62140,P3€ TFTDCFNC [iTRAQ_N1	4 149-166	4,793	801,403	2012_02_2 Nuclei_frac
P30153_CH EWAHATII [iTRAQ_N1	2 476-485	4,822	485,286	2012_02_2 Nuclei_frac
P30153_CH LNIISNLDC [iTRAQ_N1	2 382-398	6,317	696,056	2012_02_2 Nuclei_frac
P30153_CH LSTIALALC [iTRAQ_N1	1 35-46	6,761	693,928	2012_02_2 Nuclei_frac
P30153_CH SALASVIM [iTRAQ_N1	3 343-358	6,591	621,039	2012_02_2 Nuclei_frac
P30153_CH SALASVIM [iTRAQ_N1	3 343-358	6,558	931,061	2012_02_2 Nuclei_frac
AGFAGDD [iTRAQ_N1	1 682-691	6,264	560,778	2012_02_2 Nuclei_frac
AGFAGDD [iTRAQ_N1	1 682-691	5,984	560,779	2012_02_2 Nuclei_frac

	AGFAGDD/ [iTRAQ_N1	1 682-691	5,489	560,78	2012_02_2	Nuclei_frac
	AGFAGDD/ [iTRAQ_N1	1 682-691	5,253	560,779	2012_02_2	Nuclei_frac
	AGFAGDD/ [iTRAQ_N1	1 682-691	5,222	560,781	2012_02_2	Nuclei_frac
	AGFAGDD/ [iTRAQ_N1	1 682-691	5,208	560,78	2012_02_2	Nuclei_frac
	AGFAGDD/ [iTRAQ_N1	1 682-691	5,045	560,781	2012_02_2	Nuclei_frac
	AGFAGDD/ [iTRAQ_N1	1 682-691	4,84	560,78	2012_02_2	Nuclei_frac
	IWHHTFYN [iTRAQ_N1	1 748-758	8,692	830,429	2012_02_2	Nuclei_frac
	IWHHTFYN [iTRAQ_N1	1 748-758	7,853	553,956	2012_02_2	Nuclei_frac
	IWHHTFYN [iTRAQ_N1	1 748-758	7,671	553,955	2012_02_2	Nuclei_frac
	IWHHTFYN [iTRAQ_N1	1 748-758	6,661	553,954	2012_02_2	Nuclei_frac
	QEYDESGP [iTRAQ_N1	1 1023-1035	9,495	554,274	2012_02_2	Nuclei_frac
	QEYDESGP [iTRAQ_N1	1 1023-1035	5,931	554,276	2012_02_2	Nuclei_frac
P12111_CH	AAPLQGM [iTRAQ_N1	2 404-419	8,321	889,533	2012_02_2	Nuclei_frac
P12111_CH	AAPLQGM [iTRAQ_N1	2 404-419	5,736	593,355	2012_02_2	Nuclei_frac
P12111_CH	ALILVGLEF [iTRAQ_N1	1 1770-1778	4,896	564,369	2012_02_2	Nuclei_frac
P12111_CH	LLVLITGG [iTRAQ_N1	2 346-354	5,006	601,409	2012_02_2	Nuclei_frac
P12111_CH	LQPVLQPL [iTRAQ_N1	2 1010-1025	6,186	625,715	2012_02_2	Nuclei_frac
P25205	AILCLLLG [iTRAQ_N1	2 315-326	8,722	729,439	2012_02_2	Nuclei_frac
P25205	VALLDVFR [iTRAQ_N1	1 748-755	7,077	538,835	2012_02_2	Nuclei_frac
P25205	VQVVGTYI [iTRAQ_N1	1 234-241	8,585	533,314	2012_02_2	Nuclei_frac
P25205	VQVVGTYI [iTRAQ_N1	1 234-241	7,644	533,313	2012_02_2	Nuclei_frac
	AIVFVVD [iTRAQ_N1	1 138-150	9,554	783,945	2012_02_2	Nuclei_frac
	AIVFVVD [iTRAQ_N1	1 138-150	7,153	522,965	2012_02_2	Nuclei_frac
	LLTGLYR [iTRAQ_N1	1 84-90	6,201	490,307	2012_02_2	Nuclei_frac
	SAAPSTLD [iTRAQ_N1	2 209-227	8,275	693,041	2012_02_2	Nuclei_frac
	SAAPSTLD [iTRAQ_N1	2 209-227	7,135	693,042	2012_02_2	Nuclei_frac
	SAAPSTLD [iTRAQ_N1	2 209-227	7,053	693,042	2012_02_2	Nuclei_frac
Q6P2Q9	KWQQLQA [iTRAQ_N1	3 35-42	5,735	487,967	2012_02_2	Nuclei_frac
Q6P2Q9	LFPWPWK [iTRAQ_N1	3 934-953	5,27	689,158	2012_02_2	Nuclei_frac
Q6P2Q9	LLILALER [iTRAQ_N1	1 837-844	4,749	542,865	2012_02_2	Nuclei_frac
Q6P2Q9	TILQHLSE [iTRAQ_N1	1 707-717	8,202	499,947	2012_02_2	Nuclei_frac
Q13740_IS	ALFLETEQ [iTRAQ_N1	2 116-125	5,467	493,961	2012_02_2	Nuclei_frac
Q13740_IS	ESLT LIVEC [iTRAQ_N1	3 379-392	7,809	663,077	2012_02_2	Nuclei_frac
Q13740_IS	VLHPLEGA [iTRAQ_N1	2 149-162	5,028	608,384	2012_02_2	Nuclei_frac
Q13740_IS	YEKPDGSP [iTRAQ_N1	2 31-44	5,594	638,685	2012_02_2	Nuclei_frac
Q13505_IS	EARECLTL [iTRAQ_N1	2 322-333	4,863	540,62	2012_02_2	Nuclei_frac
Q13505_IS	ISNPWQSP [iTRAQ_N1	1 191-206	6,689	623,346	2012_02_2	Nuclei_frac
Q13505_IS	LLGGPPR [iTRAQ_N1	1 2-8	6,057	427,271	2012_02_2	Nuclei_frac
Q13505_IS	LLPVLVHT [iTRAQ_N1	2 253-266	6,284	657,399	2012_02_2	Nuclei_frac
Q16181	DVTNNVH [iTRAQ_N1	1 298-309	6,253	556,602	2012_02_2	Nuclei_frac
Q16181	STLINSFL [iTRAQ_N1	1 63-85	11,867	917,809	2012_02_2	Nuclei_frac
Q16181	VNIPLIAK [iTRAQ_N1	2 186-194	5,73	634,93	2012_02_2	Nuclei_frac
	DVVICPDA [iTRAQ_N1	4 49-63	9,44	698,05	2012_02_2	Nuclei_frac
	GLIAAICAG [iTRAQ_N1	3 100-122	7,564	852,489	2012_02_2	Nuclei_frac

	VTVAGLAQ [iTRAQ_N1	3 33-48	6,824	649,364	2012_02_2 Nuclei_frac
	VTVAGLAQ [iTRAQ_N1	3 33-48	5,13	649,365	2012_02_2 Nuclei_frac
O15260	LCLISTFLE [iTRAQ_N1	2 31-43	9,092	840,962	2012_02_2 Nuclei_frac
O15260	LCLISTFLE [iTRAQ_N1	2 31-43	7,974	560,976	2012_02_2 Nuclei_frac
O15260	NLALGGGL [iTRAQ_N1	1 120-135	9,127	877,538	2012_02_2 Nuclei_frac
O15260	NLALGGGL [iTRAQ_N1	1 120-135	9,125	877,542	2012_02_2 Nuclei_frac
O15260	NLALGGGL [iTRAQ_N1	1 120-135	8,34	585,362	2012_02_2 Nuclei_frac
O15260	NLALGGGL [iTRAQ_N1	1 120-135	6,265	585,361	2012_02_2 Nuclei_frac
O15260	QYLPHVAF [iTRAQ_N1	1 23-30	5,569	564,327	2012_02_2 Nuclei_frac
O14950_C1	DGFIDKEDI [iTRAQ_N1	3 44-61	4,929	609,825	2012_02_2 Nuclei_frac
O14950_C1	EAFNMIDQ [iTRAQ_N1	1 34-43	6,048	691,337	2012_02_2 Nuclei_frac
O14950_C1	ELLTTMGD [iTRAQ_N1	1 123-131	5,088	590,311	2012_02_2 Nuclei_frac
O14950_C1	GNFNIEFT [iTRAQ_N1	1 150-159	7,699	702,858	2012_02_2 Nuclei_frac
O60568	LLVITVAT, [iTRAQ_N1	1 15-30	10,703	947,048	2012_02_2 Nuclei_frac
O60568	LLVITVAT, [iTRAQ_N1	1 15-30	10,281	631,7	2012_02_2 Nuclei_frac
O60568	LSLNLDHK [iTRAQ_N1	2 184-191	5,185	409,915	2012_02_2 Nuclei_frac
O60568	VFLAVFVE [iTRAQ_N1	1 274-289	7,838	668,722	2012_02_2 Nuclei_frac
O60568	VFLAVFVE [iTRAQ_N1	1 274-289	7,319	668,722	2012_02_2 Nuclei_frac
P46777	GAVDGGLS [iTRAQ_N1	2 164-177	8,631	542,973	2012_02_2 Nuclei_frac
P46777	QFSQYIK [iTRAQ_N1	2 221-227	5,486	601,344	2012_02_2 Nuclei_frac
P46777	QFSQYIK [iTRAQ_N1	2 221-227	5,021	401,231	2012_02_2 Nuclei_frac
P46777	VGLTNYA/ [iTRAQ_N1	2 89-106	9,423	691,047	2012_02_2 Nuclei_frac
P12277	FCTGLTQIE [iTRAQ_N1	3 252-264	9,082	923,512	2012_02_2 Nuclei_frac
P12277	FCTGLTQIE [iTRAQ_N1	3 252-264	5,219	616,009	2012_02_2 Nuclei_frac
P12277	LGFSEVEL' [iTRAQ_N1	2 341-357	6,36	713,067	2012_02_2 Nuclei_frac
P12277	VLTPELYA [iTRAQ_N1	1 32-42	7,986	724,424	2012_02_2 Nuclei_frac
P50914	ALVDGPCT [iTRAQ_N1	2 35-45	6,404	680,362	2012_02_2 Nuclei_frac
P50914	ALVDGPCT [iTRAQ_N1	2 35-45	6,282	680,363	2012_02_2 Nuclei_frac
P50914	ALVDGPCT [iTRAQ_N1	2 35-45	6,073	680,361	2012_02_2 Nuclei_frac
P50914	ALVDGPCT [iTRAQ_N1	2 35-45	5,959	680,363	2012_02_2 Nuclei_frac
P50914	LVAIVDVII [iTRAQ_N1	1 23-34	9,317	749,94	2012_02_2 Nuclei_frac
P50914	LVAIVDVII [iTRAQ_N1	1 23-34	8,132	749,939	2012_02_2 Nuclei_frac
P50914	LVAIVDVII [iTRAQ_N1	1 23-34	7,768	500,295	2012_02_2 Nuclei_frac
P50914	VAYVSFGF [iTRAQ_N1	2 11-22	7,598	507,62	2012_02_2 Nuclei_frac
P62495	GFGGIGGIL [iTRAQ_N1	1 404-413	7,566	545,829	2012_02_2 Nuclei_frac
P62495	LSVLGAIT\$ [iTRAQ_N1	1 68-80	9,52	758,454	2012_02_2 Nuclei_frac
P62495	LSVLGAIT\$ [iTRAQ_N1	1 68-80	7,706	505,971	2012_02_2 Nuclei_frac
P62495	YVLHCQG1 [iTRAQ_N1	3 330-341	6,058	594,299	2012_02_2 Nuclei_frac
P42704	DLPVTEAV [iTRAQ_N1	1 168-185	9,737	676,374	2012_02_2 Nuclei_frac
P42704	KGAYDIFLM [iTRAQ_N1	3 990-1000	5,682	557,999	2012_02_2 Nuclei_frac
P42704	SLLLLGFR [iTRAQ_N1	1 483-490	7,568	518,818	2012_02_2 Nuclei_frac
	LEILTNLAM [iTRAQ_N1	1 390-407	9,395	714,749	2012_02_2 Nuclei_frac
	TVIGSVLLF [iTRAQ_N1	1 1077-1085	6,485	551,359	2012_02_2 Nuclei_frac

VVNVANV [iTRAQ_N1	1	1026-1044	7,067	697,378	2012_02_2	Nuclei_frac
P51659,P51 ATSTATSC [iTRAQ_N1	2	315-330	7,228	585,988	2012_02_2	Nuclei_frac
P51659,P51 LGLLGLAN [iTRAQ_N1	1	168-182	7,856	820,997	2012_02_2	Nuclei_frac
P51659,P51 VVLVTGA [iTRAQ_N1	1	10-22	7,744	657,406	2012_02_2	Nuclei_frac
P51659,P51 VVLVTGA [iTRAQ_N1	1	10-22	5,987	438,606	2012_02_2	Nuclei_frac
P35637 AAIDWFDG [iTRAQ_N1	2	348-356	6,797	655,852	2012_02_2	Nuclei_frac
P35637 AAIDWFDG [iTRAQ_N1	3	348-364	6,472	776,42	2012_02_2	Nuclei_frac
P35637 AAIDWFDG [iTRAQ_N1	3	348-364	5,012	582,568	2012_02_2	Nuclei_frac
P35637 AAIDWFDG [iTRAQ_N1	3	348-364	4,811	582,566	2012_02_2	Nuclei_frac
P35637 LKGEATVS [iTRAQ_N1	3	332-347	9,531	698,722	2012_02_2	Nuclei_frac
P35637 LKGEATVS [iTRAQ_N1	3	332-347	8,553	698,721	2012_02_2	Nuclei_frac
P35637 LKGEATVS [iTRAQ_N1	3	332-347	8,397	698,721	2012_02_2	Nuclei_frac
P52907 FTITPPTAC [iTRAQ_N1	2	178-192	6,893	930,066	2012_02_2	Nuclei_frac
P52907 FTITPPTAC [iTRAQ_N1	2	178-192	5,697	620,381	2012_02_2	Nuclei_frac
P52907 LLLNNDNL [iTRAQ_N1	1	37-46	6,497	671,408	2012_02_2	Nuclei_frac
P52907 TIDGQQTII [iTRAQ_N1	3	146-165	9,373	868,126	2012_02_2	Nuclei_frac
P60866 DTGKTPVE [iTRAQ_N1	2	4-18	7,701	646,362	2012_02_2	Nuclei_frac
P60866 DTGKTPVE [iTRAQ_N1	2	4-18	7,428	646,362	2012_02_2	Nuclei_frac
P60866 LIDLHSPSE [iTRAQ_N1	2	87-98	6,424	819,99	2012_02_2	Nuclei_frac
P60866 LIDLHSPSE [iTRAQ_N1	2	87-98	5,591	546,996	2012_02_2	Nuclei_frac
P60866 TPVEPEVA [iTRAQ_N1	1	8-18	8,637	464,598	2012_02_2	Nuclei_frac
P60866 TPVEPEVA [iTRAQ_N1	1	8-18	6,589	696,393	2012_02_2	Nuclei_frac
Q9UBG0 LQGAVCG [iTRAQ_N1	2	1208-1223	7,21	574,975	2012_02_2	Nuclei_frac
Q9UBG0 SCTEETHG [iTRAQ_N1	4	1067-1079	6,559	628,966	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	8,86	500,967	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	8,4	750,948	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	8,328	750,95	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	7,726	750,95	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	7,379	500,968	2012_02_2	Nuclei_frac
Q9UBG0 TLGDQLSL [iTRAQ_N1	1	95-107	5,97	750,948	2012_02_2	Nuclei_frac
Q96AE4,Q9 CQHAAEII [iTRAQ_N1	2	331-343	8,141	561,97	2012_02_2	Nuclei_frac
Q96AE4,Q9 IAQITGPPD [iTRAQ_N1	1	321-330	7,837	606,347	2012_02_2	Nuclei_frac
Q96AE4,Q9 IAQITGPPD [iTRAQ_N1	1	321-330	6,96	606,348	2012_02_2	Nuclei_frac
Q96AE4,Q9 IQIAPDSGC [iTRAQ_N1	1	133-145	6,445	748,913	2012_02_2	Nuclei_frac
Q9UMS4 IWSVPNAS [iTRAQ_N1	2	289-302	7,173	586,987	2012_02_2	Nuclei_frac
Q9UMS4 IWSVPNAS [iTRAQ_N1	2	289-302	6,574	879,974	2012_02_2	Nuclei_frac
Q9UMS4 KVTSVVFF [iTRAQ_N1	2	265-288	6,147	723,148	2012_02_2	Nuclei_frac
Q9UMS4 KVTSVVFF [iTRAQ_N1	2	265-288	4,962	723,149	2012_02_2	Nuclei_frac
Q9UMS4 VTSVVFHF [iTRAQ_N1	1	266-288	9,019	873,132	2012_02_2	Nuclei_frac
P16615_ISC DIVPGDIVE [iTRAQ_N1	2	144-164	7,359	827,137	2012_02_2	Nuclei_frac
P16615_ISC IRDEMVAT [iTRAQ_N1	1	235-246	7,89	540,943	2012_02_2	Nuclei_frac
P16615_ISC VGEATETA [iTRAQ_N1	3	437-451	7,081	637,011	2012_02_2	Nuclei_frac
P61604 VLLPEYGG [iTRAQ_N1	2	70-79	5,826	682,908	2012_02_2	Nuclei_frac

P61604	VLLPEYGG [iTRAQ_N1	2 70-79	5,557	682,907	2012_02_2 Nuclei_frac
P61604	VLQATVV, [iTRAQ_N1	2 40-53	8,573	802,487	2012_02_2 Nuclei_frac
P61604	VLQATVV, [iTRAQ_N1	2 40-53	8,085	535,327	2012_02_2 Nuclei_frac
P61604	VLQATVV, [iTRAQ_N1	2 40-53	7,425	535,327	2012_02_2 Nuclei_frac
P61604	VVLDDKD' [iTRAQ_N1	2 80-91	7,889	909,509	2012_02_2 Nuclei_frac
P61604	VVLDDKD' [iTRAQ_N1	2 80-91	5,721	606,675	2012_02_2 Nuclei_frac
P48047	LVRPPVQV [iTRAQ_N1	1 4-17	8,027	576,341	2012_02_2 Nuclei_frac
P48047	SFLSQGQV [iTRAQ_N1	2 140-149	6,017	697,916	2012_02_2 Nuclei_frac
P48047	SFLSQGQV [iTRAQ_N1	2 140-149	4,936	697,916	2012_02_2 Nuclei_frac
P48047	VAASVLNI [iTRAQ_N1	2 51-61	8,2	724,94	2012_02_2 Nuclei_frac
P61158	LGYAGNTE [iTRAQ_N1	3 18-37	7,573	827,454	2012_02_2 Nuclei_frac
P61158	LGYAGNTE [iTRAQ_N1	3 18-37	5,793	827,456	2012_02_2 Nuclei_frac
P61158	LGYAGNTE [iTRAQ_N1	3 18-37	5,377	827,456	2012_02_2 Nuclei_frac
P61158	LPACVVD([iTRAQ_N1	4 4-17	7,183	610,312	2012_02_2 Nuclei_frac
P61158	QYTGINAIS [iTRAQ_N1	3 254-264	7,437	552,334	2012_02_2 Nuclei_frac
P61158	QYTGINAIS [iTRAQ_N1	3 254-264	6,833	552,334	2012_02_2 Nuclei_frac
P99999	ADLIAYLK [iTRAQ_N1	2 92-99	4,9	597,872	2012_02_2 Nuclei_frac
P99999	KTGQAPG\ [iTRAQ_N1	3 39-53	9,192	663,7	2012_02_2 Nuclei_frac
P99999	TGQAPGYS [iTRAQ_N1	2 40-53	7,959	572,966	2012_02_2 Nuclei_frac
P99999	TGQAPGYS [iTRAQ_N1	2 40-53	7,501	572,965	2012_02_2 Nuclei_frac
P15259,P1	ALPFWNEE [iTRAQ_N1	2 162-175	6,759	986,568	2012_02_2 Nuclei_frac
P15259,P1	ALPFWNEE [iTRAQ_N1	2 162-175	4,989	493,786	2012_02_2 Nuclei_frac
P15259,P1	HYGGLTGL [iTRAQ_N1	2 90-99	6,002	449,925	2012_02_2 Nuclei_frac
P15259,P1	VLIAAHGN [iTRAQ_N1	1 180-190	9,141	647,891	2012_02_2 Nuclei_frac
P15259,P1	VLIAAHGN [iTRAQ_N1	1 180-190	8,301	647,891	2012_02_2 Nuclei_frac
P15259,P1	VLIAAHGN [iTRAQ_N1	1 180-190	7,875	432,263	2012_02_2 Nuclei_frac
Q92930_C	LLLIGDSG\ [iTRAQ_N1	2 11-21	6,471	680,428	2012_02_2 Nuclei_frac
Q92930_C	LLLIGDSG\ [iTRAQ_N1	2 11-21	5,985	680,427	2012_02_2 Nuclei_frac
Q92930_C	LLLIGDSG\ [iTRAQ_N1	2 11-21	5,355	453,953	2012_02_2 Nuclei_frac
Q92930_C	LQIWDTAC [iTRAQ_N1	1 59-69	7,713	730,884	2012_02_2 Nuclei_frac
Q92930_C	TITTAYR [iTRAQ_N1	1 72-79	7,691	566,81	2012_02_2 Nuclei_frac
P26640_CH	ALSPLEEW [iTRAQ_N1	1 138-147	8,372	679,385	2012_02_2 Nuclei_frac
P26640_CH	GALINVPPI [iTRAQ_N1	1 619-633	6,758	853,021	2012_02_2 Nuclei_frac
P26640_CH	LHEEGIIYR [iTRAQ_N1	1 462-470	6,58	425,239	2012_02_2 Nuclei_frac
P40429,Q6	LAHEVGW\ [iTRAQ_N1	2 140-147	5,269	409,908	2012_02_2 Nuclei_frac
P40429,Q6	LAHEVGW\ [iTRAQ_N1	2 140-147	4,961	614,359	2012_02_2 Nuclei_frac
P40429,Q6	VFDGIPPPY [iTRAQ_N1	3 103-114	5,919	603,351	2012_02_2 Nuclei_frac
P40429,Q6	VFDGIPPPY [iTRAQ_N1	3 103-114	5,424	603,35	2012_02_2 Nuclei_frac
P40429,Q6	VFDGIPPPY [iTRAQ_N1	3 103-114	5,068	603,349	2012_02_2 Nuclei_frac
P40429,Q6	YLAFLR [iTRAQ_N1	1 53-58	4,876	463,783	2012_02_2 Nuclei_frac
P40429,Q6	YQAVTATI [iTRAQ_N1	2 148-158	5,634	514,288	2012_02_2 Nuclei_frac
Q02818	DLELLIQT/ [iTRAQ_N1	1 127-137	5,689	708,911	2012_02_2 Nuclei_frac
Q02818	LVTLEEF\ [iTRAQ_N1	1 285-297	7,623	825,963	2012_02_2 Nuclei_frac
Q02818	LVTLEEF\ [iTRAQ_N1	1 285-297	5,931	550,978	2012_02_2 Nuclei_frac

Q02818	LVTLEEFLL [iTRAQ_N1	2	285-298	8,371	641,711	2012_02_2	Nuclei_frac
P08648_CH	KTIQFDFQI [iTRAQ_N1	3	718-729	6,491	634,048	2012_02_2	Nuclei_frac
P08648_CH	SLQWFGA [iTRAQ_N1	1	97-106	7,661	654,865	2012_02_2	Nuclei_frac
P08648_CH	VYVYLQHF [iTRAQ_N1	1	324-350	7,443	789,664	2012_02_2	Nuclei_frac
P08648_CH	VYVYLQHF [iTRAQ_N1	1	324-350	7,35	789,665	2012_02_2	Nuclei_frac
Q92520	LIADLGST [iTRAQ_N1	1	140-155	10,529	911,507	2012_02_2	Nuclei_frac
Q92520	LIADLGST [iTRAQ_N1	1	140-155	9,908	911,514	2012_02_2	Nuclei_frac
Q92520	LIADLGST [iTRAQ_N1	1	140-155	9,063	608,01	2012_02_2	Nuclei_frac
Q92520	LIADLGST [iTRAQ_N1	1	140-155	7,396	608,013	2012_02_2	Nuclei_frac
Q92520	LIADLGST [iTRAQ_N1	1	140-155	7,191	608,01	2012_02_2	Nuclei_frac
Q92520	RLIADLGST [iTRAQ_N1	1	139-155	11,039	660,047	2012_02_2	Nuclei_frac
P62879,Q9	ELPGHTGY [iTRAQ_N1	3	137-149	5,965	565,268	2012_02_2	Nuclei_frac
P62879,Q9	KACGDSTL [iTRAQ_N1	3	22-41	6,689	783,424	2012_02_2	Nuclei_frac
P62879,Q9	LIIWDSYTT [iTRAQ_N1	2	78-88	8,873	821,46	2012_02_2	Nuclei_frac
P62879,Q9	LIIWDSYTT [iTRAQ_N1	2	78-88	8,237	821,459	2012_02_2	Nuclei_frac
P62879,Q9	LIIWDSYTT [iTRAQ_N1	2	78-88	7,933	547,974	2012_02_2	Nuclei_frac
P62879,Q9	LIIWDSYTT [iTRAQ_N1	2	78-88	7,799	821,458	2012_02_2	Nuclei_frac
P62879,Q9	LIIWDSYTT [iTRAQ_N1	2	78-88	7,314	547,974	2012_02_2	Nuclei_frac
O95302	ISQSGDFLF [iTRAQ_N1	1	250-258	7,387	583,819	2012_02_2	Nuclei_frac
O95302	ISQSGDFLF [iTRAQ_N1	1	250-258	5,53	583,817	2012_02_2	Nuclei_frac
O95302	IVVPPHLG [iTRAQ_N1	1	309-322	5,163	556,307	2012_02_2	Nuclei_frac
O95302	TIQVSDFV [iTRAQ_N1	1	138-146	8,947	604,842	2012_02_2	Nuclei_frac
O95302	TIQVSDFV [iTRAQ_N1	1	138-146	5,987	604,842	2012_02_2	Nuclei_frac
O95302	TIQVSDFV [iTRAQ_N1	1	138-146	5,6	604,842	2012_02_2	Nuclei_frac
P48741	ARFEELCSI [iTRAQ_N1	2	302-313	6,733	562,953	2012_02_2	Nuclei_frac
P48741	LLQDFENG [iTRAQ_N1	2	351-359	6,356	685,392	2012_02_2	Nuclei_frac
P48741	LLQDFENG [iTRAQ_N1	2	351-359	4,962	457,264	2012_02_2	Nuclei_frac
P48741	TTPSYVAF [iTRAQ_N1	1	39-51	8,276	816,405	2012_02_2	Nuclei_frac
P48741	TTPSYVAF [iTRAQ_N1	1	39-51	5,889	544,607	2012_02_2	Nuclei_frac
P38919	EQIYDVYR [iTRAQ_N1	1	198-205	4,785	615,321	2012_02_2	Nuclei_frac
P38919	KGVAINFV [iTRAQ_N1	3	373-381	5,163	469,973	2012_02_2	Nuclei_frac
P38919	KLDYGQH [iTRAQ_N1	2	151-165	5,976	629,358	2012_02_2	Nuclei_frac
P38919	KVDWLTEI [iTRAQ_N1	3	288-295	5,416	725,937	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	8,491	1110,649	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	8,375	1110,651	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	7,155	740,768	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	7,056	740,768	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	6,738	1110,65	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	6,658	740,769	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	5,782	740,769	2012_02_2	Nuclei_frac
P18206_CH	AIPDLTAP [iTRAQ_N1	1	36-56	5,534	740,77	2012_02_2	Nuclei_frac
P18206_CH	ETVQTTEC [iTRAQ_N1	2	60-72	5,794	617,015	2012_02_2	Nuclei_frac
P18206_CH	VLQLTSWI [iTRAQ_N1	2	247-261	7,044	679,688	2012_02_2	Nuclei_frac
	DFQSGQH [iTRAQ_N1	1	28-38	7,44	477,26	2012_02_2	Nuclei_frac

FLALLR	[iTRAQ_N1	1 729-734	8,461	438,793	2012_02_2 Nuclei_frac
LLDYVPIGF	[iTRAQ_N1	1 608-617	5,265	643,884	2012_02_2 Nuclei_frac
ELVTQQLP	[iTRAQ_N1	2 40-51	6,312	854,024	2012_02_2 Nuclei_frac
ELVTQQLP	[iTRAQ_N1	2 40-51	6,29	569,686	2012_02_2 Nuclei_frac
KDSLVSNE	[iTRAQ_N1	3 30-39	6,897	533,645	2012_02_2 Nuclei_frac
KDSLVSNE	[iTRAQ_N1	3 30-39	5,77	533,643	2012_02_2 Nuclei_frac
KDSLVSNE	[iTRAQ_N1	3 30-39	5,504	533,646	2012_02_2 Nuclei_frac
SLDVNQD	[iTRAQ_N1	2 62-72	7,948	768,413	2012_02_2 Nuclei_frac
SLDVNQD	[iTRAQ_N1	2 62-72	7,673	512,611	2012_02_2 Nuclei_frac
Q96N66_IS AGGGPTLC	[iTRAQ_N1	3 272-288	6,75	656,675	2012_02_2 Nuclei_frac
Q96N66_IS KAASQPT	[iTRAQ_N1	3 456-468	5,295	587,35	2012_02_2 Nuclei_frac
Q96N66_IS LVSLASEV	[iTRAQ_N1	1 112-127	9,064	641,7	2012_02_2 Nuclei_frac
GYAFNHSA	[iTRAQ_N1	1 201-214	5,085	586,618	2012_02_2 Nuclei_frac
HIVLSGG	[iTRAQ_N1	2 300-316	9,864	644,677	2012_02_2 Nuclei_frac
HLWDYTF	[iTRAQ_N1	2 87-97	6,142	560,961	2012_02_2 Nuclei_frac
Q13492_IS ATTLSNA	[iTRAQ_N1	2 299-318	7,076	737,424	2012_02_2 Nuclei_frac
Q13492_IS ITAAQHSV	[iTRAQ_N1	2 10-24	8,812	582,332	2012_02_2 Nuclei_frac
Q13492_IS KLTGGSNV	[iTRAQ_N1	3 521-531	5,202	549,992	2012_02_2 Nuclei_frac
P12109_CH GLEQLLVG	[iTRAQ_N1	2 136-148	7,022	546,997	2012_02_2 Nuclei_frac
P12109_CH LSIIATDHT	[iTRAQ_N1	1 200-210	7,529	478,599	2012_02_2 Nuclei_frac
P12109_CH VFSVAITPI	[iTRAQ_N1	1 186-199	6,514	575,656	2012_02_2 Nuclei_frac
P08708	IAGYVTHL	3 49-58	5,122	479,611	2012_02_2 Nuclei_frac
P08708	IAGYVTHL	3 49-58	4,815	479,611	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	10,263	905,157	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	9,43	905,159	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	8,47	905,157	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	8,04	679,119	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	7,836	905,155	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	6,896	679,118	2012_02_2 Nuclei_frac
P08708	LLDFGSL	3 107-128	6,791	679,119	2012_02_2 Nuclei_frac
P08708	VCEEIAIIPS	4 33-44	5,669	607,029	2012_02_2 Nuclei_frac
P08708	VCEEIAIIPS	4 33-44	5,318	607,031	2012_02_2 Nuclei_frac
DFNHINVE	[iTRAQ_N1	2 37-50	7,967	629,692	2012_02_2 Nuclei_frac
DFNHINVE	[iTRAQ_N1	2 37-50	7,111	629,693	2012_02_2 Nuclei_frac
GVTLGFR	[iTRAQ_N1	1 83-89	6,445	447,27	2012_02_2 Nuclei_frac
TILSNQTVI	[iTRAQ_N1	2 3-21	6,57	801,119	2012_02_2 Nuclei_frac
TILSNQTVI	[iTRAQ_N1	2 3-21	6,412	801,12	2012_02_2 Nuclei_frac
Q14444	LNQDQLD	2 88-98	6,334	759,923	2012_02_2 Nuclei_frac
Q14444	QILGVIDKK	3 56-64	4,93	482,654	2012_02_2 Nuclei_frac
Q14444	TVLELQYV	2 148-165	9,656	798,446	2012_02_2 Nuclei_frac
Q14444	TVLELQYV	2 148-165	7,347	798,445	2012_02_2 Nuclei_frac
Q14444	TVLELQYV	2 148-165	5,42	599,085	2012_02_2 Nuclei_frac
P51571	FFDEESYSI	1 83-93	7,234	775,386	2012_02_2 Nuclei_frac

P51571	NNEDISIIPF [iTRAQ_N1	1 98-116	6,217	770,747	2012_02_2	Nuclei_frac
P51571	YQVSWSLI [iTRAQ_N1	2 63-72	7,446	517,611	2012_02_2	Nuclei_frac
P60891,P21	IFSGSSHQI [iTRAQ_N1	2 5-17	6,284	574,641	2012_02_2	Nuclei_frac
P60891,P21	LNVDFAII [iTRAQ_N1	2 184-193	5,923	486,629	2012_02_2	Nuclei_frac
P60891,P21	VYAILTHGI [iTRAQ_N1	1 243-259	8,687	649,378	2012_02_2	Nuclei_frac
P61803	ADFQGISPI [iTRAQ_N1	1 82-91	6,774	632,325	2012_02_2	Nuclei_frac
P61803	FLEEYLSSI [iTRAQ_N1	1 11-22	6,869	807,417	2012_02_2	Nuclei_frac
P61803	FLEEYLSSI [iTRAQ_N1	1 11-22	5,301	538,614	2012_02_2	Nuclei_frac
P61803	SASVVSVI [iTRAQ_N1	1 1-10	7,2	574,842	2012_02_2	Nuclei_frac
P24844	DGFIDKEDI [iTRAQ_N1	3 45-62	4,929	609,825	2012_02_2	Nuclei_frac
P24844	EAFNMIDQ [iTRAQ_N1	1 35-44	6,048	691,337	2012_02_2	Nuclei_frac
P24844	ELLTTMGC [iTRAQ_N1	1 124-132	5,088	590,311	2012_02_2	Nuclei_frac
P24844	NAFACFDE [iTRAQ_N1	2 104-123	4,766	628,04	2012_02_2	Nuclei_frac
Q01105_C1	EFHLNESG [iTRAQ_N1	2 142-154	6,108	578,957	2012_02_2	Nuclei_frac
Q01105_C1	IDFYFDENF [iTRAQ_N1	2 124-137	8,12	1065,007	2012_02_2	Nuclei_frac
Q01105_C1	IDFYFDENF [iTRAQ_N1	2 124-137	6,97	710,343	2012_02_2	Nuclei_frac
Q01105_C1	IDFYFDENF [iTRAQ_N1	2 124-137	6,732	710,343	2012_02_2	Nuclei_frac
Q01105_C1	IDFYFDENF [iTRAQ_N1	2 124-137	6,548	710,341	2012_02_2	Nuclei_frac
Q01105_C1	VEVTEFED [iTRAQ_N1	2 110-119	6,596	748,909	2012_02_2	Nuclei_frac
	ECADLWPI [iTRAQ_N1	2 124-131	5,282	595,791	2012_02_2	Nuclei_frac
	ISLGLPVG/ [iTRAQ_N1	3 16-35	8,432	1129,625	2012_02_2	Nuclei_frac
	ISLGLPVG/ [iTRAQ_N1	3 16-35	7,748	753,42	2012_02_2	Nuclei_frac
	ISLGLPVG/ [iTRAQ_N1	3 16-35	7,309	753,422	2012_02_2	Nuclei_frac
	ISLGLPVG/ [iTRAQ_N1	3 16-35	6,867	753,427	2012_02_2	Nuclei_frac
	NLYIISVK [iTRAQ_N1	2 36-43	6,912	413,263	2012_02_2	Nuclei_frac
	NLYIISVK [iTRAQ_N1	2 36-43	4,859	619,391	2012_02_2	Nuclei_frac
P47897	GFHQVPFA [iTRAQ_N1	1 601-615	6,16	634,36	2012_02_2	Nuclei_frac
P47897	ILQLVATG [iTRAQ_N1	1 498-508	4,857	642,911	2012_02_2	Nuclei_frac
P47897	LFTLTALR [iTRAQ_N1	1 515-522	9,596	539,841	2012_02_2	Nuclei_frac
Q5SSJ5,Q5	ALPLIVGA [iTRAQ_N1	2 14-28	7,337	616,386	2012_02_2	Nuclei_frac
Q5SSJ5,Q5	ALPLIVGA [iTRAQ_N1	3 14-32	6,007	605,379	2012_02_2	Nuclei_frac
Q5SSJ5,Q5	KYVSQYYP [iTRAQ_N1	3 282-290	7,231	536,644	2012_02_2	Nuclei_frac
P31930	ADLTEYLS [iTRAQ_N1	2 180-191	7,426	576,974	2012_02_2	Nuclei_frac
P31930	RIPLAEWE [iTRAQ_N1	1 389-398	6,789	467,597	2012_02_2	Nuclei_frac
P31930	SLLTYGR [iTRAQ_N1	1 382-388	6,344	477,28	2012_02_2	Nuclei_frac
P09211	ALPGQLKP [iTRAQ_N1	3 121-140	7,797	853,494	2012_02_2	Nuclei_frac
P09211	ASCLYGQL [iTRAQ_N1	3 45-54	5,933	712,892	2012_02_2	Nuclei_frac
P09211	PPYTVVYF [iTRAQ_N1	1 1-11	6,807	741,416	2012_02_2	Nuclei_frac
P49591_CH	KLDLEAWF [iTRAQ_N1	2 376-390	7,319	661,364	2012_02_2	Nuclei_frac
P49591_CH	VLDLDFLR [iTRAQ_N1	1 2-9	6,359	567,836	2012_02_2	Nuclei_frac
P49591_CH	YLIATSEQF [iTRAQ_N1	1 267-281	6,792	609,682	2012_02_2	Nuclei_frac

	AVPKEDIYK [iTRAQ_N1	2 173-189	6,663	632,335	2012_02_2 Nuclei_frac
	KLFVGGGLK [iTRAQ_N1	3 99-106	5,105	647,435	2012_02_2 Nuclei_frac
	KLFVGGGLK [iTRAQ_N1	3 99-106	4,865	647,435	2012_02_2 Nuclei_frac
	LFIGGLNVK [iTRAQ_N1	1 9-24	8,667	918,012	2012_02_2 Nuclei_frac
	LFIGGLNVK [iTRAQ_N1	1 9-24	5,635	612,341	2012_02_2 Nuclei_frac
	AQLGLGHK [iTRAQ_N1	1 144-154	7,443	444,911	2012_02_2 Nuclei_frac
	LIAHAGSLK [iTRAQ_N1	2 308-320	5,605	532,993	2012_02_2 Nuclei_frac
	VVSLSEYR [iTRAQ_N1	1 271-278	7,375	548,812	2012_02_2 Nuclei_frac
Q9Y6C9	EVSSSFDH [iTRAQ_N1	2 111-121	6,167	512,616	2012_02_2 Nuclei_frac
Q9Y6C9	EVSSSFDH [iTRAQ_N1	2 111-121	5,992	512,616	2012_02_2 Nuclei_frac
Q9Y6C9	GLFTGLTPK [iTRAQ_N1	1 68-76	6,562	553,329	2012_02_2 Nuclei_frac
Q9Y6C9	LCSGVLGT [iTRAQ_N1	3 77-89	7,599	538,98	2012_02_2 Nuclei_frac
	IQYQLVDISK [iTRAQ_N1	1 33-47	9,334	960,52	2012_02_2 Nuclei_frac
	IQYQLVDISK [iTRAQ_N1	1 33-47	7,218	640,682	2012_02_2 Nuclei_frac
	IQYQLVDISK [iTRAQ_N1	2 33-51	5,832	823,087	2012_02_2 Nuclei_frac
	VYSTSVTK [iTRAQ_N1	1 6-15	5,027	600,822	2012_02_2 Nuclei_frac
P06756_CH	AGTQLLAK [iTRAQ_N1	1 683-692	7,108	572,351	2012_02_2 Nuclei_frac
P06756_CH	SSASFNVIEK [iTRAQ_N1	2 916-928	5,543	592,986	2012_02_2 Nuclei_frac
P06756_CH	STGLNAVFK [iTRAQ_N1	1 374-392	7,395	714,72	2012_02_2 Nuclei_frac
	DLLFQALGK [iTRAQ_N1	1 9-17	6,048	588,85	2012_02_2 Nuclei_frac
	NPGFEIIHGK [iTRAQ_N1	1 505-517	8,835	542,302	2012_02_2 Nuclei_frac
	TTLLPGLLIK [iTRAQ_N1	2 452-460	5,159	622,416	2012_02_2 Nuclei_frac
O43175	DLPLLLFR [iTRAQ_N1	1 461-468	7,357	565,857	2012_02_2 Nuclei_frac
O43175	DLPLLLFR [iTRAQ_N1	1 461-468	5,84	565,857	2012_02_2 Nuclei_frac
O43175	DLPLLLFR [iTRAQ_N1	1 461-468	5,665	565,857	2012_02_2 Nuclei_frac
O43175	DLPLLLFR [iTRAQ_N1	1 461-468	5,556	565,857	2012_02_2 Nuclei_frac
O43175	NAGNCLSF [iTRAQ_N1	3 364-379	6,539	638,708	2012_02_2 Nuclei_frac
O43175	TLGILGLGFK [iTRAQ_N1	1 146-154	6,1	522,338	2012_02_2 Nuclei_frac
O75694	EITAIESSVK [iTRAQ_N1	3 635-656	6,437	925,513	2012_02_2 Nuclei_frac
O75694	ISLQAIQQLK [iTRAQ_N1	1 717-727	6,215	706,938	2012_02_2 Nuclei_frac
O75694	VASVSNK [iTRAQ_N1	1 256-273	7,266	624,685	2012_02_2 Nuclei_frac
P60953	NVFDEAILK [iTRAQ_N1	2 167-183	5,236	714,396	2012_02_2 Nuclei_frac
P60953	TPFLLVGT [iTRAQ_N1	1 108-120	8,586	808,98	2012_02_2 Nuclei_frac
P60953	TPFLLVGT [iTRAQ_N1	1 108-120	8,037	808,98	2012_02_2 Nuclei_frac
P60953	TPFLLVGT [iTRAQ_N1	1 108-120	6,476	539,655	2012_02_2 Nuclei_frac
P60953	TPFLLVGT [iTRAQ_N1	1 108-120	5,985	539,655	2012_02_2 Nuclei_frac
P60953	YVECSALT [iTRAQ_N1	3 154-163	5,996	496,267	2012_02_2 Nuclei_frac
P33993	ALLLLLVGK [iTRAQ_N1	1 352-366	8,038	848,022	2012_02_2 Nuclei_frac
P33993	ALLLLLVGK [iTRAQ_N1	1 352-366	7,505	565,68	2012_02_2 Nuclei_frac
P33993	ALLLLLVGK [iTRAQ_N1	1 352-366	5,896	565,681	2012_02_2 Nuclei_frac
P33993	IAQPGDHVK [iTRAQ_N1	1 263-281	6,816	726,428	2012_02_2 Nuclei_frac
P33993	TLLAILRK [iTRAQ_N1	1 604-610	4,949	472,327	2012_02_2 Nuclei_frac

FACHSASL [iTRAQ_N1	2 143-153	5,674	464,912	2012_02_2 Nuclei_frac
GIVEFSGKF [iTRAQ_N1	2 191-202	5,934	507,301	2012_02_2 Nuclei_frac
NLPQYVSN [iTRAQ_N1	1 154-176	8,183	938,154	2012_02_2 Nuclei_frac
Q15286_C1 LLIIGDSGV [iTRAQ_N1	2 11-21	6,471	680,428	2012_02_2 Nuclei_frac
Q15286_C1 LLIIGDSGV [iTRAQ_N1	2 11-21	5,985	680,427	2012_02_2 Nuclei_frac
Q15286_C1 LLIIGDSGV [iTRAQ_N1	2 11-21	5,354	453,953	2012_02_2 Nuclei_frac
Q15286_C1 LQIWDTAG [iTRAQ_N1	1 59-69	7,713	730,884	2012_02_2 Nuclei_frac
Q15286_C1 TITSTYYR [iTRAQ_N1	1 72-79	5,567	574,808	2012_02_2 Nuclei_frac
P52292 FVSFLGR [iTRAQ_N1	1 123-129	6,067	485,29	2012_02_2 Nuclei_frac
P52292 LLGASELP [iTRAQ_N1	1 300-314	7,086	847,526	2012_02_2 Nuclei_frac
P52292 NKNPAPPIL [iTRAQ_N1	2 238-257	6,575	825,157	2012_02_2 Nuclei_frac
P30041 LIALSIDSV [iTRAQ_N1	2 67-83	6,895	729,076	2012_02_2 Nuclei_frac
P30041 LSILYPATT [iTRAQ_N1	1 144-154	7,591	668,392	2012_02_2 Nuclei_frac
P30041 VVVFVGPCL [iTRAQ_N1	3 132-141	5,239	523,323	2012_02_2 Nuclei_frac
P36542_ISC HLLIGVSSI [iTRAQ_N1	1 66-75	7,005	414,241	2012_02_2 Nuclei_frac
P36542_ISC HLLIGVSSI [iTRAQ_N1	1 66-75	4,805	414,24	2012_02_2 Nuclei_frac
P36542_ISC IYGLGSLAL [iTRAQ_N1	2 43-54	7,534	807,975	2012_02_2 Nuclei_frac
P36542_ISC IYGLGSLAL [iTRAQ_N1	2 43-54	6,076	538,984	2012_02_2 Nuclei_frac
P36542_ISC THSDQFLV [iTRAQ_N1	2 119-129	5,063	527,629	2012_02_2 Nuclei_frac
A1L0T0_ISC DGHPVVVI [iTRAQ_N1	1 610-622	7,151	511,639	2012_02_2 Nuclei_frac
A1L0T0_ISC LSGTVGVV [iTRAQ_N1	2 111-134	7,19	824,815	2012_02_2 Nuclei_frac
A1L0T0_ISC NAQMAQS [iTRAQ_N1	2 135-157	5,248	843,131	2012_02_2 Nuclei_frac
P05023,P15 LIIVEGCQR [iTRAQ_N1	2 694-702	5,373	616,352	2012_02_2 Nuclei_frac
P05023,P15 LNIPVSQVI [iTRAQ_N1	1 643-653	8,255	690,908	2012_02_2 Nuclei_frac
P05023,P15 YHTEIVFAF [iTRAQ_N1	1 679-687	5,93	427,236	2012_02_2 Nuclei_frac
P29590_ISC ISQLAAVN [iTRAQ_N1	2 561-572	5,972	535,318	2012_02_2 Nuclei_frac
P29590_ISC LRQEPPQS [iTRAQ_N1	1 359-372	7,011	590,334	2012_02_2 Nuclei_frac
P29590_ISC LWGPGLPM [iTRAQ_N1	1 616-626	6,405	724,4	2012_02_2 Nuclei_frac
P30086 LYEQLSGK [iTRAQ_N1	2 179-186	5,189	613,357	2012_02_2 Nuclei_frac
P30086 LYEQLSGK [iTRAQ_N1	2 179-186	4,984	613,356	2012_02_2 Nuclei_frac
P30086 NRPTSISW [iTRAQ_N1	2 47-61	7,947	641,005	2012_02_2 Nuclei_frac
P30086 YVWLVEYC [iTRAQ_N1	2 119-131	6,235	666,376	2012_02_2 Nuclei_frac
P06748 LLSISGK [iTRAQ_N1	2 135-141	5,951	503,331	2012_02_2 Nuclei_frac
P06748 MSVQPTV [iTRAQ_N1	2 81-101	8,203	1194,167	2012_02_2 Nuclei_frac
P06748 MSVQPTV [iTRAQ_N1	2 81-101	6,915	1194,163	2012_02_2 Nuclei_frac
P06748 VTLATLK [iTRAQ_N1	2 74-80	5,173	517,348	2012_02_2 Nuclei_frac
P02768_CH KVPQVSTF [iTRAQ_N1	2 246-260	7,287	643,385	2012_02_2 Nuclei_frac
P02768_CH LVTDLT [iTRAQ_N1	2 66-72	6,404	539,343	2012_02_2 Nuclei_frac
P02768_CH YICENQDSI [iTRAQ_N1	3 95-106	5,618	866,427	2012_02_2 Nuclei_frac
P31947 DSTLIMQL [iTRAQ_N1	2 183-192	7,509	675,381	2012_02_2 Nuclei_frac
P31947 DSTLIMQL [iTRAQ_N1	1 183-192	7,419	667,386	2012_02_2 Nuclei_frac

P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	7,187	675,384	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	6,717	675,383	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	6,697	675,385	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	6,558	675,381	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	1 183-192	6,536	667,389	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	1 183-192	6,27	667,387	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	6,266	675,383	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,92	450,592	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,891	450,592	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,792	675,385	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,475	450,592	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,303	450,591	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	5,105	675,384	2012_02_2 Nuclei_frac
P31947	DSTLIMQLI [iTRAQ_N1	2 183-192	4,863	450,592	2012_02_2 Nuclei_frac
P31947	NLLSVAYK [iTRAQ_N1	2 42-49	5,612	598,368	2012_02_2 Nuclei_frac
P31947	VLSSIEQK [iTRAQ_N1	2 61-68	6,093	596,363	2012_02_2 Nuclei_frac
P31947	VLSSIEQK [iTRAQ_N1	2 61-68	6,059	596,363	2012_02_2 Nuclei_frac
Q13247	FFSGYGR [iTRAQ_N1	1 21-27	5,899	489,252	2012_02_2 Nuclei_frac
Q13247	LIVENLSSF [iTRAQ_N1	1 112-120	6,1	587,851	2012_02_2 Nuclei_frac
Q13247	LIVENLSSF [iTRAQ_N1	1 112-120	5,398	587,851	2012_02_2 Nuclei_frac
Q13247	TNEGVIIEFF [iTRAQ_N1	1 146-154	7,154	604,824	2012_02_2 Nuclei_frac
P62910_CH	GQILMPNIC [iTRAQ_N1	4 51-65	6,864	690,058	2012_02_2 Nuclei_frac
P62910_CH	KFLVHNVK [iTRAQ_N1	3 76-83	4,739	472,974	2012_02_2 Nuclei_frac
P62910_CH	SYCAEIAHI [iTRAQ_N1	3 94-106	7,546	585,297	2012_02_2 Nuclei_frac
P17813_ISC	ETVHCDLC [iTRAQ_N1	2 1-14	5,688	594,295	2012_02_2 Nuclei_frac
P17813_ISC	GFKLPDTP [iTRAQ_N1	2 264-279	6,708	663,045	2012_02_2 Nuclei_frac
P17813_ISC	GFKLPDTP [iTRAQ_N1	2 264-279	6,171	663,045	2012_02_2 Nuclei_frac
P17813_ISC	TQJLEWAA [iTRAQ_N1	1 119-128	6,731	680,872	2012_02_2 Nuclei_frac
P36871,P36	EAIQLIAR [iTRAQ_N1	1 68-75	5,399	529,328	2012_02_2 Nuclei_frac
P36871,P36	INQDPQVM [iTRAQ_N1	3 527-544	6,582	756,78	2012_02_2 Nuclei_frac
P36871,P36	SIFDFSALK [iTRAQ_N1	2 200-208	7,097	658,379	2012_02_2 Nuclei_frac
	DREDYVPY [iTRAQ_N1	2 82-93	5,158	587,296	2012_02_2 Nuclei_frac
	EHLLSYLEI [iTRAQ_N1	2 67-75	6,033	473,943	2012_02_2 Nuclei_frac
	FGYQFTQC [iTRAQ_N1	1 318-328	7,884	736,871	2012_02_2 Nuclei_frac
Q13263_C1	IVAERPQT [iTRAQ_N1	2 326-345	6,648	727,056	2012_02_2 Nuclei_frac
Q13263_C1	KLLASLVK [iTRAQ_N1	3 172-179	5,279	435,305	2012_02_2 Nuclei_frac
Q13263_C1	LTEDKADV [iTRAQ_N1	2 693-708	7,143	692,065	2012_02_2 Nuclei_frac
	FGQVYTEA [iTRAQ_N1	2 647-655	6,315	665,866	2012_02_2 Nuclei_frac
	FYSLLDPS [iTRAQ_N1	2 330-340	7,572	796,436	2012_02_2 Nuclei_frac
	IIFDDFR [iTRAQ_N1	1 500-506	5,158	535,294	2012_02_2 Nuclei_frac
	LNWLSVDI [iTRAQ_N1	2 96-107	6,451	608,663	2012_02_2 Nuclei_frac
	LTFSCLG [iTRAQ_N1	3 36-48	7,482	578,632	2012_02_2 Nuclei_frac
	SILCCLR [iTRAQ_N1	3 72-78	4,998	533,288	2012_02_2 Nuclei_frac

P51114_ISC GFLEFVED	[iTRAQ_N1	1 192-205	8,891	920,499	2012_02_2	Nuclei_frac
P51114_ISC KVPGVTAI	[iTRAQ_N1	2 161-178	9,891	746,077	2012_02_2	Nuclei_frac
P08729,P05 AKQEELEA	[iTRAQ_N1	2 351-362	6,454	558,653	2012_02_2	Nuclei_frac
P08729,P05 FASFIDKVF	[iTRAQ_N1	2 101-109	5,171	457,607	2012_02_2	Nuclei_frac
P08729,P05 KLLEGEESI	[iTRAQ_N1	2 393-401	7,146	450,263	2012_02_2	Nuclei_frac
P08729,P05 KLLEGEESI	[iTRAQ_N1	2 393-401	6,978	450,263	2012_02_2	Nuclei_frac
APDFVFYA	[iTRAQ_N1	1 264-273	7,147	663,853	2012_02_2	Nuclei_frac
APDFVFYA	[iTRAQ_N1	1 264-273	6,392	663,854	2012_02_2	Nuclei_frac
IGFPWSEIR	[iTRAQ_N1	1 238-246	6,595	624,848	2012_02_2	Nuclei_frac
IGFPWSEIR	[iTRAQ_N1	1 238-246	6,171	624,848	2012_02_2	Nuclei_frac
IGFPWSEIR	[iTRAQ_N1	1 238-246	6,021	624,847	2012_02_2	Nuclei_frac
IGFPWSEIR	[iTRAQ_N1	1 238-246	5,605	624,845	2012_02_2	Nuclei_frac
KAPDFVIFY	[iTRAQ_N1	2 263-273	4,995	533,636	2012_02_2	Nuclei_frac
P61254,Q9 FNPFTSD	[iTRAQ_N1	1 2-10	7,543	613,818	2012_02_2	Nuclei_frac
P61254,Q9 FNPFTSD	[iTRAQ_N1	1 2-10	6,11	613,818	2012_02_2	Nuclei_frac
P61254,Q9 KYVIYIER	[iTRAQ_N1	2 76-83	5,652	457,946	2012_02_2	Nuclei_frac
P61254,Q9 YVIYIER	[iTRAQ_N1	1 77-83	5,499	550,318	2012_02_2	Nuclei_frac
IFEYETQR	[iTRAQ_N1	1 38-45	6,183	615,32	2012_02_2	Nuclei_frac
KEDALLYC	[iTRAQ_N1	3 79-88	5,225	542,989	2012_02_2	Nuclei_frac
KEDALLYC	[iTRAQ_N1	3 79-88	4,75	542,988	2012_02_2	Nuclei_frac
YNIPHGPV	[iTRAQ_N1	1 19-31	7,239	514,284	2012_02_2	Nuclei_frac
P43304_CH GFITVDVC	[iTRAQ_N1	1 515-524	5,822	646,381	2012_02_2	Nuclei_frac
P43304_CH LAFLNVQA	[iTRAQ_N1	1 432-446	7,093	596,006	2012_02_2	Nuclei_frac
P43304_CH VIFFLPWQ	[iTRAQ_N1	2 214-222	5,648	489,297	2012_02_2	Nuclei_frac
P43304_CH VIFFLPWQ	[iTRAQ_N1	2 214-222	5,35	733,447	2012_02_2	Nuclei_frac
P43304_CH VIFFLPWQ	[iTRAQ_N1	2 214-222	4,861	489,297	2012_02_2	Nuclei_frac
Q13283 DFFQSYGN	[iTRAQ_N1	1 357-369	9,388	859,431	2012_02_2	Nuclei_frac
Q13283 LPNFGFVV	[iTRAQ_N1	2 376-392	9,154	742,73	2012_02_2	Nuclei_frac
P18085 DAVLLLFA	[iTRAQ_N1	2 117-126	6,466	464,621	2012_02_2	Nuclei_frac
P18085 IQEVADEL	[iTRAQ_N1	2 99-108	6,044	487,611	2012_02_2	Nuclei_frac
P18085 IQEVADEL	[iTRAQ_N1	2 99-108	5,388	730,912	2012_02_2	Nuclei_frac
P18085 LGEIVTTIP	[iTRAQ_N1	2 38-58	6,03	871,156	2012_02_2	Nuclei_frac
P18085 LGEIVTTIP	[iTRAQ_N1	2 38-58	5,941	871,159	2012_02_2	Nuclei_frac
P35222 EGLLAIFK	[iTRAQ_N1	2 217-224	6,426	589,872	2012_02_2	Nuclei_frac
P35222 LLWTTSR	[iTRAQ_N1	1 327-333	4,943	510,802	2012_02_2	Nuclei_frac
P35222 TLVTQNSC	[iTRAQ_N1	1 427-444	7,144	693,744	2012_02_2	Nuclei_frac
P49411 AEAGDNLC	[iTRAQ_N1	1 273-284	8,056	665,367	2012_02_2	Nuclei_frac
P49411 LLDVDTY	[iTRAQ_N1	1 196-209	10,425	843,98	2012_02_2	Nuclei_frac
Q92688 LKDISTLEF	[iTRAQ_N1	3 100-110	5,026	563,687	2012_02_2	Nuclei_frac
Q92688 LPNLTHLN	[iTRAQ_N1	2 87-99	6,106	570,341	2012_02_2	Nuclei_frac
Q92688 SLDLFNCE	[iTRAQ_N1	2 117-132	7,275	706,339	2012_02_2	Nuclei_frac

P63092_ISC ALWEDEG\	[iTRAQ_Nt	1 137-145	5,269	609,815	2012_02_2 Nuclei_frac
P63092_ISC LLLLGAGE	[iTRAQ_Nt	2 43-53	7,65	673,416	2012_02_2 Nuclei_frac
P63092_ISC LLLLGAGE	[iTRAQ_Nt	2 43-53	7,138	673,418	2012_02_2 Nuclei_frac
P63092_ISC LLLLGAGE	[iTRAQ_Nt	2 43-53	4,964	449,281	2012_02_2 Nuclei_frac
P63092_ISC LQEALNLF	[iTRAQ_Nt	2 251-259	5,481	455,279	2012_02_2 Nuclei_frac
P63092_ISC LQEALNLF	[iTRAQ_Nt	2 251-259	5,233	682,415	2012_02_2 Nuclei_frac
P31942_ISC ATENDIAN	[iTRAQ_Nt	1 69-85	11,525	1032,038	2012_02_2 Nuclei_frac
P31942_ISC ATENDIAN	[iTRAQ_Nt	1 69-85	9,036	688,361	2012_02_2 Nuclei_frac
P31942_ISC VHIDIGAD	[iTRAQ_Nt	1 86-95	6,856	598,831	2012_02_2 Nuclei_frac
P23528	EDLVFIFW	[iTRAQ_Nt	2 96-111	6,409	717,4 2012_02_2 Nuclei_frac
P23528	KSSTPEEV	[iTRAQ_Nt	3 21-29	5,05	479,617 2012_02_2 Nuclei_frac
P23528	NIILEEGKEI	[iTRAQ_Nt	3 45-72	6,876	1165,649 2012_02_2 Nuclei_frac
P23528	NIILEEGKEI	[iTRAQ_Nt	3 45-72	5,212	874,485 2012_02_2 Nuclei_frac
P23528	NIILEEGKEI	[iTRAQ_Nt	3 45-72	4,905	874,485 2012_02_2 Nuclei_frac
	LCFSTAQH	[iTRAQ_Nt	2 580-589	6,036	633,307 2012_02_2 Nuclei_frac
	SSSGLLEW	[iTRAQ_Nt	2 542-552	7,266	755,905 2012_02_2 Nuclei_frac
	TPASPVVF	[iTRAQ_Nt	1 98-107	5,02	407,58 2012_02_2 Nuclei_frac
	ALNRPPTY	[iTRAQ_Nt	2 45-55	5,323	515,971 2012_02_2 Nuclei_frac
	VLTLSDDL	[iTRAQ_Nt	1 225-234	6,389	652,864 2012_02_2 Nuclei_frac
	VNILDFV	[iTRAQ_Nt	2 240-248	6,601	691,922 2012_02_2 Nuclei_frac
	VNILDFV	[iTRAQ_Nt	2 240-248	5,623	461,615 2012_02_2 Nuclei_frac
Q9Y4L1	DAVVYPIL	[iTRAQ_Nt	1 407-419	7,181	833,473 2012_02_2 Nuclei_frac
Q9Y4L1	LAGLFNEQ	[iTRAQ_Nt	1 251-259	5,969	596,334 2012_02_2 Nuclei_frac
Q9Y4L1	LPATEKPV	[iTRAQ_Nt	3 846-857	5,114	576,705 2012_02_2 Nuclei_frac
Q9Y4L1	LPATEKPV	[iTRAQ_Nt	3 846-857	4,848	576,706 2012_02_2 Nuclei_frac
	GICALQCAI	[iTRAQ_Nt	4 375-388	5,293	608,664 2012_02_2 Nuclei_frac
	VLATAFDI	[iTRAQ_Nt	1 222-234	7,561	733,409 2012_02_2 Nuclei_frac
	VLTFYR	[iTRAQ_Nt	1 431-436	5,396	471,78 2012_02_2 Nuclei_frac
	LISQIVSSIT	[iTRAQ_Nt	1 169-182	9,344	816,497 2012_02_2 Nuclei_frac
	LISQIVSSIT	[iTRAQ_Nt	1 169-182	9,04	544,666 2012_02_2 Nuclei_frac
	QIFHPEQLI	[iTRAQ_Nt	2 24-35	8,844	849,994 2012_02_2 Nuclei_frac
	QIFHPEQLI	[iTRAQ_Nt	2 24-35	6,148	566,998 2012_02_2 Nuclei_frac
	QIFHPEQLI	[iTRAQ_Nt	2 24-35	5,576	566,998 2012_02_2 Nuclei_frac
O75390	DILADLIPK	[iTRAQ_Nt	2 8-16	4,85	643,402 2012_02_2 Nuclei_frac
O75390	DYIWNTLN	[iTRAQ_Nt	1 303-313	5,851	741,876 2012_02_2 Nuclei_frac
O75390	DYIWNTLN	[iTRAQ_Nt	1 303-313	5,492	741,878 2012_02_2 Nuclei_frac
O75390	VVPGYGH	[iTRAQ_Nt	1 314-324	7,453	437,927 2012_02_2 Nuclei_frac
O75390	VVPGYGH	[iTRAQ_Nt	1 314-324	7,229	656,388 2012_02_2 Nuclei_frac
O15400_Cf	ITQCSVEIQ	[iTRAQ_Nt	2 25-34	7,924	689,369 2012_02_2 Nuclei_frac
O15400_Cf	LVAEFTTS	[iTRAQ_Nt	2 93-106	10,202	629,69 2012_02_2 Nuclei_frac
O15400_Cf	LVAEFTTS	[iTRAQ_Nt	2 93-106	9,464	629,69 2012_02_2 Nuclei_frac
O15400_Cf	LVAEFTTS	[iTRAQ_Nt	2 93-106	8,623	629,69 2012_02_2 Nuclei_frac

Q03252	GLESDVAE [iTRAQ_N1	1 151-160	6,591	616,835	2012_02_2	Nuclei_frac
Q03252	KSVFEEEV [iTRAQ_N1	2 202-210	5,443	470,934	2012_02_2	Nuclei_frac
Q03252	LRAELDEV [iTRAQ_N1	2 103-112	6,047	492,289	2012_02_2	Nuclei_frac
P20591,P20591,P20591	SSVLEALS [iTRAQ_N1	1 83-96	11,962	771,955	2012_02_2	Nuclei_frac
P20591,P20591,P20591	SSVLEALS [iTRAQ_N1	1 83-96	6,684	514,972	2012_02_2	Nuclei_frac
P20591,P20591,P20591	VRPCIDLID [iTRAQ_N1	2 48-59	6,086	534,303	2012_02_2	Nuclei_frac
P17931	IALDFQR [iTRAQ_N1	1 144-150	5,023	503,794	2012_02_2	Nuclei_frac
P17931	IQVLVEPDI [iTRAQ_N1	2 199-209	6,302	538,315	2012_02_2	Nuclei_frac
P17931	VAVNDAH [iTRAQ_N1	1 210-223	6,596	449,244	2012_02_2	Nuclei_frac
	AYGDFAW [iTRAQ_N1	1 163-182	9,157	806,416	2012_02_2	Nuclei_frac
	GIFVFGNPC [iTRAQ_N1	1 439-456	8,691	1010,081	2012_02_2	Nuclei_frac
P55084	FNNWGGSI [iTRAQ_N1	2 384-403	8,788	760,368	2012_02_2	Nuclei_frac
P55084	TPFLLSGT [iTRAQ_N1	2 29-39	8,985	751,429	2012_02_2	Nuclei_frac
P55084	TPFLLSGT [iTRAQ_N1	2 29-39	5,827	501,288	2012_02_2	Nuclei_frac
	LLASINST [iTRAQ_N1	1 880-889	6,322	609,369	2012_02_2	Nuclei_frac
	LVFSNVNL [iTRAQ_N1	2 666-674	6,474	661,408	2012_02_2	Nuclei_frac
	YLAIAPPIIK [iTRAQ_N1	2 245-254	4,953	693,953	2012_02_2	Nuclei_frac
Q15005	IDKWDGSA [iTRAQ_N1	3 47-56	4,936	517,633	2012_02_2	Nuclei_frac
Q15005	IDKWDGSA [iTRAQ_N1	3 47-56	4,802	517,635	2012_02_2	Nuclei_frac
Q15005	LHDSLAIEF [iTRAQ_N1	1 214-222	5,142	599,341	2012_02_2	Nuclei_frac
Q15005	LTFISGR [iTRAQ_N1	1 173-179	7,668	469,282	2012_02_2	Nuclei_frac
	AVIVLVEN [iTRAQ_N1	2 11-21	6,191	528,32	2012_02_2	Nuclei_frac
	AVIVLVEN [iTRAQ_N1	2 11-21	5,836	528,322	2012_02_2	Nuclei_frac
	AVIVLVEN [iTRAQ_N1	2 11-21	4,83	528,322	2012_02_2	Nuclei_frac
	ISFDEYWTI [iTRAQ_N1	2 74-92	5,134	790,443	2012_02_2	Nuclei_frac
	LIQNLDAN [iTRAQ_N1	1 62-73	6,396	503,935	2012_02_2	Nuclei_frac
Q02952_ISC	LVQNIIQT [iTRAQ_N1	1 1444-1458	9,971	944,552	2012_02_2	Nuclei_frac
Q02952_ISC	LVQNIIQT [iTRAQ_N1	1 1444-1458	8,515	630,034	2012_02_2	Nuclei_frac
Q02952_ISC	TEGTQEAC [iTRAQ_N1	3 1156-1171	7,737	749,379	2012_02_2	Nuclei_frac
P16070_ISC	ALSIGFETC [iTRAQ_N1	2 69-78	9,187	649,339	2012_02_2	Nuclei_frac
P16070_ISC	ALSIGFETC [iTRAQ_N1	2 69-78	8,39	649,339	2012_02_2	Nuclei_frac
P16070_ISC	ALSIGFETC [iTRAQ_N1	2 69-78	5,433	433,229	2012_02_2	Nuclei_frac
P16070_ISC	YGFIEGHV [iTRAQ_N1	1 79-90	8,505	765,933	2012_02_2	Nuclei_frac
P16070_ISC	YGFIEGHV [iTRAQ_N1	1 79-90	6,093	510,957	2012_02_2	Nuclei_frac
	EQVIAALR [iTRAQ_N1	1 205-212	5,077	522,321	2012_02_2	Nuclei_frac
	EQVIAALR [iTRAQ_N1	1 205-212	4,774	522,321	2012_02_2	Nuclei_frac
	NFVVVMV [iTRAQ_N1	3 68-78	5,726	565,353	2012_02_2	Nuclei_frac
	NFVVVMV [iTRAQ_N1	4 68-78	5,494	570,684	2012_02_2	Nuclei_frac
	NFVVVMV [iTRAQ_N1	4 68-78	5,055	570,684	2012_02_2	Nuclei_frac
	QIIQQNPSL [iTRAQ_N1	1 290-308	6,872	1137,677	2012_02_2	Nuclei_frac
	QIIQQNPSL [iTRAQ_N1	1 290-308	5,847	758,783	2012_02_2	Nuclei_frac

Q8NBJS	FISAPTK	[iTRAQ_N1	2	298-304	6,083	526,324	2012_02_2	Nuclei_frac
Q8NBJS	KLLAAEPL	[iTRAQ_N1	3	479-488	5,658	501,329	2012_02_2	Nuclei_frac
Q8NBJS	VLIALLAR	[iTRAQ_N1	1	25-32	5,896	506,854	2012_02_2	Nuclei_frac
Q0ZGT2,Q0	EAENFHEE	[iTRAQ_N1	1	471-487	5,19	543,758	2012_02_2	Nuclei_frac
Q0ZGT2,Q0	LTFEELER	[iTRAQ_N1	1	235-242	7,574	590,821	2012_02_2	Nuclei_frac
Q0ZGT2,Q0	TISQEFLLP	[iTRAQ_N1	3	349-369	4,801	721,167	2012_02_2	Nuclei_frac
	FGAPPHAG	[iTRAQ_N1	1	461-475	5,544	527,287	2012_02_2	Nuclei_frac
	LQSGICHLF	[iTRAQ_N1	2	198-207	5,939	458,92	2012_02_2	Nuclei_frac
	LQSGICHLF	[iTRAQ_N1	2	198-207	4,933	458,92	2012_02_2	Nuclei_frac
	VFSIGPVFF	[iTRAQ_N1	1	265-273	6,059	583,346	2012_02_2	Nuclei_frac
P56134_CH	DFSPSGIFC	[iTRAQ_N1	1	28-40	10,431	786,903	2012_02_2	Nuclei_frac
P56134_CH	DFSPSGIFC	[iTRAQ_N1	1	28-40	10,116	786,904	2012_02_2	Nuclei_frac
P56134_CH	DFSPSGIFC	[iTRAQ_N1	1	28-40	9,644	786,905	2012_02_2	Nuclei_frac
P56134_CH	DFSPSGIFC	[iTRAQ_N1	1	28-40	9,434	786,901	2012_02_2	Nuclei_frac
P56134_CH	DFSPSGIFC	[iTRAQ_N1	1	28-40	8,825	786,901	2012_02_2	Nuclei_frac
P56134_CH	LGELPSWII	[iTRAQ_N1	2	17-27	7,107	492,279	2012_02_2	Nuclei_frac
P56134_CH	LGELPSWII	[iTRAQ_N1	2	17-27	5,972	737,916	2012_02_2	Nuclei_frac
P40227	ALQFLEEV	[iTRAQ_N1	2	129-137	5,853	682,906	2012_02_2	Nuclei_frac
P40227	AQLGVQAI	[iTRAQ_N1	2	432-448	6,4	686,087	2012_02_2	Nuclei_frac
P40227	AQLGVQAI	[iTRAQ_N1	2	432-448	5,376	686,086	2012_02_2	Nuclei_frac
P40227	GLQDVLR	[iTRAQ_N1	1	28-34	5,228	472,787	2012_02_2	Nuclei_frac
P40227	GLQDVLR	[iTRAQ_N1	1	28-34	4,87	472,787	2012_02_2	Nuclei_frac
	QGIFQVVIS	[iTRAQ_N1	1	227-236	10,131	645,888	2012_02_2	Nuclei_frac
	QLGTAYVS	[iTRAQ_N1	2	149-169	7,326	761,103	2012_02_2	Nuclei_frac
	TSILAAAN	[iTRAQ_N1	1	497-512	6,146	610,658	2012_02_2	Nuclei_frac
	YLQLAEEL	[iTRAQ_N1	1	46-58	4,744	592,004	2012_02_2	Nuclei_frac
	YTQPNICR	[iTRAQ_N1	2	174-181	6,46	598,304	2012_02_2	Nuclei_frac
Q07021	AFVDFLSD	[iTRAQ_N1	2	8-21	11,189	662,685	2012_02_2	Nuclei_frac
Q07021	AFVDFLSD	[iTRAQ_N1	2	8-21	9,11	662,687	2012_02_2	Nuclei_frac
Q07021	AFVDFLSD	[iTRAQ_N1	2	8-21	8,435	662,687	2012_02_2	Nuclei_frac
Q07021	VEEQEPEL	[iTRAQ_N1	2	82-101	6,147	859,132	2012_02_2	Nuclei_frac
P35268	AGNLGGG\	[iTRAQ_N1	1	52-64	10,199	693,896	2012_02_2	Nuclei_frac
P35268	AGNLGGG\	[iTRAQ_N1	1	52-64	9,696	693,896	2012_02_2	Nuclei_frac
P35268	AGNLGGG\	[iTRAQ_N1	1	52-64	6,618	462,933	2012_02_2	Nuclei_frac
P35268	ITVTSEVPF	[iTRAQ_N1	2	69-79	7,118	748,435	2012_02_2	Nuclei_frac
	EVLDSFLD	[iTRAQ_N1	1	179-189	9,077	711,393	2012_02_2	Nuclei_frac
	NIFPSNLVS	[iTRAQ_N1	1	190-202	8,232	790,44	2012_02_2	Nuclei_frac
	NIFPSNLVS	[iTRAQ_N1	1	190-202	7,972	790,441	2012_02_2	Nuclei_frac
	GITNLCVIG	[iTRAQ_N1	2	118-138	7,288	760,405	2012_02_2	Nuclei_frac
	GITNLCVIG	[iTRAQ_N1	2	118-138	6,861	760,407	2012_02_2	Nuclei_frac
	IIEVVDAIM	[iTRAQ_N1	2	194-210	10,011	691,37	2012_02_2	Nuclei_frac
	IIEVVDAIM	[iTRAQ_N1	1	194-210	8,527	686,039	2012_02_2	Nuclei_frac

P07996	FVFGTTPE [iTRAQ_N1	1 199-210	8,424	769,919	2012_02_2 Nuclei_frac
P07996	TIVTTLQD [iTRAQ_N1	1 271-281	8,847	695,906	2012_02_2 Nuclei_frac
P07996	TIVTTLQD [iTRAQ_N1	1 271-281	8,397	695,906	2012_02_2 Nuclei_frac
P30533	FSGEELDK [iTRAQ_N1	2 130-140	5,741	556,64	2012_02_2 Nuclei_frac
P30533	FSGEELDK [iTRAQ_N1	2 130-140	5,194	556,639	2012_02_2 Nuclei_frac
P30533	LAELHADL [iTRAQ_N1	2 42-50	5,179	433,263	2012_02_2 Nuclei_frac
P30533	VHEYNVLL [iTRAQ_N1	1 149-161	6,324	572,987	2012_02_2 Nuclei_frac
P50991	ALIAGGGA [iTRAQ_N1	1 419-434	9,791	848,001	2012_02_2 Nuclei_frac
P50991	ALIAGGGA [iTRAQ_N1	1 419-434	7,054	565,671	2012_02_2 Nuclei_frac
P50991	ALIAGGGA [iTRAQ_N1	1 419-434	6,842	565,67	2012_02_2 Nuclei_frac
P50991	SIHDALCV [iTRAQ_N1	2 403-412	7,412	443,248	2012_02_2 Nuclei_frac
P50991	SIHDALCV [iTRAQ_N1	2 403-412	7,085	443,247	2012_02_2 Nuclei_frac
P34897	AALEALGS [iTRAQ_N1	3 54-66	4,876	550,3	2012_02_2 Nuclei_frac
P34897	GYSLVSGG [iTRAQ_N1	2 340-360	6,449	632,858	2012_02_2 Nuclei_frac
P34897	VLELVSIT [iTRAQ_N1	2 370-380	5,771	492,309	2012_02_2 Nuclei_frac
	AITIANQTM [iTRAQ_N1	3 239-254	9,48	703,726	2012_02_2 Nuclei_frac
	VFNLVPR [iTRAQ_N1	1 391-397	7,61	526,804	2012_02_2 Nuclei_frac
P61769_CH	SNFLNCYV [iTRAQ_N1	3 19-40	9,745	948,15	2012_02_2 Nuclei_frac
P61769_CH	VEHSDLSF [iTRAQ_N1	2 48-57	7,252	718,888	2012_02_2 Nuclei_frac
P61769_CH	VEHSDLSF [iTRAQ_N1	2 48-57	7,17	479,593	2012_02_2 Nuclei_frac
Q9UBQ0_1S	LVLVLGDL [iTRAQ_N1	1 2-14	5,042	542,671	2012_02_2 Nuclei_frac
Q9UBQ0_1S	TLAGDVHI [iTRAQ_N1	1 51-60	4,908	408,911	2012_02_2 Nuclei_frac
Q9UBQ0_1S	VVTVGQFI [iTRAQ_N1	2 74-81	7,038	583,362	2012_02_2 Nuclei_frac
P49755	ISFHLPIN [iTRAQ_N1	1 1-10	6,634	443,259	2012_02_2 Nuclei_frac
P49755	ITDSAGHIL [iTRAQ_N1	2 45-56	5,585	531,634	2012_02_2 Nuclei_frac
P49755	LKPLEVEL [iTRAQ_N1	2 113-121	4,72	692,942	2012_02_2 Nuclei_frac
	IVALNAHT [iTRAQ_N1	1 245-255	7,188	466,95	2012_02_2 Nuclei_frac
	LAAAILGG [iTRAQ_N1	3 144-162	4,888	576,859	2012_02_2 Nuclei_frac
	NLVPGESV [iTRAQ_N1	2 110-122	4,842	579,328	2012_02_2 Nuclei_frac
	ALAGGVTI [iTRAQ_N1	2 646-660	5,498	566,687	2012_02_2 Nuclei_frac
	AVITNILLR [iTRAQ_N1	1 29-37	5,783	578,881	2012_02_2 Nuclei_frac
	LFLELLDHI [iTRAQ_N1	1 10-25	5,543	698,387	2012_02_2 Nuclei_frac
Q14554	GFPTICYFE [iTRAQ_N1	3 205-214	6,569	775,402	2012_02_2 Nuclei_frac
Q14554	LLSTVAQA [iTRAQ_N1	2 45-54	5,36	659,418	2012_02_2 Nuclei_frac
Q14554	YAVPVLR [iTRAQ_N1	1 343-349	4,81	481,301	2012_02_2 Nuclei_frac
P12270	GQNLLLTM [iTRAQ_N1	1 810-827	10,392	1084,633	2012_02_2 Nuclei_frac
P12270	GQNLLLTM [iTRAQ_N1	1 810-827	7,346	723,424	2012_02_2 Nuclei_frac
P12270	IAVEAQNK [iTRAQ_N1	2 1073-1083	6,342	536,971	2012_02_2 Nuclei_frac
Q9HDC9	EPPLLLGVI [iTRAQ_N1	2 74-87	5,401	606,037	2012_02_2 Nuclei_frac

Q9HDC9	LLEYDTVT [iTRAQ_N1	1 239-247	5,861	627,347	2012_02_2	Nuclei_frac
Q9HDC9	LLLSSETPI [iTRAQ_N1	2 184-195	5,471	525,647	2012_02_2	Nuclei_frac
P24539	HYLFDVQR [iTRAQ_N1	1 122-129	5,034	407,888	2012_02_2	Nuclei_frac
P24539	LAQLEEAK [iTRAQ_N1	2 90-97	5,365	595,357	2012_02_2	Nuclei_frac
P24539	QASIQHIQN [iTRAQ_N1	2 98-112	6,329	662,029	2012_02_2	Nuclei_frac
P38159	ALEAVFGK [iTRAQ_N1	2 22-29	5,051	561,843	2012_02_2	Nuclei_frac
P38159	ALEAVFGK [iTRAQ_N1	2 22-29	4,72	561,843	2012_02_2	Nuclei_frac
P38159	IVEVLLMK [iTRAQ_N1	3 33-40	4,864	416,934	2012_02_2	Nuclei_frac
P38159	LFIGGLNTE [iTRAQ_N1	2 9-21	6,794	575,323	2012_02_2	Nuclei_frac
P38159	LFIGGLNTE [iTRAQ_N1	2 9-21	6,291	862,48	2012_02_2	Nuclei_frac
P38159	LFIGGLNTE [iTRAQ_N1	2 9-21	4,997	575,323	2012_02_2	Nuclei_frac
P20618	LSEGFSIHT [iTRAQ_N1	1 29-38	9,5	430,902	2012_02_2	Nuclei_frac
P20618	TVIGCSGF [iTRAQ_N1	4 50-66	7,191	718,701	2012_02_2	Nuclei_frac
	FLSVLER [iTRAQ_N1	1 448-454	5,307	504,304	2012_02_2	Nuclei_frac
	IPLLTDPK [iTRAQ_N1	2 160-168	4,971	649,422	2012_02_2	Nuclei_frac
	VISYWR [iTRAQ_N1	1 93-98	6,367	484,278	2012_02_2	Nuclei_frac
Q9UKV3_IS	KPSISITTE [iTRAQ_N1	3 861-872	6,485	579,358	2012_02_2	Nuclei_frac
Q9UKV3_IS	KSLSPGVS [iTRAQ_N1	3 654-662	5,127	649,866	2012_02_2	Nuclei_frac
Q9UKV3_IS	LLDDLFR [iTRAQ_N1	1 1210-1216	5,025	518,302	2012_02_2	Nuclei_frac
Q9UKV3_IS	LLDDLFR [iTRAQ_N1	1 1210-1216	4,889	518,302	2012_02_2	Nuclei_frac
P37108	KGTVEGFE [iTRAQ_N1	3 42-54	5,707	608,668	2012_02_2	Nuclei_frac
P37108	VLLESEQF [iTRAQ_N1	1 1-14	10,868	911,51	2012_02_2	Nuclei_frac
P37108	VLLESEQF [iTRAQ_N1	1 1-14	9,534	608,008	2012_02_2	Nuclei_frac
	ISLISEK [iTRAQ_N1	2 93-99	5,504	539,342	2012_02_2	Nuclei_frac
	LVTDLLQR [iTRAQ_N1	1 308-315	5,944	551,34	2012_02_2	Nuclei_frac
	LVTDLLQR [iTRAQ_N1	1 308-315	5,755	551,34	2012_02_2	Nuclei_frac
	LVTDLLQR [iTRAQ_N1	1 308-315	4,933	551,341	2012_02_2	Nuclei_frac
	VENQYQLL [iTRAQ_N1	2 72-80	5,097	711,915	2012_02_2	Nuclei_frac
	VLIDWIND [iTRAQ_N1	1 100-113	9,581	893,007	2012_02_2	Nuclei_frac
	VLYNLFTK [iTRAQ_N1	2 360-367	6,959	643,392	2012_02_2	Nuclei_frac
	FEHCNFND [iTRAQ_N1	2 42-53	7,096	842,389	2012_02_2	Nuclei_frac
	FEHCNFND [iTRAQ_N1	2 42-53	5,575	561,928	2012_02_2	Nuclei_frac
	LQCYNCPL [iTRAQ_N1	5 1-14	9,435	1014,963	2012_02_2	Nuclei_frac
	LQCYNCPL [iTRAQ_N1	5 1-14	7,664	676,978	2012_02_2	Nuclei_frac
	LQCYNCPL [iTRAQ_N1	5 1-14	7,615	676,978	2012_02_2	Nuclei_frac
	LQCYNCPL [iTRAQ_N1	5 1-14	6,278	676,977	2012_02_2	Nuclei_frac
Q99439	GLQSGVDI [iTRAQ_N1	2 134-144	7,429	680,905	2012_02_2	Nuclei_frac
Q99439	TWIEGLTG [iTRAQ_N1	2 35-51	9,078	717,396	2012_02_2	Nuclei_frac
Q99439	TWIEGLTG [iTRAQ_N1	2 35-51	7,137	717,397	2012_02_2	Nuclei_frac
	ELLTVGQE [iTRAQ_N1	2 415-425	7,35	543,307	2012_02_2	Nuclei_frac
	GFLGCFPD [iTRAQ_N1	3 498-511	9,07	617,334	2012_02_2	Nuclei_frac

O75380	VIACDGGG [iTRAQ_N1	3 56-70	9,395	566,306	2012_02_2 Nuclei_frac
O75380	VIACDGGG [iTRAQ_N1	3 56-70	8,85	566,307	2012_02_2 Nuclei_frac
O75380	VTHTGQV' [iTRAQ_N1	2 11-24	6,969	662,339	2012_02_2 Nuclei_frac
O75380	VTHTGQV' [iTRAQ_N1	2 11-24	5,037	497,006	2012_02_2 Nuclei_frac
P09669	AGIFQSVK [iTRAQ_N1	2 67-74	5,73	569,347	2012_02_2 Nuclei_frac
P09669	AGIFQSVK [iTRAQ_N1	2 67-74	5,339	569,349	2012_02_2 Nuclei_frac
P09669	AYADFYR [iTRAQ_N1	1 47-53	5,01	525,263	2012_02_2 Nuclei_frac
P09669	KAYADFYR [iTRAQ_N1	2 46-53	5,56	441,244	2012_02_2 Nuclei_frac
Q9Y2D5_IS	LWAEDGEf [iTRAQ_N1	1 430-441	6,667	763,375	2012_02_2 Nuclei_frac
Q9Y2D5_IS	SPGALETP [iTRAQ_N1	2 393-414	9,631	768,733	2012_02_2 Nuclei_frac
Q13641	AGAFEHLP [iTRAQ_N1	1 104-114	5,116	447,918	2012_02_2 Nuclei_frac
Q13641	DVLAQLP\$ [iTRAQ_N1	1 197-206	5,332	628,38	2012_02_2 Nuclei_frac
Q13641	NLFLTGNQ [iTRAQ_N1	1 64-82	5,843	706,405	2012_02_2 Nuclei_frac
P09525	GLGTDDN1 [iTRAQ_N1	1 259-269	7,929	659,858	2012_02_2 Nuclei_frac
P09525	ISQTYQQQ [iTRAQ_N1	1 123-133	8,353	758,387	2012_02_2 Nuclei_frac
P09661	KLDGFPLL [iTRAQ_N1	2 55-63	5,8	449,618	2012_02_2 Nuclei_frac
P09661	NAIANAST [iTRAQ_N1	1 205-218	10,394	801,935	2012_02_2 Nuclei_frac
Q6IAA8	KLLLDPSSI [iTRAQ_N1	3 19-30	6,757	576,694	2012_02_2 Nuclei_frac
Q6IAA8	KLLLDPSSI [iTRAQ_N1	3 19-30	5,684	576,693	2012_02_2 Nuclei_frac
Q6IAA8	LAVLSSSL [iTRAQ_N1	2 91-102	9,434	543,99	2012_02_2 Nuclei_frac
P62888	LVILANNC [iTRAQ_N1	2 44-55	9,115	499,961	2012_02_2 Nuclei_frac
P62888	LVILANNC [iTRAQ_N1	2 44-55	8,308	749,44	2012_02_2 Nuclei_frac
P62888	VCTLAIDP [iTRAQ_N1	2 90-105	7,074	951,512	2012_02_2 Nuclei_frac
P62888	VCTLAIDP [iTRAQ_N1	2 90-105	5,877	634,676	2012_02_2 Nuclei_frac
P07093_IS	ASAATTAI [iTRAQ_N1	1 335-346	10,852	651,898	2012_02_2 Nuclei_frac
P07093_IS	LVLVNAV^ [iTRAQ_N1	2 162-171	5,289	727,456	2012_02_2 Nuclei_frac
O75534	EAFGFIER [iTRAQ_N1	1 164-171	4,938	556,798	2012_02_2 Nuclei_frac
O75534	IKVDFVIPK [iTRAQ_N1	3 256-264	4,936	497,661	2012_02_2 Nuclei_frac
O75534	IKVDFVIPK [iTRAQ_N1	3 256-264	4,775	497,661	2012_02_2 Nuclei_frac
O75534	VTLLEGDH [iTRAQ_N1	1 277-286	6,225	428,247	2012_02_2 Nuclei_frac
Q10713	GLDTVVAI [iTRAQ_N1	1 126-142	6,14	641,718	2012_02_2 Nuclei_frac
Q10713	LYLNVLNR [iTRAQ_N1	1 330-337	4,748	574,85	2012_02_2 Nuclei_frac
Q10713	YLSGIAHFL [iTRAQ_N1	2 71-81	5,187	522,635	2012_02_2 Nuclei_frac
Q92598_IS	FICEQDHQI [iTRAQ_N1	2 612-623	4,759	584,286	2012_02_2 Nuclei_frac
Q92598_IS	GCALQCAI [iTRAQ_N1	4 375-388	5,293	608,664	2012_02_2 Nuclei_frac
Q92598_IS	IEVPLYSLL [iTRAQ_N1	2 317-331	6,013	691,073	2012_02_2 Nuclei_frac
O00231	EASIDILHS [iTRAQ_N1	2 20-31	5,419	538,324	2012_02_2 Nuclei_frac
O00231	EASIDILHS [iTRAQ_N1	2 20-32	5,448	443,019	2012_02_2 Nuclei_frac
O00231	YQEALHLC [iTRAQ_N1	1 142-154	5,165	557,982	2012_02_2 Nuclei_frac

P30049	AQAELVG	[iTRAQ_N1	1 115-128	10,771	788,409	2012_02_2	Nuclei_frac
P30049	AQAELVG	[iTRAQ_N1	1 115-128	7,554	525,942	2012_02_2	Nuclei_frac
P30049	IEANEALVI	[iTRAQ_N1	2 135-143	5,246	637,884	2012_02_2	Nuclei_frac
P30049	IEANEALVI	[iTRAQ_N1	2 135-143	4,773	425,592	2012_02_2	Nuclei_frac
P30049	IEANEALVI	[iTRAQ_N1	2 135-143	4,728	425,592	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	10,462	918,031	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	10,016	918,033	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	9,182	612,357	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	8,81	612,357	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	8,76	612,357	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	8,313	612,356	2012_02_2	Nuclei_frac
P62913_ISC	VLEQLTGC	[iTRAQ_N1	2 38-51	7,843	612,357	2012_02_2	Nuclei_frac
P62913_ISC	YDGIILPGK	[iTRAQ_N1	2 169-177	5,409	632,382	2012_02_2	Nuclei_frac
Q15437	AVLNPLCC	[iTRAQ_N1	2 68-79	8,354	796,425	2012_02_2	Nuclei_frac
Q15437	FSWNVWP	[iTRAQ_N1	1 19-28	7,486	705,359	2012_02_2	Nuclei_frac
P30455_CH	FIAVGYVD	[iTRAQ_N1	1 22-35	9,324	887,469	2012_02_2	Nuclei_frac
P30455_CH	FIAVGYVD	[iTRAQ_N1	1 22-35	8,367	591,981	2012_02_2	Nuclei_frac
P30455_CH	KWEAVHA	[iTRAQ_N1	2 146-156	6,486	403,976	2012_02_2	Nuclei_frac
P30455_CH	KWEAVHA	[iTRAQ_N1	2 146-156	5,75	403,976	2012_02_2	Nuclei_frac
P30455_CH	KWEAVHA	[iTRAQ_N1	2 146-156	5,655	403,976	2012_02_2	Nuclei_frac
	GVFVQSVI	[iTRAQ_N1	2 224-238	5,75	648,382	2012_02_2	Nuclei_frac
	TFVDFFSQ	[iTRAQ_N1	2 207-221	10,057	708	2012_02_2	Nuclei_frac
	TFVDFFSQ	[iTRAQ_N1	2 207-221	9,159	707,999	2012_02_2	Nuclei_frac
	GSLITSLLR	[iTRAQ_N1	1 259-267	10,433	552,349	2012_02_2	Nuclei_frac
	VAASALNI	[iTRAQ_N1	1 34-41	5,31	473,278	2012_02_2	Nuclei_frac
	ILGGVISAIS	[iTRAQ_N1	1 61-84	10,932	864,47	2012_02_2	Nuclei_frac
	ILGGVISAIS	[iTRAQ_N1	1 61-84	7,641	648,605	2012_02_2	Nuclei_frac
	YLWNNIKR	[iTRAQ_N1	2 166-173	4,809	465,61	2012_02_2	Nuclei_frac
	LPFAAAQI	[iTRAQ_N1	1 319-331	7,538	768,429	2012_02_2	Nuclei_frac
	TFFSFPV	[iTRAQ_N1	2 603-615	8,195	873,501	2012_02_2	Nuclei_frac
Q8IVL6	AYAAGAW	[iTRAQ_N1	1 27-41	9,632	822,971	2012_02_2	Nuclei_frac
Q8IVL6	LLLEVSR	[iTRAQ_N1	1 514-521	6,074	551,834	2012_02_2	Nuclei_frac
P02533	APSTYGGG	[iTRAQ_N1	1 41-55	9,173	785,406	2012_02_2	Nuclei_frac
P02533	APSTYGGG	[iTRAQ_N1	1 41-55	7,99	523,938	2012_02_2	Nuclei_frac
P02533	APSTYGGG	[iTRAQ_N1	1 41-55	6,838	523,939	2012_02_2	Nuclei_frac
P02533	LASYLDKV	[iTRAQ_N1	2 125-133	6,521	451,61	2012_02_2	Nuclei_frac
P02533	LASYLDKV	[iTRAQ_N1	2 125-133	5,626	676,913	2012_02_2	Nuclei_frac
Q8N4C6_IS	LGTLNGSC	[iTRAQ_N1	3 831-843	5,2	601,636	2012_02_2	Nuclei_frac
Q8N4C6_IS	LQQENSILF	[iTRAQ_N1	1 806-814	5,74	622,859	2012_02_2	Nuclei_frac
Q8N4C6_IS	LQTMVQN	[iTRAQ_N1	3 1145-1153	4,735	456,269	2012_02_2	Nuclei_frac

Q96I24	RPLDDGVC [iTRAQ_N1	1 57-74	5,704	523,041	2012_02_2	Nuclei_frac
Q96I24	SINQQSGA [iTRAQ_N1	1 378-391	9,905	570,972	2012_02_2	Nuclei_frac
	ISLISEK [iTRAQ_N1	2 93-99	5,504	539,342	2012_02_2	Nuclei_frac
	VENQYQLL [iTRAQ_N1	2 72-80	5,097	711,915	2012_02_2	Nuclei_frac
	VSQDLIET [iTRAQ_N1	3 286-296	4,97	574,673	2012_02_2	Nuclei_frac
Q00688	ARLEIEPEV [iTRAQ_N1	2 187-199	4,886	617,342	2012_02_2	Nuclei_frac
Q00688	AWTVEQL [iTRAQ_N1	1 8-15	4,836	573,824	2012_02_2	Nuclei_frac
Q00688	FLQEHGSD [iTRAQ_N1	2 27-41	5,848	509,015	2012_02_2	Nuclei_frac
	FLAVGLVC [iTRAQ_N1	1 604-615	6,538	724,426	2012_02_2	Nuclei_frac
	LGAVFNQ [iTRAQ_N1	1 770-786	9,016	689,052	2012_02_2	Nuclei_frac
Q16630,Q1	AVSDASA [iTRAQ_N1	2 359-383	7,064	914,172	2012_02_2	Nuclei_frac
Q16630,Q1	AVSDASA [iTRAQ_N1	2 359-383	6,192	685,879	2012_02_2	Nuclei_frac
Q16630,Q1	VLISSLQD [iTRAQ_N1	3 395-410	8,466	696,388	2012_02_2	Nuclei_frac
P49748_ISC	AGLGSGLS [iTRAQ_N1	1 473-491	10,242	665,379	2012_02_2	Nuclei_frac
P49748_ISC	GILLFGTK [iTRAQ_N1	2 148-155	5,276	568,868	2012_02_2	Nuclei_frac
Q9BUJ2_ISC	AEPYCSVL [iTRAQ_N1	2 273-294	9,04	902,467	2012_02_2	Nuclei_frac
Q9BUJ2_ISC	EALGGQAL [iTRAQ_N1	2 247-261	6,452	628,373	2012_02_2	Nuclei_frac
P15313	IPIFSAAGL [iTRAQ_N1	2 189-208	7,658	774,756	2012_02_2	Nuclei_frac
P15313	QIYPPINVL [iTRAQ_N1	1 387-400	7,795	871,011	2012_02_2	Nuclei_frac
P15313	QIYPPINVL [iTRAQ_N1	1 387-400	7,356	581,008	2012_02_2	Nuclei_frac
Q969X5	LSFGDTLQ [iTRAQ_N1	1 61-84	8,285	882,454	2012_02_2	Nuclei_frac
Q969X5	LTSNPLAS [iTRAQ_N1	2 85-98	7,15	620,687	2012_02_2	Nuclei_frac
P08779	APSTYGGC [iTRAQ_N1	1 41-54	8,887	741,887	2012_02_2	Nuclei_frac
P08779	LASYLDKV [iTRAQ_N1	2 127-135	6,521	451,61	2012_02_2	Nuclei_frac
P08779	LASYLDKV [iTRAQ_N1	2 127-135	5,626	676,913	2012_02_2	Nuclei_frac
Q9UQ80	AAHLCAE [iTRAQ_N1	2 144-154	6,973	663,859	2012_02_2	Nuclei_frac
Q9UQ80	LVKPGNQ [iTRAQ_N1	3 155-171	8,325	787,109	2012_02_2	Nuclei_frac
Q9UQ80	LVKPGNQ [iTRAQ_N1	3 155-171	6,929	787,109	2012_02_2	Nuclei_frac
	NNLCPSGS [iTRAQ_N1	3 172-187	10,143	1033,551	2012_02_2	Nuclei_frac
	NNLCPSGS [iTRAQ_N1	3 172-187	8,252	689,372	2012_02_2	Nuclei_frac
	TFHETLDC [iTRAQ_N1	4 149-171	5,144	944,152	2012_02_2	Nuclei_frac
	FNFLNPND [iTRAQ_N1	1 81-95	5,788	692,336	2012_02_2	Nuclei_frac
	VMQQQQC [iTRAQ_N1	3 116-131	9,476	749,403	2012_02_2	Nuclei_frac
Q9Y230	AVLIAGQP [iTRAQ_N1	2 71-82	6,2	700,43	2012_02_2	Nuclei_frac
Q9Y230	YAIQLITAA [iTRAQ_N1	2 400-413	9,033	861,988	2012_02_2	Nuclei_frac
P62826	LVLVGDGC [iTRAQ_N1	2 12-22	8,017	652,397	2012_02_2	Nuclei_frac
P62826	NLQYYDIS [iTRAQ_N1	2 142-151	7,213	751,91	2012_02_2	Nuclei_frac
P62826	NLQYYDIS [iTRAQ_N1	2 142-151	5,343	501,609	2012_02_2	Nuclei_frac

P09874	KPPLLNNAL [iTRAQ_N1	3 747-760	5,482	643,05	2012_02_2	Nuclei_frac
P09874	TTNFAGILS [iTRAQ_N1	1 865-877	9,738	761,429	2012_02_2	Nuclei_frac
P09874	TTNFAGILS [iTRAQ_N1	1 865-877	8,253	507,956	2012_02_2	Nuclei_frac
	DFYPAIADI [iTRAQ_N1	3 256-272	7,407	759,388	2012_02_2	Nuclei_frac
	TLPAFQVP [iTRAQ_N1	1 122-133	7,794	765,435	2012_02_2	Nuclei_frac
	TLPAFQVP [iTRAQ_N1	1 122-133	7,439	765,436	2012_02_2	Nuclei_frac
P62917	ASGNYATV [iTRAQ_N1	2 128-143	9,685	659,681	2012_02_2	Nuclei_frac
P62917	ASGNYATV [iTRAQ_N1	2 128-143	6,457	495,013	2012_02_2	Nuclei_frac
P62917	ASGNYATV [iTRAQ_N1	2 128-143	5,903	495,013	2012_02_2	Nuclei_frac
P62917	ASGNYATV [iTRAQ_N1	3 128-144	5,432	563,061	2012_02_2	Nuclei_frac
P20674	LNDFASTV [iTRAQ_N1	1 58-66	5,114	583,819	2012_02_2	Nuclei_frac
P20674	RLNDFAST [iTRAQ_N1	1 57-66	9,927	661,87	2012_02_2	Nuclei_frac
P20674	RLNDFAST [iTRAQ_N1	1 57-66	8,362	441,583	2012_02_2	Nuclei_frac
P24534	LVPVGYGII [iTRAQ_N1	2 176-184	5,443	617,394	2012_02_2	Nuclei_frac
P24534	SIQADGLV [iTRAQ_N1	2 163-175	9,577	818,454	2012_02_2	Nuclei_frac
P24534	SIQADGLV [iTRAQ_N1	2 163-175	9,364	818,455	2012_02_2	Nuclei_frac
P24534	SIQADGLV [iTRAQ_N1	2 163-175	6,458	545,971	2012_02_2	Nuclei_frac
Q93008	KLPPVLAIK [iTRAQ_N1	3 1788-1798	5,108	551,378	2012_02_2	Nuclei_frac
Q93008	LYSVVSQL [iTRAQ_N1	1 2228-2237	9,889	661,403	2012_02_2	Nuclei_frac
Q14019	FALITWIGE [iTRAQ_N1	1 75-90	9,334	974,547	2012_02_2	Nuclei_frac
Q14019	FALITWIGE [iTRAQ_N1	1 75-90	7,592	650,032	2012_02_2	Nuclei_frac
Q14019	LFAFVR [iTRAQ_N1	1 57-62	5,648	448,777	2012_02_2	Nuclei_frac
O76094	EALNVINTI [iTRAQ_N1	2 62-72	7,659	509,964	2012_02_2	Nuclei_frac
O76094	KTNLSAVV [iTRAQ_N1	3 147-162	7,217	726,746	2012_02_2	Nuclei_frac
Q13423	GITHIGYTD [iTRAQ_N1	1 324-336	7,111	525,288	2012_02_2	Nuclei_frac
Q13423	ILIVGGGVA [iTRAQ_N1	2 187-204	7,726	605,044	2012_02_2	Nuclei_frac
P47813_CH	KVWINTSC [iTRAQ_N1	2 67-81	6,333	672,416	2012_02_2	Nuclei_frac
P47813_CH	VWINTSDII [iTRAQ_N1	1 68-81	8,502	872,021	2012_02_2	Nuclei_frac
P46063	LIYVTPEK [iTRAQ_N1	2 185-192	4,757	625,884	2012_02_2	Nuclei_frac
P46063	QFPNASLIK [iTRAQ_N1	2 243-266	10,077	933,846	2012_02_2	Nuclei_frac
P46063	QFPNASLIK [iTRAQ_N1	2 243-266	4,774	700,637	2012_02_2	Nuclei_frac
P54136	LQEVFGHA [iTRAQ_N1	2 8-17	5,191	477,286	2012_02_2	Nuclei_frac
P54136	VEIAGPGFI [iTRAQ_N1	1 82-95	9,627	555,991	2012_02_2	Nuclei_frac
	DIEAQTQK [iTRAQ_N1	3 348-364	7,683	777,084	2012_02_2	Nuclei_frac
	EAQGNSSV [iTRAQ_N1	1 302-324	7,115	844,07	2012_02_2	Nuclei_frac
	ANVELDHV [iTRAQ_N1	1 132-143	7,374	494,612	2012_02_2	Nuclei_frac
	LQQQLTQV [iTRAQ_N1	2 428-440	7,421	606,354	2012_02_2	Nuclei_frac

O94874_ISCIIISGHIDLDN [iTRAQ_N1	1	164-174	5,543	466,261	2012_02_2	Nuclei_frac
O94874_ISCTYDLPGNF [iTRAQ_N1	1	145-160	9,163	661,357	2012_02_2	Nuclei_frac
AIGSASEG [iTRAQ_N1	2	169-187	8,547	750,725	2012_02_2	Nuclei_frac
AIGSASEG [iTRAQ_N1	2	169-187	8,31	750,726	2012_02_2	Nuclei_frac
LFQVEYAI [iTRAQ_N1	2	21-32	6,156	571,334	2012_02_2	Nuclei_frac
LFQVEYAI [iTRAQ_N1	2	21-32	5,07	571,336	2012_02_2	Nuclei_frac
FSPAGPILS [iTRAQ_N1	1	31-41	8,653	651,39	2012_02_2	Nuclei_frac
FSPAGPILS [iTRAQ_N1	1	31-41	5,025	434,596	2012_02_2	Nuclei_frac
SGVGNIFI [iTRAQ_N1	2	96-104	6,042	611,874	2012_02_2	Nuclei_frac
SGVGNIFI [iTRAQ_N1	2	96-104	4,872	408,252	2012_02_2	Nuclei_frac
LDQWLTTI [iTRAQ_N1	2	272-282	5,732	775,434	2012_02_2	Nuclei_frac
NSQSFFSG [iTRAQ_N1	2	23-37	8,691	613,316	2012_02_2	Nuclei_frac
P11177_ISCTYYMSGGL [iTRAQ_N1	2	100-115	7,814	994,527	2012_02_2	Nuclei_frac
P11177_ISCTYYMSGGL [iTRAQ_N1	2	100-115	7,353	663,358	2012_02_2	Nuclei_frac
P11177_ISCVLLGEEV [iTRAQ_N1	2	23-38	6,6	697,375	2012_02_2	Nuclei_frac
Q16795_FGPIPLGSL [iTRAQ_N1	2	188-199	7,315	780,468	2012_02_2	Nuclei_frac
Q16795_VFEISPFEP [iTRAQ_N1	1	269-281	7,097	882,978	2012_02_2	Nuclei_frac
Q9Y3B3_KQYDSFTF [iTRAQ_N1	3	57-68	6,328	619,002	2012_02_2	Nuclei_frac
Q9Y3B3_SVIDYQTH [iTRAQ_N1	1	126-135	8,075	705,37	2012_02_2	Nuclei_frac
Q9Y3B3_SVIDYQTH [iTRAQ_N1	1	126-135	6,564	470,581	2012_02_2	Nuclei_frac
P09622_EANLAASF [iTRAQ_N1	2	461-470	6,667	648,366	2012_02_2	Nuclei_frac
P09622_EANLAASF [iTRAQ_N1	2	461-470	6,328	432,579	2012_02_2	Nuclei_frac
P09622_IPNIYAIGD [iTRAQ_N1	3	312-330	7,737	761,763	2012_02_2	Nuclei_frac
P04181_CHIVFAAGNF [iTRAQ_N1	1	135-145	9,13	691,379	2012_02_2	Nuclei_frac
P04181_CHLPSDVVTA [iTRAQ_N1	1	328-337	5,273	600,857	2012_02_2	Nuclei_frac
ALLNHLDV [iTRAQ_N1	1	34-45	5,882	469,945	2012_02_2	Nuclei_frac
SSLGAPAI [iTRAQ_N1	1	1-20	8,505	733,411	2012_02_2	Nuclei_frac
O75131_DIVQFVPFI [iTRAQ_N1	1	484-492	6,495	632,864	2012_02_2	Nuclei_frac
O75131_DIVQFVPFI [iTRAQ_N1	1	484-492	5,286	632,862	2012_02_2	Nuclei_frac
O75131_DIVQFVPFI [iTRAQ_N1	1	484-492	4,788	632,864	2012_02_2	Nuclei_frac
O75131_LYGPTNFS [iTRAQ_N1	1	390-405	7,881	648,36	2012_02_2	Nuclei_frac
O14776_LIVAYVDD [iTRAQ_N1	1	1049-1060	8,286	531,303	2012_02_2	Nuclei_frac
O14776_VFFYNPTT [iTRAQ_N1	1	523-531	6,084	644,845	2012_02_2	Nuclei_frac
GFGFITFTN [iTRAQ_N1	2	48-65	8,215	714,691	2012_02_2	Nuclei_frac
YYDSRPGG [iTRAQ_N1	1	117-131	6,139	625,624	2012_02_2	Nuclei_frac
P18621_EQIVPKPEE [iTRAQ_N1	3	153-166	5,516	686,061	2012_02_2	Nuclei_frac
P18621_GLDVDSL [iTRAQ_N1	2	105-120	8,83	689,73	2012_02_2	Nuclei_frac
P18621_GLDVDSL [iTRAQ_N1	2	105-120	7,813	689,729	2012_02_2	Nuclei_frac

Q08431	ISLYPTSCHT [iTRAQ_N1	3	132-144	7,177	575,284	2012_02_2	Nuclei_frac
Q08431	ISVTFLGLQH [iTRAQ_N1	1	18-32	7,141	637,361	2012_02_2	Nuclei_frac
	ESETTTSL [iTRAQ_N1	1	1-12	8,307	754,901	2012_02_2	Nuclei_frac
	QATTIADM [iTRAQ_N1	2	112-129	6,004	760,764	2012_02_2	Nuclei_frac
	QATTIADM [iTRAQ_N1	2	112-129	5,322	760,763	2012_02_2	Nuclei_frac
Q16881	ISKIGLETVG [iTRAQ_N1	3	299-308	5,096	492,654	2012_02_2	Nuclei_frac
Q16881	ISVVGFBHVL [iTRAQ_N1	2	435-457	9,188	857,482	2012_02_2	Nuclei_frac
P24752	LNVTPLAR [iTRAQ_N1	1	271-278	6,333	514,323	2012_02_2	Nuclei_frac
P24752	TPIGSFLGS [iTRAQ_N1	2	17-33	7,926	995,586	2012_02_2	Nuclei_frac
P24752	TPIGSFLGS [iTRAQ_N1	2	17-33	5,174	664,068	2012_02_2	Nuclei_frac
Q14676	ISAVLALGG [iTRAQ_N1	1	885-907	9,153	770,756	2012_02_2	Nuclei_frac
Q14676	ISVGLPLLSP [iTRAQ_N1	2	1032-1048	5,1	695,443	2012_02_2	Nuclei_frac
	AIKPKQYVC [iTRAQ_N1	3	166-178	6,053	649,066	2012_02_2	Nuclei_frac
	AIKPKQYVC [iTRAQ_N1	3	166-178	5,855	649,068	2012_02_2	Nuclei_frac
	TQAIVCQC [iTRAQ_N1	3	196-210	8,185	686,055	2012_02_2	Nuclei_frac
Q6UVK1	ALLHVWA [iTRAQ_N1	1	2016-2033	8,989	692,055	2012_02_2	Nuclei_frac
Q6UVK1	ITVAALDA [iTRAQ_N1	1	1694-1713	5,22	723,081	2012_02_2	Nuclei_frac
P08574	GLLSSLDH [iTRAQ_N1	1	16-27	7,756	481,609	2012_02_2	Nuclei_frac
P08574	LFDYFPKP [iTRAQ_N1	2	87-102	6,449	735,054	2012_02_2	Nuclei_frac
P59190	IQIWDTAG [iTRAQ_N1	1	59-69	7,713	730,884	2012_02_2	Nuclei_frac
P59190	LLLIGDSG [iTRAQ_N1	2	11-21	6,471	680,428	2012_02_2	Nuclei_frac
P59190	LLLIGDSG [iTRAQ_N1	2	11-21	5,985	680,427	2012_02_2	Nuclei_frac
P59190	LLLIGDSG [iTRAQ_N1	2	11-21	5,355	453,953	2012_02_2	Nuclei_frac
	APVPGTPE [iTRAQ_N1	1	322-337	8,643	829,929	2012_02_2	Nuclei_frac
	APVPGTPE [iTRAQ_N1	1	322-337	6,69	829,93	2012_02_2	Nuclei_frac
	ESAINVAE [iTRAQ_N1	3	212-222	5,537	526,649	2012_02_2	Nuclei_frac
Q13243	LIVENLSSF [iTRAQ_N1	1	107-115	6,1	587,851	2012_02_2	Nuclei_frac
Q13243	LIVENLSSF [iTRAQ_N1	1	107-115	5,398	587,851	2012_02_2	Nuclei_frac
Q13243	QAGEVTF [iTRAQ_N1	2	127-140	8,077	605,665	2012_02_2	Nuclei_frac
Q13243	QAGEVTF [iTRAQ_N1	2	127-140	5,106	454,501	2012_02_2	Nuclei_frac
Q29865	CFAYLEGTCV [iTRAQ_N1	2	158-169	8,312	820,914	2012_02_2	Nuclei_frac
Q29865	CFYFDTAVSR [iTRAQ_N1	1	7-17	5,86	471,586	2012_02_2	Nuclei_frac
Q03135	CFEIDLVRDI [iTRAQ_N1	2	17-26	5,724	743,929	2012_02_2	Nuclei_frac
Q03135	CFEIDLVRDI [iTRAQ_N1	2	17-26	4,797	496,287	2012_02_2	Nuclei_frac
Q03135	CFIDFEDVIAE [iTRAQ_N1	2	35-55	8,439	898,45	2012_02_2	Nuclei_frac
	RYESHPVC [iTRAQ_N1	3	176-189	7,922	654,678	2012_02_2	Nuclei_frac
	YESHPVCA [iTRAQ_N1	3	177-189	6,225	602,643	2012_02_2	Nuclei_frac
P42766	QLDDLKVE [iTRAQ_N1	2	19-31	7,307	923,039	2012_02_2	Nuclei_frac

P42766	QLDDLKVE [iTRAQ_N1	2 19-31	5,101	615,695	2012_02_2 Nuclei_frac
P42766	VLTVINQT [iTRAQ_N1	2 56-65	6,824	716,442	2012_02_2 Nuclei_frac
P42766	VLTVINQT [iTRAQ_N1	2 56-65	5,905	477,964	2012_02_2 Nuclei_frac
P42766	VLTVINQT [iTRAQ_N1	2 56-65	5,729	477,964	2012_02_2 Nuclei_frac
Q15008	FLLSLPEHF [iTRAQ_N1	1 23-31	7,054	419,249	2012_02_2 Nuclei_frac
Q15008	GAEILEVL [iTRAQ_N1	1 242-256	7,063	583,345	2012_02_2 Nuclei_frac
	TALALAIA [iTRAQ_N1	2 77-90	5,819	558,675	2012_02_2 Nuclei_frac
	YSVQLLTP [iTRAQ_N1	2 405-418	8,269	910,052	2012_02_2 Nuclei_frac
	YSVQLLTP [iTRAQ_N1	2 405-418	5,697	607,036	2012_02_2 Nuclei_frac
	AYVVLGQF [iTRAQ_N1	2 42-53	6,476	819,518	2012_02_2 Nuclei_frac
	AYVVLGQF [iTRAQ_N1	2 42-53	4,885	546,68	2012_02_2 Nuclei_frac
	AYVVLGQF [iTRAQ_N1	3 42-54	7,576	637,417	2012_02_2 Nuclei_frac
	DGVGGDP [iTRAQ_N1	1 1-14	6,355	502,272	2012_02_2 Nuclei_frac
	YVSSLTEE [iTRAQ_N1	2 332-343	7,637	567,321	2012_02_2 Nuclei_frac
	YVSSLTEE [iTRAQ_N1	2 332-343	7,46	567,321	2012_02_2 Nuclei_frac
	YVSSLTEE [iTRAQ_N1	2 332-343	7,197	567,321	2012_02_2 Nuclei_frac
	VYIASSSG [iTRAQ_N1	2 5-17	5,743	524,635	2012_02_2 Nuclei_frac
	VYIASSSG [iTRAQ_N1	2 5-17	4,744	524,634	2012_02_2 Nuclei_frac
	VYIASSSG [iTRAQ_N1	3 5-18	8,243	615,367	2012_02_2 Nuclei_frac
	VYIASSSG [iTRAQ_N1	3 5-18	6,118	615,368	2012_02_2 Nuclei_frac
P49773	AQVARPG [iTRAQ_N1	2 7-20	7,629	568,993	2012_02_2 Nuclei_frac
P49773	KCAADLGL [iTRAQ_N1	4 82-91	6,347	507,965	2012_02_2 Nuclei_frac
P33176	ELQTLHNL [iTRAQ_N1	1 791-799	6,758	423,248	2012_02_2 Nuclei_frac
P33176	KLFVQDLA [iTRAQ_N1	2 800-809	7,21	493,637	2012_02_2 Nuclei_frac
Q15293	TFDQLTPD [iTRAQ_N1	2 42-54	8,331	618,655	2012_02_2 Nuclei_frac
Q15293	YIFDNVAK [iTRAQ_N1	2 86-93	5,634	629,359	2012_02_2 Nuclei_frac
P30084	ALNALCD [iTRAQ_N1	3 30-47	8,236	753,746	2012_02_2 Nuclei_frac
P30084	AQFAQPEI [iTRAQ_N1	1 131-151	5,726	757,088	2012_02_2 Nuclei_frac
P30084	AQFAQPEI [iTRAQ_N1	1 131-151	4,952	757,087	2012_02_2 Nuclei_frac
P17301	AVIDQCNH [iTRAQ_N1	2 265-277	7,577	571,295	2012_02_2 Nuclei_frac
P17301	IPLLYDAEI [iTRAQ_N1	1 901-913	6,375	566,662	2012_02_2 Nuclei_frac
O14737	NSILAQVL [iTRAQ_N1	1 40-52	9,107	520,295	2012_02_2 Nuclei_frac
O14737	NSILAQVL [iTRAQ_N1	1 40-52	8,971	779,94	2012_02_2 Nuclei_frac
O14737	VSEQGLIE [iTRAQ_N1	2 86-96	4,842	506,313	2012_02_2 Nuclei_frac
	ILLLGAGES [iTRAQ_N1	2 51-61	7,65	673,416	2012_02_2 Nuclei_frac
	ILLLGAGES [iTRAQ_N1	2 51-61	7,138	673,418	2012_02_2 Nuclei_frac
	ILLLGAGES [iTRAQ_N1	2 51-61	4,963	449,281	2012_02_2 Nuclei_frac
	VFLQYLPA [iTRAQ_N1	1 141-150	6,251	682,413	2012_02_2 Nuclei_frac
O14653_IS	QSVHIVEN [iTRAQ_N1	1 28-47	8,543	819,761	2012_02_2 Nuclei_frac

O14653_IS(YDVQHLQ[[iTRAQ_N1	1 75-85	5,352	496,608	2012_02_2 Nuclei_frac
P22102_CH AFAHITGG[[iTRAQ_N1	1 677-692	7,656	604,01	2012_02_2 Nuclei_frac
P22102_CH AIAFLQQPI [iTRAQ_N1	1 425-433	6,23	594,354	2012_02_2 Nuclei_frac
FYNLVLLP[[iTRAQ_N1	1 249-257	8,922	639,891	2012_02_2 Nuclei_frac
QQQEELEA[[iTRAQ_N1	2 64-83	4,925	620,567	2012_02_2 Nuclei_frac
Q16666_IS(GLEVINDY[[iTRAQ_N1	1 13-23	6,406	502,934	2012_02_2 Nuclei_frac
Q16666_IS(IFEDIPTLE[[iTRAQ_N1	3 68-84	7,438	803,129	2012_02_2 Nuclei_frac
Q10567_IS(LAPPLVTL [iTRAQ_N1	1 284-304	6,547	813,146	2012_02_2 Nuclei_frac
Q10567_IS(LASQANIA [iTRAQ_N1	2 345-359	7,244	929,061	2012_02_2 Nuclei_frac
Q10567_IS(LASQANIA [iTRAQ_N1	2 345-359	5,693	619,708	2012_02_2 Nuclei_frac
Q10567_IS(LASQANIA [iTRAQ_N1	2 345-359	4,834	619,708	2012_02_2 Nuclei_frac
P14927 KWYYNAA [iTRAQ_N1	3 18-28	6,744	598,663	2012_02_2 Nuclei_frac
P14927 KWYYNAA [iTRAQ_N1	3 18-28	5,424	598,665	2012_02_2 Nuclei_frac
P14927 RLPENLYN [iTRAQ_N1	1 49-58	7,002	478,594	2012_02_2 Nuclei_frac
Q13177 IISIFSGTEK [iTRAQ_N1	2 53-62	6,062	691,912	2012_02_2 Nuclei_frac
Q13177 LLQTSNIT[[iTRAQ_N1	2 105-113	7,672	653,403	2012_02_2 Nuclei_frac
P62249 EIKDILIQY[[iTRAQ_N1	2 106-116	7,181	565,331	2012_02_2 Nuclei_frac
P62249 EIKDILIQY[[iTRAQ_N1	2 106-116	6,007	565,33	2012_02_2 Nuclei_frac
P62249 LLEPVLLL[[iTRAQ_N1	2 50-59	6,545	691,967	2012_02_2 Nuclei_frac
P62249 LLEPVLLL[[iTRAQ_N1	2 50-59	6,263	691,966	2012_02_2 Nuclei_frac
P62249 LLEPVLLL[[iTRAQ_N1	2 50-59	5,682	461,646	2012_02_2 Nuclei_frac
O43294_IS(DFLQLFAP [iTRAQ_N1	1 337-345	7,334	625,853	2012_02_2 Nuclei_frac
O43294_IS(RDFLQLFA [iTRAQ_N1	1 336-345	6,386	469,607	2012_02_2 Nuclei_frac
A0FGR8_IS(ITVPLVSE[[iTRAQ_N1	1 161-175	7,474	905,553	2012_02_2 Nuclei_frac
A0FGR8_IS(ITVPLVSE[[iTRAQ_N1	1 161-175	5,52	604,037	2012_02_2 Nuclei_frac
A0FGR8_IS(VGNQIFQS [iTRAQ_N1	1 216-224	6,243	596,832	2012_02_2 Nuclei_frac
FYLGGPTS[[iTRAQ_N1	1 337-346	7,271	627,854	2012_02_2 Nuclei_frac
WSYGAGIV [iTRAQ_N1	1 424-433	6,445	633,367	2012_02_2 Nuclei_frac
Q8WUM4 FYNELTEIL [iTRAQ_N1	1 675-685	6,943	770,93	2012_02_2 Nuclei_frac
Q8WUM4 NIQVSHQE [iTRAQ_N1	2 627-637	6,768	535,626	2012_02_2 Nuclei_frac
P09496_ISC AIKELEEW[[iTRAQ_N1	2 139-149	7,439	565,984	2012_02_2 Nuclei_frac
P09496_ISC SVLISLK [iTRAQ_N1	2 206-212	6,24	524,355	2012_02_2 Nuclei_frac
P63000_CH LTPITYPQC[[iTRAQ_N1	3 134-147	7,423	603,346	2012_02_2 Nuclei_frac
P63000_CH TVFDEAIR [iTRAQ_N1	1 167-174	6,237	547,802	2012_02_2 Nuclei_frac
ELFSPLHA[[iTRAQ_N1	1 61-79	7,815	730,384	2012_02_2 Nuclei_frac
IIVLGLLP[[iTRAQ_N1	1 134-142	5,816	569,4	2012_02_2 Nuclei_frac
O15145 AYLQQLR [iTRAQ_N1	1 130-136	6,961	518,308	2012_02_2 Nuclei_frac

O15145	LIGNMALLI [iTRAQ_N1	2 14-24	6,654	457,616	2012_02_2	Nuclei_frac
O15145	LIGNMALLI [iTRAQ_N1	2 14-24	4,873	685,92	2012_02_2	Nuclei_frac
P26368	CH ELLTSFGPI [iTRAQ_N1	2 277-286	7,261	464,951	2012_02_2	Nuclei_frac
P26368	CH ELLTSFGPI [iTRAQ_N1	2 277-286	6,464	464,95	2012_02_2	Nuclei_frac
P26368	CH ELLTSFGPI [iTRAQ_N1	2 277-286	6,315	696,922	2012_02_2	Nuclei_frac
P26368	CH ELLTSFGPI [iTRAQ_N1	2 277-286	6,3	696,921	2012_02_2	Nuclei_frac
P26368	CH NFAFLEFR [iTRAQ_N1	1 196-203	6,353	594,32	2012_02_2	Nuclei_frac
O43684	TPCNAGTF [iTRAQ_N1	3 127-139	8,411	575,623	2012_02_2	Nuclei_frac
O43684	VYTLVSVG [iTRAQ_N1	1 140-149	5,189	620,837	2012_02_2	Nuclei_frac
P13073	DHPLPEVA [iTRAQ_N1	2 21-31	6,318	510,629	2012_02_2	Nuclei_frac
P13073	VNPIQGLA [iTRAQ_N1	2 128-137	7,235	657,904	2012_02_2	Nuclei_frac
P62995	GFAFVYFE [iTRAQ_N1	2 60-73	6,693	637,325	2012_02_2	Nuclei_frac
P62995	IRVDFSITK [iTRAQ_N1	2 89-97	6,831	456,282	2012_02_2	Nuclei_frac
P26373	GFSLEELR [iTRAQ_N1	1 74-81	5,463	547,803	2012_02_2	Nuclei_frac
P26373	LATQLTGF [iTRAQ_N1	1 145-157	8,037	763,946	2012_02_2	Nuclei_frac
P26373	LATQLTGF [iTRAQ_N1	2 145-157	7,85	771,943	2012_02_2	Nuclei_frac
P26373	LATQLTGF [iTRAQ_N1	2 145-157	6,721	514,965	2012_02_2	Nuclei_frac
	IVLFDTLLE [iTRAQ_N1	2 277-292	7,699	728,753	2012_02_2	Nuclei_frac
	NEEVLA VL [iTRAQ_N1	2 326-341	5,792	530,546	2012_02_2	Nuclei_frac
	GVIDVFLH, [iTRAQ_N1	2 252-262	6,216	524,976	2012_02_2	Nuclei_frac
	LTFVGELA [iTRAQ_N1	1 507-517	7,258	448,59	2012_02_2	Nuclei_frac
	IATLG YLPT [iTRAQ_N1	1 167-181	7,865	916,526	2012_02_2	Nuclei_frac
	VTTFEHQY [iTRAQ_N1	2 121-133	5,609	604,337	2012_02_2	Nuclei_frac
P62750	LAPDYDAL [iTRAQ_N1	2 139-151	8,364	846,956	2012_02_2	Nuclei_frac
P62750	LAPDYDAL [iTRAQ_N1	2 139-151	4,835	564,972	2012_02_2	Nuclei_frac
P62750	VNTLIRPD ([iTRAQ_N1	2 123-133	5,053	510,635	2012_02_2	Nuclei_frac
P42224	FSLENNFLI [iTRAQ_N1	1 71-84	8,235	630,343	2012_02_2	Nuclei_frac
P42224	YLYPNIDKI [iTRAQ_N1	3 666-679	5,167	529,041	2012_02_2	Nuclei_frac
P30837	LLNLLADL [iTRAQ_N1	1 87-97	7,812	471,625	2012_02_2	Nuclei_frac
P30837	LLNLLADL [iTRAQ_N1	1 87-97	7,184	706,934	2012_02_2	Nuclei_frac
P30837	VLGYIQLG ([iTRAQ_N1	2 353-362	5,55	469,625	2012_02_2	Nuclei_frac
P23497	ISC TFPFLEGLF [iTRAQ_N1	1 71-79	6,845	612,35	2012_02_2	Nuclei_frac
P23497	ISC VVYNVLSE [iTRAQ_N1	2 105-115	6,486	790,963	2012_02_2	Nuclei_frac
P23497	ISC VVYNVLSE [iTRAQ_N1	2 105-115	4,781	527,643	2012_02_2	Nuclei_frac
Q9UHX1	IS AVTPPMPL [iTRAQ_N1	3 242-272	6,713	1033,587	2012_02_2	Nuclei_frac
Q9UHX1	IS QAFAPFGP [iTRAQ_N1	2 87-96	6,605	682,404	2012_02_2	Nuclei_frac
Q9NP72	IIQTPGLWE [iTRAQ_N1	2 169-183	7,991	682,369	2012_02_2	Nuclei_frac
Q9NP72	TLTPSYR [iTRAQ_N1	1 72-79	5,321	572,81	2012_02_2	Nuclei_frac

	DIPFSAIYFI [iTRAQ_N1	3 493-508	7,39	739,389	2012_02_2 Nuclei_frac
	FGLGSVAC [iTRAQ_N1	2 332-353	5,883	798,468	2012_02_2 Nuclei_frac
Q9UL25	FHALGPIYY [iTRAQ_N1	1 80-89	6,672	460,924	2012_02_2 Nuclei_frac
Q9UL25	GIEELFLDL [iTRAQ_N1	3 167-178	6,59	594,335	2012_02_2 Nuclei_frac
Q9UL25	GIEELFLDL [iTRAQ_N1	3 167-178	6,193	594,334	2012_02_2 Nuclei_frac
	LTDYISK [iTRAQ_N1	2 179-185	5,681	564,331	2012_02_2 Nuclei_frac
	LTDYISK [iTRAQ_N1	2 179-185	5,441	564,332	2012_02_2 Nuclei_frac
	LTDYISK [iTRAQ_N1	2 179-185	5,433	564,331	2012_02_2 Nuclei_frac
	TPMGIVLD [iTRAQ_N1	1 160-178	7,573	753,058	2012_02_2 Nuclei_frac
P62244	ILGFFF [iTRAQ_N1	1 124-129	6,557	444,261	2012_02_2 Nuclei_frac
P62244	ILGFFF [iTRAQ_N1	1 124-129	5,618	444,261	2012_02_2 Nuclei_frac
P62244	ILGFFF [iTRAQ_N1	1 124-129	5,338	444,262	2012_02_2 Nuclei_frac
P62244	IVVNL TGR [iTRAQ_N1	1 60-67	6,691	508,323	2012_02_2 Nuclei_frac
Q9P0L0,Q9	FKGPFTDV [iTRAQ_N1	3 24-37	7,487	667,06	2012_02_2 Nuclei_frac
Q9P0L0,Q9	FKGPFTDV [iTRAQ_N1	3 24-37	7,23	667,06	2012_02_2 Nuclei_frac
Q9P0L0,Q9	FKGPFTDV [iTRAQ_N1	3 24-37	6,724	667,06	2012_02_2 Nuclei_frac
Q9P0L0,Q9	QDGPMPKF [iTRAQ_N1	3 154-172	5,761	604,058	2012_02_2 Nuclei_frac
P14314	LGSPTSLS [iTRAQ_N1	4 425-450	6,62	795,912	2012_02_2 Nuclei_frac
P14314	LWEEQLA [iTRAQ_N1	2 183-192	6,592	723,915	2012_02_2 Nuclei_frac
P14314	LWEEQLA [iTRAQ_N1	2 183-192	6,285	482,946	2012_02_2 Nuclei_frac
P14314	LWEEQLA [iTRAQ_N1	2 183-192	6,067	482,945	2012_02_2 Nuclei_frac
	EYTINIHK [iTRAQ_N1	2 24-31	5,551	435,918	2012_02_2 Nuclei_frac
	LYTLVTYV [iTRAQ_N1	2 102-115	7,631	967,07	2012_02_2 Nuclei_frac
	LYTLVTYV [iTRAQ_N1	2 102-115	6,024	645,048	2012_02_2 Nuclei_frac
	LYTLVTYV [iTRAQ_N1	2 102-115	5,726	484,038	2012_02_2 Nuclei_frac
	LYTLVTYV [iTRAQ_N1	2 102-115	5,145	645,047	2012_02_2 Nuclei_frac
P46776	LWTLVSEC [iTRAQ_N1	1 77-86	5,241	688,888	2012_02_2 Nuclei_frac
P46776	TGAAPIDV [iTRAQ_N1	1 94-104	7,928	628,381	2012_02_2 Nuclei_frac
P46776	TGAAPIDV [iTRAQ_N1	1 94-104	7,035	628,38	2012_02_2 Nuclei_frac
P46776	TGAAPIDV [iTRAQ_N1	1 94-104	4,999	419,256	2012_02_2 Nuclei_frac
P51572	LDVGNAE [iTRAQ_N1	2 167-181	7,528	668,361	2012_02_2 Nuclei_frac
P51572	LKDELAST [iTRAQ_N1	3 190-198	5,62	718,942	2012_02_2 Nuclei_frac
P51572	LKDELAST [iTRAQ_N1	3 190-198	5,476	479,629	2012_02_2 Nuclei_frac
P51572	LKDELAST [iTRAQ_N1	3 190-198	5,395	718,939	2012_02_2 Nuclei_frac
	LSDQFHDII [iTRAQ_N1	1 126-136	6,196	500,951	2012_02_2 Nuclei_frac
	YITDWQNV [iTRAQ_N1	1 91-100	6,944	743,384	2012_02_2 Nuclei_frac
Q969H8	ESDVPLKT [iTRAQ_N1	3 100-114	5,561	728,399	2012_02_2 Nuclei_frac
Q969H8	SYLYFTQFI [iTRAQ_N1	2 70-78	7,558	742,904	2012_02_2 Nuclei_frac
Q969H8	SYLYFTQFI [iTRAQ_N1	2 70-78	5,911	495,604	2012_02_2 Nuclei_frac
Q01844	AAVEWFD [iTRAQ_N1	3 352-366	6,423	706,374	2012_02_2 Nuclei_frac

Q01844	AAVEWFD [iTRAQ_N1	3 352-366	5,388	530,033	2012_02_2	Nuclei_frac
Q01844	AAVEWFD [iTRAQ_N1	3 352-366	5,135	530,033	2012_02_2	Nuclei_frac
Q01844	GDATVSYE [iTRAQ_N1	2 338-351	6,659	580,298	2012_02_2	Nuclei_frac
Q9UJ70	IGLPILCVG [iTRAQ_N1	3 261-273	7,484	865,524	2012_02_2	Nuclei_frac
Q9UJ70	LGILTHLYR [iTRAQ_N1	1 197-205	5,592	410,588	2012_02_2	Nuclei_frac
	DLSHIGDA' [iTRAQ_N1	3 150-164	7,652	625,009	2012_02_2	Nuclei_frac
	DLSHIGDA' [iTRAQ_N1	3 150-164	6,656	625,009	2012_02_2	Nuclei_frac
	DLSHIGDA' [iTRAQ_N1	3 150-164	6,617	625,01	2012_02_2	Nuclei_frac
	YLNFFTK [iTRAQ_N1	2 211-217	5,41	610,85	2012_02_2	Nuclei_frac
P35221,P35	AHVLAAS' [iTRAQ_N1	2 57-74	8,213	749,075	2012_02_2	Nuclei_frac
P35221,P35	LVYDGIR [iTRAQ_N1	1 616-622	4,843	490,29	2012_02_2	Nuclei_frac
P35221,P35	LVYDGIR [iTRAQ_N1	1 616-622	4,801	490,29	2012_02_2	Nuclei_frac
P16152	IGVTVLSR [iTRAQ_N1	1 198-205	5,246	494,818	2012_02_2	Nuclei_frac
P16152	LFSGDVVL [iTRAQ_N1	1 27-37	7,81	661,385	2012_02_2	Nuclei_frac
A2RRP1	IVDHLLASI [iTRAQ_N1	1 2192-2204	7,815	531,979	2012_02_2	Nuclei_frac
A2RRP1	LLVFFR [iTRAQ_N1	1 2006-2011	5,221	469,802	2012_02_2	Nuclei_frac
Q14498_C1	GIFEPFGR [iTRAQ_N1	1 268-275	6,415	533,795	2012_02_2	Nuclei_frac
Q14498_C1	VLGVPIIVC [iTRAQ_N1	2 218-232	6,586	614,045	2012_02_2	Nuclei_frac
Q14498_C1	VLGVPIIVC [iTRAQ_N1	2 218-232	5,579	614,045	2012_02_2	Nuclei_frac
Q14498_C1	VLGVPIIVC [iTRAQ_N1	2 218-232	5,478	614,043	2012_02_2	Nuclei_frac
Q99805	DTFYIFNH [iTRAQ_N1	2 176-187	5,462	600,658	2012_02_2	Nuclei_frac
Q99805	RPSENLGQ [iTRAQ_N1	1 63-76	7,514	582,652	2012_02_2	Nuclei_frac
	ATATISAK [iTRAQ_N1	3 558-572	5,442	658,4	2012_02_2	Nuclei_frac
	AVSILPLL [iTRAQ_N1	1 179-192	7,487	524,996	2012_02_2	Nuclei_frac
P35613_CH	FFVSSSQG [iTRAQ_N1	1 158-166	6,248	579,806	2012_02_2	Nuclei_frac
P35613_CH	GGVVLKEE [iTRAQ_N1	3 58-71	6,666	615,041	2012_02_2	Nuclei_frac
P35613_CH	GGVVLKEE [iTRAQ_N1	3 58-71	6,019	615,04	2012_02_2	Nuclei_frac
O75489	ILTDYGFEC [iTRAQ_N1	1 151-163	6,318	565,958	2012_02_2	Nuclei_frac
O75489	QLSAFGEY [iTRAQ_N1	2 21-35	6,57	651,705	2012_02_2	Nuclei_frac
Q9BXP5_IS1	LLLYLR [iTRAQ_N1	1 575-580	6,605	467,814	2012_02_2	Nuclei_frac
Q9BXP5_IS1	LTPLLSVR [iTRAQ_N1	1 633-640	6,269	521,841	2012_02_2	Nuclei_frac
Q8N163_IS	ILLTLGIR [iTRAQ_N1	1 728-735	5,039	521,86	2012_02_2	Nuclei_frac
Q8N163_IS	VLLLSSPG [iTRAQ_N1	1 310-323	7,817	867,007	2012_02_2	Nuclei_frac
	ISEIEDAAF [iTRAQ_N1	1 242-253	8,093	739,904	2012_02_2	Nuclei_frac
	LALQQDLT [iTRAQ_N1	2 150-169	4,72	762,1	2012_02_2	Nuclei_frac
O43747,O4	VLAINILGR [iTRAQ_N1	1 306-314	5,644	556,867	2012_02_2	Nuclei_frac
O43747,O4	VLTTAGSY [iTRAQ_N1	1 424-433	7,165	605,85	2012_02_2	Nuclei_frac

	AFGYYGPL [iTRAQ_N1	1 29-37	6,782	594,32	2012_02_2 Nuclei_frac
	NPPGFAFV [iTRAQ_N1	1 44-57	5,902	883,436	2012_02_2 Nuclei_frac
	NPPGFAFV [iTRAQ_N1	1 44-57	5,255	589,295	2012_02_2 Nuclei_frac
O00629	DAQVVQV [iTRAQ_N1	2 423-439	6,692	700,416	2012_02_2 Nuclei_frac
O00629	SGILPILVH [iTRAQ_N1	2 112-124	5,975	550,987	2012_02_2 Nuclei_frac
O94826	GLLQLQWI [iTRAQ_N1	2 516-523	5,891	637,399	2012_02_2 Nuclei_frac
O94826	LRPESALA [iTRAQ_N1	2 429-440	6,758	533,986	2012_02_2 Nuclei_frac
P60903	EFPGFLEN [iTRAQ_N1	3 37-53	6,161	793,769	2012_02_2 Nuclei_frac
P60903	EFPGFLEN [iTRAQ_N1	3 37-53	6,066	793,769	2012_02_2 Nuclei_frac
P60903	EFPGFLEN [iTRAQ_N1	3 37-53	5,312	595,578	2012_02_2 Nuclei_frac
P60903	EFPGFLEN [iTRAQ_N1	3 37-53	5,067	595,579	2012_02_2 Nuclei_frac
P60903	EFPGFLEN [iTRAQ_N1	3 37-53	4,735	595,578	2012_02_2 Nuclei_frac
P60903	FAGDKGYL [iTRAQ_N1	3 18-27	6,46	766,446	2012_02_2 Nuclei_frac
P10301	LFTQILR [iTRAQ_N1	1 122-128	5,895	517,828	2012_02_2 Nuclei_frac
P10301	LNVDFAFE [iTRAQ_N1	1 177-188	6,695	788,926	2012_02_2 Nuclei_frac
P11387	AGNEKEEG [iTRAQ_N1	4 488-507	6,475	824,386	2012_02_2 Nuclei_frac
P11387	LNTGILNK [iTRAQ_N1	2 567-574	6,115	580,867	2012_02_2 Nuclei_frac
Q96CW1_1	DIILPFR [iTRAQ_N1	1 282-288	6,161	509,315	2012_02_2 Nuclei_frac
Q96CW1_1	DIILPFR [iTRAQ_N1	1 282-288	5,562	509,315	2012_02_2 Nuclei_frac
Q96CW1_1	TFITQQGIK [iTRAQ_N1	2 131-139	6,425	662,399	2012_02_2 Nuclei_frac
Q9HBR0	EELEQAQIH [iTRAQ_N1	2 370-378	4,784	688,372	2012_02_2 Nuclei_frac
Q9HBR0	QVEVHQEF [iTRAQ_N1	1 665-678	7,789	554,301	2012_02_2 Nuclei_frac
Q16698	EQWDTIEE [iTRAQ_N1	1 286-296	5,197	788,413	2012_02_2 Nuclei_frac
Q16698	VAFITGGG [iTRAQ_N1	2 27-39	7,358	489,292	2012_02_2 Nuclei_frac
Q92804_1	AAIDWFDG [iTRAQ_N1	2 298-306	6,797	655,852	2012_02_2 Nuclei_frac
Q92804_1	AAIDWFDG [iTRAQ_N1	3 298-314	5,746	599,082	2012_02_2 Nuclei_frac
P23634_1	NVFSGIYR [iTRAQ_N1	1 974-981	7,079	550,304	2012_02_2 Nuclei_frac
P23634_1	NVFSGIYR [iTRAQ_N1	1 974-981	7,06	550,304	2012_02_2 Nuclei_frac
P23634_1	TICIAAYR [iTRAQ_N1	2 625-631	5,453	520,787	2012_02_2 Nuclei_frac
	LADFGVLH [iTRAQ_N1	1 434-442	5	586,338	2012_02_2 Nuclei_frac
	VNTPTTTV [iTRAQ_N1	1 244-253	7,485	648,357	2012_02_2 Nuclei_frac
	DNTINLIHT [iTRAQ_N1	1 238-248	7,52	496,609	2012_02_2 Nuclei_frac
	DNTINLIHT [iTRAQ_N1	1 238-248	7,264	744,41	2012_02_2 Nuclei_frac
	IIEETLALK [iTRAQ_N1	2 10-18	4,901	659,415	2012_02_2 Nuclei_frac
Q9P0K7,Q9	IQQLQEILQ [iTRAQ_N1	2 423-435	6,917	629,041	2012_02_2 Nuclei_frac
Q9P0K7,Q9	IQQLQEILQ [iTRAQ_N1	2 423-436	5,481	681,075	2012_02_2 Nuclei_frac
	IKDLSTIEPI [iTRAQ_N1	3 100-110	5,066	563,687	2012_02_2 Nuclei_frac
	SLDLFNCE [iTRAQ_N1	2 117-132	7,275	706,339	2012_02_2 Nuclei_frac

P63173_CHDFLLTAR	[iTRAQ_N1	1 10-16	6,189	490,289	2012_02_2 Nuclei_frac
P63173_CHDFLLTAR	[iTRAQ_N1	1 10-16	5,708	490,289	2012_02_2 Nuclei_frac
P63173_CHYLYTLVITE	[iTRAQ_N1	3 41-52	6,139	640,049	2012_02_2 Nuclei_frac
P63173_CHYLYTLVITE	[iTRAQ_N1	3 41-52	6,046	640,05	2012_02_2 Nuclei_frac
Q9H0S4	LFALVLTP	[iTRAQ_N1	1 92-101	7,539	637,902 2012_02_2 Nuclei_frac
Q9H0S4	TGAFALPIL	[iTRAQ_N1	1 74-91	4,787	690,404 2012_02_2 Nuclei_frac
	NVTDVVN	[iTRAQ_N1	3 477-492	7,318	673,349 2012_02_2 Nuclei_frac
	VFNTTPDE	[iTRAQ_N1	2 335-357	5,003	729,382 2012_02_2 Nuclei_frac
Q96FJ2	NFGSYVTH	[iTRAQ_N1	2 61-71	6,131	524,276 2012_02_2 Nuclei_frac
Q96FJ2	NFGSYVTH	[iTRAQ_N1	2 61-71	5,643	524,274 2012_02_2 Nuclei_frac
Q96FJ2	YNPTWHCI	[iTRAQ_N1	2 50-60	6,17	516,263 2012_02_2 Nuclei_frac
	FYFHLGDA	[iTRAQ_N1	2 527-537	4,809	515,585 2012_02_2 Nuclei_frac
	LIFIVDVW	[iTRAQ_N1	1 736-752	7,486	745,752 2012_02_2 Nuclei_frac
Q9Y3U8	EVCGFAPY	[iTRAQ_N1	2 45-54	6,473	686,328 2012_02_2 Nuclei_frac
Q9Y3U8	EVCGFAPY	[iTRAQ_N1	2 45-54	5,878	686,329 2012_02_2 Nuclei_frac
Q9Y3U8	YPMAGVGL	[iTRAQ_N1	3 4-12	5,761	648,864 2012_02_2 Nuclei_frac
Q8TAQ2	KYIQAEPP	[iTRAQ_N1	3 37-47	5,139	574,344 2012_02_2 Nuclei_frac
Q8TAQ2	TQDECILHI	[iTRAQ_N1	2 662-672	7,091	525,94 2012_02_2 Nuclei_frac
	LDDTVHVN	[iTRAQ_N1	1 212-225	5,753	546,311 2012_02_2 Nuclei_frac
	SGAYLIPL	[iTRAQ_N1	1 147-157	6,469	688,409 2012_02_2 Nuclei_frac
	SGAYLIPL	[iTRAQ_N1	1 147-157	6,368	688,409 2012_02_2 Nuclei_frac
P16949_CHDLSLEEIQK	[iTRAQ_N1	2 44-52	6,154	681,89	2012_02_2 Nuclei_frac
P16949_CHDLSLEEIQK	[iTRAQ_N1	2 44-52	5,602	454,93	2012_02_2 Nuclei_frac
P16949_CHDLSLEEIQK	[iTRAQ_N1	3 44-53	6,068	545,664	2012_02_2 Nuclei_frac
P36957	GLVVPVIR	[iTRAQ_N1	1 259-266	5,003	498,838 2012_02_2 Nuclei_frac
P36957	TPAFAESV	[iTRAQ_N1	1 8-21	7,215	811,911 2012_02_2 Nuclei_frac
Q02880	LLFPAVDD	[iTRAQ_N1	2 832-843	4,89	823,49 2012_02_2 Nuclei_frac
Q02880	YGVFPLR	[iTRAQ_N1	1 497-503	7,298	498,295 2012_02_2 Nuclei_frac
P42892_ISCALNFGGIG	[iTRAQ_N1	1 579-602	4,971	664,098	2012_02_2 Nuclei_frac
P42892_ISCDNFQDTLC	[iTRAQ_N1	1 202-216	7,215	650,997	2012_02_2 Nuclei_frac
P05161	LAVHPSGV	[iTRAQ_N1	1 44-56	5,918	502,955 2012_02_2 Nuclei_frac
P05161	LTQTVAH	[iTRAQ_N1	2 99-107	6,261	433,606 2012_02_2 Nuclei_frac
P05161	LTQTVAH	[iTRAQ_N1	2 99-107	6,125	433,606 2012_02_2 Nuclei_frac
	DGIILCELIN	[iTRAQ_N1	3 54-64	6,254	788,456 2012_02_2 Nuclei_frac
	DGIILCELIN	[iTRAQ_N1	3 54-64	6,237	788,454 2012_02_2 Nuclei_frac
	DGIILCELIN	[iTRAQ_N1	3 54-64	5,545	525,972 2012_02_2 Nuclei_frac
	VNESSLN	[iTRAQ_N1	2 73-91	5,914	830,782 2012_02_2 Nuclei_frac
	VNESSLN	[iTRAQ_N1	2 73-91	4,844	830,782 2012_02_2 Nuclei_frac

P49821_ISC AAYIYIR [iTRAQ_N1	1	133-139	5,355	507,299	2012_02_2	Nuclei_frac
P49821_ISC IFTNLYGR [iTRAQ_N1	1	21-28	6,744	564,319	2012_02_2	Nuclei_frac
P25786_ISC FVFDRPLP' [iTRAQ_N1	1	97-107	5,323	492,953	2012_02_2	Nuclei_frac
P25786_ISC NVSIGIVGK [iTRAQ_N1	2	209-217	6,774	587,874	2012_02_2	Nuclei_frac
FQSIVIGCA [iTRAQ_N1	3	155-168	5,299	632,677	2012_02_2	Nuclei_frac
LLESLDQL [iTRAQ_N1	1	28-38	6,787	736,924	2012_02_2	Nuclei_frac
LLVATSVV [iTRAQ_N1	1	672-681	5,969	572,862	2012_02_2	Nuclei_frac
VVTVVTTI [iTRAQ_N1	3	264-272	6,078	469,65	2012_02_2	Nuclei_frac
VVTVVTTI [iTRAQ_N1	3	264-272	4,882	469,65	2012_02_2	Nuclei_frac
ILLSWVR [iTRAQ_N1	1	155-161	5,851	515,83	2012_02_2	Nuclei_frac
QLGLLLHD [iTRAQ_N1	1	2990-3003	6,19	577,685	2012_02_2	Nuclei_frac
AGLVELLL [iTRAQ_N1	1	25-33	5,631	564,368	2012_02_2	Nuclei_frac
AGLVELLL [iTRAQ_N1	1	25-33	5,621	564,367	2012_02_2	Nuclei_frac
ILVQGCHA [iTRAQ_N1	3	431-444	6,379	604,353	2012_02_2	Nuclei_frac
O60264,P2: LLNILMQLF [iTRAQ_N1	2	449-457	5,578	637,395	2012_02_2	Nuclei_frac
O60264,P2: LRLDSIVIQ [iTRAQ_N1	1	628-639	6,421	514,647	2012_02_2	Nuclei_frac
Q8WUJ3 IFQVVPIPV [iTRAQ_N1	2	1317-1327	6,017	763,997	2012_02_2	Nuclei_frac
Q8WUJ3 VGLCYPR [iTRAQ_N1	2	1050-1056	5,878	504,774	2012_02_2	Nuclei_frac
Q9H3N1 RPQYPYP' [iTRAQ_N1	2	187-196	5,187	507,621	2012_02_2	Nuclei_frac
Q9H3N1 VDVTEQP' [iTRAQ_N1	1	57-68	6,682	701,379	2012_02_2	Nuclei_frac
FLILPDMK [iTRAQ_N1	3	70-78	5,276	697,423	2012_02_2	Nuclei_frac
FLILPDMK [iTRAQ_N1	3	70-78	4,842	465,285	2012_02_2	Nuclei_frac
VAQLEQV' [iTRAQ_N1	1	55-64	6,583	681,898	2012_02_2	Nuclei_frac
IVLQIDNAF [iTRAQ_N1	1	151-159	5,333	593,361	2012_02_2	Nuclei_frac
LASYLDKV [iTRAQ_N1	2	91-99	6,521	451,61	2012_02_2	Nuclei_frac
LASYLDKV [iTRAQ_N1	2	91-99	5,626	676,913	2012_02_2	Nuclei_frac
P13473,P1: GILTVDELI [iTRAQ_N1	1	105-116	6,182	728,946	2012_02_2	Nuclei_frac
P13473,P1: YLDFVFAV [iTRAQ_N1	2	253-261	5,633	695,405	2012_02_2	Nuclei_frac
Q99733 KYAALYQF [iTRAQ_N1	3	93-104	5,839	630,37	2012_02_2	Nuclei_frac
Q99733 VLAALQEF [iTRAQ_N1	1	36-43	5,964	522,323	2012_02_2	Nuclei_frac
DYLHLPPEI [iTRAQ_N1	1	81-95	6,16	626,693	2012_02_2	Nuclei_frac
IAIYELLFK [iTRAQ_N1	2	9-17	5,629	699,441	2012_02_2	Nuclei_frac
IAIYELLFK [iTRAQ_N1	2	9-17	5,58	699,438	2012_02_2	Nuclei_frac
IAIYELLFK [iTRAQ_N1	2	9-17	5,104	699,438	2012_02_2	Nuclei_frac
P68871_CH LHVDPENF [iTRAQ_N1	1	96-104	5,197	424,228	2012_02_2	Nuclei_frac
P68871_CH LLVVYPW' [iTRAQ_N1	1	31-40	6,574	709,919	2012_02_2	Nuclei_frac

	GSPHYFSP [iTRAQ_N1	1 210-221	5,719	533,601	2012_02_2 Nuclei_frac
	IYVGNLPT [iTRAQ_N1	1 16-26	6,027	695,896	2012_02_2 Nuclei_frac
	IYVGNLPT [iTRAQ_N1	1 16-26	5,231	695,896	2012_02_2 Nuclei_frac
	ILSFVYPIR [iTRAQ_N1	1 409-417	6,935	626,38	2012_02_2 Nuclei_frac
	RFDGYLNQ [iTRAQ_N1	2 459-471	4,793	595,646	2012_02_2 Nuclei_frac
P17655	RPTEICADF [iTRAQ_N1	2 58-75	6,101	716,045	2012_02_2 Nuclei_frac
P17655	SDTFINLR [iTRAQ_N1	1 443-450	5,537	555,31	2012_02_2 Nuclei_frac
P23526	IILLAEGR [iTRAQ_N1	1 335-342	6,654	514,833	2012_02_2 Nuclei_frac
P23526	YPQLLPGR [iTRAQ_N1	1 142-150	4,891	600,865	2012_02_2 Nuclei_frac
P61353_CH	VVLVLAGE [iTRAQ_N1	1 10-17	5,284	485,831	2012_02_2 Nuclei_frac
P61353_CH	YSVDIPLD [iTRAQ_N1	2 85-93	6,256	669,385	2012_02_2 Nuclei_frac
P48735	DLAGCIHG [iTRAQ_N1	3 375-387	4,997	557,973	2012_02_2 Nuclei_frac
P48735	NILGGTVFI [iTRAQ_N1	1 102-110	6,526	560,833	2012_02_2 Nuclei_frac
Q8TCS8	ALYPVIPR [iTRAQ_N1	1 412-419	4,834	536,837	2012_02_2 Nuclei_frac
Q8TCS8	YTQQIIQGI [iTRAQ_N1	2 206-219	6,68	650,054	2012_02_2 Nuclei_frac
Q08945	LFDFVNAK [iTRAQ_N1	2 413-420	5,147	621,363	2012_02_2 Nuclei_frac
Q08945	SDHPGISIT [iTRAQ_N1	2 566-578	6,357	553,308	2012_02_2 Nuclei_frac
O43854_IS	DFGHVQF [iTRAQ_N1	2 382-393	5,679	557,962	2012_02_2 Nuclei_frac
O43854_IS	DFGHVQF [iTRAQ_N1	2 382-393	4,934	557,962	2012_02_2 Nuclei_frac
O43854_IS	LYPQVCR [iTRAQ_N1	2 280-286	5,715	540,292	2012_02_2 Nuclei_frac
O00410,O0	ITFLLQAIR [iTRAQ_N1	1 41-49	6,597	609,889	2012_02_2 Nuclei_frac
O00410,O0	QMAAVLLI [iTRAQ_N1	2 59-66	4,774	531,315	2012_02_2 Nuclei_frac
Q12841	IQVDYDGH [iTRAQ_N1	3 70-79	6,29	508,259	2012_02_2 Nuclei_frac
Q12841	LSFQEFLK [iTRAQ_N1	2 193-200	5,047	650,383	2012_02_2 Nuclei_frac
Q00325_IS	FGFYEVFK [iTRAQ_N1	2 89-96	4,818	662,862	2012_02_2 Nuclei_frac
Q00325_IS	IQTQPGYA [iTRAQ_N1	1 141-152	6,48	502,611	2012_02_2 Nuclei_frac
Q00325_IS	IQTQPGYA [iTRAQ_N1	1 141-152	6,168	753,414	2012_02_2 Nuclei_frac
	LLTVNPEH [iTRAQ_N1	1 332-340	4,97	408,24	2012_02_2 Nuclei_frac
	RMGSSMS [iTRAQ_N1	1 67-78	6,323	685,342	2012_02_2 Nuclei_frac
	KVESLWPI [iTRAQ_N1	2 42-51	6,435	521,648	2012_02_2 Nuclei_frac
	YIFDLFYK [iTRAQ_N1	2 59-66	4,848	698,893	2012_02_2 Nuclei_frac
P20908	TGPIGPQG [iTRAQ_N1	2 1385-1403	5,225	687,388	2012_02_2 Nuclei_frac
P20908	VLDFHNLP [iTRAQ_N1	2 8-20	5,935	586,336	2012_02_2 Nuclei_frac
	ASSVTTFT [iTRAQ_N1	2 113-128	6,017	623,635	2012_02_2 Nuclei_frac
	TVYFAEK [iTRAQ_N1	2 11-17	5,032	573,327	2012_02_2 Nuclei_frac
Q9BVK6	DKLSELQL [iTRAQ_N1	2 124-132	5,618	463,948	2012_02_2 Nuclei_frac

Q9BVK6	DKLSELQL [iTRAQ_N1	2 124-132	5,598	463,949	2012_02_2	Nuclei_frac
Q9BVK6	DKLSELQL [iTRAQ_N1	2 124-132	5,252	463,948	2012_02_2	Nuclei_frac
Q9BVK6	DKLSELQL [iTRAQ_N1	2 124-132	5,162	463,949	2012_02_2	Nuclei_frac
Q9BVK6	QLVEQVEC [iTRAQ_N1	2 135-145	5,373	543,987	2012_02_2	Nuclei_frac
	AILQATLRI [iTRAQ_N1	2 36-46	5,541	520,653	2012_02_2	Nuclei_frac
	AILQATLRI [iTRAQ_N1	2 36-46	5,381	520,652	2012_02_2	Nuclei_frac
	IGCIITAR [iTRAQ_N1	2 159-166	5,445	524,308	2012_02_2	Nuclei_frac
P07942	CHIPSWTGAG [iTRAQ_N1	1 580-590	5,641	667,872	2012_02_2	Nuclei_frac
P07942	CHISGVIGPYR [iTRAQ_N1	1 1209-1217	5,338	553,327	2012_02_2	Nuclei_frac
Q07666	ILGPQGNTI [iTRAQ_N1	2 151-160	5,415	664,912	2012_02_2	Nuclei_frac
Q07666	KDDEENYL [iTRAQ_N1	3 114-127	5,445	547,037	2012_02_2	Nuclei_frac
P05783	IVLQIDNAF [iTRAQ_N1	1 149-157	5,333	593,361	2012_02_2	Nuclei_frac
P05783	LASYLDR [iTRAQ_N1	1 90-96	5,526	491,279	2012_02_2	Nuclei_frac
P37235	LRPEVLQD [iTRAQ_N1	1 7-16	5,131	461,614	2012_02_2	Nuclei_frac
P37235	LSLEEFIR [iTRAQ_N1	1 163-170	5,68	575,834	2012_02_2	Nuclei_frac
P37235	LSLEEFIR [iTRAQ_N1	1 163-170	5,276	575,833	2012_02_2	Nuclei_frac
P55265	ISC FQYCVAVC [iTRAQ_N1	4 351-371	4,766	676,867	2012_02_2	Nuclei_frac
P55265	ISC LVDQSGPF [iTRAQ_N1	2 451-462	6,043	531,295	2012_02_2	Nuclei_frac
Q9Y2H6	FVSLYR [iTRAQ_N1	1 941-946	4,942	464,773	2012_02_2	Nuclei_frac
Q9Y2H6	LNPFCFYR [iTRAQ_N1	2 572-579	5,812	585,795	2012_02_2	Nuclei_frac
	RPLFLAPDI [iTRAQ_N1	1 99-109	5,33	497,614	2012_02_2	Nuclei_frac
	VELSDVQI [iTRAQ_N1	2 23-43	5,349	661,117	2012_02_2	Nuclei_frac
Q9NSK0	NLGALYR [iTRAQ_N1	1 487-493	5,233	475,781	2012_02_2	Nuclei_frac
Q9NSK0	QGKYAEAF [iTRAQ_N1	3 410-421	5,415	611,682	2012_02_2	Nuclei_frac
Q04637	ISG AALSEEEL [iTRAQ_N1	3 1039-1049	5,141	560,325	2012_02_2	Nuclei_frac
Q04637	ISG GVIDLIFEK [iTRAQ_N1	2 600-608	5,372	661,403	2012_02_2	Nuclei_frac
P36776	DIIALNPLY [iTRAQ_N1	1 235-244	5,019	666,396	2012_02_2	Nuclei_frac
P36776	DIIALNPLY [iTRAQ_N1	1 235-244	4,961	666,396	2012_02_2	Nuclei_frac
P36776	LGLLDNHS [iTRAQ_N1	1 378-392	5,457	615,991	2012_02_2	Nuclei_frac
Q13561,Q1	LTPVLLAK [iTRAQ_N1	2 132-139	4,912	571,892	2012_02_2	Nuclei_frac
Q13561,Q1	QQLVASHI [iTRAQ_N1	2 146-155	5,536	480,953	2012_02_2	Nuclei_frac
P11413,P11	IFGPIWNR [iTRAQ_N1	1 219-226	5,373	573,831	2012_02_2	Nuclei_frac
P11413,P11	LQFHDVAC [iTRAQ_N1	3 370-385	5,037	558,537	2012_02_2	Nuclei_frac
P11413,P11	LQFHDVAC [iTRAQ_N1	3 370-385	5,022	558,537	2012_02_2	Nuclei_frac
Q9Y6M1	ENSGAAEK [iTRAQ_N1	3 233-256	5,342	700,852	2012_02_2	Nuclei_frac
Q9Y6M1	KLPLAGQV [iTRAQ_N1	3 27-37	5,036	538,034	2012_02_2	Nuclei_frac
	LKDIVSLVI [iTRAQ_N1	2 221-230	5,536	476,645	2012_02_2	Nuclei_frac

	VLSEAAIS	[iTRAQ_N1	3	661-679	4,803	616,618	2012_02_2	Nuclei_frac
	IVVLLQR	[iTRAQ_N1	1	110-116	4,739	492,838	2012_02_2	Nuclei_frac
	LEGFHTQIS	[iTRAQ_N1	2	167-176	5,513	483,275	2012_02_2	Nuclei_frac
	LEGFHTQIS	[iTRAQ_N1	2	167-176	4,765	483,276	2012_02_2	Nuclei_frac
Q13557,Q1	DLKPENLL	[iTRAQ_N1	3	135-146	5,083	591,701	2012_02_2	Nuclei_frac
Q13557,Q1	FYFENALS	[iTRAQ_N1	2	396-404	5,158	703,893	2012_02_2	Nuclei_frac
Q9BS26	ALADYIR	[iTRAQ_N1	1	102-108	5,208	483,281	2012_02_2	Nuclei_frac
Q9BS26	QFVFDLHS	[iTRAQ_N1	2	317-326	4,927	489,273	2012_02_2	Nuclei_frac
Q96AC1	INQGWLDS	[iTRAQ_N1	1	248-257	5,318	660,349	2012_02_2	Nuclei_frac
Q96AC1	TSTILGDIT	[iTRAQ_N1	2	362-380	4,783	780,106	2012_02_2	Nuclei_frac
O15042	AAAEIYEEF	[iTRAQ_N1	3	112-133	4,79	698,619	2012_02_2	Nuclei_frac
O15042	KPGQSFQE	[iTRAQ_N1	2	865-878	5,293	506,015	2012_02_2	Nuclei_frac
	FLELLR	[iTRAQ_N1	1	241-246	5,1	467,797	2012_02_2	Nuclei_frac
	LTNQELLR	[iTRAQ_N1	1	445-452	4,93	565,837	2012_02_2	Nuclei_frac
P56385	VPPVQVSF	[iTRAQ_N1	2	1-11	4,966	488,985	2012_02_2	Nuclei_frac
P56385	YNYLKPR	[iTRAQ_N1	2	29-35	4,997	621,368	2012_02_2	Nuclei_frac
	KAAMAEPI	[iTRAQ_N1	3	235-244	5,231	731,922	2012_02_2	Nuclei_frac
	MWTFGLIA	[iTRAQ_N1	3	1-16	4,72	817,103	2012_02_2	Nuclei_frac
P78357	LHGISGWS	[iTRAQ_N1	1	36-45	4,734	418,567	2012_02_2	Nuclei_frac
P78357	VSYPLLIR	[iTRAQ_N1	1	451-458	5,216	552,848	2012_02_2	Nuclei_frac
Q16851_C1	EFPTVPLV	[iTRAQ_N1	2	412-420	4,927	659,403	2012_02_2	Nuclei_frac
Q16851_C1	IFNTNNLW	[iTRAQ_N1	2	315-329	5,011	664,722	2012_02_2	Nuclei_frac
	KIASFPTA	[iTRAQ_N1	3	340-348	4,818	465,629	2012_02_2	Nuclei_frac
	YIEIFPSRR	[iTRAQ_N1	1	318-326	5,117	442,255	2012_02_2	Nuclei_frac
	EADGDVVI	[iTRAQ_N1	2	473-482	4,802	682,361	2012_02_2	Nuclei_frac
	RTPNETTS	[iTRAQ_N1	2	484-496	5,002	587,336	2012_02_2	Nuclei_frac
Q07157	ISKPGAVS	[iTRAQ_N1	3	346-357	4,806	539,342	2012_02_2	Nuclei_frac
Q07157	LGSWLAIR	[iTRAQ_N1	1	554-561	4,92	530,323	2012_02_2	Nuclei_frac
O60762	FIPEFIR	[iTRAQ_N1	1	126-132	4,912	533,315	2012_02_2	Nuclei_frac
O60762	GLLTLFAT	[iTRAQ_N1	1	251-259	4,8	540,826	2012_02_2	Nuclei_frac
	ILLGGYQSF	[iTRAQ_N1	1	719-727	4,77	575,84	2012_02_2	Nuclei_frac
	LGLLGLPA	[iTRAQ_N1	2	478-487	4,883	633,926	2012_02_2	Nuclei_frac

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1	[P21333_	141166,14	250641,03	63251,168	26352,684	146024,2	259683,28	52206,213
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1	[P21333_	98021,313	215620,5	63084,668	17680,889	100513,69	224608,16	54456,771
1	[P21333_	154338,91	191368,06	49713,484	27015,312	161413,46	195263,61	41161,922
1	[P21333_	160603,76	190622,7	75536,511	30501,894	168163,68	193223,5	68947,946

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1	[P21333_	1174510	1236585,3	730655,5	480558,44	1233292,6	1237273	695101,65
1	[P21333_	242870,66	176686,15	102244,29	42111,326	256692,23	172070,51	98243,313
1	[P21333_	610291,99	714789,38	399293,9	251368,63	639297,04	720296,4	377946,71
1	[P21333_	819903,26	1388157,5	425226,91	179658,85	849608,24	1433393,3	368629,81
1	[P21333_	895444,18	1298456	438498,22	175088,3	932543,7	1331267,7	388685,56
1	[P21333_	309464,72	661502,5	150678,38	78888,276	317715,31	689913,56	119740,01
1	[P21333_	345565,53	250464,76	84512,338	36488,362	365212,19	245793,82	75024,175
1	[P21333_	11672,703	13461,533	3237,2367	1516,0718	12229,152	13691,955	2632,691
1	[P21333_	172581,05	251444,34	82251,238	33103,926	179704,31	257936,67	72426,086
1	[P21333_	25437,868	35424,484	9659,0681	4010,1732	26521,405	36329,974	8150,8027
1	[P21333_	39036,354	48049,023	11961,222	5114,0079	40832,887	49025,524	9844,9205
1	[P21333_	541072,4	717395,64	179227,44	73675,397	564878,14	734612,37	147737,9
1	[P21333_	323742,09	610526,5	193198,49	59787,764	334146,98	632563,77	169576,74
1	[P21333_	283253,64	550764,75	188260,46	60016,735	292013,17	570753,43	167790,7
1	[P21333_	175268,26	271410,47	118477,17	22928,606	182180,21	278154,41	110776,85
1	[P21333_	447927,76	1188622,3	295308,67	78602,762	454954,49	1245746,8	244247,29
1	[P21333_	651019,25	1669316,3	385978,43	93441,199	662455,02	1749074,2	312735,6
1	[P21333_	226527,97	571713,25	151383,61	32181,011	230714,51	598180,08	127827,12
1	[P21333_	170738,1	341961,91	109865,85	31549,803	175801,55	354925,54	96835,623
1	[P21333_	428560,18	1078043,6	280601,16	69562,484	436553,23	1128019,9	235414,05
1	[P21333_	40085,275	79610,023	16227,475	4147,2879	41282,389	82908,921	12586,695
1	[P21333_	138331,25	287432,63	74298,554	15234,528	142201,28	299241,44	62386,112
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1	[P21333_	30952,187	46822,016	10951,608	3957,0282	32190,221	48247,362	8867,4851
1	[P21333_	734300,95	1105563,3	459834,78	232998,2	763912,39	1132505,9	420660,03
1	[P21333_	144246,89	235229,88	66435,231	31888,541	149660,67	242739,75	56341,418
1	[P21333_	1382611,6	1671272,4	431028,86	189925,75	1446903,3	1703174,3	358128,82
1	[P21333_	487749,68	574766,69	134805,19	59164,467	510737,3	585391,77	108945,69
1	[P21333_	403825,25	517736,96	155462,09	69706,287	421986,32	528470,04	134124,83
1	[P21333_	224312,95	329474,38	80912,787	30362,354	233497,63	338965,5	66454,91
1	[P21333_	99538,004	133322,56	33787,14	10855,114	103889	136570,71	28094,179
1	[P21333_	199222,65	289347,91	65303,947	27540,602	207446,07	297727,94	52113,289
1	[P21333_	92607,69	131354,33	32541,349	13464,712	96499,33	134926,98	26745,71
1	[P21333_	23240,046	32498,934	7288,2731	2758,3894	24226,077	33386,608	5818,6762
1	[P21333_	64543,315	97661,188	22784,626	8843,0306	67124,359	100637,24	18407,48

1	[Q15149]	317632,63	189442,04	119806,83	80190,602	336594,1	180527,6	114898,29
1	[Q15149]	1446584,1	495137,22	378808,56	247330,06	1540730	430477,16	370456,77
1	[Q15149]	285115,66	126365,14	87868,565	57350,03	303061,75	115499,29	85165,236
1	[Q15149]	359487,13	209129,59	103956,25	57431,791	381040,23	199636,26	97633,897
1	[Q15149]	146640,62	185363,75	50080,336	21271,598	153288,08	189255,36	42157,892
1	[Q15149]	73139,921	96264,875	24753,175	12450,873	76373,456	98518,815	20473,93
1	[Q15149]	40953,606	41806,805	15440,748	11846,938	43024,998	42050,003	13691,612
1	[Q15149]	19999,737	29128,73	6029,8029	1862,5203	20823,193	29993,367	4697,6496
1	[Q15149]	30198,81	60265,496	14791,594	3901,5636	31096,091	62690,99	12202,384
1	[Q15149]	473019,88	250672,91	163403,25	89509,485	501923,32	235359,28	158086,96
1	[Q15149]	141502,86	91484,017	43256,944	32787,99	149791,26	88407,707	39961,525
1	[Q15149]	60951,26	107429,14	20677,182	6651,9168	63061,542	111484	15630,921
1	[Q15149]	186031,38	317964,56	71340,133	28317,561	192690,68	329280,73	56848,902
1	[Q15149]	441858,63	297007,93	158113,04	72292,432	467511,49	287556,67	150272,54
1	[Q15149]	245722,88	345815,66	115929,23	44584,589	256126,24	354120,67	102692,94

1 [Q15149]	17609,673	31049,855	7422,4413	1918,2753	18220,037	32175,377	6079,4548
1 [Q15149]	106826,19	203875,14	52936,62	16106,054	110200,63	211690,2	44289,706
1 [Q15149]	415193,65	655855,56	173242,86	66847,693	431220,77	676349,65	145113,54
1 [Q15149]	319777,06	151749,76	95500,048	66830,289	339687,58	140465,06	91510,722
1 [Q15149]	161203,52	83060,838	50796,844	36912,569	171101,39	77812,287	48461,786
1 [Q15149]	83520,844	48814,348	27722,642	17780,532	88525,764	46512,118	26333,409
1 [Q15149]	83991,109	56927,55	32547,497	23440,693	88858,816	55089,994	30809,155
1 [Q15149]	45152,518	88637,016	17849,32	8715,5608	46522,935	92284,705	13602,298
1 [Q15149]	42535,985	77154,102	30648,948	5646,8549	43972,249	79633,186	28245,579
1 [Q15149]	88251,156	72207,299	34363,385	20482,58	93099,673	71262,775	31979,765
1 [Q15149]	157761,81	87286,02	51499,597	30244,143	167320,69	82570,735	49247,933
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1 [Q15149]	91738,299	138152,47	31202,857	8548,3847	95420,236	142367,23	25100,328
1 [Q15149]	85711,184	103977,78	24281,507	6101,9751	89687,235	106063,05	19789,905
1 [Q15149]	77524,121	100158,95	30138,396	10022,999	80994,317	102270,59	26164,127
1 [Q15149]	43182,397	56129,562	13814,139	4521,8326	45106,164	57429,093	11388,512
1 [Q15149]	26113,218	45280,016	9466,0633	2175,5998	27033,733	46937,681	7426,7007
1 [Q15149]	41304,838	72878,188	17287,496	3856,7505	42735,379	75525,886	14152,451
1 [Q15149]	110360,78	189463,75	45785,28	16983,797	114295,62	196131,6	37406,318
1 [Q15149]	211115,77	129670,48	67997,916	46435,245	223630,41	124421,91	63876,628
1 [Q15149]	234320,61	310499,63	82862,253	24867,5	244637,39	317769,63	69957,975
1 [Q15149]	188824,24	193956,25	56088,607	14935,974	198339,47	195654,48	48458,532
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1 [Q15149]	288930,11	375675	68174,346	23729,702	301783,78	385164,13	50284,625
1 [Q15149]	355692,63	445545,36	83072,479	26620,641	371879,64	455897,89	62116,455
1 [Q15149]	27121,133	14278,81	9595,6795	5211,7259	28780,506	13385,94	9311,1871
1 [Q15149]	243806,63	83406,435	43960,457	14832,832	259662,17	73143,823	42127,8
1 [Q15149]	29709,105	63917,113	14243,754	5066,0276	30492,197	66684,242	11339,194
1 [Q15149]	8155,9698	11582,484	3855,738	1109,0892	8499,0426	11866,157	3426,7159
1 [Q15149]	11832,878	23865,646	5354,2911	1006,4423	12178,774	24850,387	4311,8535
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1 [Q15149]	4514,1089	8308,0254	1936,356	398,43968	4663,1044	8623,3537	1577,7255
1 [Q15149]	58197,354	107046,59	24203,28	8520,6968	60119,104	111132,24	19376,891
1 [Q15149]	918385,88	838529,53	357652,36	149447,84	966971,17	835660,94	330333,17
1 [Q15149]	1854289,5	1032545,8	690381,2	295742,14	1966555	974882,77	672877,35
1 [Q15149]	243600,11	172336,92	87318,11	41645,161	257558,21	167810,2	82410,757
1 [Q15149]	43934,14	74632,5	15490,418	6017,3649	45515,838	77312,031	12016,512
1 [Q15149]	17871,875	38426,555	6263,9552	2868,4187	18341,974	40163,925	4342,0332
1 [Q15149]	51068,943	82645,297	17719,648	4641,8412	52995,562	85439,801	14008,514
1 [Q15149]	311674,49	480485,5	133356,72	38932,921	323962,28	494811,37	113705,95
1 [Q15149]	226648,17	111726,57	55826,464	26269,981	240662,98	104442,25	52710,761
1 [Q15149]	158697,64	97689,778	40904,173	12159,064	168093,9	94087,643	37959,879
1 [Q15149]	196959,5	179763,42	95319,037	36361,694	207392,71	178540,16	90763,098
1 [Q15149]	597685,25	348082,01	159908,09	87081,542	633503,05	332746,21	148704,67
1 [Q15149]	695264	425041,46	258448,05	127042,55	736543,59	406472,02	248865,13
1 [Q15149]	216249,14	122437,45	80358,68	37423,123	229298,14	115880,22	78056,377
1 [Q15149]	164009,16	113358,76	57256,181	31521,156	173463,13	110147,58	53841,213
1 [Q15149]	1680350,5	900671,84	528887,94	431674,64	1782774,3	848784,08	500368,76
1 [Q15149]	539893,81	391261,02	189811,55	158585,05	570626,68	382108,6	175217,59
1 [Q15149]	142910,83	212666,5	50107,842	20261,917	148702,28	218981,07	40575,406
1 [Q15149]	62590,316	56016,788	25116,459	9620,8547	65926,305	55706,54	23406,448
1 [Q15149]	50031,41	25940,239	12790,245	10076,184	53097,954	24420,343	11878,02

1 [Q15149]	422594,2	260235,97	135611,94	71035,798	447630,31	249795,13	128226,87
1 [Q15149]	209420,06	162066,17	61892,213	35482,366	221112,37	159715,58	55795,618
1 [Q15149]	62286,304	99734,813	19208,871	5028,0967	64657,409	103135,7	14582,552
1 [Q15149]	309228,09	383852,78	103693,64	29726,309	323395,82	391554,71	87912,314
1 [Q15149]	125012,78	97649,434	41818,819	17800,902	131976,2	96160,035	38659,181
1 [Q15149]	297692,94	181153,09	89683,034	54515,883	315372,2	173815	83952,35
1 [Q15149]	54359,587	81524,117	21321,63	4627,463	56550,414	83902,593	17970,797
1 [Q15149]	58003,897	64964,898	26472,854	10405,858	60817,096	65619,467	24289,786
1 [Q15149]	15386,284	32125,41	7797,0207	1936,7033	15813,11	33466,475	6414,9665
1 [Q15149]	28676,17	55196,816	13425,67	2378,4347	29571,424	57357,245	11097,478
1 [Q15149]	93320,054	138247,59	35681,664	12240,751	97117,126	142224,91	29773,564
1 [Q15149]	38815,752	63592,652	30575,958	10050,38	40274,423	65225,776	28791,417
1 [Q15149]	236839,75	386965,25	80809,024	27305,295	245694,65	400265,95	63016,952
1 [Q15149]	208757,51	329490,44	116702,9	35269,188	216840,76	338814,13	104864,95
1 [Q15149]	209142,34	332108,16	73483,759	21854,35	217169,36	343014,93	58619,77
1 [Q15149]	283629,57	419200,06	121530,73	36546,516	295199,55	430785,84	104705,03
1 [Q15149]	464710,06	236147,75	163302,29	106864,55	493324,88	220206,87	158095,79
1 [Q15149]	69137,539	59581,805	29339,343	15207,03	72872,786	59004,609	27518,898
1 [Q15149]	108660,46	143976,94	46999,582	15470,518	113450,33	147070,39	41530,076

2 [P35579,	217969,12	907147,38	127837,48	17482,544	214316,42	961783,34	82747,574
2 [P35579,	51367,56	151580,45	32180,589	20374,203	51844,188	159411,52	24777,449
2 [P35579,	42137,501	154893,87	23907,736	3661,8909	41870,671	163842,42	16352,31
1 [P35579]	214180,4	252990,19	66190,213	58441,384	224266,21	257484,15	53956,412
1 [P35579]	565294,15	1399318,6	262353,95	58660,384	576255,29	1466909,7	196952,69
1 [P35579]	114950,16	140059,84	34808,124	28567,94	120270,8	142837,17	28047,052
1 [P35579]	155494,34	220815,34	56011,072	39559,723	162023,82	226794,3	45642,233
1 [P35579]	121230,56	173807,17	55298,006	23404,895	126293,35	178222,2	48362,541
1 [P35579]	454758,92	618434,88	221337,87	103884,47	474479,96	631862,41	197764,76
1 [P35579]	91798,804	116481,71	44310,954	20866,957	95959,029	118534,85	40032,666
1 [P35579]	882694,1	1181486,4	339277,03	243638,39	921320,64	1208972,7	285647,52
1 [P35579]	129940,16	175307,75	50879,169	28889,106	135597,25	179432,91	43276,293
1 [P35579]	174698,06	218956,39	58912,829	38745,54	182657,13	223469,72	48949,932
1 [P35579]	311069,38	301526,15	97664,588	70252,005	327134,6	302721,67	84633,892
1 [P35579]	100956,33	120466,41	44730,983	27528,451	105692,97	122243,54	39970,891
1 [P35579]	557,28085	571,104	173,3084	120,11319	585,39645	575,77458	148,21026
1 [P35579]	363086,65	609352,19	156573,58	116375,95	376336,19	629990,07	127716,55
1 [P35579]	409362,87	699975,06	178052,5	139114,7	424023,66	724233,53	144514,63
4 [P35579,	29623,641	107651,21	22440,925	5349,4235	29466,369	113660,73	17534,001
4 [P35579,	137316,58	273428,63	90231,125	33820,793	141424,3	283668,09	79632,887
1 [P35579]	250046,05	320399,5	90288,779	75603,501	261291,14	327231,54	75212,237
1 [P35579]	396383,79	1529006	187983,96	58124,9	392304,62	1620146,8	108597,01
1 [P35579]	67234,84	249286,28	40644,452	8354,6394	66764,783	263655,37	28550,63
1 [P35579]	42267,166	132852,5	27732,85	8213,6648	42485,632	139904,55	21618,787
1 [P35579]	75065,938	266730,06	47019,718	11054,104	74791,185	281791,61	34274,445
1 [P35579]	62586,067	126357,91	49174,387	15469,51	64426,204	130902,91	44878,635
1 [P35579]	867979,59	899272,25	255829,39	202280,03	911551,5	907789,07	214367,83
1 [P35579]	306257,95	401741,13	127014,51	114306,74	319841,44	410327,2	108359,64
1 [P35579]	65380,739	74264,633	20867,497	17935,87	68523,616	75377,699	17360,81
4 [P35579,	208584,84	197051,83	60282,73	49456,609	219464,15	197611,54	51338,963
1 [P35579]	131259,7	158135,64	46244,635	34872,817	137378,01	160953,03	39053,991
1 [P35579]	357451,73	436600,81	146006,42	102130,21	373998,26	444101,51	127356,14

1 [P35579]	48017,733	64734,656	14170,187	9672,0836	50106,288	66405,108	11037,442
1 [P35579]	91534,657	156186,25	47757,868	15539,011	94825,129	161323,19	41583,718
1 [P35579]	40390,247	57509,008	20077,22	7679,9914	42086,627	58894,447	17927,572
1 [P35579]	165058,64	217968,33	59820,705	48680,922	172342,87	222988,9	49547,87
1 [P35579]	287406,92	393468,63	107773,47	94312,965	299793,51	403211,56	88919,922
1 [P35579]	207658,54	243474,89	64102,63	52821,641	217476,12	247688,42	52510,749
1 [P35579]	1742031,1	2153722,5	468504,92	342657,37	1821956,5	2200200,5	363347,52
1 [P35579]	1822235,3	2049831	443326,07	278769,51	1910172,5	2083684,9	345309,25
1 [P35579]	799369,88	884173,75	270109,47	179113,24	838317,28	895381,22	231602,17
1 [P35579]	161658,13	420385,84	112195,18	24551,159	164382,27	440131,32	94898,97
1 [P35579]	160634,28	422742,81	97721,938	35125,237	163224,42	443213,64	78671,444
1 [P35579]	68443,44	140863,34	37889,608	16401,495	70387,991	146563,14	31785,02
1 [P35579]	80362,66	151232,86	42615,971	21614,705	82948,84	156852,29	36053,408
1 [P35579]	19484,922	24950,876	6870,7561	3838,055	20361,453	25486,86	5772,3004
1 [P35579]	29141,247	104943,8	18469,989	3253,9504	29004,722	110895,45	13499,73
1 [P35579]	46432,298	158441,3	26031,966	3922,6767	46401	167331,75	18426,305
1 [P35579]	55618,936	148621,81	31283,889	6422,15	56465,832	155971,33	24595,818
1 [P35579]	44536,503	127233,14	28079,19	5100,8886	45039,913	133678,78	22469,893
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1 [P35579]	222307,09	281165,28	85740,316	43540,99	232387,62	286761,49	74016,587
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1 [P35579]	77752,248	116109,63	24112,799	15991,289	80892,377	119680,79	18436,634
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1 [P35579]	643233,73	726294,69	166330,85	99095,676	674222,69	738144,01	132322,17
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1 [P35579]	531733,04	556184,99	117078,32	72749,937	558286,84	563099,41	90404,274
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1 [P35579]	274332,72	354135,38	90228,72	50050,646	286608,3	362119,58	74244,273
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1 [P35579]	35266,375	105123	22316,649	6460,9101	35571,106	110575,09	17512,649
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1	[P02545_	95186,756	122413,47	54914,642	31866,685	99471,181	124384,69	50653,814
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1	[Q13813_	17424,099	30645,227	9898,1499	3642,1274	18031,333	31670,285	8702,4619
1	[Q13813_	68079,824	97536,156	51507,508	20301,079	70937,589	99348,566	48939,49
1	[Q13813_	56161,591	101029,09	29390,28	7352,0236	58068,837	104594,03	25388,883
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1	[Q13813_	383018,67	457633,63	140471,85	52688,254	400957,64	465359,89	122277,09
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1	[Q13813_	80811,772	91124,222	26871,791	13565,201	84711,511	92409,635	23035,008
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3	[P21333_	670451,51	2114357	337689,01	69301,265	673700,43	2230080,3	234760,1
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1	[O75369_	122983,41	235717,81	72910,314	28005,616	126854,27	244409,69	63440,97
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1	[O75369_	41745,444	56506,91	25740,245	13234,787	43564,913	57543,471	23865,157
2	[O75369_	142176,76	234403,41	87350,014	32644,256	147472,17	241301,14	78938,7
1	[O75369_	116676,33	224510,81	58562,684	26477,068	120322,9	233171,37	48683,581
1	[O75369_	84685,619	199186,06	34965,216	9582,8016	86549,22	208616,14	25418,656

1	[O75369_	63793,914	155799,36	37509,884	10018,064	65081,399	163002,27	30740,883
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1	[P02751_	3283,1753	8348,7734	2325,4228	805,60449	3342,5897	8733,2044	1976,0659
1	[P02751_	2881,3952	11603,35	2452,0487	699,18116	2841,9437	12269,884	1920,0722
1	[P02751_	4876,4252	24757,324	5485,2327	1291,0183	4700,5335	26252,146	4377,2731
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1	[Q07065]	704963,09	821716,75	265589,45	190621,72	738426,78	834081,12	229868,06
1	[Q07065]	87212,254	157777,06	40993,336	31925,397	90151,758	163539,38	33470,696
1	[Q07065]	587135,7	1031355,7	288180,38	229132,62	607595,52	1067286,7	239761,02
1	[Q07065]	167593,83	170464,95	51463,792	57039,842	176076,28	171792,36	43039,145
1	[Q07065]	101829,85	114550,73	35685,999	38827,037	106750,82	116094,09	30076,065
1	[Q07065]	148026,96	168158,36	66833,065	65486,908	155154,82	170050,34	59381,768
1	[Q07065]	59130,17	89406,625	25682,247	21622,393	61499,159	91975,038	21476,41
1	[Q07065]	172667,88	331561	105529,72	59922,12	178091,29	343715,48	91561,438
1	[Q07065]	2096655,9	2341855,5	541446,48	400766,71	2198214	2378473,5	428726,38
1	[Q07065]	42413,106	44435,203	13520,37	15867,469	44532,252	44859,106	11287,835
1	[Q07065]	4642865,5	4190733,5	1397209,9	1307464,6	4889259,5	4185790,8	1205450,9
1	[Q07065]	100615,87	128666,34	40168,02	30413,208	105148,82	131270,38	34423,418
1	[Q07065]	138525,76	211115,88	74982,296	46737,984	144049,54	216784,9	66379,368
1	[Q07065]	421121,54	707197,75	188142,27	177255,21	436483,26	730967,33	153344,04
1	[Q07065]	601068,68	1012459,3	275069,71	261326,21	622932,71	1046421,9	225378,13
1	[Q07065]	273043,54	292612	85246,699	71586,832	286544,26	295917,12	71653,416
1	[Q07065]	105792,58	137070,69	38443,615	25838,101	110517,99	140073,16	32258,039
1	[Q07065]	49897,918	120070,27	39955,207	11778,626	50950,273	125217,45	35445,614
1	[Q07065]	92751,611	111446,88	31304,599	14249,12	97080,491	113456,28	26580,125
1	[Q07065]	1097559,6	1253416,4	293675,92	203897,7	1150139,3	1274454,4	234077,6
1	[Q07065]	95395,439	130705,48	42229,002	52551,543	99508,554	133743,16	35563,338
1	[Q07065]	176250,06	203885,38	54171,187	69038,944	184641,84	207253,14	43436,823
1	[Q07065]	52645,076	93098,891	29818,27	8299,4204	54468,821	96238,912	26284,589
1	[Q07065]	1525280	1661946,4	518754,55	418162,91	1600137,7	1681225	443771,74
1	[Q07065]	218492,18	406731,63	141843,9	58982,593	225635,78	420811,95	126332,67
1	[Q07065]	42159,706	44659,129	11852,986	9430,9331	44254,683	45169,748	9751,1828
1	[Q07065]	70497,28	95329,406	34745,821	19324,302	73566,349	97354,26	31019,916

1 [Q07065]	1559142,9	1628030,8	507965,84	475909,87	1637169,1	1642799,6	431729,86
1 [Q07065]	51969,59	67574,586	19304,61	6092,8965	54286,051	69053,712	16569,611
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1 [Q07065]	66722,947	107432,13	29505,313	19800,859	69255,895	110836,51	24603,964
1 [Q07065]	86240,997	131498,38	37819,441	20643,251	89672,818	135318,34	32117,478
1 [Q07065]	85824,699	135534,86	35739,19	20709,363	89138,385	139772,04	29623,87
1 [Q07065]	171478,75	256360,97	85592,526	31216,152	178418,89	263208,52	75816,508
1 [Q07065]	52953,582	59346,945	19568,875	16379,936	55518,019	60098,155	16910,03
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1 [Q07065]	4084,8462	6909,1494	1629,4199	358,44531	4232,6727	7149,7113	1331,9947
1 [Q07065]	59187,8	95929,828	24669,273	5971,3333	61420,24	99046,449	20663,419
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1 [Q07065]	693361,32	711948,19	226134,1	186749,72	728319,16	717537,98	194052,3
1 [Q07065]	428018,84	439326,31	127095,67	113297,17	449594,19	443168,32	106390,07
1 [Q07065]	628282,82	774354,38	208143,66	105362,23	657185,87	789650,58	174273,16
1 [Q07065]	1046053,6	1532263,8	357252,53	187773,89	1088962,1	1576848,9	286491
1 [Q07065]	667615,49	1105995,3	203450,2	90749,513	692233,88	1145497	149842,85
1 [Q07065]	252065,72	279180,19	100140,76	83979,797	264348,53	282264,97	87983,29
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1 [Q07065]	66093,452	70188,648	19758,111	14459,004	69374,692	70965,11	16560,304
1 [Q07065]	2776,2512	6455,4805	1005,5373	906,91053	2838,8516	6763,3548	660,28304
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2	[P04264_	80833,711	52509,776	18867,247	8791,7862	85559,389	50959,65	16932,265
2	[P04264_	80428,813	53323,738	17930,995	8710,1179	85107,142	51894,904	15875,09
2	[P04264_	118032,79	75229,943	24300,838	11220,21	124962,13	72955,734	21373,352
2	[P04264_	59627,684	39686,812	14022,367	6868,281	63093,225	38616,32	12529,27
2	[P04264_	469935,75	294048,86	131676,3	43034,548	497664,29	283423,76	123207,63
1	[P04264_	25167,361	15721,002	5168,5093	2590,5713	26651,72	15210,94	4554,049
1	[P04264_	110171,23	109111,49	35699,351	13029,557	115811,96	109682,2	31543,666
1	[P04264_	54462,396	58831,786	17537,051	5837,699	57145,672	59509,26	15204,109
1	[P04264_	1536,5847	904,16138	428,33494	192,1549	1628,4803	864,91261	401,71339
1	[P04264_	8889,6652	3619,1594	934,85457	1057,3838	9454,9402	3313,0196	757,53469
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1	[P04264_	97405,281	67551,859	26465,961	13683,207	103010,27	65906,238	24040,05
1	[P04264_	250375,42	245337,66	103754,46	46003,969	263265,57	245694,32	95566,535
1	[P04264_	516637,25	466652,3	189717,73	87902,33	544070,18	465006,09	173574,59
1	[P04264_	48989,922	32672,867	10219,906	8866,5988	51834,924	31841,525	8746,3928
1	[P04264_	44313,859	30885,657	11191,806	10685,345	46859,951	30177,753	9818,8239
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3	[P12814,	35879,958	83097,82	18290,581	7126,0467	36699,564	86877,535	14469,11
1	[P12814]	162284,28	501034	82265,907	21820,581	163301,95	528168,06	57826,074
1	[P12814]	79768,173	264264,72	45981,901	11332,165	79885,521	278863,17	33297,514
3	[P12814,	70833,683	217578,55	45573,3	8896,8401	71308,003	229019,48	35771,026
3	[P12814,	243074,63	730376,31	142526,67	25091,966	245042,94	768782,33	109001,46
3	[P12814,	96885,122	270347,94	60284,765	9963,8472	98117,996	283880,03	48456,456
1	[P12814]	84159,556	140126,58	31334,504	11222,158	87251,474	144978,22	24997,154
2	[P12814,	47217,03	106841,27	23338,041	5176,9998	48349,141	111636,81	18583,82
2	[P12814,	212343,31	481835,34	117259,32	22221,951	217413,52	503110,91	96824,078
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1	[P12814]	4661,6209	11313,792	1821,6707	422,77161	4756,6344	11864,178	1271,3493
1	[P12814]	29213,652	105614,38	16341,468	2361,8602	29066,587	111683,93	11199,49
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3	[P12814,	72331,712	159660,03	22532,619	2724,8735	74143,634	167112,49	14662,301
3	[P12814,	65110,074	135702,28	22249,948	6079,7586	66914,565	141705,63	15650,504
1	[P12814]	71625,599	165678,75	41461,905	11940,652	73269,365	173046,64	34338,973
1	[P12814]	48080,381	130107,37	21173,004	4674,5203	48773,701	136781,35	14862,534
1	[P12814]	23539,859	62294,824	10835,604	2169,9851	23909,788	65434,603	7873,5223
1	[P12814]	484287,61	1095527,8	221573,33	38679,068	495894,37	1145263,2	172031,98
1	[P12814]	145431,5	300519,84	76408,267	21188,558	149534,84	312857,69	63626,141
1	[P12814]	116133,57	201917,81	43726,33	22320,815	120216,7	209283,47	34208,233
1	[P12814]	36769,716	69703,055	17376,183	7365,9481	37940,769	72383,056	14282,42
1	[P12814]	36993,118	70706,789	15792,494	3465,7256	38157,751	73503,442	12680,278
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1	[P12814]	107678,1	281407,25	57154,572	14833,633	109451,33	295240,48	44213,222
2	[P12814,	291789,09	338384,06	44537,22	3934,7653	305635,28	345466,49	27874,392
1	[P12814]	55886,933	177009,75	32385,417	6034,8658	56144,095	186579,96	24086,191
1	[P12814]	77772,659	264788,56	50481,361	9505,0254	77737,455	279409,77	38200,155
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4	[P12814,	19197,787	53475,641	12686,772	3146,0887	19444,569	56125,736	10357,251
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1	[P12814]	53328,6	129006,74	29317,265	7861,8591	54430,069	134995,19	23592,785
1	[P12814]	48839,147	148012,98	21788,863	4574,8193	49203,059	156052,7	14450,461
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1	[P12814]	9364,1466	21743,943	4766,6094	1556,9538	9576,8323	22735,089	3778,3441
2	[P12814,	54634,93	100781,22	23777,058	7425,7557	56433,556	104605,45	19337,638
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2 [P12814,	5852,6799	13335,376	2783,8434	766,90994	5990,9589	13940,732	2174,8856
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2 [P12814,	2726,967	6057,3037	1417,3735	355,15178	2794,827	6322,9582	1152,7631
2 [P12814,	4844,3105	10640,131	2318,1155	639,03159	4967,3165	11108,891	1839,0413
2 [P12814,	13624,445	17179,619	4556,0324	1185,496	14242,921	17540,749	3848,9074
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1 [Q09666]	1801641,1	2401093,3	1160374,3	367044,47	1881006,3	2441168	1094474,7
1 [Q09666]	246662,38	153525,19	77940,315	29761,611	261239,88	147598,31	73939,077
1 [Q09666]	38340,523	27689,554	14104,181	5681,204	40525,501	27010,465	13364,103
1 [Q09666]	364656,88	346878,32	140863,24	105625,9	383648,12	346902,09	127085,97
1 [Q09666]	99508,359	94492,047	31757,49	14239,999	104690,03	94698,741	28103,978
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1 [Q09666]	175702,34	173846,68	44562,322	10975,854	184693,88	175142,46	37380,96
1 [Q09666]	33432,641	25646,952	4428,9062	3326,1072	35300,595	25429,802	3135,3299
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1 [Q09666]	21282,477	21755,434	13079,709	9740,6968	22361,532	21721,098	12417,563
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1 [Q09666]	206193,45	195024,95	80118,673	41699,417	216956,31	194929,96	73210,638
1 [Q09666]	123269,37	91771,95	34330,267	13932,83	130228,24	90164,705	31093,062
1 [Q09666]	136559,38	101249,32	29123,196	15592,785	144271,72	99724,183	24844,892
1 [Q09666]	289203,97	119904,39	56127,553	25493,089	307563,97	109282,76	52663,033
1 [Q09666]	242267,92	192056,18	79347,23	59472,637	255700,94	189455,77	71841,342
1 [Q09666]	253661,7	191608,02	82729,654	63362,599	267929,89	188137,59	75368,88
1 [Q09666]	208599	148767,02	56482,679	30082,986	220514,19	145577,77	50990,319
1 [Q09666]	270728,34	213300,43	73851,162	39436,083	285758,27	210763,43	65526,914
1 [Q09666]	185262,03	146474,71	57139,709	31822,285	195540,41	144566,59	51730,469
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1 [Q09666]	664684,13	442352,94	215957,81	145611,57	703354,48	428497,91	201095,7
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1 [Q09666]	170625,17	133247,43	52999,332	17965,737	180127,33	131342,96	48636,518
1 [Q09666]	95214,164	108195,8	41382,276	14598,239	99797,336	109461,48	37646,481
1 [Q09666]	65586,508	40904,861	22462,994	7623,3111	69461,943	39279,162	21545,262
1 [Q09666]	50016,443	55728,188	19276,281	7299,4289	52446,211	56384,075	17200,367
1 [Q09666]	233947,12	293090,63	68936,162	32270,544	244601,87	299443,13	55653,796
1 [Q09666]	1935004,4	1674246	587361,91	286859,18	2039251,8	1666174,4	523346,94
1 [Q09666]	367716,03	253252,27	113807,86	24353,138	388922,48	246442,31	107042,2
1 [Q09666]	3425023,3	2896973,8	1016236,6	544463,84	3610958	2878127,8	903497,04
1 [Q09666]	1745020,8	1544739,7	591594,81	301207,24	1838323,5	1538256,5	534860,09
1 [Q09666]	976911,13	903617,37	295446,4	137948,79	1028287,6	904249,56	259809,67
1 [Q09666]	2193536	1852267,6	638410,23	312520,77	2312675,2	1840346	566961,96
1 [Q09666]	928994,19	647765,98	305333,94	139656,02	982410,28	630637,83	285811,27
1 [Q09666]	661262,38	523288,89	178624,01	70712,116	697923,09	517327,56	159117,26
1 [Q09666]	1278053,6	1121147,9	649621,99	209922,6	1346747,6	1108566,8	626401,85
1 [Q09666]	241107,81	153516,71	44732,51	19235,353	255262,73	149016,83	38529,497
1 [Q09666]	57504,953	47552,771	13585,509	5438,9228	60647,846	47261,233	11640,724
1 [Q09666]	109888,42	75089,877	26789,46	10784,714	116233,82	73242,167	24076,243

1 [Q09666]	205186,33	121907,63	40575,799	24085,258	217421,65	117298,79	35692,358
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1	[O43707]	179411,14	242268,13	75386,503	24035,026	187220,72	247811,28	65969,322
1	[O43707]	333684,93	771353,63	175256,83	29300,439	341342,12	806213,2	141810,84
3	[P12814,	70833,683	217578,55	45573,3	8896,8401	71308,003	229019,48	35771,026
3	[P12814,	243074,63	730376,31	142526,67	25091,966	245042,94	768782,33	109001,46
3	[P12814,	96885,122	270347,94	60284,765	9963,8472	98117,996	283880,03	48456,456
1	[O43707]	70093,965	75694,172	20704,146	8377,7889	73546,676	76624,908	17516,883
2	[P12814,	47217,03	106841,27	23338,041	5176,9998	48349,141	111636,81	18583,82
2	[P12814,	212343,31	481835,34	117259,32	22221,951	217413,52	503110,91	96824,078
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1	[O43707]	7083,41	15045,383	3257,1461	650,44114	7274,2013	15693,975	2589,3193
1	[O43707]	31241,116	73278,348	13978,683	2472,4626	31933,667	76705,702	10601,1
1	[O43707]	53993,241	73730,57	22720,61	8359,8632	56325,896	75463,661	19790,988
4	[P12814,	192853,16	341273,56	109590,11	20553,168	199529,42	352780,78	97084,896
4	[P12814,	60510,765	139196,98	30069,584	4867,2396	61912,857	145519,29	23928,355
3	[P12814,	46898,69	102132,88	17658,138	2022,4026	48105,291	106755,02	12871,157
3	[P12814,	215952,92	484989,22	85545,77	11746,766	221195,84	507313,23	62847,447
3	[P12814,	72331,712	159660,03	22532,619	2724,8735	74143,634	167112,49	14662,301

3 [P12814,	65110,074	135702,28	22249,948	6079,7586	66914,565	141705,63	15650,504
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1 [O43707]	666912,9	930745,75	198936,69	41439,367	695242,43	956392,43	157689,17
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2 [P12814,	291789,09	338384,06	44537,22	3934,7653	305635,28	345466,49	27874,392
4 [P12814,	19197,787	53475,641	12686,772	3146,0887	19444,569	56125,736	10357,251
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1 [O43707]	531775,36	914383,75	188238,74	66344,201	550683,5	947675,07	145862,82
1 [O43707]	236892,55	358893,41	82842,268	35718,399	246355,56	369878,44	66546,554
1 [O43707]	56802,849	100682,97	27897,228	8041,0584	58762,906	104227,91	23768,861
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2 [P12814,	54634,93	100781,22	23777,058	7425,7557	56433,556	104605,45	19337,638
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2 [P12814,	5852,6799	13335,376	2783,8434	766,90994	5990,9589	13940,732	2174,8856
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2 [P12814,	1244,6664	2817,7122	576,12342	174,46626	1274,4558	2945,5056	445,96424
2 [P12814,	2726,967	6057,3037	1417,3735	355,15178	2794,827	6322,9582	1152,7631
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2 [P12814,	13624,445	17179,619	4556,0324	1185,496	14242,921	17540,749	3848,9074
2 [P12814,	1173,4429	2508,1672	625,31314	193,17192	1204,7664	2614,1136	516,88245
1 [O43707]	54639,93	72825,766	19352,84	7835,6502	57036,586	74554,267	16232,84
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1 [O43707]	233551,25	327160,63	97917,134	37032,193	243464,17	335328,62	84680,628
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6 [P60709_	75,481362	133,56972	56,09181				
6 [P60709_	212,054	336,50269	129,03285	31,298038	220,23281	345,77762	117,93028
6 [P60709_	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
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3 [P60709_	125046,53	474705,56	109764,85	18455,601	123956,49	501209,57	89202,495
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2 [P60709_	7405,8837	17782,137	4935,5278	1456,2272	7562,268	18575,156	4201,8194
1 [P60709_	26723,373	58399,695	12815,895	2213,7445	27408,311	60960,681	10249,808
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8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2

8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
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2 [P06753_	307228,69	190603,84	135411,89	54259,935	325423,53	181933,36	132781,43
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56
1 [P06753_	5880634,5	2651244,2	2453255	1253349,6	6250228,7	2409969,3	2442859,9
1 [P06753_	655692,56	305358,39	233181,97	123966,82	696667,17	280541,17	228895,93
1 [P06753_	399154,66	194187,72	156415,25	66580,836	423929,13	179274,13	154841,21
1 [P06753_	3896278,5	1681179,2	1628983,1	778031,38	4142780	1515152,3	1629198,5
1 [P06753_	262171	149238,72	119502,88	54707,882	277988,02	140639,53	118021,46
1 [P07355_	569135,11	1490285,3	293059,04	54233,006	578439,54	1563921	224803,94
1 [P07355_	108215,52	247134,03	51689,489	13163,182	110760,31	258364,95	40456,936
1 [P07355_	77985,073	217636,2	41539,741	9274,3437	78972,355	228757,32	31406,069
1 [P07355_	17647,988	47659,02	8883,7616	1564,5969	17905,276	50064,856	6668,5849
1 [P07355_	2413707,2	7408809,5	1424345,6	252454,57	2429901,8	7802397,6	1082579,6
1 [P07355_	454753,35	1123159,5	225351,99	73344,986	463634,5	1176873,1	172904,93
1 [P07355_	1243763,9	3488727	701715,58	116384,53	1259154,9	3666234,9	543513,02
1 [P07355_	83464,139	219833,89	45599,645	11953,253	84802,769	230651,2	35549,084
1 [P07355_	113259,43	265043,13	42775,367	6179,3464	115778,3	277674,67	30057,555
1 [P07355_	6091,717	14337,469	1710,5317	215,86333	6225,0543	15042,532	979,49766
1 [P07355_	21792,165	58070,297	7751,3265	1859,1369	22124,557	61082,902	4809,5863
1 [P07355_	77357,663	183497,56	29404,225	7069,6866	79025,138	192317,38	20460,62
1 [P07355_	104481,06	246736,56	39919,689	11466,963	106756,93	258554,51	27840,374
1 [P07355_	523285,13	865039,75	132420,97	33599,008	542603,85	896721,79	89976,585
1 [P07355_	305755,39	522774,19	91313,47	23961,765	316679,98	542223,17	66390,531
1 [P07355_	184930,57	316427,84	61489,462	18926,908	191537,02	328008,27	46708,961
1 [P07355_	209824,31	319518,53	62096,582	15512,706	218163,75	329741,32	47359,948
1 [P07355_	34203,498	64530,98	10227,374	1707,919	35295,62	67190,612	7116,5391
1 [P07355_	2705181,8	4934175	727413,93	139842,36	2795150,1	5133583,8	484926,43
1 [P07355_	23404,475	44980,09	6432,9872	1450,805	24133,73	46884,327	4197,3031
1 [P07355_	18703,621	33312,629	4938,25	863,77477	19342,836	34630,021	3307,3705
1 [P07355_	483674,29	861333,88	160718,38	36013,299	500228,33	894324,1	120595
1 [P07355_	622,04057	1088,5789	237,82213	65,680418	643,76183	1128,4676	189,02603
1 [P07355_	340,87565	549,98853	101,36984	23,351441	353,76012	569,0552	75,679544
1 [P07355_	41225,051	117369,62	19884,535	5217,814	41695,756	123501,75	14208,238
1 [P07355_	57882,274	213736,48	33590,15	6519,9011	57495,463	226082,1	23148,717
1 [P07355_	25953,815	89824,336	12625,724	2879,9726	25907,969	94957,359	8114,9942
1 [P07355_	1216,0212	3080,9758	610,49343	112,20652	1238,1077	3230,5497	469,80573
1 [P07355_	608390,56	1464100,3	274581,59	46139,395	621082,44	1533737	206840,07
1 [P07355_	20831,864	68111,406	9509,1532	1484,5662	20880,296	71932,261	6115,4135
1 [P07355_	26962,517	84831,547	11654,681	2129,4071	27096,196	89531,804	7402,1183
1 [P07355_	79905,271	180572,91	36182,52	6126,377	81824,051	188776,41	28000,582
1 [P07355_	113967,23	270910,31	44609,444	6874,0536	116412,39	283907,39	31654,262
1 [P07355_	132637,77	143104,58	99329,59	20201,246	139212,84	142906,64	97916,07

1	[P07355_	624707,37	1665227,4	269687,27	66566,068	634254,66	1750096,3	188538,98
1	[P07355_	181698,36	460786	71984,352	14731,969	184977	483792,49	49490,61
1	[P07355_	83339,18	150161,44	32764,252	7924,6475	86157,185	155821,92	26075,376
1	[P07355_	38520,658	73054,297	28643,364	15613,507	39753,483	75527,815	25892,371
1	[P07355_	90585,935	217239,61	45214,648	10284,08	92494,717	227407,89	35372,221
1	[P07355_	126567,41	310102,59	60142,478	12312,247	129091,22	324934,09	45840,083
1	[P07355_	124833,08	229339,81	52548,055	11771,515	128961,56	238059,62	42543,065
1	[P07355_	225062,79	543241,38	88781,803	25470,023	229714,73	569548,84	62241,091
1	[P07355_	57618,945	141763,23	26195,529	5817,0809	58754,428	148600,94	19545,158
1	[P07355_	1732881,3	4652032,5	904758,28	189491,66	1758760,1	4885004,6	689961,14
1	[P07355_	1863588,9	4416436	824111,06	200407,62	1903922,3	4624835,1	616837,17
1	[P07355_	3545117,1	8656827	1553397,1	307423,43	3616348,1	9074169,4	1145700,6
1	[P07355_	70750,926	166064,17	31939,037	6366,3867	72317,088	173826,06	24272,502
1	[P07355_	62633,577	123672,25	32562,528	6870,5208	64524,168	128535,7	27475,198
1	[P07355_	55043,924	130256,84	31518,253	8155,5498	56243,915	136164,93	25883,488
1	[P07355_	574877,69	355532,57	172650,98	36297,226	608895,66	341821,39	164171,69
1	[P07355_	699012,5	385857,1	296966,03	54149,024	741429,86	362646,6	295972,98
1	[P07355_	474958,94	224569,83	237555,78	30000,823	504611,3	204625,88	242300,76
1	[P07355_	64969,766	32740,532	28035,232	3781,7029	68979,621	30318,789	28220,274

6	[P60709_	13510,768	22746,746	10148,038	3039,745	14005,035	23380,125	9470,2272
6	[P60709_	409431	784178,56	290998,43	113476,5	422360,82	811510	262484,16
6	[P60709_	416,08235	762,12024	289,98635	85,621849	429,96614	787,28841	263,93553
6	[P60709_	221,99668	366,86652	164,68984	43,033489	230,26468	376,78708	154,10339
6	[P60709_	75,481362	133,56972	56,09181				
6	[P60709_	212,054	336,50269	129,03285	31,298038	220,23281	345,77762	117,93028
6	[P60709_	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
6	[P60709_	509,74009	871,26935	383,647	101,0475	528,1078	896,18435	357,93432
5	[P60709_	5581146,7	16381216	3923600,4	733096,8	5635108,9	17210844	3222494,6
5	[P60709_	2404345,9	6616989	1661626,9	298420,38	2437026,2	6940076,7	1384656,1
5	[P60709_	3435994,8	9739154	2255721,6	466492,01	3476542,1	10227395	1831596,3
5	[P60709_	5275789,7	15097403	3245935,8	598961,66	5334826,8	15865587	2573746,9
5	[P60709_	76825,314	159564,39	47267,741	9136,1857	78979,943	165922,79	41105,743
3	[P60709_	688643,33	2485118	398540,76	61261,368	685281,7	2627402,7	278424,43
3	[P60709_	30539,341	52604,922	19305,372	11714,331	31628,666	54250,605	17202,763
3	[P60709_	6518,4565	17878,439	5425,4894	1234,8299	6608,9579	18719,736	4733,3361
3	[P60709_	69509,467	249253,78	61720,251	11692,168	69218,058	262793,07	51168,535
3	[P60709_	125046,53	474705,56	109764,85	18455,601	123956,49	501209,57	89202,495
3	[P60709_	80038,377	288088,72	68784,654	11702,116	79678,176	303838,98	56463,12
3	[P60709_	137622,84	502697,13	119008,03	21249,002	136846,29	530343,32	97387,956
3	[P60709_	40923,377	143488,63	36437,312	7645,9553	40821,868	151195,79	30397,095
3	[P60709_	65953,674	131771,64	34276,735	9625,0207	67911,303	137017,44	28722,373
3	[P60709_	114933,24	350499,09	86230,324	19485,324	115765,3	368462,49	71240,787
2	[P68032_	71451,478	346851,75	74572,762	12347,147	69212,15	367667,41	59120,653
2	[P68032_	46822,094	178727,22	42207,296	7598,3112	46393,607	188694,03	34507,398
2	[P68032_	7198,1007	32513,996	6762,1846	1237,6741	7024,1866	34440,835	5292,7345
3	[P60709_	1141,7166	3746,9072	857,95194	245,13095	1144,2871	3946,5525	690,90621
3	[P60709_	670,17996	2177,1887	484,35245	161,93607	672,15369	2293,2277	385,32664
3	[P60709_	125,62992	344,70508	86,678443	20,783655	127,35974	361,50924	72,033956
3	[P60709_	14972,925	27260,914	17689,279	8227,3937	15480,725	27919,435	17118,343
3	[P60709_	528,83159	1067,375	302,52025	58,903463	544,31423	1109,4007	260,32704
3	[P60709_	744,78627	1426,9027	345,9752	71,137174	768,17991	1482,5688	285,29005

3 [P60709_	99108,042	291672,28	66396,734	9755,7218	100047,42	306572,54	53778,902
5 [P60709_	89164,326	241555,5	43800,138	9595,7238	90447,125	253807,39	32402,661
5 [P60709_	515509,33	1282652,7	206123,63	47308,175	525342,66	1345889,7	143709,91
5 [P60709_	245846,38	629859,33	110487,06	27615,526	250153,58	661077,72	80377,987
5 [P60709_	48015,281	122457,09	26248,995	6819,9116	48871,499	128358,46	20713,204
2 [P68032_	25595,175	131265,52	28004,564	6525,2893	24643,094	139242,64	22057,467
2 [P68032_	23114,837	93360,969	21256,533	4949,2724	22793,412	98678,667	17127,111
2 [P68032_	46141,967	248849,89	51919,238	11053,374	44164,241	264161,95	40604,934
2 [P68032_	30000,257	62014,754	13589,759	2375,8448	30844,844	64631,607	10864,476
2 [P68032_	12474,196	56866,438	13415,352	2620,6895	12162,723	60192,393	10952,161
2 [P68032_	186862,57	512721,34	154539,33	63151,318	189451,77	536893,15	133409,11
2 [P68032_	14907,893	61248,691	14845,832	4146,7612	14679,072	64724,648	12169,42
4 [P60709_	4642888,9	16503489	3155465,1	347982,29	4625926,7	17427453	2400995,3
4 [P60709_	146782,24	389429	67725,317	14648,31	149067,73	409081,44	49159,997
4 [P60709_	2210550,1	6327004	946631,99	149791,94	2234994,6	6662347	636304,69
4 [P60709_	142498,52	233338,92	74865,98	21455,102	147832,05	240533,14	66006,398
4 [P60709_	1050,6501	2704,783	598,61666	123,34594	1068,8593	2835,1432	479,00994
2 [P68032_	268818,79	1310272,8	267157,58	57799,529	260270,73	1389450,2	207142,31
2 [P68032_	375926,28	1983919,6	412428,43	79601,79	360741,12	2105525,8	322486,74
2 [P68032_	158071,8	597334,75	132430,87	25935,654	156748,69	630824,45	105987
2 [P68032_	19260,391	52653,328	14871,689	5176,849	19530,761	55163,202	12678,636

1 [P13645]	29123,375	40309,676	12773,626	4390,1792	30370,315	41270,922	11207,24
1 [P13645]	63716,55	74692,898	24885,696	8854,201	66732,593	75814,002	22062,936
1 [P13645]	47538,074	85428,922	27155,854	7453,8142	49155,805	88365,896	23902,777
1 [P13645]	157625,17	177026,23	72356,125	29797,18	165259,86	178830,66	66362,037
1 [P13645]	194282,21	201136,91	76835,37	32134,061	204050,91	202394,04	69691,793
1 [P13645]	80708,016	68653,809	17592,17	9341,6166	85076,99	68446,076	14555,678
1 [P13645]	23626,797	17670,67	5420,5795	2014,0302	24958,108	17406,531	4731,0613
1 [P13645]	129750,3	67301,105	15146,344	4899,5193	137690,87	63941,3	12257,153
1 [P13645]	6631,4883	4907,2638	1231,1299	430,10359	7006,097	4838,3034	1023,4487
1 [P13645]	7380,6972	6056,2224	1528,1343	483,83786	7784,9583	6021,9699	1273,4211
1 [P13645]	195275,97	259532,59	86444,472	26535,477	203868,29	265090,59	76780,034
4 [P13645,	451944,03	446936,27	141966,96	75470,67	475094,64	449374,46	123652,5
4 [P13645,	91560,734	80761,94	29345,135	15175,245	96461,444	80453,357	26277,709
1 [P13645]	118717,67	137463,91	41776,156	15663,114	124370,88	139564,84	36289,625
1 [P13645]	664323,68	670298,63	254242,14	85206,291	698096,33	673468,31	231258,53
1 [P13645]	252776,83	206558,54	70910,419	29520,021	266652,44	204717,56	63161,608
1 [P13645]	71216,461	64134,978	21654,039	7506,0917	74999,214	64037,524	19280,477
1 [P13645]	154130,03	172514,25	60523,671	23054,195	161601,48	174561,88	54144,553
1 [P13645]	247980,8	238576,29	75936,05	23463,262	260825,3	239440,67	66907,019
1 [P13645]	515723,34	293700,92	181321,43	54881,221	546800,2	278526,54	176386,69
1 [P13645]	120172,11	181513,5	60668,525	24850,164	124996,31	186439,33	53631,701
1 [P13645]	513820,5	472193,08	163769,01	77623,089	540914,17	472008,77	145660,79
1 [P13645]	194684,38	158557,66	66038,318	27402,351	205389,87	156728,03	60812,241
1 [P13645]	138327,81	134934,62	52664,475	22000,397	145459,49	135233,05	47953,502
1 [P13645]	88844,155	92455,961	43015,999	16379,698	93306,151	92814,024	40276,197
1 [P13645]	548992,94	471652,38	171330,79	74364,193	578644,89	468939,88	154048,38
1 [P13645]	218899,05	221407,47	66903,571	24702,242	230004,91	223041,22	58097,679

4 [P07951,	261498,81	543151,38	469942,07	145036,5	269030,96	554803,66	468700,4
4 [P07951,	305431,51	731014,69	465094,41	143174,25	312099,83	755072,54	452251,68

3 [P07951,	503728,59	261603,39	177983,05	78231,861	534625,89	244735,23	173698,41
2 [P07951,	170286,4	190210,13	184529,21	52502,675	178625,08	188633,52	185722,96
2 [P07951,	730692,71	1235422,6	1134787,6	283658,05	757688,7	1251129,3	1139403,1
2 [P07951,	525528,04	905755,55	931070,5	230064,27	544648,21	914712,04	941390,25
2 [P07951,	237524,33	431461,44	266889,43	119290,71	245592,42	442270,76	257281,89
8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
4 [P07951,	464198,53	772619,13	720110,36	219759,98	481610,67	781652,73	722011,51
4 [P07951,	15049934	25158040	23432953	7393748,3	15612177	25456897	23483285
4 [P07951,	15616965	26098812	24415215	7095559,9	16200611	26405014	24500675
4 [P07951,	162585,2	234481,75	196419,37	68367,891	169423,92	236559,09	195190,04
4 [P07951,	1940534,9	2403826	1706999,3	764523,03	2030229,3	2417646,2	1667582,5
4 [P07951,	2356409,8	3955201,5	3950456,5	1240351,6	2444276,3	3994180,8	3976245,5
4 [P07951,	700911,05	1227550,4	861329,57	251988,29	725747,8	1253379,1	845935,48
4 [P07951,	717603,04	1210133,8	1031539,1	281207,45	744129,79	1227994,4	1029536,1
4 [P07951,	494,90426	762,58691	426,19158	155,939	514,56169	778,37511	408,05367
4 [P07951,	580146,66	727732,42	741913,13	243074,97	606916,1	725088,2	747424,18
4 [P07951,	24673,978	31057,32	30323,086	10576,904	25809,417	30993,332	30442,571
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
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8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
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8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
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4 [P07951,	419108,78	410503,13	237661,7	65338,483	440730,88	409009,87	229572,53
2 [P07951,	573580,04	777314,5	703578,72	211878,48	598785,26	780295	704371,39
2 [P07951,	61143,168	119030,16	111715	30950,618	63076,693	121056,41	112180,38
2 [P07951,	94290,027	157540,63	138735,63	36943,053	97809,08	159666,46	138816,21
2 [P07951,	488500,86	990723,31	969315,59	248467,64	503144,56	1007606,2	976703,31
2 [P07951,	799944,67	1403600,8	1348710,1	373841,03	828470,05	1421453,7	1356428,2
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56
1 [P07951]	285217,29	308306,32	311870,75	87004,817	299406,65	304751,3	314755,14
1 [P07951]	238906,95	243264,77	222698,18	58864,06	251089,46	240333,03	223551,05
4 [P07951,	261498,81	543151,38	469942,07	145036,5	269030,96	554803,66	468700,4

4 [P07951,	305431,51	731014,69	465094,41	143174,25	312099,83	755072,54	452251,68
2 [P07951,	170286,4	190210,13	184529,21	52502,675	178625,08	188633,52	185722,96
2 [P07951,	730692,71	1235422,6	1134787,6	283658,05	757688,7	1251129,3	1139403,1
2 [P07951,	525528,04	905755,55	931070,5	230064,27	544648,21	914712,04	941390,25
2 [P07951,	237524,33	431461,44	266889,43	119290,71	245592,42	442270,76	257281,89
8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
4 [P07951,	464198,53	772619,13	720110,36	219759,98	481610,67	781652,73	722011,51
4 [P07951,	15049934	25158040	23432953	7393748,3	15612177	25456897	23483285
4 [P07951,	15616965	26098812	24415215	7095559,9	16200611	26405014	24500675
4 [P07951,	162585,2	234481,75	196419,37	68367,891	169423,92	236559,09	195190,04
4 [P07951,	1940534,9	2403826	1706999,3	764523,03	2030229,3	2417646,2	1667582,5
4 [P07951,	2356409,8	3955201,5	3950456,5	1240351,6	2444276,3	3994180,8	3976245,5
4 [P07951,	700911,05	1227550,4	861329,57	251988,29	725747,8	1253379,1	845935,48
4 [P07951,	717603,04	1210133,8	1031539,1	281207,45	744129,79	1227994,4	1029536,1
4 [P07951,	494,90426	762,58691	426,19158	155,939	514,56169	778,37511	408,05367
4 [P07951,	580146,66	727732,42	741913,13	243074,97	606916,1	725088,2	747424,18
4 [P07951,	24673,978	31057,32	30323,086	10576,904	25809,417	30993,332	30442,571
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
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2 [P07951,	61143,168	119030,16	111715	30950,618	63076,693	121056,41	112180,38
2 [P07951,	94290,027	157540,63	138735,63	36943,053	97809,08	159666,46	138816,21
2 [P07951,	488500,86	990723,31	969315,59	248467,64	503144,56	1007606,2	976703,31
2 [P07951,	799944,67	1403600,8	1348710,1	373841,03	828470,05	1421453,7	1356428,2
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
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1 [P07951_	257241,48	371532,94	282036,45	103564,62	268031,64	375793,15	277965,71
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6 [P60709_	13510,768	22746,746	10148,038	3039,745	14005,035	23380,125	9470,2272
6 [P60709_	409431	784178,56	290998,43	113476,5	422360,82	811510	262484,16
6 [P60709_	416,08235	762,12024	289,98635	85,621849	429,96614	787,28841	263,93553
6 [P60709_	221,99668	366,86652	164,68984	43,033489	230,26468	376,78708	154,10339
6 [P60709_	75,481362	133,56972	56,09181				
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6 [P60709_	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
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5 [P60709_	2404345,9	6616989	1661626,9	298420,38	2437026,2	6940076,7	1384656,1
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5 [P60709_	5275789,7	15097403	3245935,8	598961,66	5334826,8	15865587	2573746,9
5 [P60709_	76825,314	159564,39	47267,741	9136,1857	78979,943	165922,79	41105,743
3 [P60709_	688643,33	2485118	398540,76	61261,368	685281,7	2627402,7	278424,43
3 [P60709_	30539,341	52604,922	19305,372	11714,331	31628,666	54250,605	17202,763
3 [P60709_	6518,4565	17878,439	5425,4894	1234,8299	6608,9579	18719,736	4733,3361
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3 [P60709_	125046,53	474705,56	109764,85	18455,601	123956,49	501209,57	89202,495
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3 [P60709_	137622,84	502697,13	119008,03	21249,002	136846,29	530343,32	97387,956
3 [P60709_	40923,377	143488,63	36437,312	7645,9553	40821,868	151195,79	30397,095
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3 [P60709_	114933,24	350499,09	86230,324	19485,324	115765,3	368462,49	71240,787
2 [P68032_	71451,478	346851,75	74572,762	12347,147	69212,15	367667,41	59120,653
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2 [P68032_	7198,1007	32513,996	6762,1846	1237,6741	7024,1866	34440,835	5292,7345
3 [P60709_	1141,7166	3746,9072	857,95194	245,13095	1144,2871	3946,5525	690,90621
3 [P60709_	670,17996	2177,1887	484,35245	161,93607	672,15369	2293,2277	385,32664
3 [P60709_	125,62992	344,70508	86,678443	20,783655	127,35974	361,50924	72,033956
3 [P60709_	14972,925	27260,914	17689,279	8227,3937	15480,725	27919,435	17118,343
3 [P60709_	528,83159	1067,375	302,52025	58,903463	544,31423	1109,4007	260,32704
3 [P60709_	744,78627	1426,9027	345,9752	71,137174	768,17991	1482,5688	285,29005
3 [P60709_	99108,042	291672,28	66396,734	9755,7218	100047,42	306572,54	53778,902
2 [P68032_	25595,175	131265,52	28004,564	6525,2893	24643,094	139242,64	22057,467
2 [P68032_	23114,837	93360,969	21256,533	4949,2724	22793,412	98678,667	17127,111
2 [P68032_	46141,967	248849,89	51919,238	11053,374	44164,241	264161,95	40604,934
2 [P68032_	30000,257	62014,754	13589,759	2375,8448	30844,844	64631,607	10864,476
2 [P68032_	12474,196	56866,438	13415,352	2620,6895	12162,723	60192,393	10952,161
2 [P68032_	186862,57	512721,34	154539,33	63151,318	189451,77	536893,15	133409,11
2 [P68032_	14907,893	61248,691	14845,832	4146,7612	14679,072	64724,648	12169,42
4 [P60709_	4642888,9	16503489	3155465,1	347982,29	4625926,7	17427453	2400995,3
4 [P60709_	146782,24	389429	67725,317	14648,31	149067,73	409081,44	49159,997
4 [P60709_	2210550,1	6327004	946631,99	149791,94	2234994,6	6662347	636304,69
4 [P60709_	142498,52	233338,92	74865,98	21455,102	147832,05	240533,14	66006,398
4 [P60709_	1050,6501	2704,783	598,61666	123,34594	1068,8593	2835,1432	479,00994
2 [P68032_	268818,79	1310272,8	267157,58	57799,529	260270,73	1389450,2	207142,31
2 [P68032_	375926,28	1983919,6	412428,43	79601,79	360741,12	2105525,8	322486,74
2 [P68032_	158071,8	597334,75	132430,87	25935,654	156748,69	630824,45	105987
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2 [P14618_	6042,4776	14938,33	4512,9767	1339,5028	6161,151	15604,06	3920,5955
2 [P14618_	423872,56	1385382,8	395604,03	46027,06	424999,02	1456539	342018,36

1 [P14618_	13371,797	26308,27	7357,4082	1663,3191	13777,721	27325,884	6300,9029
2 [P14618_	45707,433	98991,984	24022,653	8033,9893	46899,494	103233,42	19672,187
2 [P14618_	1280355,8	2297115,8	605259,74	111204,39	1323926,6	2379985,6	511673,71
2 [P14618_	104360,17	227444,36	64776,885	7519,2285	107057,77	236918,39	56016,372
2 [P14618_	120346,3	321536,63	82881,84	10582,125	122189,58	336942,48	69767,674
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2 [P14618_	134930,89	300199,38	68759,224	17355,818	138277,36	313427,12	55536,955
2 [P14618_	114404,4	301074,63	77655,881	15196,645	116254,45	315390,36	65154,491
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2 [P14618_	39908,316	107676,2	25622,46	5771,0589	40495,789	112929,97	20964,053
2 [P14618_	65298,258	161256,58	38859,412	7043,5052	66578,109	168756,4	31998,554
2 [P14618_	334711,19	716993,06	281832,08	209082,97	343678,22	744018,22	252419,58
2 [P14618_	383473,78	728114,25	311653,76	265052,7	395744,77	751971,36	281602,04
1 [P14618_	231235,47	718858,44	194449,2	32488,538	232629,07	755414,37	165425,64
1 [P14618_	26828,966	83702,641	23412,088	4542,0717	26984,812	87940,424	20061,228
1 [P14618_	77428,205	171245,06	48665,832	10795,562	79376,379	178455,6	41838,506
1 [P14618_	95392,295	246828,94	62288,751				
1 [P14618_	13001,937	31552,322	7613,4487	1560,1349	13268,649	33005,147	6264,284
2 [P14618_	1490087,7	3036115,3	885783,12	327251,82	1533120,1	3155772,8	760873,66
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2 [P14618_	172346,12	279797,91	87521,714	35158,234	178846,72	288405,59	76313,964
2 [P14618_	59364,867	101892,65	29402,752	6507,3136	61485,063	105322,25	25391,086
2 [P14618_	42972,182	92621,539	27294,787	6383,0572	44105,54	96420,488	23657,745
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1 [Q9NZM1_	65061,925	152402,09	34996,191	6139,6275	66512,418	159332,84	28401,141
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1 [Q9NZM1_	41980,234	159233,86	24907,342	6021,906	41609,444	168508,11	17067,273
1 [Q9NZM1_	119052,38	345738,5	68649,253	11230,575	120273,09	363626,46	52907,153
1 [Q9NZM1_	18893,154	38525,598	10021,924	2429,2724	19437,355	40083,985	8414,1067
1 [Q9NZM1_	31654,896	63448,223	15852,056	3969,3272	32589,716	66001,563	13154,148
1 [Q9NZM1_	12977,293	40750,688	9085,9177	1562,8002	13045,579	42894,035	7297,9865
1 [Q9NZM1_	14618,302	32487,191	8380,1912	2611,29	14982,23	33887,365	6992,6019
1 [Q9NZM1_	77382,55	133128,06	40010,927	6558,9007	80140,671	137568,4	34980,217
1 [Q9NZM1_	32723,32	69247,055	14587,628	3882,673	33609,969	72237,76	11443,571
1 [Q9NZM1_	38414,782	72406,797	17604,495	4810,7268	39646,796	75190,657	14478,017
1 [Q9NZM1_	62731,482	156196,22	27788,162	5482,2118	63927,416	163812,67	20413,956
1 [Q9NZM1_	66685,276	88848,125	24808,929	6444,8488	69611,743	90915,87	21232,438
1 [Q9NZM1_	83619,858	210705,47	46579,05	7687,0808	85166,482	220749,12	37342,643
1 [Q9NZM1_	108213,21	251629,16	58500,003	10954,225	110665,67	262999,01	47634,151
1 [Q9NZM1_	138178,16	305193,51	62628,589	12493,024	141648,09	318812,16	48829,774
1 [Q9NZM1_	43399,536	91404,094	26124,006	6753,651	44589,173	95116,362	22451,802
1 [Q9NZM1_	112842,01	221353,44	47677,2	11092,727	116272,37	230354,71	37778,927
1 [Q9NZM1_	53231,928	104683,35	26376,036	8518,0852	54847,012	108825,41	21858,921
1 [Q9NZM1_	450196,07	711120,35	172176,7	57462,66	467564,87	733844,74	141075,55

4 [P07951,	261498,81	543151,38	469942,07	145036,5	269030,96	554803,66	468700,4
4 [P07951,	305431,51	731014,69	465094,41	143174,25	312099,83	755072,54	452251,68
1 [P09493]	114868,56	237671,7	118660,63	45938,643	118140,43	245557,67	111937,09
8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
4 [P07951,	464198,53	772619,13	720110,36	219759,98	481610,67	781652,73	722011,51
4 [P07951,	15049934	25158040	23432953	7393748,3	15612177	25456897	23483285
4 [P07951,	15616965	26098812	24415215	7095559,9	16200611	26405014	24500675
4 [P07951,	162585,2	234481,75	196419,37	68367,891	169423,92	236559,09	195190,04
4 [P07951,	1940534,9	2403826	1706999,3	764523,03	2030229,3	2417646,2	1667582,5
4 [P07951,	2356409,8	3955201,5	3950456,5	1240351,6	2444276,3	3994180,8	3976245,5
4 [P07951,	700911,05	1227550,4	861329,57	251988,29	725747,8	1253379,1	845935,48
4 [P07951,	717603,04	1210133,8	1031539,1	281207,45	744129,79	1227994,4	1029536,1
4 [P07951,	494,90426	762,58691	426,19158	155,939	514,56169	778,37511	408,05367
2 [P09493,	100402,67	143832,08	129258,4	42401,051	104651,8	144779,25	129185,02
2 [P09493,	36336,81	60228,414	53759,996	17079,346	37703,52	60999,984	53721,21
2 [P09493,	255929,62	421707,99	429540,28	126844,86	265642,12	425294,22	433194,56
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
2 [P09493,	125696,17	244827,27	131376,06	36891,794	129605,04	252182,92	125639,5
2 [P09493,	247370,08	429967,19	222772,26	61541,429	256153,59	441447,5	212241,08
2 [P09493,	149791,87	316730,88	216810,1	82442,154	153952,33	325551,95	211609,94
2 [P09493,	44749,831	90089,484	71660,309	24688,725	46094,567	92138,449	70927,659
2 [P09493,	147259,22	178521,89	82021,618	24568,372	154118,93	180791,59	76918,912
2 [P09493,	1446004,1	1798622,4	1002953,7	269121,61	1512509,7	1818167,6	964642,19
2 [P09493,	133821,61	195661,78	144176,37	38206,905	139382,06	198147,99	142387,51
2 [P09493,	458469,6	662632,81	572754,47	157996,83	477735,67	667985,32	572207,91
2 [P09493,	636435,93	976721,36	983497,75	261730,57	662080,2	982608,49	992499,14
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56
1 [P09493_	306827,84	433212,81	381560,08	102735,7	319940,6	436030,18	381803,68
1 [P09493_	407834,59	485520,69	454042,28	155877,62	427169,56	483759,35	454754,72

4 [P07951,	261498,81	543151,38	469942,07	145036,5	269030,96	554803,66	468700,4
4 [P07951,	305431,51	731014,69	465094,41	143174,25	312099,83	755072,54	452251,68
8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
4 [P07951,	464198,53	772619,13	720110,36	219759,98	481610,67	781652,73	722011,51
4 [P07951,	15049934	25158040	23432953	7393748,3	15612177	25456897	23483285
4 [P07951,	15616965	26098812	24415215	7095559,9	16200611	26405014	24500675
4 [P07951,	162585,2	234481,75	196419,37	68367,891	169423,92	236559,09	195190,04
4 [P07951,	1940534,9	2403826	1706999,3	764523,03	2030229,3	2417646,2	1667582,5
4 [P07951,	2356409,8	3955201,5	3950456,5	1240351,6	2444276,3	3994180,8	3976245,5
4 [P07951,	700911,05	1227550,4	861329,57	251988,29	725747,8	1253379,1	845935,48
4 [P07951,	717603,04	1210133,8	1031539,1	281207,45	744129,79	1227994,4	1029536,1
4 [P07951,	494,90426	762,58691	426,19158	155,939	514,56169	778,37511	408,05367
2 [P09493,	100402,67	143832,08	129258,4	42401,051	104651,8	144779,25	129185,02
2 [P09493,	36336,81	60228,414	53759,996	17079,346	37703,52	60999,984	53721,21
2 [P09493,	255929,62	421707,99	429540,28	126844,86	265642,12	425294,22	433194,56
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
2 [P09493,	125696,17	244827,27	131376,06	36891,794	129605,04	252182,92	125639,5
2 [P09493,	247370,08	429967,19	222772,26	61541,429	256153,59	441447,5	212241,08
2 [P09493,	149791,87	316730,88	216810,1	82442,154	153952,33	325551,95	211609,94
2 [P09493,	44749,831	90089,484	71660,309	24688,725	46094,567	92138,449	70927,659
2 [P09493,	147259,22	178521,89	82021,618	24568,372	154118,93	180791,59	76918,912
2 [P09493,	1446004,1	1798622,4	1002953,7	269121,61	1512509,7	1818167,6	964642,19
2 [P09493,	133821,61	195661,78	144176,37	38206,905	139382,06	198147,99	142387,51
2 [P09493,	458469,6	662632,81	572754,47	157996,83	477735,67	667985,32	572207,91
2 [P09493,	636435,93	976721,36	983497,75	261730,57	662080,2	982608,49	992499,14
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56

1 [Q9Y490]	18952,101	52674,129	15188,712	3696,1128	19199,957	55194,699	13083,116
1 [Q9Y490]	61394,543	202870,47	52815,109	16237,148	61507,32	213501,23	44149,656
1 [Q9Y490]	303750,81	285238,26	84299,993	22796,235	319628,63	286018,12	73224,492

1 [Q9Y490]	10454,445	23562,207	6199,9078	2133,9829	10707,785	24583,233	5192,6851
1 [Q9Y490]	6025,4415	16063,079	3691,1018	1537,2611	6118,1918	16846,654	2956,6269
1 [Q9Y490]	17072,3	45990,609	11428,591	2839,5824	17325,46	48217,267	9461,4332
1 [Q9Y490]	13539,378	33088,949	8823,0367	2051,6892	13812,697	34591,526	7457,0066
1 [Q9Y490]	30317,601	37085,314	7334,3776	3392,8896	31716,605	37888,385	5573,7984
1 [Q9Y490]	47271,274	148833,36	29683,999	5986,273	47509,344	156783	22862,594
1 [Q9Y490]	37928,608	95497,758	16629,78	4859,7393	38628,833	100193,48	12026,889
1 [Q9Y490]	121933,22	164494,67	51400,47	13328,25	127244,36	168243,29	45152,702
1 [Q9Y490]	9039,8011	30807,438	7585,7656	2692,8937	9036,1634	32453,979	6224,9915
1 [Q9Y490]	23432,385	39598,25	13547,934	5007,9766	24283,837	40839,847	12051,657
1 [Q9Y490]	45283,362	89328,281	22057,24	9381,4204	46651,096	92886,759	18075,495
1 [Q9Y490]	88726,102	133802,36	45502,012	14132,31	92292,999	137398,23	40557,801
1 [Q9Y490]	5046,1971	17188,836	2974,4801	929,39423	5043,5391	18148,005	2139,6372
1 [Q9Y490]	87626,527	212699,33	59620,293	19455,553	89428,222	222227,45	50801,519
1 [Q9Y490]	60729,386	156661,88	40149,331	9405,222	61778,585	164043,27	33560,817
1 [Q9Y490]	76665,074	143274,94	50000,896	17932,017	79159,768	148252,26	44662,01

1 [P04843_	55398,336	97713,195	21212,762	5474,1844	57316,392	101325,81	16839,539
1 [P04843_	26082,145	49374,215	11280,022	2980,7091	26913,631	51303,135	9103,0628
1 [P04843_	162562,55	223867,22	59733,092	16629,806	169539,77	229515,03	50475,518
1 [P04843_	122943,77	192104,73	55064,472	18768,428	127737,17	197882,68	47206,651
1 [P04843_	48874,198	88680,253	22239,253	3672,1957	50515,49	91951,102	18562,489
1 [P04843_	71098,488	143959,58	28844,086	5915,5409	73162,612	150029,24	22286,899
1 [P04843_	124600,7	174372,44	65517,995	18887,544	129901,49	178285,96	59563,022
1 [P04843_	216507,7	466176,38	117810,69	23637,041	222215,59	485915,18	98310,85
1 [P04843_	27498,76	48020,902	12880,562	1800,9589	28462,727	49699,123	10965,939
1 [P04843_	102197	145626,91	41079,374	12023,405	106480,53	149455,11	35177,541
1 [P04843_	2043185,3	1544023,8	364208,69	124232,7	2157904,7	1525833,8	297434,62
1 [P04843_	12967,072	18858,043	4322,4566	768,24409	13501,837	19402,924	3512,311
1 [P04843_	298217,27	515138,09	146689,84	27768,12	308796,81	532661,34	126470,25
1 [P04843_	373901,22	701760	161323,7	26607,567	385950,69	728936,8	131146,24
1 [P04843_	298980,93	403851,78	96970,767	21850,302	311974,22	414023,93	79769,565
1 [P04843_	111199,49	176418,42	53786,64	11855,614	115480,34	181727,65	47056,786
1 [P04843_	52905,112	70118,555	22423,763	4921,2214	55236,547	71640,514	19835,594
1 [P04843_	10391,309	29968,457	4560,3146	733,68029	10501,42	31559,407	3095,367
1 [P04843_	26705,431	41007,594	9598,7793	2113,0664	27760,606	42281,074	7831,805
1 [P04843_	15605,766	28464,443	7300,3639	1494,8248	16126,777	29514,339	6119,3762
1 [P04843_	61444,012	102962,18	26530,681	5189,4008	63689,638	106437,87	22285,068

1 [P68371]	232574,84	167753,49	89943,854	30184,066	245836,39	163473,98	86001,789
1 [P68371]	422889,56	229819,05	139079,5	48334,785	448602,76	216806,07	134789,24
3 [P07437,	70664,569	189358,77	54993,907	10606,331	71738,934	198245,43	47574,921
3 [P07437,	556535,8	1213665,5	320911,38	83020,278	570889,74	1265052,8	270340,33
5 [P07437,	158186,74	246368,5	69009,986	10936,114	164370,38	253795,04	59371,464
5 [P07437,	136489,58	202216,13	60065,519	8333,243	142047,95	207777,19	52464,434
5 [P07437,	260674,66	442854,69	119786,23	15546,875	270076,61	457848,23	102264,85
1 [P68371]	200047,99	244548,31	78284,083	31677,057	209301,76	248868,07	68659,596
4 [P07437,	116552,53	177057,78	60513,25	17427,031	121210,81	181860,62	54048,46
4 [P07437,	15843,876	20495,275	6197,9324	2951,8947	16552,566	20927,825	5348,2592
4 [P07437,	177082,12	244977,52	70715,363	33047,814	184662,13	251039,28	60369,856
1 [P68371]	37711,881	67652,992	22305,311	8572,2717	38998,232	69949,325	19677,894
3 [P07437,	8168,3202	15423,864	4927,4639	1485,8789	8430,4565	15979,744	4335,4669

4 [P07437,	494240,21	925059,56	261904,6	39573,212	510254,1	959201,91	225860,3
4 [P07437,	224387,44	506487,63	113417,86	15052,142	229796,02	529093,78	91512,16
5 [P07437,	142060,43	331430,47	88009,635	13514,525	145263,67	346080,8	74610,418
5 [P07437,	12295,527	22303,764	6912,1196	1253,9214	12709,411	23083,525	6078,3207
4 [P07437,	10040,13	27931,853	4760,2053	1107,8709	10168,739	29375,653	3417,6823
3 [P07437,	5451,9918	11537,499	2540,4274	407,56661	5599,7801	12032,186	2035,6746
3 [P07437,	5552,5221	11163,377	2405,0858	384,51191	5715,5249	11626,083	1913,2909
5 [P07437,	74820,007	159661,33	43147,626	6331,1586	76824,994	166288,08	36769,329
5 [P07437,	23134,843	46218,926	12852,986	2664,718	23822,135	48031,719	11001,7
5 [P07437,	29211,637	46072,637	12031,622	2959,7036	30340,687	47513,549	10119,5
5 [P07437,	237519,66	267284,03	81602,755	18582,71	248995,17	270928,79	71486,026
3 [P07437,	8314,8314	14322,511	3903,2987	1117,2526	8610,5556	14813,975	3312,3032
3 [P07437,	11032,725	19651,848	4963,4066	1490,1348	11411,06	20362,826	4122,5363
3 [P07437,	3874,5038	6825,2148	1774,7752	509,0701	4009,0258	7067,7663	1487,2243
3 [P07437,	56085,149	95496,055	22774,702	6048,4933	58101,47	98836,876	18636,276
2 [P07437,	43796,674	89062,469	27628,57	3867,1076	45066,295	92512,528	24342,971

1 [P50454_	124233,76	312824,5	97645,982	36284,626	126554,52	326812,16	85132,907
1 [P50454_	139985,72	290063,38	92625,009	36553,685	143930,52	301388,17	81097,989
1 [P50454_	32650,564	80351,719	23862,382	12137,345	33299,355	83937,577	20430,612
1 [P50454_	901681,75	2478093,7	686172,57	429522,97	914050,31	2597010,6	573837,51
1 [P50454_	75636,756	161813,31	57377,177	25788,164	77663,627	168103,42	51165,633
1 [P50454_	73689,44	239387,29	56555,39	20817,581	73908,679	252039,67	45800,5
1 [P50454_	35680,598	98074,117	26357,43	7404,0453	36169,284	102804,54	22261,718
1 [P50454_	10684,66	29810,494	9411,1836	2110,7576	10822,485	31213,188	8283,683
1 [P50454_	27985,227	109210,69	19464,94	3539,0929	27674,143	115545,47	14302,169
1 [P50454_	16591,395	86761,328	16503,322	3806,71	15937,256	92119,574	12433,866
1 [P50454_	24015,029	74903,867	19142,97	4119,9798	24153,783	78754,391	15997,771
1 [P50454_	23751,665	65799,781	16864,644	3668,0539	24065,489	69011,69	14107,213
1 [P50454_	245235,72	1128753,5	256664,06	45128,349	238875,99	1195232,1	207298,27
1 [P50454_	130732,42	467325,91	127152,86	28479,864	130222,96	492315,5	107999,05
1 [P50454_	40475,606	212034,48	56848,354	16866,656	38882,393	224600,29	47894,008
1 [P50454_	29347,824	143024,25	39511,13	14352,267	28421,723	151332,95	33438,606
1 [P50454_	159692,36	777465,88	198352,12	50211,019	154659,28	823147,35	165231,9
1 [P50454_	69992,912	287259,94	108735,03	21089,695	68950,281	302290,46	99230,799
1 [P50454_	10931,946	61255,398	15912,398	2927,1301	10416,347	64950,169	13367,652
1 [P50454_	1982,0551	10440,205	1461,0697	159,5067	1901,9613	11102,841	942,38241
1 [P50454_	6308,2861	30859,549	4624,0007	584,5427	6104,2328	32779,695	3110,9517
1 [P50454_	32069,531	117934,36	29825,715	5248,4979	31872,878	124372,35	24893,925
1 [P50454_	66879,775	326910,84	81120,274	12465,338	64742,647	346208,31	67384,28
1 [P50454_	4824,2692	19967,715	5151,5887	1399,4928	4747,2805	21093,104	4301,8055
1 [P50454_	56657,956	122650,63	33797,003	16059,622	58139,414	127774,65	28465,155
1 [P50454_	116963,44	207443,81	69533,811	27993,672	121004,45	214363,96	61496,419
1 [P50454_	106740,09	433032,06	126849,54	27753,668	105233,29	456812,17	109742,21
1 [P50454_	55376,242	291377,5	83585,325	15382,926	53172,681	308482,22	72051,943
1 [P50454_	56064,148	274028,72	87872,999	20030,526	54285,721	289562,25	77530,852

1 [P35527]	180557,63	98305,872	31797,483	19719,071	191514,49	93658,271	27794,345
1 [P35527]	85140,203	73595,352	26740,769	10058,507	89729,217	73204,85	24110,512
1 [P35527]	10203,36	8804,4118	1743,8726	919,05115	10752,707	8803,6663	1325,4352
1 [P35527]	49458,316	32770,82	24684,928	10415,059	52344,381	31448,994	24293,017
1 [P35527]	161,77538	231,86711	94,772207				

1 [P35527]	62817,473	41426,842	17337,284	9372,159	66478,276	40185,74	15899,876
1 [P35527]	258268,25	157267,69	61531,842	36075,021	273593,47	151434,92	55739,753
1 [P35527]	381827,81	226646,6	92836,957	48555,951	404611,97	217492,44	84983,11
1 [P35527]	120598,5	67726,761	20155,497	10595,259	127871,77	64822,527	17381,543
1 [P35527]	83827,719	49344,211	19819,606	8694,4279	88838,378	47319,071	18160,353
1 [P35527]	85085,557	107965,63	32029,097	13135,507	88935,695	110160,51	27610,095
1 [P35527]	288459,63	181726,81	66309,136	38449,595	305444,31	175776,6	59359,541
1 [P35527]	420678,72	247319,36	78858,779	38398,675	445817,43	237798,44	69133,164
1 [P35527]	22241,767	37664,168	14697,994	6371,2852	23049,461	38789,682	13349,882
1 [P35527]	86061,104	138553,16	37829,47				

1 [P67936_	359716,96	525483,75	291636,32	95015,624	374611,76	535236,96	279537,6
3 [P07951,	503728,59	261603,39	177983,05	78231,861	534625,89	244735,23	173698,41
2 [P67936_	93572,609	52063,599	33962,782	15726,418	99238,164	49178,995	32977,543
2 [P67936_	265938,53	180509,67	108957,06	41551,934	281349,33	174514,03	105316,91
8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
1 [P67936_	507368,35	581765,5	289878,13	131084,98	531723,05	586691,45	272888,99
4 [P07951,	580146,66	727732,42	741913,13	243074,97	606916,1	725088,2	747424,18
4 [P07951,	24673,978	31057,32	30323,086	10576,904	25809,417	30993,332	30442,571
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
4 [P07951,	77615,694	113833,86	36589,863	14044,931	80802,893	116826,63	32130,125
4 [P07951,	419108,78	410503,13	237661,7	65338,483	440730,88	409009,87	229572,53
2 [P67936_	48879,516	33956,022	22525,385	8747,2031	51696,908	32835,598	21960,713
2 [P67936_	281010	185696,21	143568,54	46523,116	297420,83	178035,73	142182,08
3 [P67936_	7794,958	5234,1462	3327,7633	1602,9493	8247,9708	5049,5952	3218,5899
1 [P67936_	361873,28	257018,1	163576,29	51379,538	382608,57	249274,42	159378,36
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56

1 [P78527_	223905,11	139107,86	161813,7	41143,729	237201,76	130759	164850,35
1 [P78527_	10859,315	19158,561	3476,0929	883,36394	11234,759	19889,148	2572,3485

1	[P78527_	25781,654	49146,363	10061,205	2137,2937	26595,537	51115,487	7836,7675
1	[P78527_	4743,6665	7209,0732	1411,1057	266,53429	4932,5202	7438,7709	1083,0294
1	[P78527_	23860,838	38218,121	8198,7976	2181,8642	24769,464	39494,677	6481,8259
1	[P78527_	17957,999	26089,156	6461,405	2266,1047	18699,477	26826,435	5327,1405
1	[P78527_	19594,122	32920,594	7806,9045	1250,3551	20307,959	34057,002	6413,0917
1	[P78527_	78962,558	105352,59	32887,72	9912,3355	82426,91	107699,47	28825,556
1	[P78527_	10167,036	19562,721	3636,9235	621,26238	10483,875	20364,477	2731,9043
1	[P78527_	25870,012	43255,457	10839,269	2310,4506	26817,326	44721,983	9025,654
1	[P78527_	100402,94	166101,7	39501,738	10665,404	104115,98	171734,74	32292,4
1	[P78527_	21500,878	38943,313	8415,0786	1413,4465	22223,524	40421,007	6701,3384
1	[P78527_	69629,421	111630,2	29807,276	7439,347	72282,477	115173,29	25213,471
1	[P78527_	1374,6475	3483,6902	355,1198	77,16634	1399,382	3663,6881	171,45483
1	[P78527_	43909,066	67879,18	18035,076	4637,2224	45635,669	69936,669	15231,854
1	[P78527_	29855,793	49758,43	13536,687	2983,1947	30953,187	51404,745	11521,684
1	[P78527_	159231,57	295410,28	59539,18	10135,349	164431,12	307004,77	46216,69

3	[P07951,	503728,59	261603,39	177983,05	78231,861	534625,89	244735,23	173698,41
2	[P67936_	93572,609	52063,599	33962,782	15726,418	99238,164	49178,995	32977,543
2	[P67936_	265938,53	180509,67	108957,06	41551,934	281349,33	174514,03	105316,91
1	[P67936_	158273,27	100136,12	80583,712	36410,86	167611,78	95476,064	79609,579
1	[P67936_	1140319,8	1163271,6	615973,05	272288,13	1198133,4	1163936,4	584639,22
8	[P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8	[P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8	[P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8	[P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
1	[P67936_	446924,88	308113,59	195579,77	91779,843	472729,37	298019,07	189222,69
1	[P67936_	186466,77	107356,56	91197,167	37878,901	197694,45	101136,28	90609,374
1	[P67936_	106627,47	60772,91	48931,458	21992,26	113058,98	57270,926	48361,674
1	[P67936_	5256775,5	3165099,9	2552555,7	1077209,7	5570312,2	3001437,2	2525736,1
1	[P67936_	2500638	1573965,6	1343488,4	562593,99	2648402	1497406,1	1334743,5
1	[P67936_	5797659	3493344,1	2836698,9	1239153,7	6143414,6	3312362,2	2806474,6
1	[P67936_	200172,25	119698,17	101753,7	37392,88	212132,07	113251,54	101302,02
1	[P67936_	509847,25	899931,31	791857,97	355677,62	527869,06	913958,99	785987,26
4	[P07951,	580146,66	727732,42	741913,13	243074,97	606916,1	725088,2	747424,18
4	[P07951,	24673,978	31057,32	30323,086	10576,904	25809,417	30993,332	30442,571
8	[P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8	[P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8	[P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8	[P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8	[P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8	[P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8	[P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8	[P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537
8	[P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8	[P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8	[P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8	[P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8	[P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8	[P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8	[P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8	[P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8	[P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609

8 [P06753_	1167640,2	1192010,1	1233745,3	494870,1	1227208,1	1173261,9	1240382,7
8 [P06753_	242235,48	359109,05	165410,66	72297,706	252133,04	367102,9	154116,96
4 [P07951,	77615,694	113833,86	36589,863	14044,931	80802,893	116826,63	32130,125
4 [P07951,	419108,78	410503,13	237661,7	65338,483	440730,88	409009,87	229572,53
2 [P67936_	48879,516	33956,022	22525,385	8747,2031	51696,908	32835,598	21960,713
2 [P67936_	281010	185696,21	143568,54	46523,116	297420,83	178035,73	142182,08
3 [P67936_	7794,958	5234,1462	3327,7633	1602,9493	8247,9708	5049,5952	3218,5899
8 [P06753_	194887,5	191683,4	125455,72	42663,069	204934,32	190571,26	122308,04
8 [P06753_	203593,08	212140,34	118744,59	47386,255	213825,23	212330,91	113633,56

3 [P07437,	122748,1	229252,5	72119,309	29728,633	126740,32	237467,58	62903,071
3 [P07437,	72523,03	128076,52	36738,33	15457,667	75036,339	132529,65	31361,348
3 [P07437,	232574,84	167753,49	89943,854	30184,066	245836,39	163473,98	86001,789
3 [P07437,	422889,56	229819,05	139079,5	48334,785	448602,76	216806,07	134789,24
3 [P07437,	70664,569	189358,77	54993,907	10606,331	71738,934	198245,43	47574,921
3 [P07437,	556535,8	1213665,5	320911,38	83020,278	570889,74	1265052,8	270340,33
5 [P07437,	158186,74	246368,5	69009,986	10936,114	164370,38	253795,04	59371,464
5 [P07437,	136489,58	202216,13	60065,519	8333,243	142047,95	207777,19	52464,434
5 [P07437,	260674,66	442854,69	119786,23	15546,875	270076,61	457848,23	102264,85
4 [P07437,	116552,53	177057,78	60513,25	17427,031	121210,81	181860,62	54048,46
4 [P07437,	15843,876	20495,275	6197,9324	2951,8947	16552,566	20927,825	5348,2592
4 [P07437,	177082,12	244977,52	70715,363	33047,814	184662,13	251039,28	60369,856
3 [P07437,	8168,3202	15423,864	4927,4639	1485,8789	8430,4565	15979,744	4335,4669
4 [P07437,	494240,21	925059,56	261904,6	39573,212	510254,1	959201,91	225860,3
4 [P07437,	224387,44	506487,63	113417,86	15052,142	229796,02	529093,78	91512,16
5 [P07437,	142060,43	331430,47	88009,635	13514,525	145263,67	346080,8	74610,418
5 [P07437,	12295,527	22303,764	6912,1196	1253,9214	12709,411	23083,525	6078,3207
4 [P07437,	10040,13	27931,853	4760,2053	1107,8709	10168,739	29375,653	3417,6823
3 [P07437,	5451,9918	11537,499	2540,4274	407,56661	5599,7801	12032,186	2035,6746
3 [P07437,	5552,5221	11163,377	2405,0858	384,51191	5715,5249	11626,083	1913,2909
5 [P07437,	74820,007	159661,33	43147,626	6331,1586	76824,994	166288,08	36769,329
5 [P07437,	23134,843	46218,926	12852,986	2664,718	23822,135	48031,719	11001,7
5 [P07437,	29211,637	46072,637	12031,622	2959,7036	30340,687	47513,549	10119,5
5 [P07437,	237519,66	267284,03	81602,755	18582,71	248995,17	270928,79	71486,026
3 [P07437,	8314,8314	14322,511	3903,2987	1117,2526	8610,5556	14813,975	3312,3032
3 [P07437,	11032,725	19651,848	4963,4066	1490,1348	11411,06	20362,826	4122,5363
3 [P07437,	3874,5038	6825,2148	1774,7752	509,0701	4009,0258	7067,7663	1487,2243
3 [P07437,	56085,149	95496,055	22774,702	6048,4933	58101,47	98836,876	18636,276
1 [Q13885]	8590,6846	15276,835	5859,3127	910,77779	8887,1051	15763,724	5375,9212

3 [P07900_	122186,62	232096,64	78936,665	11215,546	126081,64	240350,27	70889,882
3 [P07900_	56157,411	116752,67	44219,293	5803,8799	57736,156	121096,17	40516,83
3 [P07900_	25286,983	50557,582	18598,504	2428,8311	26040,305	52394,567	16956,374
3 [P07900_	23515,33	46398,074	16775,4	4271,9403	24228,791	48074,206	15157,331
3 [P07900_	20579,424	46136,738	9904,6325	2559,7447	21081,91	48201,169	7824,103
1 [P07900_	52087,121	95647,734	34102,119	4399,1726	53818,571	98887,714	30923,444
1 [P07900_	362915,57	556301,31	190561,29	33594,333	377314,63	571581,8	171192,02
1 [P07900_	1147963,2	1835194,9	559323,85	100357,65	1191859,6	1890985,1	490279,45
1 [P07900_	585020,78	1073939	345453,66	65507,049	604450,64	1111523,3	306082,03
1 [P07900_	161597,61	290722,19	98930,057	17280,053	167094,22	300515,39	88727,743
1 [P07900_	207661,12	261184,98	85600,218	22695,313	217112,44	266113,41	75951,609
1 [P07900_	78042,262	118539,88	30294,625	3655,263	81155,182	122084,18	25497,033

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2 [P07900_	305346,6	575230,88	183330,43	34821,223	315174,07	595926,9	162106,24
2 [P07900_	147317,96	241247,19	70157,693	19530,379	152826,87	248920,14	60534,334
1 [P07900_	349039,97	475552,65	144818,94	57414,37	364141,29	486737,23	125636
1 [P07900_	69329,271	115823,59	33641,157	10985,706	71873,012	119598,14	28946,249
1 [P07900_	6911,157	12775,315	3275,7013	705,52902	7138,2762	13252,479	2743,9644
1 [P07900_	52370,733	72077,305	28954,411	6034,7791	54625,679	73578,722	26719,902
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1 [P07900_	91970,515	134921,42	44427,092	10143,981	95747,159	138434,35	39506,083
3 [P07900_	1510868	2087383,5	782609,22	164114,37	1575716,4	2133044,9	713888,53
3 [P07900_	806877,96	1300636	504243,81	128462,82	837572,89	1337119,4	461429,19
3 [P07900_	503039,57	865610,44	317257,04	76576,656	521001,93	892645,35	287637,54

1 [P11021_	84207,26	170792,52	53013,494	16131,209	86657,831	177395,49	46339,685
1 [P11021_	256757,71	677830,88	209996,27	66563,511	260886,91	708979,69	183259,08
1 [P11021_	377382,69	791711,13	222260,44	60826,577	387790,61	823902,6	190034,33
1 [P11021_	357840,06	892218,75	268547,03	65064,277	364706,49	932204,44	233726,4
1 [P11021_	44528,682	82158,797	23992,179	7960,2855	45997,141	85128,104	20658,389
1 [P11021_	47010,668	88190,047	27427,047	6736,7366	48531,151	91372,784	24058,87
1 [P11021_	260199,56	565739,38	137446,18	31012,518	266938,75	590035,71	113237,02
1 [P11021_	20940,12	48588,805	10719,843	2047,465	21416,526	50800,121	8578,7011
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1 [P11021_	158498,83	312400,13	85572,333	18714,87	163297,21	324560	72927,98
1 [P11021_	38434,676	77697,289	22866,107	4943,4241	39557,872	80733,075	19833,753
1 [P11021_	52913,928	79982,391	29893,296	4331,0765	55038,929	82051,531	27330,039
1 [P11021_	74425,89	120901,5	37784,232	9736,0357	77231,539	124623,72	33173,855
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1 [P11021_	539346,5	738540,75	209591,42	93837,716	562592,78	756581,02	178373,26
1 [P11021_	1391824,5	1733903	326113,09	169487,74	1455369	1773630,5	241953,92
1 [P11021_	365127,82	511687,53	126165,4	35860,994	380603,59	525341,87	104262,59
1 [P11021_	73741,402	133772	53405,522	18015,44	76231,144	138064,04	48904,922
1 [P11021_	179632,28	244728,88	61768,624	23278,369	187396,2	250896,25	51149,548
1 [P11021_	109408	214964,17	62651,938	20366,605	112737,06	223189	53929,393
1 [P11021_	208956,02	327218,28	108661,44	41108,856	217097,22	336609,27	96067,919
1 [P11021_	430966,28	831573,38	217482,6	44010,721	444387,17	863697,42	183266,38
1 [P11021_	1439914,7	2864880	783448,31	207976,75	1482934,1	2977308,8	665802,29
1 [P11021_	871812,15	1752715,3	378269,47	108276,23	897407,2	1825349,8	299041,09
1 [P11021_	1061626,7	2124330	634284,13	146053,7	1093121	2206352,9	551647,22
1 [P11021_	475007	642174,88	167109,33	56434,956	495646,57	657962,11	139851,11
1 [P11021_	14827,013	25509,816	7908,8594	2229,0922	15355,606	26353,093	6922,2482
1 [P11021_	167111,1	249160,31	79076,409	21812,271	173886,14	255918,4	69615,431
1 [P11021_	331257,03	498377,78	144801,46	35476,652	344583,02	512518,27	125158,47
1 [P11021_	1176620,2	2208765,5	662261,56	194336,23	1214628,6	2289333,8	574831,14
1 [P11021_	205335,1	371218,94	112935,07	33074,589	212272,22	384224,11	98363,916
1 [P11021_	1341795,1	1811567,9	569077,13	181648,4	1400212,4	1852827,9	499005,58
1 [P11021_	638218,21	1199664,6	368217,49	97834,234	658806,21	1243200,6	321741,7
1 [P11021_	23886,48	41927,676	12356,649	3768,1023	24719,946	43365,268	10678,659
1 [P11021_	108311,21	189518,66	59371,883	19025,739	112105,5	195881,44	51982,241
1 [P11021_	193071,52	339742,69	108492,92	31270,734	199795,7	351151,28	95530,811
1 [P11021_	157239,61	315660,13	94976,009	20156,98	161883,02	327856,77	82820,599
1 [P11021_	514799,01	1192544,5	328450,95	53475,566	526595,49	1244646,5	280973,53
1 [P11021_	12531,423	32393,219	8947,4309	1536,3606	12746,93	33900,099	7654,1872

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2 [P14618_	42972,182	92621,539	27294,787	6383,0572	44105,54	96420,488	23657,745
2 [P14618_	110253,18	212517,91	102467,15	38475,692	113721,45	219206,42	96288,074
2 [P14618_	74676,952	194023,7	47815,763	11984,122	75936,434	203261,5	39488,51
2 [P14618_	54952,279	166349,66	39313,277	10889,748	55375,336	174902,12	32000,289
2 [P14618_	61395,254	163972,84	36252,399	8829,6219	62333,013	172023,55	28936,893
2 [P14618_	272387,88	765603,13	244613,12	58194,58	275783,49	801662,6	215713,78
2 [P14618_	812869,04	946801,19	351361,73	114741,95	851499,3	959517,5	318344,06

1 [P06576_	52018,099	78117,742	28778,768	7971,201	54117,683	80131,488	26081,085
1 [P06576_	13060,351	15026,24	3898,4517	1328,6295	13683,894	15272,166	3262,0892
1 [P06576_	75362,963	105861,45	29439,397	6225,4368	78554,048	108589,21	25225,403
1 [P06576_	27763,99	42481,051	12142,597	2409,3498	28865,649	43722,762	10478,142
1 [P06576_	18627,262	25832,557	7773,7238	1530,3106	19423,467	26463,984	6792,3106
1 [P06576_	107357,28	163163,88	50574,993	12636,224	111643,13	167760,43	44351,176
1 [P06576_	61746,717	89109,313	27849,267	6848,2568	64312,641	91413,909	24475,119
1 [P06576_	104404,29	158936,78	57558,266	9242,2198	108572,06	163155,71	52289,156
1 [P06576_	511388,13	403637,5	143839,89	39528,208	539766,01	398755,25	129926,1
1 [P06576_	411512,93	459011,53	213879,76	85711,788	431528,66	462662,02	200072,1
1 [P06576_	211504,93	286334,16	90670,728	29303,155	220697,03	292869,11	79626,631
1 [P06576_	41089,772	48569,555	18590,113	5793,9623	43027,786	49242,311	16944,591
1 [P06576_	87428,268	105944,59	39960,872	13688,648	91496,23	107571,51	36276,076
1 [P06576_	75309,991	117284,1	39407,596	19626,433	78258,242	120609,85	34720,04
1 [P06576_	510823,75	641974,19	223870,1	90339,693	534092,41	653632,83	199739,04
1 [P06576_	1015207,9	1256283,6	467556,62	180878,69	1061886,9	1277153	422529,65
1 [P06576_	3410,6404	5409,4595	1681,3063	330,1912	3541,9937	5571,1464	1478,9473
1 [P06576_	72495,353	119091,09	40248,302	8333,778	75201,975	122711,04	36001,65
1 [P06576_	33139,829	50955,879	17490,871	3394,3984	34451,371	52360,958	15705,73
1 [P06576_	15364,703	23893,715	7824,7687	1796,3784	15966,816	24575,963	6948,5658
1 [P06576_	39479,544	70570,852	18257,135	4651,7655	40828,364	73118,703	15302,048
1 [P06576_	33097,662	55695,875	16391,939	5004,9227	34303,62	57519,223	14163,093
1 [P06576_	153202,87	256758,08	86341,552	30540,325	158814,24	264776,46	76604,698
1 [P06576_	989150,94	1235823,4	437915,31	145554,27	1034367,5	1257666	393248,03
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1 [P06576_	394742,34	499003,59	163642,98	53938,573	412654,79	508546,01	144757,92
1 [P06576_	415594	512538,81	185489,35	57530,983	434736,63	521130,49	167402,81
1 [P06576_	196715,52	247085,88	90276,868	27727,463	205681,71	251431,44	81621,115
1 [P06576_	529306,03	680219,19	229892,05	75819,59	553092,71	693565,88	204581,55
1 [P06576_	339710,73	427540,25	150779,58	54483,954	355173,1	435279,68	135087,7
1 [P06576_	541494,13	670858,94	242078,2	77138,155	566370,53	682285,39	218265,73
1 [P06576_	957434,31	1273672,5	504276,95	71383,488	999588,84	1298398,5	465768,61
1 [P06576_	1082414,3	1432629	539067,49	145133,29	1130208,2	1461017,6	490719,78
1 [P06576_	477880,38	808108,19	215490,34	50148,569	495194,33	835432,28	182335,02
1 [P06576_	735208,58	1217700,3	348962,15	78332,125	762405,94	1257126,1	300837,98

3 [P07900_	122186,62	232096,64	78936,665	11215,546	126081,64	240350,27	70889,882
3 [P07900_	56157,411	116752,67	44219,293	5803,8799	57736,156	121096,17	40516,83
3 [P07900_	25286,983	50557,582	18598,504	2428,8311	26040,305	52394,567	16956,374
3 [P07900_	23515,33	46398,074	16775,4	4271,9403	24228,791	48074,206	15157,331
3 [P07900_	20579,424	46136,738	9904,6325	2559,7447	21081,91	48201,169	7824,103
1 [P08238]	17662,502	39692,387	15098,42	2449,7332	18095,976	41258,027	13822,327
2 [P08238,	121501,82	319108,97	86006,123	12023,741	123482,77	334145,88	73227,335
2 [P08238,	261421,42	634655,06	227322,12	68829,014	266826,29	661488,03	204485,63

2 [P08238,	110238,87	236913,84	73908,09	14047,616	113163,75	246477,47	65030,093
2 [P08238,	402082,34	823289	296096,18	57638,197	413644,48	854043,22	268022,15
2 [P08238,	247866,68	487884,34	151983,55	36641,735	255396,41	506260,56	133380,11
2 [P07900_	177906,72	256225,45	69682,092	11588,071	185304,13	263164,4	59500,938
2 [P07900_	305346,6	575230,88	183330,43	34821,223	315174,07	595926,9	162106,24
2 [P07900_	147317,96	241247,19	70157,693	19530,379	152826,87	248920,14	60534,334
1 [P08238]	751272,15	1184362,3	442964,01	155856,63	780406,77	1217065,5	401031,22
1 [P08238]	16041,413	29395,264	7261,7422	2088,3393	16573,884	30493,353	5996,4198
1 [P08238]	10212,06	21465,932	5056,6946	1339,7076	10492,181	22371,384	4118,9339
1 [P08238]	501870,03	829914,13	230619,41	52749,565	520458,94	856967,62	197274,08
1 [P08238]	342335,3	686683,94	283064,91	41310,352	352505,9	710720,08	262829,67
2 [P08238,	132455,66	198660,66	49185,353	13259,53	137791,85	204547,49	40713,314
2 [P08238,	108206,43	176112,91	62466,597	11872,13	112283,15	181306,87	56442,552
2 [P08238,	104732,75	169881,75	56269,022	16129,794	108688,28	174999,61	49938,855
2 [P07900_	432118,79	659328,19	185845,85	30368,524	449302,7	678606,54	160108,9
1 [P08238]	91970,515	134921,42	44427,092	10143,981	95747,159	138434,35	39506,083
3 [P07900_	1510868	2087383,5	782609,22	164114,37	1575716,4	2133044,9	713888,53
3 [P07900_	806877,96	1300636	504243,81	128462,82	837572,89	1337119,4	461429,19
3 [P07900_	503039,57	865610,44	317257,04	76576,656	521001,93	892645,35	287637,54

1 [P02452]	27663,304	196596,09	42083,65	12758,875	25466,334	209218,77	33044,163
1 [P02452]	34687,504	88264,289	30565,748	19093,745	35317,815	92138,411	26893,114
1 [P02452]	328804,6	6191885,5	1163027,4	935726,54	220301,26	6629355,9	841581,64
1 [P02452]	41958,679	333558,88	77129,245	49507,944	37875,059	355112,63	61040,363
1 [P02452]	103369,58	1339156,8	240626,15	196924,16	82226,982	1432070,1	170515,6
1 [P02452]	4436,7338	58978,809	9817,2812	2143,5922	3496,7302	63102,127	6948,6997
1 [P02452]	28109,144	134577,97	33311,884	12708,927	27270,976	142489,65	27324,665
1 [P02452]	16319,697	106492,12	21507,685	7394,5071	15225,29	113286,43	16489,475
1 [P02452]	15685,348	96643,633	23352,337	7055,7491	14757,848	102629,72	19090,317
1 [P02452]	20838,318	129098,19	28064,03	8417,5687	19589,065	137203,04	22164,386
1 [P02452]	113417,44	239718,27	65462,124	21173,683	116506,3	249579,44	55438,121
1 [P02452]	5745,9985	30247,859	5451,8783	2020,0522	5514,9784	32128,289	3979,1293
1 [P02452]	15241,53	167242,8	32895,339	8890,712	12771,531	178602,38	25046,842
1 [P02452]	84110,801	110330,56	35836,752	13220,704	87842,15	112653,51	31573,417
1 [P02452]	21885,093	182887,42	38321,275	12533,894	19562,612	194901,94	29812,001
1 [P02452]	88407,874	361199,06	79300,051	22201,881	87088,724	381933,23	62956,478
1 [P02452]	82315,169	163248,16	36916,827	10376,354	84780,718	169887,86	29660,847
1 [P02452]	6233,9985	40324,086	9682,7526	3719,0681	5824,5127	42843,67	7865,7223
1 [P02452]	13918,102	115050,8	23434,487	14239,793	12467,501	122622,49	17753,95
1 [P02452]	10834,14	51688,648	12653,469	6995,9657	10514,863	54729,973	10251,505
1 [P02452]	11542,135	47958,273	12833,684	7492,628	11354,269	50650,034	10651,175
1 [P02452]	83511,767	151556,19	42910,026	18541,939	86318,778	156990,84	36488,328
1 [P02452]	126010,65	286773,56	76619,125	29388,91	129005,92	299241,77	64303,789

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1 [P10809_	86317,844	82781,015	38186,742	13462,137	90802,004	82680,952	35768,926
1 [P10809_	42435,621	16925,578	16239,89	5639,5292	45149,138	15054,495	16328,4
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1	[P10809_	108572,72	127676,3	37569,091	10884,346	113700,35	129774,52	32530,533
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1	[P10809_	185033,45	96698,877	66459,74	29490,084	196370,59	90516,27	64903,091
1	[P10809_	12807,867	9731,7542	7450,3979	3024,5487	13529,18	9454,9676	7343,8771
1	[P10809_	33470,977	21918,721	19361,593	8223,0839	35431,395	20917,599	19273,188
1	[P10809_	24692,854	22653,488	14547,374	5562,349	26000,035	22425,495	14133,002
1	[P10809_	108766,95	38410,125	28627,191	8528,3311	115820,43	33636,144	28373,617
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1	[P10809_	97738,942	118990,33	47637,141	11230,089	102276,74	120756,34	43896,476
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1	[P10809_	248320,84	232918,3	106899,02	38610,171	261331,36	232307,59	100028,65
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1	[P04083_	209263,72	232247,22	48322,879	10126,763	219428,51	235961,58	37994,897
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1	[P04083_	35925,805	32359,034	7811,5894	2098,9078	37831,932	32410,819	6438,48
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1	[P04083_	8257,9006	16746,748	3057,6755	667,27833	8496,8913	17463,3	2272,0168
1	[P04083_	28747,146	53279,07	10055,023	1452,8845	29686,556	55390,442	7613,9565
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1	[P04083_	43963,127	77503,609	18810,743	4269,1234	45487,392	80303,239	15503,526
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1	[P04083_	8162,7226	18363,484	4328,5169	1489,8267	8360,921	19174,564	3510,8694
1	[P04083_	11103,818	26803,342	5912,6095	1243,1771	11334,28	28051,724	4725,8768
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1	[P04083_	107103,05	92515,112	50951,197	8607,9657	112888,43	91456,663	49201,57
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1 [Q08211]	44956,449	74761,422	19878,232	6999,5134	46612,08	77244,191	16705,557
1 [Q08211]	24288,037	40965,77	12183,466	4520,4499	25171,07	42306,537	10517,929
1 [Q08211]	37763,931	62430,613	17342,936	5392,1709	39163,043	64465,537	14772,677
1 [Q08211]	39556,156	73481,164	23806,128	2681,8182	40851,58	76076,937	21202,736
1 [Q08211]	57534,914	56029,1	19725,28	5435,8582	60501,846	56215,502	17757,939
1 [Q08211]	204876,74	287732,97	95292,133	23247,471	213562,81	294650,81	84783,906
1 [Q08211]	51226,183	60081,68	19113,539	7314,776	53649,75	61014,497	16762,511
1 [Q08211]	26218,545	32107,433	9712,1739	1628,9383	27429,798	32695,332	8512,4644
1 [Q08211]	211899,07	358864,22	126162,16	19937,545	219584,53	370030,49	113968,61
1 [Q08211]	163540,74	258441,16	75015,955	20238,944	169855,78	266301,08	64732,933
1 [Q08211]	70606,741	122592,44	44336,293	5551,032	73104,314	126479,94	40321,376
1 [Q08211]	41049,258	65102,711	24966,717	3059,4389	42633,311	66894,883	22948,19
1 [Q08211]	124563,45	166578,72	61916,927	15752,294	130026,67	169986,47	56281,063
1 [Q08211]	35041,562	46116,266	12200,927	3296,1	36591,088	47184,122	10293,365
1 [Q08211]	319954,85	450131,54	158415,52	23510,648	333509,3	460683,73	143275,04
1 [Q08211]	181322,45	266337,51	86346,881	11394,022	188760,22	273328,68	76896,706
1 [Q08211]	30480,212	52790,707	15911,682	5410,8833	31559,114	54563,667	13798,963
1 [Q08211]	40578,748	51770,336	15720,303	3431,1353	42409,235	52824,475	13753,599
1 [Q08211]	96695,904	119015,64	37053,003	5167,7467	101150,98	121191,82	32726,675

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4 [Q71U36,	24738,721	44769,582	12803,323	3067,5145	25573,019	46365,894	11020,576
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3 [Q71U36,	78872,53	143924,84	52750,12	16674,679	81514,565	148724,31	47648,543

3 [Q71U36,	100510,57	235033,67	72198,332	15179,757	102771,7	245121,69	63235,115
3 [Q71U36,	79089,781	206720,44	64780,117	13988,864	80406,344	216144,75	56958,057
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3 [Q71U36,	84027,475	207729,73	36586,009	8275,4078	85661,034	217833,14	26707,7
3 [Q71U36,	37637,952	87655,938	21026,82	5694,1814	38488,456	91599,791	17212,262
3 [Q71U36,	36476,236	90930,07	19842,52	2667,3655	37171,705	95247,829	15864,495
4 [Q71U36,	20662,967	32072,461	8148,1932	1302,1364	21472,484	33061,85	6832,141
4 [Q71U36,	19576,468	29485,15	7823,9683	1454,2181	20362,837	30347,036	6630,3759
4 [Q71U36,	250864,98	383934,34	97417,538	15899,247	260809,29	395558,66	81644,965
4 [Q71U36,	223075,4	339203,44	89257,316	13745,313	231967,1	349278,46	75591,765
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2	[P35579,	42137,501	154893,87	23907,736	3661,8909	41870,671	163842,42	16352,31
1	[P35580]	209041,36	179245,71	55841,124	35655,875	220333,36	178491,28	48215,387

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3 [Q71U36,	93408,696	130479,02	41903,683	18841,757	97383,037	133628,28	36676,862
3 [Q71U36,	78872,53	143924,84	52750,12	16674,679	81514,565	148724,31	47648,543
3 [Q71U36,	100510,57	235033,67	72198,332	15179,757	102771,7	245121,69	63235,115
3 [Q71U36,	79089,781	206720,44	64780,117	13988,864	80406,344	216144,75	56958,057
3 [Q71U36,	40701,653	105593,66	34397,786	8708,6298	41396,838	110346,35	30439,562
3 [Q71U36,	84027,475	207729,73	36586,009	8275,4078	85661,034	217833,14	26707,7
3 [Q71U36,	37637,952	87655,938	21026,82	5694,1814	38488,456	91599,791	17212,262
3 [Q71U36,	36476,236	90930,07	19842,52	2667,3655	37171,705	95247,829	15864,495
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4 [Q71U36,	19576,468	29485,15	7823,9683	1454,2181	20362,837	30347,036	6630,3759
4 [Q71U36,	250864,98	383934,34	97417,538	15899,247	260809,29	395558,66	81644,965
4 [Q71U36,	223075,4	339203,44	89257,316	13745,313	231967,1	349278,46	75591,765
4 [Q71U36,	78931,167	121357,69	33808,343	5585,1831	82050,05	124957,6	29038,66
5 [P68363,	4815,985	9767,1973	3636,2349	502,92132	4956,5462	10125,096	3320,887
5 [P68363,	21966,947	41645,738	15138,724	1972,3411	22669,553	43092,386	13774,41
5 [Q71U36,	157228,19	346137,75	89010,857	16492,117	161212,24	360968,57	74695,338
5 [Q71U36,	1511366	3237278,3	813316,75	126506,97	1551569	3373997,4	679155,24
5 [Q71U36,	46717,622	93865,258	25005,94	3251,8862	48093,47	97598,887	21251,484
5 [Q71U36,	254242,43	528366,75	145953,13	27632,215	261359,44	549772,75	124819,07
5 [Q71U36,	59621,132	80387,5	21936,591	3292,2784	62217,009	82319,773	18768,503
5 [Q71U36,	442962,46	578032,5	161938,25	21413,039	462660,98	590882,69	139610,5
5 [Q71U36,	101665,65	144591,16	42640,658	7197,605	105934,06	148318,58	37133,344
3 [Q71U36,	28615,612	44211,766	14647,633	8582,6593	29743,225	45458,013	12813,287
3 [Q71U36,	266313,72	346343,59	140301,83	56597,102	278209,42	352592,69	128488,32
3 [Q71U36,	331530,15	520180,83	196964,51	101276,43	344440,85	534373,61	177326,19
3 [Q71U36,	77518,426	126130,14	42418,468	14823,129	80438,208	129925,13	37646,56
3 [Q71U36,	76678,043	120474,43	29483,111	3773,184	79650,295	124286,84	24496,846
3 [Q71U36,	95541,57	95473,949	14408,103	2475,3147	100404,35	96571,598	9813,3701
3 [Q71U36,	29388,169	67618,367	20375,161	3531,3067	30072,519	70503,288	17801,602
3 [Q71U36,	11530,401	17346,255	4270,0597	1809,0736	11993,781	17863,442	3500,2125
5 [Q71U36,	95126,339	198042,02	56250,081	7725,736	97782,754	206025,52	48565,027
5 [Q71U36,	43715,218	93434,344	24171,424	3758,989	44882,81	97351,754	20350,366
5 [Q71U36,	112431,9	216602,83	60210,308	9390,427	115942,75	224843,15	51671,628
5 [Q71U36,	1571097,1	3085342	839422,9	148652,08	1618897,1	3205249	715657,13
5 [Q71U36,	204764,31	180094,33	88541,945	44671,923	215750,04	178622,18	83078,063
5 [Q71U36,	103957,55	203355,98	57830,406	19683,077	107138,98	211154,24	49446,863
5 [Q71U36,	709104,75	532368,68	276194,22	161144,87	749090,31	520945,96	260087,22
5 [Q71U36,	118519,67	217848,3	57263,412	17610,74	122441,77	225898,11	48068,441
5 [Q71U36,	290521,56	225207,33	112651,33	66531,544	306750,99	221112,14	105561,02
5 [Q71U36,	225912,52	480820,75	131700,83	21669,806	231994,44	500683,04	112521,6

5 [Q71U36,	284046,22	460863,66	150192,84	31168,059	294769,82	474829,49	133367,01
1 [Q14315_	824412,56	752933,2	508068,51	182466,36	868142,32	744323,55	496363,75
3 [P21333_	670451,51	2114357	337689,01	69301,265	673700,43	2230080,3	234760,1
1 [Q14315_	182140,59	118801,94	43551,014	28991,478	192779,1	115316,1	38848,569
1 [Q14315_	305518,44	202337,62	68690,242	61025,862	323294,59	196879,83	59734,896
2 [O75369_	142176,76	234403,41	87350,014	32644,256	147472,17	241301,14	78938,7
2 [P21333_	53641,529	55249,438	16427,374	6126,0136	56341,721	55728,295	14208,897
1 [Q14315_	105754,34	132679,58	32788,548	11133,087	110567,74	135512,93	27051,572
1 [Q14315_	113986,25	123157,27	34141,512	12063,441	119599,96	124660,29	29059,535
1 [Q14315_	42432,416	72564,766	20905,238	3832,5651	43953,508	74998,316	18080,301
1 [Q14315_	77450,414	69899,302	24359,328	11610,506	81561,571	69779,85	21684,814
3 [P21333_	54794,336	168935,64	41395,498	7581,8041	55151,786	177637,06	34234,699
3 [P21333_	1168,69	3484,7849	753,74871	148,07896	1178,7738	3665,0767	598,46171
3 [P21333_	14250,103	44145,824	10946,46	2173,0008	14338,635	46419,881	9077,1482
3 [P21333_	68381,779	211661,66	50016,972	10208,117	68808,871	222641,06	40866,779
3 [P21333_	21601,959	66204,742	16756,752	3080,862	21751,665	69589,305	13988,536
2 [O75369_	2530,1782	5753,2974	1248,5065	331,89978	2590,2387	6012,6006	989,5318
2 [O75369_	14558,737	32336,938	7303,9123	1951,2499	14920,898	33763,611	5867,9517
1 [Q14315_	34912,612	41153,332	15380,101	5546,1448	36561,47	41729,368	13928,884
1 [Q14315_	19868,777	27580,547	5514,2466	1327,5621	20715,696	28346,124	4257,4534
1 [P19338_	283383,04	321420,81	156927,41	49951,882	297058,4	324046,94	148257,11
1 [P19338_	158238,28	95739,945	57025,528	14006,26	167653,62	91488,764	55404,537
1 [P19338_	43171,023	60222,695	19835,075	5979,4392	45009,917	61655,924	17579,327
1 [P19338_	359880,78	286900,32	176144,85	46408,992	379838,29	281268,24	171354,48
1 [P19338_	186537,49	206753,58	96881,808	23210,825	195638,83	208301,88	91371,446
1 [P19338_	1123048	737460,28	484315,81	121041,22	1188676,3	709356,77	474721,49
1 [P19338_	223494,09	188840,8	116441,64	36815,574	235663,48	185970,8	113039,34
1 [P19338_	441820,94	408383,77	216761,61	59031,496	465116,44	405950,97	207437,66
1 [P19338_	71181,234	47003,161	27720,711	7932,9321	75333,367	45339,353	26848,174
1 [P19338_	5836,875	4409,0023	3710,161	1478,8687	6166,357	4270,5981	3683,9628
1 [P19338_	475904,25	417819,6	188117,37	66536,156	501441,62	414902,8	175662,8
1 [P19338_	103752,69	172088,42	56541,807	16299,795	107590,17	177436,59	50091,289
1 [P19338_	53063,445	76142,43	30017,022	8854,6633	55281,798	77891,485	27500,873
1 [P19338_	235563,16	168294,96	148230,31	67289,52	249066,44	161987,41	147307,97
1 [P19338_	158769,42	124118,39	58334,264	19436,937	167614,35	122064,93	54868,661
1 [P19338_	136645,94	99070,297	57820,117	21277,535	144429,82	96436,233	55717,183
1 [P19338_	69523,477	56827,777	37320,664	15191,137	73350,92	55746,75	36304,478
1 [P19338_	235961,91	224100,3	107340,75	34573,111	248269,01	223554,95	101195,4
1 [P19338_	7247,4556	6019,7032	5363,2626	2276,5676	7645,3368	5867,0906	5339,1179
1 [P19338_	59896,039	56125,047	48911,034	20224,477	63050,29	55226,044	48631,078
1 [P19338_	29020,453	41370,285	12818,569	3760,6529	30237,203	42421,433	11218,66
3 [P35908,	405655,88	235232,8	129998,88	55128,792	430001,48	224046,3	124339,86
2 [PO4264_	522755,84	294946,86	99426,719	37294,798	554261,43	282075,18	88653,59
2 [PO4264_	80833,711	52509,776	18867,247	8791,7862	85559,389	50959,65	16932,265
2 [PO4264_	80428,813	53323,738	17930,995	8710,1179	85107,142	51894,904	15875,09
2 [PO4264_	118032,79	75229,943	24300,838	11220,21	124962,13	72955,734	21373,352
2 [PO4264_	59627,684	39686,812	14022,367	6868,281	63093,225	38616,32	12529,27
2 [PO4264_	469935,75	294048,86	131676,3	43034,548	497664,29	283423,76	123207,63
1 [P35908]	11351,692	11274,122	3177,3547	1004,7957	11931,895	11351,623	2721,8644

1 [P35908]	2860,1425	2660,1323	701,03724	227,9696	3010,1414	2668,4265	590,33197
2 [P04264_	188551,03	141664,36	49142,498	18480,021	199165,33	139417,93	43966,314
2 [P35908,	151998,31	148126,89	28065,021	11269,572	159818,71	149406,6	21076,699
2 [P35908,	129274,52	118208,59	33781,09	16131,12	136099,1	118354,59	28815,595
1 [P35908]	13830,807	19843,114	5927,2255	1669,4863	14407,861	20360,082	5147,8636
1 [P35908]	470184,25	416832,94	117060,89	36646,281	495283,78	416497,9	100280
1 [P35908]	190771,06	195477,41	60987,018	21591,448	200397,44	197016,2	53371,349
1 [P35908]	66568,57	65969,325	15960,087	4936,5109	69972,375	66498,666	13125,804
1 [P35908]	99090,393	133162,34	36608,275	7750,672	103414,32	136334,05	31283,261
1 [P35908]	363388,47	461520,56	127120,36	48991,898	379816,76	471239,74	107757,59
1 [P61978_	123472,47	138671,27	84141,083	26222,636	129470,61	139195,34	81511,615
1 [P61978_	279174,82	293817,81	213972,17	69124,558	293175,71	292656,36	210687,24
1 [P61978_	263848,8	308544,03	245709,61	80732,101	276446,21	308511,46	243543,47
1 [P61978_	387262,11	426898,56	347251,85	113839,84	406301,01	425204,18	344775,19
1 [P61978_	173065,55	204231,55	123202,5	38628,911	181264,4	205585,72	119259,86
1 [P61978_	24302,848	16771,793	11338,961	2802,9245	25706,136	16200,969	11142,724
1 [P61978_	31760,641	23549,42	16121,266	4123,314	33560,358	22891,918	15850,269
1 [P61978_	21048,316	15467,752	9994,2576	2401,8926	22243,56	15043,173	9782,3228
1 [P61978_	160288,71	235234,11	88587,509	23173,969	166876	241003,2	80658,61
1 [P61978_	35801,957	24199,613	16603,959	3574,1082	37880,071	23321,147	16361,528
1 [P61978_	149511,45	184717,72	75914,907	23174,152	156396,9	187537,88	70013,92
1 [P61978_	91837,8	121270,89	36706,802	9686,8862	95893,112	123949,16	32014,786
1 [P61978_	333340,59	368112,47	144378,96	37132,562	349615,16	371701,68	132508,48
1 [P61978_	53427,635	144541,38	43972,374	9264,4874	54211,995	151292,95	38417,26
1 [P61978_	14710,158	19344,59	8135,4295	2353,0615	15362,889	19694,227	7534,0728
1 [P61978_	27081,314	37976,082	16234,542	4281,4543	28233,042	38768,234	15087,064
1 [P61978_	24094,095	33630,707	14565,07	4292,2161	25122,217	34319,127	13542,461
1 [P61978_	60466,055	91806,063	36986,939	11497,027	62887,371	94112,996	33976,236
1 [P61978_	14130,951	20807,66	7731,2409	2292,4061	14710,135	21324,432	7011,0051
1 [P61978_	22264,376	34401,832	13351,022	4206,3714	23142,925	35307,822	12186,1
1 [P61978_	16348,033	24127,355	9673,804	2701,8934	17017,377	24705,981	8893,2748
1 [P61978_	13025,786	20638,186	15416,755	3243,1782	13533,696	20962,84	15277,156
1 [P61978_	14768,846	44596,906	13175,212	3357,4334	14886,607	46802,083	11406,03
1 [P61978_	77408,35	234997,17	77696,709	19844,033	78004,279	246375,76	68940,542
1 [P61978_	5977,1805	16025,483	5297,4673	1439,1182	6068,2868	16757,032	4697,5447
1 [P61978_	27186,773	72070,164	23932,555	6604,4844	27618,685	75337,124	21237,954
1 [P61978_	18491,444	51873,453	17247,928	4322,4801	18724,534	54292,615	15327,302
1 [P61978_	51370,836	121899,84	35667,898	9629,0086	52487,577	127238,28	30800,558
1 [P61978_	13434,583	34018,52	8496,5421	1677,4782	13680,152	35612,717	7064,2711
1 [P61978_	49630,216	117753,76	35766,687	7824,8662	50710,304	122867,36	31233,225
1 [P61978_	65027,95	88071,297	36164,169	12967,422	67858,627	89815,694	33256,619
1 [P61978_	94074,767	118316,78	61069,048	18222,008	98370,862	119828,26	58133,638
1 [P61978_	327033,74	487941,5	170989,87	58422,804	340295,5	500671,16	153070,8
1 [P61978_	44678,595	106782,05	33284,549	7680,1443	45634,937	111412,59	29215,654
3 [P07437,	122748,1	229252,5	72119,309	29728,633	126740,32	237467,58	62903,071
3 [P07437,	72523,03	128076,52	36738,33	15457,667	75036,339	132529,65	31361,348
3 [P07437,	232574,84	167753,49	89943,854	30184,066	245836,39	163473,98	86001,789
3 [P07437,	422889,56	229819,05	139079,5	48334,785	448602,76	216806,07	134789,24
5 [P07437,	158186,74	246368,5	69009,986	10936,114	164370,38	253795,04	59371,464
5 [P07437,	136489,58	202216,13	60065,519	8333,243	142047,95	207777,19	52464,434

5 [P07437,	260674,66	442854,69	119786,23	15546,875	270076,61	457848,23	102264,85
4 [P07437,	116552,53	177057,78	60513,25	17427,031	121210,81	181860,62	54048,46
4 [P07437,	15843,876	20495,275	6197,9324	2951,8947	16552,566	20927,825	5348,2592
4 [P07437,	177082,12	244977,52	70715,363	33047,814	184662,13	251039,28	60369,856
4 [P07437,	494240,21	925059,56	261904,6	39573,212	510254,1	959201,91	225860,3
4 [P07437,	224387,44	506487,63	113417,86	15052,142	229796,02	529093,78	91512,16
5 [P07437,	142060,43	331430,47	88009,635	13514,525	145263,67	346080,8	74610,418
5 [P07437,	12295,527	22303,764	6912,1196	1253,9214	12709,411	23083,525	6078,3207
5 [P07437,	74820,007	159661,33	43147,626	6331,1586	76824,994	166288,08	36769,329
5 [P07437,	23134,843	46218,926	12852,986	2664,718	23822,135	48031,719	11001,7
5 [P07437,	29211,637	46072,637	12031,622	2959,7036	30340,687	47513,549	10119,5
5 [P07437,	237519,66	267284,03	81602,755	18582,71	248995,17	270928,79	71486,026
2 [Q13509,	99283,801	193625,91	52918,787	14380,014	102333,35	201100,48	44953,86
2 [Q13509,	9125,2804	23680,621	5097,4882	909,81103	9279,3177	24831,213	4046,1123

1 [P60174_	53641,68	143278,05	37849,686	8761,6817	54464,702	150113,16	31904,617
1 [P60174_	31380,391	56720,852	16016,486	4476,2894	32439,991	58747,665	13716,119
1 [P60174_	25895,042	58120,93	17592,247	4587,3287	26529,176	60558,022	15320,409
1 [P60174_	65374,541	151168,17	38680,597	8113,8869	66876,498	157861,2	32369,278
1 [P60174_	153679,76	368705,5	93554,294	18333,82	156925,51	385422,76	78152,46
1 [P60174_	379472,89	800057,81	232186,22	82218,92	389858,87	832467,61	199327,47
1 [P60174_	24272,46	57824,422	17192,396	4235,0561	24795,451	60353,945	14919,503
1 [P60174_	44797,304	101192,8	30768,81	8285,1259	45880,666	105449,83	26811,225
1 [P60174_	30250,563	73160,688	20487,161	5196,255	30878,243	76431,312	17516,899
1 [P60174_	513055,76	1200635,1	340881,45	78070,591	524560,38	1253098,5	292843,1
1 [P60174_	564533,74	1216808,5	331223,15	77984,848	579404,81	1267603,1	281512,94
1 [P60174_	43548,605	97285,781	26533,087	6119,2928	44622,935	101446,22	22565,524
1 [P60174_	67714,028	179786,16	43311,044	9873,4779	68773,274	188472,51	35566,431
1 [P60174_	243119,38	613508	144573,65	30227,208	247602,72	642486,18	118055,1
1 [P60174_	848,98533	1888,1611	437,53001	114,31026	870,05938	1971,177	354,54767
1 [P60174_	16316,968	41793,504	9185,0189	2129,5386	16604,26	43804,674	7322,208
1 [P60174_	27377,549	62777,824	16174,297	3274,1604	28017,874	65539,176	13566,579
1 [P60174_	14918,575	31808,371	7739,6596	1523,7052	15318,377	33155,589	6389,3505
1 [P60174_	29106,573	69965,367	18336,386	2913,9729	29718,844	73122,129	15484,576
1 [P60174_	35878,399	78285,438	19485,092	3525,0035	36802,054	81640,341	16205,113
1 [P60174_	4752,182	12367,973	3417,9748	663,21693	4832,1226	12945,333	2920,9962

8 [P06753_	129397,76	143649,73	44375,525	15309,766	135691,57	145481,85	38752,632
8 [P06753_	285873,01	317958,13	214642,73	66128,617	299839,84	318281,23	210090,6
8 [P06753_	967052,27	1067027	810549,74	300555	1014537,3	1064713,4	799089,41
8 [P06753_	77242,993	79225,867	59468,717	19780,561	81161,41	78730,355	58677,864
2 [P06753_	200640,16	99596,027	83748,695	35085,83	213054,01	92092,753	83176,397
2 [P06753_	103214,26	59877,689	50643,802	21182,314	109419,45	56465,618	50294,832
2 [P06753_	278983,69	181047,89	159450,89	58140,135	295358,13	172631,86	159108,21
8 [P06753_	791,66017	834,1037	679,74929	260,01769	831,38971	828,53206	673,43912
8 [P06753_	109989,21	127074,23	97452,682	33333,607	115270,65	127097,95	96260,261
8 [P06753_	45404,438	41829,974	43166,119	16384,532	47814,829	40894,022	43437,361
8 [P06753_	31676,865	27313,733	29397,255	10987,077	33398,195	26534,219	29661,369
8 [P06753_	914178,94	741174,28	757435,32	290320,6	964808,64	717849,08	761804,1
8 [P06753_	43418,25	38581,178	39126,533	13891,96	45752,302	37641,871	39376,703
8 [P06753_	820156,5	697376,59	768838,1	281320,33	864939,8	676157,69	777019,8
8 [P06753_	1663374,3	1418913,5	1427392,1	539332,26	1754017,4	1380512,1	1434537

8 [P06753_	812582,19	667407,58	669389,18	272156,4	857397,82	647492,09	671835,64
8 [P06753_	267720,75	212391,86	207855,96	76508,82	282639,07	205638,17	208670,94
8 [P06753_	1530499	1330597,1	1294117,9	483368,55	1613351,3	1297889,1	1298199,2
8 [P06753_	228071,16	230592,02	228118,44	92928,534	239746,18	227166,84	228685,25
8 [P06753_	2196336,5	2069756,2	2032929,5	732968,39	2311903,3	2029965,9	2041422,9
8 [P06753_	1098729,8	1076744,9	1096195	422613,53	1155705,5	1057594,9	1101849,6
8 [P06753_	329496,36	327073,35	382026,38	141871,16	346527,44	319940,48	387067,43
8 [P06753_	1935365,1	1797300,5	1902241,6	755298,67	2037840,9	1756544	1915452
8 [P06753_	2213363,9	2129071,3	2281946,3	898264,7	2329046,8	2084912	2299609
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1 [P08758_	36702,274	106318,09	19981,04	2835,4105	37083,61	111849,4	15076,908
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1 [P08758_	80690,267	241448,16	56043,671	8903,3019	81370,88	253833,92	45647,098
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1 [P08758_	6339,2952	20767,385	4040,9308	488,48302	6353,9014	21896,172	3095,6501
1 [P08758_	4818,1283	16491,188	2373,8846	412,76026	4813,5902	17428,357	1555,2767
1 [P08758_	68308,29	172591,17	24456,474	6152,2898	69552,9	181273,78	15804,403
1 [P08758_	16386,94	54434,438	4509,583	1491,8103	16404,732	57604,945	1537,3287
1 [P08758_	174617,79	408095,34	82474,62	23002,304	178523,34	426994,46	63636,079
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1 [P08758_	7893,602	23893,797	3758,2812	931,50566	7953,188	25183,282	2584,5421
1 [P08758_	241235,29	704446,13	140178,44	25530,874	243626,18	740968,75	108011,93
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1 [P08758_	109092,49	305414,19	52611,736	10222,1	110449,32	321226,3	38057,71
1 [P08758_	39349,262	65721,336	16965,846	4534,8708	40792,01	67930,921	14205,79
1 [P08758_	49691,423	130769,43	33843,562	8606,9148	50495,096	136984,04	28336,266

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1 [P08123]	23356,973	120216,51	23597,366	7751,7168	22477,648	127594,33	17910,657
1 [P08123]	127557,8	161386,77	52219,686	13696,12	133342,7	164501,94	46217,18
1 [P08123]	124458,79	390440,75	89528,539	29450,977	125123,31	410891,85	71971,113
1 [P08123]	140513,87	159719,53	48968,371	15517,582	147268,76	161982,17	42747,016
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1 [P08123]	21020,411	31689,541	10338,599	3374,364	21865,388	32554,96	9131,5179
1 [P08123]	6832,1368	49579,934	9343,0997	2727,0555	6266,8326	52813,517	6983,0799
1 [P08123]	6564,2181	58640,633	13466,985	6638,9515	5787,5574	62484,108	10719,036

1 [P08123]	79602,634	399766,03	88645,037	45609,267	76824,614	423851,67	69693,402
1 [P08123]	15613,985	137943,27	33635,867	13443,945	13800,755	146909,58	27421,767
1 [P25705_	342127	497092,09	139052,64	27343,215	356262,47	510622,21	119394,96
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1 [P25705_	305623,4	426543,75	135245,37	33392,722	318633,89	436872,32	119236,5
1 [P25705_	74001,555	116960,58	37914,334	7388,1454	76861,29	120389,47	33653,234
1 [P25705_	145712,82	224451,13	67204,038	14617,229	151464,65	230975,77	58570,099
1 [P25705_	70066,867	132551,41	26838,427	6211,5121	72300,209	137838,16	20796,701
1 [P25705_	2379,0836	2582,0834	582,37668	104,1799	2495,9189	2618,5705	471,58797
1 [P25705_	16713,937	18225,069	4140,433	1162,5594	17532,953	18486,715	3342,2999
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1 [P25705_	195939,03	258530,17	85287,044	19376,438	204600,08	264001,64	75900,594
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1 [P25705_	203618,98	123671,44	62648,396	26126,26	215717,37	118588,66	59328,482
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1 [P25705_	209635,71	325665,03	81665,556	19595,263	217842,08	335758,7	67941,724
1 [P25705_	178596,93	318673,44	91460,861	20114,61	184716,75	329865,72	78874,824
1 [P25705_	285278,25	172390,48	84297,523	29334,754	302245,22	165310,05	79735,618
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1 [P25705_	588101,25	424920,75	169519,31	48213,364	621582,21	416029,01	156100,32
1 [P25705_	76216,039	64536,712	27999,215	8396,7573	80355,549	63947,688	26076,044
1 [P25705_	134558,77	110100,99	37525,922	11460,813	141941,82	109138,88	33558,073
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1 [P30101_	212057,52	556405,88	174564,77	55592,536	215542	581821,67	152752,34
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1 [P30101_	28031,22	84529,07	14609,038	4503,623	28250,521	89041,825	10509,488
1 [P30101_	28299,688	59447,559	16929,171	2833,3654	29078,68	61858,929	14603,285
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1 [P30101_	227520,38	573474,5	138754,47	40412,957	231732,62	600430,32	113730,64
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1 [P30101_	137410,33	235438,25	70056,947	23424,502	142327,96	243280,81	60594,817
1 [P30101_	143605,77	285045	74074,783	19634,616	147908,1	296335,02	62106,477
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2 [P08238,	247866,68	487884,34	151983,55	36641,735	255396,41	506260,56	133380,11
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1 [Q05682_	547480,97	936557,75	287626,39	177358,15	567111,36	967427,75	247070,72
1 [Q05682_	787162,6	1215938,8	355272,68	216849,14	818155,79	1251741,6	301857,19
1 [Q05682_	31987,548	73447,984	15340,859	4289,833	32731,268	76797,648	11984,327
1 [Q05682_	263395,68	459655,13	112725,83	29218,113	272628,76	476052,77	93039,939
1 [Q05682_	54005,693	84448,328	23861,723	5826,4523	56109,762	87001,456	20484,491
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1 [Q05682_	5109,8106	7013,0498	5607,5189	2417,0711	5332,0309	7068,1891	5533,7379
1 [Q05682_	192566,97	247959,7	137180,98	37463,925	201244,78	251121,18	131787,44
1 [Q05682_	285561,83	451279,94	201275,51	53218,83	296633,66	462730,81	188154,18
1 [Q05682_	141092,84	227349,08	92112,897	22556,998	146464,58	233594,29	84941,423
1 [Q05682_	86503,504	143935,38	63830,7	19101,369	89703,906	147891,27	59518,287
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1 [Q05682_	101806,84	128289,78	79339,219	26367,93	106459,21	129517,34	76917,603
1 [Q05682_	98482,184	127932,17	81730,217	26772,615	102903,52	129265,32	79498,779
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1 [Q05682_	465587,97	423768,72	293066,13	113413	490319,48	418593,62	286585,75
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1 [Q05682_	310329,28	283993,6	230627,26	65354,832	326803,38	279521,39	229470,96
1 [Q05682_	1659235,4	723917,25	492209,2	162149,05	1763907,7	660348,28	483044,62

1 [P53621]	51664,682	103483,83	23678,485	4330,756	53190,554	107716,12	19197,134
1 [P53621]	305399,45	475661,59	116777,39	15536,518	317326,81	490532,91	97096,202
1 [P53621]	84151,733	145935,13	40965,198	8037,1252	87124,531	150939,62	35182,162
1 [P53621]	2551,0936	5916,9019	1084,7156	154,79665	2609,0463	6193,2469	810,45558
1 [P53621]	34352,773	75441,125	13879,664	2052,9716	35223,67	78846,721	10385,911
1 [P53621]	41289,916	91434,281	16635,902	2346,0024	42320,354	95589,845	12392,288
1 [P53621]	18634,645	32309,898	7100,8095	1309,9212	19291,808	33481,377	5683,6807
1 [P53621]	17155,765	29287,23	9548,9552	1868,3038	17772,562	30231,546	8483,637
1 [P53621]	22522,424	42090,664	11830,984	1793,6973	23253,484	43644,757	10184,453
1 [P53621]	24953,577	39377,141	14300,446	2245,8223	25920,207	40479,201	12998,822
1 [P53621]	78024,879	120060,13	34689,297	7175,0298	81106,703	123585,62	29998,467
1 [P53621]	99173,018	209859,84	55829,161	10387,665	101867,72	218546,42	47287,021
1 [P53621]	6810,6227	12119,74	3586,7749	781,63135	7044,7595	12540,733	3116,0541
1 [P53621]	161875,59	253121,95	72454,984	12546,873	168182,95	260743,22	62618,68
1 [P53621]	54721,131	74766,695	20611,897	4631,5685	57082,787	76603,971	17613,286
1 [P53621]	150130,76	177162,16	46803,143	10309,356	157204,56	180278,58	39592,835

1 [Q99623_	178185,36	207725,27	62738,493	6841,1408	186640,3	210986,21	55140,579
1 [Q99623_	128802,17	152076,66	49093,601	12196,59	134874,98	154467,99	43471,009
1 [Q99623_	56120,02	50107,21	16320,351	2480,4123	59109,731	50019,134	14564,914
1 [Q99623_	40625,735	43818,895	14420,123	2819,1554	42629,591	44275,236	12856,859
1 [Q99623_	67939,404	76324,867	25021,978	4342,7122	71225,666	77302,45	22311,954
1 [Q99623_	68085,607	67825,147	21118,392	4032,0702	71562,505	68239,153	18624,463
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1 [Q99623_	13856,444	16932,689	3373,5467	371,04	14496,23	17297,425	2622,4942

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1 [P13639_ 27394,421 38819,391 14801,183 2080,5438 28549,747 39705,131 13583,775
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1	[P26641_	36797,753	75315,25	19704,74	4087,6846	37851,79	78366,752	16598,856
1	[P26641_	54297,485	75346,237	21001,719	4360,7603	56616,329	77244,203	18010,247
1	[P26641_	80337,368	114464,26	32120,963	6487,0371	83704,861	117477,46	27596,501
1	[P26641_	33891,492	8856,7873	18809,719	1677,3737	36162,56	6799,2607	19749,817
1	[P26641_	5832,2666	1153,4838	3150,3905	203,25612	6230,9934	772,51214	3331,3587
1	[P04075_	696153,51	2009642,3	693795,59	174342,35	703738,35	2103823,4	621103,65
1	[P04075_	32059,098	97171,563	25897,818	4826,6328	32305,175	102074,59	21926,079
1	[P04075_	704125,36	1975298,6	635588,2	134998,94	712986,7	2068099,9	562038,17
1	[P04075_	398969,68	933251,88	357946,82	103623,95	407984,39	971016,19	326170,52
1	[P04075_	50939,629	109375,41	34722,152	8020,0599	52293,648	113768,55	30605,289
1	[P04075_	30370,037	67712,07	20839,286	5008,2644	31123,623	70527,265	18234,759
1	[P04075_	52870,074	117646,77	31693,886	9037,0428	54183,961	122677,83	26794,346
1	[P04075_	94245,112	170178,48	46185,672	9541,799	97429,897	176313,15	39302,757
1	[P04075_	284641,67	488147,19	129925,33	43806,426	294809,09	504919,86	109289,5
1	[P04075_	150349,94	251830,45	71860,022	25760,287	155851,68	260104,16	61468,231
1	[P04075_	71206,286	158176,88	45219,392	14297,188	72983,312	164849,37	38747,407
1	[P04075_	149397,1	184807,39	57582,147	17599,33	156260,57	188235,02	50453,901
1	[P04075_	23966,525	41429,328	9487,1088	1416,3084	24814,642	42914,412	7711,9309
1	[P04075_	55799,602	134394,19	28703,411	4334,8579	56963,53	140675,93	22759,891
1	[P04075_	4153,1362	10455,985	2135,3909	299,14168	4230,0331	10959,847	1666,5622
1	[P04075_	34977,86	81888,672	18508,664	3187,5347	35758,407	85621,055	14946,278
1	[P11142_	153394,79	208755,36	68837,074	14328,914	160039,98	213480,93	61305,45
1	[P11142_	177648,06	259105,52	79784,701	11902,384	184971,42	265964,21	70221,251
1	[P11142_	149266,92	202314,72	56884,988	6847,3195	155744,5	207173,03	49106,348
1	[P11142_	109832,12	166747,75	56325,207	9037,2408	114223,55	171286,63	50502,051
1	[P11142_	612681,79	890035,06	280379,94	39997,934	638019,28	913233,59	248074,74
1	[P11142_	105350,96	158962,7	50394,083	7555,0243	109581,97	163355,28	44626,131
1	[P11142_	63276,476	97434,031	32622,032	6929,352	65777,199	100153,27	29123,949
1	[P11142_	55890,097	97234,367	28568,885	7310,2642	57858,71	100539,29	24732,793
1	[P11142_	73573,213	112648,02	35004,312	11447,418	76492,74	115853,99	30596,147
1	[P11142_	143074,15	206212,28	49708,496	6733,6952	149015,85	212009,56	41118,074
1	[P11142_	455986,38	357495,48	118226,63	30323,232	481335,31	353272,9	105378,46
2	[P11142_	76678,125	60244,932	23163,883	4409,0132	80940,122	59438,633	21287,158
2	[P11142_	29083,632	38917,437	14464,057	2434,8216	30358,705	39714,497	13200,931
1	[P11142_	134350,38	177335,75	72517,548	26052,727	140296,58	180640,61	66646,371
1	[P11142_	120507,96	135269,95	36373,974	4465,9559	126334,24	137253,88	31074,672
1	[P11142_	101584,84	115660,8	31038,011	4970,8472	106461,41	117451,99	26450,138
1	[P11142_	42735,775	43856,328	13882,713	3973,3597	44890,96	44199,01	12227,514
4	[P11142_	292485,47	385919,53	160695,99	39658,933	305435,58	393007,4	148883,96
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1	[P11142_	65038,134	87137,789	29850,273	8092,7041	67885,552	89010,369	26705,854
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1	[P11142_	70831,728	91230,188	26871,79	2066,4205	74008,021	93156,933	23510,497
1	[P11142_	42272,579	67057,781	20794,636	4952,3509	43900,342	69064,29	18245,261
1	[P11142_	222440,14	279153,13	92660,975	17292,704	232578,08	284349,72	82743,105
1	[P11142_	228692,19	257419,03	99364,451	21987,13	239753,12	260260,72	91101,394
1	[P11142_	171282,84	144807,52	57413,168	19127,004	180587,05	143644,19	52654,395
1	[Q01995_	125136,54	347094,66	117867,17	21744,41	126799,47	363110,91	105523,54

1 [Q01995_	257547,3	824060,38	208613,35	46887,696	258591,54	866910,73	173775,84
1 [Q01995_	144048,7	330106,59	83204,387	20374,715	147420,93	344681,56	69208,879
1 [Q01995_	8743,5119	54002,406	8866,1088	1292,5925	8221,0332	57483,648	6265,2604
1 [Q01995_	8371,904	48841,535	8372,5723	1157,7892	7933,1159	51949,077	6049,6344
1 [Q01995_	4515,4266	25425,564	4319,0817	694,84752	4298,343	27034,554	3102,9251
1 [Q01995_	15369,32	74175,797	15684,288	2660,4855	14896,699	78630,188	12358,039
1 [Q01995_	58174,676	246635,42	59978,66	9560,1307	57119,278	260742,58	49522,332
1 [Q01995_	189900,15	975919,25	211531,18	26363,111	182795,62	1035139,1	168536,35
1 [Q01995_	105570,56	404871,69	87150,388	13281,622	104558,64	427754,55	69201,727
1 [Q01995_	13487,02	69464,32	14688,38	1778,4679	12978,944	73693,295	11602,91
1 [Q01995_	43109,082	183143,63	43698,929	6526,6525	42318,365	193651,93	35892,014
1 [Q01995_	118075,16	233815,78	49994,311	13436,808	121617,47	243407,4	39433,738
1 [Q01995_	170223,53	579478	169913,49	39727,966	170186,27	609552,09	146960,73
1 [Q01995_	21265,37	79088,055	15645,697	4678,8362	21113,278	83562,202	11940,663
1 [Q01995_	178629,62	194583,61	40813,936	21288,696	187384,78	197477,54	31639,379
1 [Q01995_	30102,39	98586,781	29894,979	8906,2851	30179,222	103599,04	25977,771
1 [Q01995_	62753,044	100800,63	36614,565	10745,467	65146,179	103694,23	33066,064
1 [Q01995_	54236,785	195306,81	62132,19	19328,034	54000,769	205486,16	54523,666
1 [Q01995_	140945,71	190884,03	52872,281	13302,955	147064,88	195488,07	45174,472
1 [Q01995_	211651,41	421969,22	129982,92	33856,805	217965,78	438084,39	113678,64
1 [Q01995_	56500,191	182447,69	53370,289	19385,003	56698,326	191737,09	45841,043
1 [Q01995_	217068,68	459077,38	158316,1	49487,161	222995,6	476904,64	141361,77

1 [P35232]	23527,119	15304,423	5698,4407	2444,7751	24902,235	14848,208	5155,4076
1 [P35232]	896781,78	516343,71	196396,73	79516,381	950623,18	494258,75	178678,95
1 [P35232]	417840,76	316073,45	109847,09	44441,42	441317,4	311236,48	98172,038
1 [P35232]	209367,91	154220,72	54566,86	23002,071	221220,31	151479,86	48898,501
1 [P35232]	58116,509	74150,8	17572,324	5826,1697	60734,802	75821,377	14321,78
1 [P35232]	4770,9333	6441,9058	1183,5739	399,83407	4978,0901	6615,8303	878,01635
1 [P35232]	201998,62	272918,81	91757,952	14942,665	210792,67	278946,19	82217,527
1 [P35232]	147171,26	149427,42	62192,93	22995,74	154636,84	150014,96	57335,299
1 [P35232]	422965,23	503197,79	138411,72	57268,039	442810,86	512097,96	117156,93
1 [P35232]	138919,84	73788,879	26501,487	7157,1408	147391	69997,372	24041,257
1 [P35232]	121324,62	52271,452	19209,575	5031,5857	128981,77	48112,663	17535,454
1 [P35232]	133338,36	50724,651	16717,208	4489,9664	141895,32	45757,849	14978,081
1 [P35232]	147378,15	157270,95	48860,318	9558,9712	154681,65	158902,72	43045,018
1 [P35232]	464189,41	497438,25	122277,84	47792,346	487127,52	503773,68	100551,17
1 [P35232]	28804,711	26403,581	10498,56	4605,6768	30325,877	26345,188	9581,626
1 [P35232]	39804,834	50079,797	17676,06	4600,4169	41616,964	50984,674	15916,012
1 [P35232]	19076,109	16367,22	5547,2741	2148,7447	20106,641	16284,312	4934,4419
1 [P35232]	68111,105	80772,813	27612,351	4017,2507	71315,898	82011,661	24854,316
1 [P35232]	35098,708	42141,227	13525,407	4168,1622	36738,604	42844,351	11926,243
1 [P35232]	17173,76	15841,983	6298,559	2730,5077	18078,581	15813,889	5749,6283
1 [P35232]	12950,061	13112,248	4414,8466	1877,7191	13607,079	13195,288	3911,5348
1 [P35232]	8126,0905	11995,701	3854,0281	1547,9042	8458,1246	12314,521	3380,9222
1 [P35232]	214459,03	233239,69	91044,988	17963,924	225005,45	235319,77	83733,581
1 [P35232]	115152,21	128972,4	50703,367	12268,454	120735,93	130330,16	46583,537
1 [P35232]	306424,77	324526,59	119180,17	19958,519	321674,35	327151,6	108637,63
1 [P35232]	83820,191	124350,54	57589,144	22070,043	87243,354	127111,69	53831,053

1 [P63244_	141107,95	214026,02	84639,19	46629,772	146762,05	219450,7	76638,82
1 [P63244_	94826,177	180534,09	50507,778	11611,185	97833,277	187321,49	43255,125

1	[P63244_	107892,31	120635,67	83097,936	73257,979	113151,09	120751,14	79425,002
1	[P63244_	6982,0241	13750,58	3506,9298	561,69161	7193,4642	14293,813	2940,9819
1	[P63244_	104745,8	234309,52	70571,788	13183,962	107327,51	244122,21	61614,66
1	[P63244_	114513,63	205786,34	51320,218	12136,262	118401,53	213316,61	42610,887
1	[P63244_	91432,815	148709,23	41299,804	13641,22	94872,389	153462,75	35144,298
1	[P63244_	77793,231	179082,58	42670,07	7899,9958	79595,571	187091,28	35016,167
1	[P63244_	50252,216	123151,73	33507,184	5944,9336	51259,849	128730,88	28549,159
1	[P63244_	71373,851	98033,898	34059,182	8630,2638	74447,773	100239,49	30577,489
1	[P63244_	35459,315	84758,375	20945,374	4497,8986	36214,575	88611,242	17348,011
1	[P63244_	121120,1	138898,75	39528,148	10279,503	126914,67	141033,36	34011,165
1	[P63244_	47224,09	118828,84	29215	4735,2792	48102,993	124393,41	24223,89
1	[P63244_	28523,657	64348,504	17010,789	3367,8912	29213,605	67135,594	14372,406
1	[P63244_	102231,15	189989,16	41943,849	10916,849	105564,75	197339,81	33476,981
1	[P63244_	235612,62	494730,5	121612,76	17149,736	242090,24	515415,28	100996,7
1	[P63244_	48214,477	95111,57	21100,219	2449,4164	49669,21	98976,144	16995,641

1	[P09382]	4007,1639	9794,9795	3607,7422	1406,8291	4088,6557	10207,712	3248,319
1	[P09382]	86163,856	187072,17	47939,412	16954,9	88402,838	195019,04	39844,024
1	[P09382]	2198707	4601251,5	1146078,2	438169,7	2259494,6	4792734,2	943527,17
1	[P09382]	77032,475	157291,08	46225,5	18151,605	79250,198	163489,95	39729,262
1	[P09382]	204396,78	144058,45	50123,098	13822,686	216105,41	140962,22	45103,561
1	[P09382]	2875,1492	4472,5673	1229,5923	377,44556	2987,639	4607,9613	1045,0519
1	[P09382]	1397,1417	2384,4761	667,85784	182,50047	1447,3155	2464,8943	571,07259
1	[P09382]	270,322	501,93198	152,46723	44,761138	279,173	519,98981	132,73458
1	[P09382]	317,99541	522,45197	149,05759	64,635236	329,8485	539,23311	127,02246
1	[P09382]	169561,51	412254,17	126930,69	38246,237	173040,91	430370,62	110721,73
1	[P09382]	34475,043	67065,531	20369,565	6485,1036	35538,861	69583,164	17708,741
1	[P09382]	23318,143	57296,852	16756,848	5351,6735	23783,216	59859,234	14431,608
1	[P09382]	5777,338	14740,753	3691,884	1150,9263	5880,5664	15434,11	3053,7211
1	[P09382]	12375,007	28765,441	9260,7689	2658,7906	12657,337	29981,825	8163,1888
1	[P09382]	18209,321	49126,199	13260,363	4554,7263	18478,466	51472,596	11177,373
1	[P09382]	72972,408	117697,58	33372,796	14141,672	75738,982	121399,67	28412,21
1	[P09382]	26504,22	39048,121	9965,385	4515,8661	27587,172	40166,117	8242,1865
1	[P09382]	421996,4	743077,25	231918,04	96962,391	436679,17	768228,4	201906,4
1	[P09382]	294520,34	333199	86131,944	29121,042	308702	338349,56	72017,486
1	[P09382]	257811,17	311551,25	85772,818	26393,383	269804,79	317316,05	73004,341
1	[P09382]	6106540,3	9587083	2747581,1	1209400,2	6343658,1	9877355,6	2343593
1	[P09382]	87797,453	141746,56	38560,731	17194,48	91122,1	146263,43	32449,308
1	[P09382]	150760,79	211047,16	62825,853	35264,558	157162,44	216323,33	53769,611
1	[P09382]	405,93696	597,98267	133,59409	79,247067	422,51271	615,7189	105,2533
1	[P09382]	748,27664	887,91791	306,59683	122,89021	783,47507	901,48304	273,1262
1	[P09382]	280079,64	311637,19	90624,147	22751,046	293683,82	315833,22	78425,818
1	[P09382]	4099426,4	6643058	2035660,2	850548,7	4254282,3	6848320,3	1765516,2
1	[P09382]	59864,74	134129,86	20975,335	7860,3768	61323,121	140382,89	14285,111
1	[P09382]	99458,567	235028,69	73504,647	27168,501	101644,57	245143,53	64127,364
1	[P09382]	451089,32	948085,94	237798,37	88808,055	463474,47	987611,42	196255,31
1	[P09382]	212022,55	436387,03	125179,65	50151,465	218050,87	453792,48	106918,45
1	[P09382]	147003,43	162355,94	38774,288	16911,518	154164,08	164747,31	31529,548
1	[P09382]	42161,464	125296,67	29658,896	10015,724	42535,835	131688,28	24077,332
1	[P09382]	470604,37	1706788,6	291957,94	69607,999	468136,78	1804075,2	209725,36
1	[P09382]	19517,294	40311,09	12277,25	12921,031	20069,652	41901,911	10289,741
1	[P09382]	193766,4	275220,16	89082,597	37437,129	201914,29	282047,49	78207,918

1 [P09382]	88438,391	216658,22	78101,271	47809,814	90225,505	225858,84	69295,346
1 [P09382]	14228,993	27512,035	9085,1993	5891,1584	14672,101	28516,4	7912,5844
1 [P09382]	32274,805	59639,227	48851,771	30479,512	33357,405	60784,186	47873,489
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1 [O60506_	110186,39	225362,7	77323,61	17112,715	113357,79	233894,52	69284,026
2 [O60506_	335867,68	703514,38	172287,36	29955,616	345137,98	732898,27	142680,33
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1 [O60506_	35965,668	35662,285	17657,874	9637,6931	37810,032	35658,573	16545,274
1 [O60506_	77554,238	141955,84	59326,687	20067,859	80147,527	146469,11	54720,447
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1 [O60506_	243455,16	399651,69	98395,363	24864,836	252526,95	412976,73	81353,532
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1 [P78371_	240450,98	285182,66	74571,471	17101,218	251749,31	290301,85	62879,994
1 [P78371_	89445,976	163000,62	65459,85	20002,616	92450,517	168243,49	60090,12
1 [P78371_	80707,428	144996,1	55180,046	15450,263	83460,623	149685,52	50262,899
1 [P78371_	99285,635	144482,3	38993,377	5349,7573	103382,05	148470,34	33278,106
1 [P78371_	46195,637	67955,258	19922,225	3680,8269	48087,067	69811,903	17309,378
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1 [P78371_	41643,029	49829,961	15935,016	3781,7658	43592,247	50654,063	14089,109
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1 [P78371_	238653,28	204904,07	114940,52	44176,345	251572,1	202405,76	110151,32
1 [P78371_	50222,461	45942,62	23671,338	9099,9439	52880,151	45659,621	22460,132
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1 [P78371_	79120,475	122808,77	37621,397	7033,8575	82224,319	126389,58	33005,886
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1 [Q14697_	29349,979	54219,281	22346,477	9372,6615	30320,646	55970,895	20488,141
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1	[Q14697_	225306,79	347594,88	95952,298	22780,259	234183,77	357984,86	81926,893
1	[P15144_	66585,039	109352,35	28079,198	6493,8989	69065,91	112962,64	23521,762
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1	[P15144_	72351,019	87980,742	30797,461	10896,26	75709,401	89425,197	27567,001
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1	[P15144_	40703,689	77069,672	15731,409	2415,4915	41999,752	80141,453	12280,195
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1	[P21796_	112431,35	189784,96	40968,618	7038,4799	116505,86	196500,68	32617,941
1	[P21796_	88660,364	105156,99	29828,134	7263,5709	92827,78	106969,43	25661,665
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1	[P21796_	54616,931	84082,516	32810,617	4820,8354	56778,803	86277,162	30213,445
1	[P21796_	67000,868	83956,672	30896,386	7368,9442	70059,137	85415,47	28061,679
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1	[P21796_	20969,168	31357,113	5509,1753	797,31176	21814,481	32355,146	4048,0974
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1	[P21796_	728827,68	730587,56	201996,13	29827,308	765933,26	736160,76	173680,37
1	[P21796_	450479,01	606349,44	135903,89	29263,112	470095,62	621834,51	109460
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1	[Q92945_	8088,4847	26328,572	6271,9034	2690,9605	8111,4645	27719,556	5075,8409
1	[Q92945_	143815,98	351833,22	99297,466	32098,953	146715	367643,97	84766,06
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1	[Q92945_	91053,94	160020,8	70128,159	48818,703	94241,578	164777,57	64070,315

1	[Q92945_	76119,344	139569,48	46728,035	14932,785	78652,101	144390,22	41480,711
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1	[P36578_	81044,545	222992,06	63583,5	14323,888	82152,06	233633,95	54670,665
1	[P36578_	41018,968	130259,84	18909,538	6156,1986	41197,247	137469,24	12335,488
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1	[P36578_	78628,096	134567,67	36574,28	7047,61	81443,085	139155,51	31163,131
1	[P36578_	8625,716	15566,158	4140,5154	915,25786	8917,345	16129,7	3502,4084
1	[P22314]	15038,34	20250,143	5853,5433	1183,1088	15693,869	20725,12	5066,376
1	[P22314]	42026,276	135132,19	29068,607	3548,1939	42179,244	142337,84	23124,148
1	[P22314]	120016,61	308324,09	91252,811	16326,132	122125,26	322422,69	79356,779
1	[P22314]	61698,435	154980,77	52854,58	8901,1935	62861,969	161753,92	47404,092
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1	[P22314]	58680,227	162258,59	54228,143	9139,0205	59470,193	169762,28	48432,745
1	[P22314]	12434,991	27738,563	7529,9273	957,11402	12742,606	28924,619	6429,8584
1	[P22314]	11875,001	33561,648	7516,1455	1140,2559	12017,05	35250,2	6054,2777
1	[P22314]	271411,39	622878,63	203811,15	26777,435	277776,19	648885,42	181639,18
1	[P22314]	44203,414	83880,453	27473,854	7809,4368	45613,629	86895,469	24319,715
1	[P22314]	21786,198	54248,371	16922,845	2330,201	22206,169	56658,096	14923,289
1	[P22314]	9469,8786	24792,426	8000,0684	1201,4325	9626,8054	25916,106	7100,8833
2	[P11940_	251739,07	288422,25	132021,33	33997,007	263820,52	291223,86	124003,07
2	[P11940_	12349,653	23501,988	6468,8578	1331,8468	12741,423	24388,651	5523,988
2	[P11940_	31153,08	41044,496	14949,826	3105,5064	32532,321	41864,567	13570,845
2	[P11940_	24115,382	36876,711	12656,687	2935,569	25074,09	37885,304	11344,193
1	[P11940_	80098,172	77208,343	24785,455	5250,2515	84243,966	77490,513	21981,128
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2	[P11940_	80280,151	85366,773	29856,668	16393,919	84267,062	86128,793	26483,237
1	[P11940_	141020,88	82662,973	35211,329	13996,119	149458,83	79167,597	32617,29
1	[P11940_	178979,47	104204,92	46395,41	22788,476	189704,96	99657,734	43065,313
1	[P60842]	44440,205	72016,945	23232,212	3251,0102	46119,662	74203,257	20653,885
1	[P60842]	97469,119	134793,02	40542,18	10253,24	101643,38	138071,56	35322,12
1	[P60842]	298783,41	420849,97	136507,46	12506,485	311422,82	431112,55	121834,64
1	[P60842]	82046,932	115364,63	35805,23	5340,8092	85521,008	118221,45	31572,019

1 [P60842]	78204,353	105232,54	28947,112	2825,7917	81613,982	107744,26	24882,498
1 [P60842]	87478,11	151118,84	41382,565	9458,387	90580,203	156313,51	35262,836
1 [P60842]	321386,46	393646,38	115503,19	33013,775	336230,04	400976,59	99947,011
1 [P60842]	125893,19	174168,56	53024,02	15837,973	131283,72	178387,77	46218,267
1 [P60842]	1153164	1766055,5	548728,57	118106,59	1198914,5	1816324,6	482260,53
2 [P60842]	49742,966	82555,5	28240,77	4802,3916	51582,472	85086,245	25365,38
1 [P60842]	567298,5	464960,48	142624,4	26081,123	598398,78	461466,69	125565,26
1 [P60842]	153006,78	198600,31	59313,312	16748,563	159835,93	202846,5	51531,107
1 [P60842]	507647,63	735048,25	261793,41	39598,834	528712,07	753123,04	237244,42
1 [P60842]	184901,29	308974,94	101712,82	15082,174	191691,67	318655,77	90756,628
1 [P60842]	44096,768	68465,898	21220,804	3819,1519	45826,389	70454,994	18671,736
1 [P60842]	21295,902	36536,512	12437,932	2164,4138	22058,027	37704,271	11157,849
1 [P60842]	94754,896	108489,19	27155,937	4540,1491	99289,449	110266,54	22700,95
6 [P60709]	13510,768	22746,746	10148,038	3039,745	14005,035	23380,125	9470,2272
6 [P60709]	409431	784178,56	290998,43	113476,5	422360,82	811510	262484,16
6 [P60709]	416,08235	762,12024	289,98635	85,621849	429,96614	787,28841	263,93553
6 [P60709]	221,99668	366,86652	164,68984	43,033489	230,26468	376,78708	154,10339
6 [P60709]	75,481362	133,56972	56,09181				
6 [P60709]	212,054	336,50269	129,03285	31,298038	220,23281	345,77762	117,93028
6 [P60709]	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
6 [P60709]	509,74009	871,26935	383,647	101,0475	528,1078	896,18435	357,93432
5 [P60709]	5581146,7	16381216	3923600,4	733096,8	5635108,9	17210844	3222494,6
5 [P60709]	2404345,9	6616989	1661626,9	298420,38	2437026,2	6940076,7	1384656,1
5 [P60709]	3435994,8	9739154	2255721,6	466492,01	3476542,1	10227395	1831596,3
5 [P60709]	5275789,7	15097403	3245935,8	598961,66	5334826,8	15865587	2573746,9
5 [P60709]	76825,314	159564,39	47267,741	9136,1857	78979,943	165922,79	41105,743
2 [P60709]	7405,8837	17782,137	4935,5278	1456,2272	7562,268	18575,156	4201,8194
5 [P60709]	89164,326	241555,5	43800,138	9595,7238	90447,125	253807,39	32402,661
5 [P60709]	515509,33	1282652,7	206123,63	47308,175	525342,66	1345889,7	143709,91
5 [P60709]	245846,38	629859,33	110487,06	27615,526	250153,58	661077,72	80377,987
5 [P60709]	48015,281	122457,09	26248,995	6819,9116	48871,499	128358,46	20713,204
2 [P60709]	2853,0737	9612,4766	2019,8756	346,1686	2854,0652	10135,3	1588,9677
2 [P60709]	19861,427	66283,531	13937,783	2148,4671	19881,847	69876,375	10977,744
2 [P60709]	561588,37	1832418,8	393042,38	72290,577	563062,29	1930698,9	311289,56
2 [P60709]	3902,927	4795,7977	1833,731				
2 [P60709]	42878,886	124948,14	28764,31	6726,2746	43312,027	131294,45	23275,351
2 [P60709]	61795,051	198401,88	43701,403	6919,9697	62026,927	208942,64	34981,635
2 [P60709]	91070,884	288137,41	68368,249	18235,626	91506,617	303204,14	55744,297
2 [P60709]	3821,0899	11426,803	2637,7636	494,66025	3853,4595	12013,312	2141,4143
2 [P60709]	2106,1144	4733,9136	1210,058	325,85261	2157,4026	4939,8173	1009,3041
2 [P60709]	7386,6797	24535,771	4378,5693	623,72641	7396,2431	25888,771	3228,0538
2 [P60709]	293868,79	780953,88	218732,06	53485,833	298470,32	817713,13	187073,94
2 [P60709]	3674,0797	8758,9082	2128,792	458,58645	3752,8077	9157,5991	1754,4766
2 [P60709]	2836,1583	5830,4468	1638,6364	436,31919	2916,9246	6063,8275	1402,0395
2 [P60709]	6592,4227	17766,404	4571,649	880,73343	6690,1272	18621,618	3833,5471
2 [P60709]	38578,174	117109,08	24365,396	4119,405	38866,088	123243,37	19105,867
2 [P60709]	1606,4551	4318,4155	1228,707	273,14074	1630,5726	4522,2354	1056,1281
2 [P60709]	271271,84	852088	166389,11	26128,049	272678,69	897673,42	127404,39
2 [P60709]	10352,715	28401,873	7555,9248	2376,3861	10495,613	29773,076	6353,6885
2 [P60709]	29674,489	70953,242	18017,974	3554,1636	30306,373	74163,426	15054,239
2 [P60709]	26319,903	77790,07	17609,034	3128,4509	26562,237	81774,519	14213,03

2 [P60709_	7837,0183	25097,705	5801,9948	1071,0817	7867,9705	26421	4712,3736
2 [P60709_	42184,701	127413,45	26797,367	3940,327	42513,462	134064,54	21121,685
2 [P60709_	3914,6076	8942,1973	2124,9569	598,06195	4006,7773	9340,4098	1733,5785
2 [P60709_	6513,2587	15034,835	3316,4204	822,38034	6663,1114	15716,995	2645,7407
2 [P60709_	2860,0696	7299,2075	1890,3838	456,54824	2911,1751	7640,5409	1584,2375
2 [P60709_	1548,7189	4448,0039	1127,0203	275,03185	1565,8147	4669,1741	938,33482
2 [P60709_	7950,112	15798,384	3545,6933	1240,3932	8187,5444	16442,883	2831,1346
2 [P60709_	49373,664	75356,477	16169,683	2941,0589	51333,354	77725,025	12846,519
2 [P60709_	2812,1088	6546,6878	1538,4778	471,63488	2875,6865	6842,2159	1249,0381
4 [P60709_	146165,42	482749,5	157402,75	35841,937	146459,39	507013	139433,32
4 [P60709_	215,04315	357,79355	151,64598	78,690837	222,99499	367,86064	139,02002
4 [P60709_	4642888,9	16503489	3155465,1	347982,29	4625926,7	17427453	2400995,3
4 [P60709_	146782,24	389429	67725,317	14648,31	149067,73	409081,44	49159,997
4 [P60709_	2210550,1	6327004	946631,99	149791,94	2234994,6	6662347	636304,69
4 [P60709_	142498,52	233338,92	74865,98	21455,102	147832,05	240533,14	66006,398
4 [P60709_	1050,6501	2704,783	598,61666	123,34594	1068,8593	2835,1432	479,00994

1 [P04844_	8292,0585	19271,873	5046,719	965,0181	8480,5553	20124,078	4254,2548
1 [P04844_	35431,398	69790,414	20962,025	5256,1958	36506,181	72445,927	18238,078
1 [P04844_	40099,773	73922,367	25260,768	7295,4537	41425,923	76472,719	22548,499
1 [P04844_	18004,093	38924,727	9351,7933	1056,0613	18475,045	40593,101	7724,3773
1 [P04844_	24575,817	51633,391	12045,703	1449,7706	25250,416	53813,988	9857,1496
1 [P04844_	313076,77	676873,88	163523,97	17024,382	321266,74	705856,31	135354,12
1 [P04844_	23422,85	47091,859	12594,384	1828,2962	24112,039	48964,431	10706,184
1 [P04844_	16967,967	30990,496	8198,4489	1998,9259	17533,732	32126,98	6916,5594
1 [P04844_	46314,398	72685,508	15369,646	3194,3107	48109,866	75060,884	12128,912
1 [P04844_	7972,6574	15880,694	3769,1274	520,62398	8210,0981	16522,953	3098,4879
1 [P04844_	26980,713	49776,055	13038,708	2146,7151	27869,64	51622,77	11014,954
1 [P04844_	114391	168490,17	42350,076	6803,4692	119065,46	173330,85	35409,767
1 [P04844_	57048,465	124930,12	32203,054	4488,3356	58508,2	130261	27105,898
1 [P04844_	252642,23	564012	147192,85	18235,12	258878,73	588332,42	124405,91
1 [P04844_	4750,1711	9579,7891	2558,0996	569,04554	4889,3066	9961,8274	2165,1501
1 [P04844_	102611,19	180201,98	54214,655	11162,246	106190,41	186346,94	47308,035
1 [P04844_	43838,188	67363,727	20272,531	4233,2435	45572,186	69311,838	17696,239
1 [P04844_	68010,757	101417,43	32782,822	7358,8123	70768,142	104149,19	29044,9

4 [Q71U36,	44104,15	98462,547	23700,33	4677,5723	45191,528	102773,37	19498,668
4 [Q71U36,	24738,721	44769,582	12803,323	3067,5145	25573,019	46365,894	11020,576
4 [Q71U36,	20662,967	32072,461	8148,1932	1302,1364	21472,484	33061,85	6832,141
4 [Q71U36,	19576,468	29485,15	7823,9683	1454,2181	20362,837	30347,036	6630,3759
4 [Q71U36,	250864,98	383934,34	97417,538	15899,247	260809,29	395558,66	81644,965
4 [Q71U36,	223075,4	339203,44	89257,316	13745,313	231967,1	349278,46	75591,765
4 [Q71U36,	78931,167	121357,69	33808,343	5585,1831	82050,05	124957,6	29038,66
5 [P68363,	4815,985	9767,1973	3636,2349	502,92132	4956,5462	10125,096	3320,887
5 [P68363,	21966,947	41645,738	15138,724	1972,3411	22669,553	43092,386	13774,41
5 [Q71U36,	157228,19	346137,75	89010,857	16492,117	161212,24	360968,57	74695,338
5 [Q71U36,	1511366	3237278,3	813316,75	126506,97	1551569	3373997,4	679155,24
5 [Q71U36,	46717,622	93865,258	25005,94	3251,8862	48093,47	97598,887	21251,484
5 [Q71U36,	254242,43	528366,75	145953,13	27632,215	261359,44	549772,75	124819,07
5 [Q71U36,	59621,132	80387,5	21936,591	3292,2784	62217,009	82319,773	18768,503
5 [Q71U36,	442962,46	578032,5	161938,25	21413,039	462660,98	590882,69	139610,5
5 [Q71U36,	101665,65	144591,16	42640,658	7197,605	105934,06	148318,58	37133,344

2 [P68363,	303022,48	557981,81	156935,78	27016,978	313035,54	578298,17	134982,54
2 [P68363,	33410,105	55395,832	20039,993	6174,1394	34647,434	57057,271	18070,245
2 [P68363,	7991,351	15710,048	4629,5537	742,39716	8234,3619	16309,609	4028,3141
2 [P68363,	39913,826	81872,594	23773,221	3812,8668	41054,812	85118,962	20611,653
2 [P68363,	58600,276	94037,047	29273,214	8539,29	60833,875	96890,812	25637,383
2 [P68363,	299707,77	595298,75	167750	29860,644	308686,64	618464,86	144276,08
2 [P68363,	62478,844	123090,77	36858,269	6581,0272	64373,515	127778,2	32160,963
2 [P68363,	12965,462	25309,646	7607,8219	1290,2327	13363,638	26264,953	6647,1755
5 [Q71U36,	95126,339	198042,02	56250,081	7725,736	97782,754	206025,52	48565,027
5 [Q71U36,	43715,218	93434,344	24171,424	3758,989	44882,81	97351,754	20350,366
5 [Q71U36,	112431,9	216602,83	60210,308	9390,427	115942,75	224843,15	51671,628
5 [Q71U36,	1571097,1	3085342	839422,9	148652,08	1618897,1	3205249	715657,13
5 [Q71U36,	204764,31	180094,33	88541,945	44671,923	215750,04	178622,18	83078,063
5 [Q71U36,	103957,55	203355,98	57830,406	19683,077	107138,98	211154,24	49446,863
5 [Q71U36,	709104,75	532368,68	276194,22	161144,87	749090,31	520945,96	260087,22
5 [Q71U36,	118519,67	217848,3	57263,412	17610,74	122441,77	225898,11	48068,441
5 [Q71U36,	290521,56	225207,33	112651,33	66531,544	306750,99	221112,14	105561,02
5 [Q71U36,	225912,52	480820,75	131700,83	21669,806	231994,44	500683,04	112521,6
5 [Q71U36,	284046,22	460863,66	150192,84	31168,059	294769,82	474829,49	133367,01

1 [P17987]	37380,118	54970,98	14853,338	4023,6658	38910,137	56513,307	12593,951
1 [P17987]	24822,597	29176,18	9875,6704	3331,3513	25996,036	29613,255	8790,8096
1 [P17987]	18888,846	31190,639	6432,8541	1323,1283	19587,992	32277,948	5029,9016
1 [P17987]	53417,145	83300,563	23660,712	5301,931	55503,21	85805,637	20358,627
1 [P17987]	369768,21	535660,56	147385,83	33264,759	385078,04	550251,08	125844,75
1 [P17987]	129066,46	225278,22	58078,95	10926,156	133591,69	233223,79	48803,018
1 [P17987]	17281,114	32066,543	10571,165	2502,9792	17847,922	33192,474	9392,163
1 [P17987]	182990,25	232040,19	60759,704	16110,248	191268,79	237008,73	51141,093
1 [P17987]	71196,149	109919,36	33932,927	6247,3428	74001,842	113091,72	29825,198
1 [P17987]	73204,746	101828,47	28761,522	4446,2544	76326,07	104392,21	24810,962
1 [P17987]	90173,34	124936,8	37165,004	5212,2135	94029,933	127998,81	32478,572

1 [Q02878]	52128,296	105762,73	26527,65	4780,9976	53640,552	110055,76	22117,004
1 [Q02878]	39531,658	83513,047	21471,077	3831,1398	40608,304	86989,747	18025,41
1 [Q02878]	26721,771	58584,652	13707,725	1817,7193	27403,197	61131,56	11218,664
1 [Q02878]	9572,0883	21028,707	5065,2555	727,30558	9815,3616	21939,474	4180,1205
1 [Q02878]	21612,905	47290,5	11090,227	1685,6815	22166,06	49342,924	9073,6602
1 [Q02878]	30473,253	66170,656	16896,74	2940,3802	31264,877	68983,171	14160,291
1 [Q02878]	92422,73	177306,8	58314,306	13866,769	95330,492	183736,19	51778,688
1 [Q02878]	118141,84	221555	58887,497	14823,758	121958,07	229872,49	49717,649
1 [Q02878]	52745,587	87297,109	26329,278	5471,4513	54698,989	90078,553	22990,17
1 [Q02878]	211280,58	376662,16	113670,33	21485,141	218530,95	389698,43	99336,988
1 [Q02878]	293241,09	539083,06	182109,44	31906,191	302969,47	557693,66	163081,74
1 [Q02878]	77417,226	132408,27	39211,675	8349,3401	80192,792	136815,04	34083,562
1 [Q02878]	56734,717	100109,32	25747,55	4186,5541	58700,804	103681,5	21648,563
1 [Q02878]	2070,9359	4468,2573	867,61059	49,493594	2125,1689	4666,1643	667,47396
1 [Q02878]	5070,5828	7025,3281	1947,4222	972,8068	5287,3513	7202,2679	1643,2258
1 [Q02878]	6194,0863	12005,418	2974,1379	669,65396	6385,7298	12476,337	2465,4296
1 [Q02878]	125172,95	335995,09	94775,902	16598,715	127062,09	351867,42	81483,604
1 [Q02878]	914855,24	1579485,3	378825,09	79233,921	947282,55	1635481,7	311426,15
1 [Q02878]	392991,79	678133,19	169992,44	34326,8	406933,96	701923,14	141628,55
1 [Q02878]	184873,03	301579,97	91737,444	26306,281	191813,75	310996,11	79948,573

1 [Q14152_	49805,219	73574,836	19755,286	4252,4261	51836,674	75657,289	16769,841
1 [Q14152_	102934,57	65586,122	27025,686	17690,965	108981,71	63413,798	24598,173
1 [Q14152_	7922,5769	12924,89	3383,3233	555,26669	8219,6444	13346,124	2859,0318
1 [Q14152_	27579,173	44183,305	11762,368	2598,6031	28630,664	45585,476	9956,2623
1 [Q14152_	204643,41	170343,44	65860,958	30884,678	215815,29	168830,22	59772,092
1 [Q14152_	33108,19	60907,832	15206,089	2455,7397	34202,196	63185,81	12677,558
1 [Q14152_	2674,2849	4852,8447	1104,8226	275,72532	2764,0101	5035,5035	891,44757
1 [Q14152_	29341,274	48906,801	13390,571	2799,4297	30419,687	50522,362	11422,598
1 [Q14152_	130382,74	196550,31	54270,661	10086,625	135617,76	202234,58	46465,701
1 [Q14152_	17363,332	32535,803	7434,435	1203,8107	17923,985	33795,469	6033,0457

1 [O75533]	21413,961	36552,863	9100,6426	2065,3358	22182,115	37822,565	7557,8467
1 [O75533]	11039,284	18552,004	5034,33	740,985	11441,769	19172,019	4297,923
1 [O75533]	85077,797	116249,93	37266,73	12819,486	88752,793	118938,96	32778,273
1 [O75533]	13176,902	17501,646	7006,1057	2083,6293	13757,693	17837,84	6435,5518
1 [O75533]	14368,637	20407,67	6335,5416	1593,2102	14972,694	20922,363	5558,6631
1 [O75533]	140645,62	172623,88	53904,647	19016,032	147135,99	175752,38	47146,196
1 [O75533]	98858,177	125067,77	50523,387	21367,865	103348,12	127157,9	46209,859
1 [O75533]	26261,845	47200,535	11984,504	2018,2783	27153,469	48920,887	10036,895
1 [O75533]	71402,531	65712,677	32648,592	14874,825	75171,896	65374,968	30738,971
1 [O75533]	147446,8	126429,43	69364,952	32151,332	155430,9	124927,08	66075,089

1 [P13010]	171412,46	355311,28	95683,991	16612,502	176228,79	369757,55	81360,899
1 [P13010]	74675,102	147008,31	43908,045	12031,632	76941,888	152607,52	38109,222
1 [P13010]	21463,076	39099,766	12308,047	2901,0514	22182,133	40466,538	10831,117
1 [P13010]	11373,721	11031,555	3243,1971	750,44038	11960,769	11086,039	2818,6228
1 [P13010]	32032,402	70066,906	13430,545	2459,0967	32850,77	73204,452	10205,07
1 [P13010]	207362,88	396030,06	104186,72	14855,434	213908	411172,83	88206,625
1 [P13010]	45682,029	115649,7	31800,699	4384,6419	46519,453	120973,94	27220,946
1 [P13010]	44767,987	92714,617	22177,417	2829,1407	46025,839	96571,796	18282,421
1 [P13010]	20999,249	38896,203	9874,4402	1500,4586	21687,597	40354,776	8275,4797
1 [P13010]	155154,91	346566,09	89731,32	24826,509	158980,36	361541,66	75084,99
1 [P13010]	44553,809	84308,258	26194,295	7989,9694	45979,33	87376,742	22904,952
1 [P13010]	39947,25	62248,148	18876,654	5206,0787	41509,05	64079,716	16450,844
1 [P13010]	150775,55	281220,06	86368,852	21333,45	155686,09	291349,21	75549,092

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1 [P23396_	265895,12	740443,25	195784,61	38718,158	269330,6	776479,48	165342,8
1 [P23396_	576553,81	1660841,5	435841,07	76827,152	582822,51	1743041,5	367699,09
1 [P23396_	480723,13	906055,88	221211,93	46357,51	496142,16	940857,17	182759,38
1 [P23396_	445662,54	1186020,3	305439,97	49661,403	452588,13	1242746	256588,95
1 [P23396_	122670,49	323321,41	93153,84	13748,265	124650	338389,99	80617,733
1 [P23396_	22097,098	39768,461	12123,42	4603,5852	22847,482	41154,779	10518,805
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1 [P23396_	222460,83	464026,88	120694,84	24830,622	228646,96	483121,33	101511,87
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1	[P46940_	44184,444	65767,781	19156,167	3893,8481	45977,029	67602,144	16602,443
1	[P46940_	7515,8761	15757,986	2900,4684	497,72686	7722,383	16447,646	2168,3123
1	[P46940_	84385,522	119038,36	20506,448	7624,728	87939,809	122536,89	14735,796
1	[P46940_	96754,092	142865,88	34783,571	7518,8232	100699,56	147022,54	28733,151
1	[P46940_	41542,931	65213,277	18433,623	3875,7624	43156,07	67194,807	15852,855
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1	[P62805_	77121,216	111753,52	25671,251	8139,4121	80310,356	114963,78	20720,472
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1	[P62805_	49475,998	76036,164	11700,138	5305,2107	51425,591	78598,013	7877,6001
1	[P62805_	25204,572	36071,039	7404,4246	3207,0108	26255,911	37116,066	5711,5684
1	[P62805_	48814,632	63961,555	12276,556	5715,1284	50976,18	65579,88	9211,3049
1	[P62805_	30161,332	43749,883	8456,9079	3429,165	31406,602	45060,279	6381,1894
1	[P62805_	79013,952	130769,1	23031,67	10464,182	81929,679	135467,84	16623,254
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1	[P20700_	225709,91	219685,4	85650,688	42685,309	237356,96	220143,9	77678,041
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1	[P08865_	8940,0094	21817,307	5695,1032	841,2333	9121,0701	22811,079	4806,7264
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1	[P08865_	271696,27	504444,13	147625,17	43543,563	280589,51	522772,34	127408,92
1	[P08865_	124242,66	285368,72	76961,136	19470,607	127140,59	297823,74	65183,288
1	[P08865_	52425,041	88159,93	18834,664	3974,683	54331,919	91273,476	14909,773
1	[P08865_	129276,24	255652,25	69398,789	13297,989	133171,43	265650,67	59087,514
1	[O60701]	104112,3	121560,93	38268,162	6564,4214	109049,43	123429,74	33835,081
1	[O60701]	2522,5914	6997,0132	1226,5603	459,15243	2555,3722	7357,1451	885,15202
1	[O60701]	80207,194	220239,59	49004,231	10003,912	81303,944	231185,96	39280,167
1	[O60701]	42003,276	105170,5	27307,276	5942,075	42797,055	110035,65	22930,286
1	[O60701]	327160,03	689487,56	222248,94	45469,952	336134,52	716686,39	196793,12
1	[O60701]	300067,56	495032,44	131086,17	31712,406	311202,65	511334,27	110670,02
1	[O60701]	3862,2395	10004,444	2394,4358	853,79121	3927,9788	10482,385	1949,2321
1	[O60701]	68293,96	164556,83	34657,636	11219,32	69716,679	172267,34	27086,278
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1	[P68104]	151646,82	253866,09	69940,739	19568,614	157197,34	262281,14	59541,69
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1	[P68104]	158954,01	366555,97	109492,06	16062,72	162637,37	382248,24	95596,652
1	[P68104]	61995,232	123922,5	27281,956	5420,747	63830,919	129017,48	21819,979
1	[P68104]	158773,55	374665,97	84128,621	10761,252	162253,33	391840,18	67948,501
1	[P68104]	7219,3467	11207,545	3849,7185	1439,6233	7502,7823	11521,082	3427,3081
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1	[P68104]	437352,44	579827,63	149807,26	33289,794	456599,11	593574,48	125883,36
1	[P68104]	24230,839	44322,539	10935,53	3061,7583	25036,833	45975,918	9030,3758
1	[P68104]	357515,83	651390,5	169133,21	44426,779	369468,16	675327,13	141831,9
1	[P68104]	497607,02	944884	229776,58	66776,282	513417,54	981446,95	188802,99
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1	[P68104]	67545,446	101155,68	36170,313	11770,929	70276,992	103787,26	32527,433
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1 [Q8WWI1_	111626,41	291334,69	82767,142	15851,07	113488,22	304881,7	71230,054
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1 [Q8WWI1_	53921,557	90122,641	29339,781	10494,926	55901,164	92959,023	25854,961
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1 [Q8WWI1_	291512,48	323956,78	190491,52	104506,9	305742,25	325192,39	182003,29
1 [Q8WWI1_	164097,07	168720,92	141192,2	57789,808	172422,14	167223,11	139991,94
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1	[P15880_	406211,23	583145,56	130898,72	21512,017	423124,04	599750,93	105730,36
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1	[Q12906_	44211,083	90433,141	27666,562	14281,585	45481,188	93967,615	23852,543
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1	[Q12906_	68881,289	179990,86	50400,594	9621,775	70025,062	188389,45	43221,528
1	[P19367_	103295,12	184420,78	55195,425	11347,709	106833,77	190828,32	48104,958
1	[P19367_	69486,687	139269,41	33801,657	8371,5821	71538,269	144905,9	27815,188
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1	[P19367_	144653,26	271726,56	73883,344	13428,129	149317,28	281888,11	62974,044
1	[P19367_	172819,53	307941,16	77650,34	10557,037	178743,53	319087,27	65015,719
1	[P19367_	82867,963	180670,97	42450,567	6538,6195	85002,777	188490,65	34748,994
1	[P19367_	83259,811	158754,3	44949,924	6668,2097	85895,355	164712,78	38767,538
1	[P19367_	9903,9687	26573,979	4618,745	504,79064	10051,819	27922,152	3372,8442
1	[P19367_	24329,925	57437,474	11193,43	1620,568	24861,524	60126,224	8578,3277
1	[Q9ULV4]	6601,8917	24416,652	2865,8069	537,48931	6556,3255	25859,085	1604,458
1	[Q9ULV4]	283112,35	452712,41	79662,55	26787,115	293898,11	468369,98	57892,003
1	[Q9ULV4]	865330,35	1146976,8	325291,28	204225,24	903434,54	1173249,4	274307,94
1	[Q9ULV4]	92192,156	208498,56	47194,982	8046,5085	94406,07	217799,87	38137,669
1	[Q9ULV4]	49940,092	110831,51	29559,34	6093,4665	51187,28	115571,82	25024,384
1	[Q9ULV4]	97341,251	224320,92	52958,038	9451,4658	99591,091	234375,12	43350,523
1	[Q9ULV4]	74617,552	183812,64	41307,079	7149,1467	76087,913	192446,35	33286,449
1	[Q9ULV4]	1416009,9	1333285,8	476768,72	448756,91	1490003,9	1334566,3	416832,03
1	[Q9ULV4]	863585,75	794168,76	345413,57	283888,32	909155,31	791661,78	313924,45

1 [Q9ULV4]	46827,716	85284,203	18387,558	4906,6904	48391,58	88538,459	14552,776
1 [Q9ULV4]	45816,866	105135,55	27849,781	4403,4986	46887,346	109737,21	23589,894
1 [Q9ULV4]	142988,22	181990,94	48866,798	10872,475	149443,45	185882,02	41494,832
2 [P17844,	53902,28	74552,102	21720,558	7105,401	56210,075	76388,92	18715,492
2 [P17844,	63390,037	88860,469	27517,873	9369,2019	66079,838	91051,808	24025,923
2 [P17844,	39761,312	51745,656	18980,104	6204,7123	41535,346	52744,799	17154,101
1 [P17844]	52518,873	64143,273	20336,799	6957,2336	54949,399	65279,356	17855,043
1 [P17844]	264160,71	311814,94	62975,141	24486,715	276592,84	317935,15	48463,678
2 [P17844,	110788,3	156870,38	41807,435	6167,5931	115451,67	161027,25	35548,635
2 [P17844,	74281,641	38555,14	21426,798	9388,3154	78835,239	36221,688	20504,58
1 [P17844]	77168,287	85509,32	27399,134	4595,6306	80925,72	86557,959	24325,565
1 [P17844]	99299,997	114091,82	38942,335	7279,8277	104050,24	115647,1	34976,912
1 [P17844]	220322,46	222498,04	58973,637	21348,393	231502,66	224384,82	49616,025
1 [P17844]	93600,429	115093,2	35663,886	9315,8254	97915,153	117198,22	31280,626
1 [P17844]	47326,517	60448,723	20542,028	4703,757	49461,318	61612,323	18389,866
1 [P17844]	42879,382	54723,035	16313,762	3784,2867	44813,08	55848,032	14203,9
1 [P48643_	24183,388	44631,77	12534,022	2867,1523	24980,341	46261,082	10745,988
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1 [P48643_	152272,74	193231,41	63066,089	22176,773	159166,57	196973,88	55672,591
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1 [Q01518_	4072,4154	10635,054	3122,8521	755,3946	4140,2668	11126,488	2702,1613
1 [Q01518_	122936,75	338516,63	140936,74	27055,177	124639,83	353239,33	130719,42
1 [Q01518_	169532,02	313484,97	131410,79	31961,912	175133,91	323546,49	121800,86
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1 [Q01518_	119834,17	318988,34	107247,09	25330,888	121710,82	333436,17	95593,377
1 [Q01518_	102362,88	236149,77	73277,541	18867,849	104734,57	246175,07	64176,467
1 [Q01518_	13174,941	46483,68	19749,343	3750,9383	13141,223	48728,435	18371,204
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1 [Q01518_	274817,68	540036,38	186681,55	40779,438	283197,11	559749,89	167552,23
1 [Q01518_	148093,63	271217,31	77346,839	17175,478	153019,44	281007,61	66587,772
1 [O76021]	359679	392711,5	147904,13	17112,797	377330,87	396475,49	135728,27
1 [O76021]	79553,616	100939,77	38757,391	7169,9411	83159,27	102704,77	35549,23
1 [O76021]	129334,2	158115,81	57367,39	6996,1419	135321,08	160687,64	52264,637
1 [O76021]	39227,028	45491,805	14611,496	2477,7735	41093,993	46164,892	12975,121
1 [O76021]	20091,204	22796,201	7232,3583	1216,6289	21058,08	23108,737	6406,9092
1 [O76021]	40543,661	58234,723	19632,07	5988,5252	42235,259	59682,579	17476,217

1 [O76021]	16424,346	16824,279	5137,664	903,37363	17253,168	16959,795	4514,515
1 [O76021]	23484,493	25092,598	8226,8704	1285,8841	24647,899	25340,81	7343,7058
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1 [O75643]	241295,02	206306,88	85988,456	37622,731	254355,97	204689,73	79091,773
1 [O75643]	21435,102	20665,641	9218,6073	4682,3565	22546,129	20658,362	8532,7805
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1 [O75643]	54770,799	73188,58	16920,346	4303,562	57167,566	75015,887	13736,934
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1 [Q9BQGO]	26615,879	21438,324	5836,1392	1214,2145	28082,536	21272,001	4990,706
1 [Q9BQGO]	33564,633	31363,321	9809,5793	1653,0245	35322,806	31420,818	8671,9188

1 [Q9BQG0]	80404,958	96206,711	24240,295	4130,6846	84164,463	98008,321	20292,731
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3 [P12814,	35879,958	83097,82	18290,581	7126,0467	36699,564	86877,535	14469,11
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3 [P12236_	41960,044	59388,574	13775,967	2230,827	43725,453	61027,67	11247,374

1 [Q99832]	100205,81	174398,52	47670,661	8684,9554	103731,66	180443,38	40696,417
1 [Q99832]	67446,937	110463,38	34357,774	6523,1201	69970,275	113904,28	30233,871
1 [Q99832]	41887,568	67529,578	21397,84	4009,4286	43477,766	69578,627	18908,178
1 [Q99832]	36333,597	58030,078	19750,394	3828,071	37725,432	59725,257	17703,605
1 [Q99832]	9215,6536	17219,555	5866,5333	1518,9069	9515,5079	17822,144	5240,9287
1 [Q99832]	17660,714	29047,439	9981,7721	4905,1175	18319,418	29927,034	8835,2022
1 [Q99832]	25933,842	40861,738	14115,705	6073,2566	26939,285	42027,109	12545,905
1 [Q99832]	64930,978	93992,338	25768,906	8227,9681	67620,774	96553,023	21878,63
1 [Q99832]	35415,769	52092,371	14041,56	2436,8991	36865,152	53555,175	11957,118

1 [P63104]	107075,06	270235,34	62885,086	15296,019	109048,39	283026,59	51055,334
1 [P63104]	37728,224	108062,56	40556,905	7636,3348	38159,47	113002,4	36982,713
4 [P63104,	161857,69	327951,88	117754,95	25383,247	166585,44	340101,77	106454,3
4 [P63104,	17331,97	42488,875	13986,94	3246,2065	17680,765	44335,72	12418,334
4 [P63104,	374942,26	985718,38	313352,7	67796,007	381064,95	1030651,9	276359,6
4 [P63104,	79175,538	162033,38	56059,267	13864,788	81452,618	168155,96	50248,542
4 [P63104,	40150,962	105845,82	34122,592	7792,3713	40800,761	110662,48	30165,92
4 [P63104,	181306,25	305822,41	113912,04	20782,076	187912,4	315085,45	103868,47
4 [P63104,	5050,6447	11932,093	4021,4808	976,54269	5161,9051	12436,051	3585,8903

4 [P63104,	10281,669	22831,688	7389,229	1685,6517	10538,985	23766,561	6540,1139
4 [P63104,	206607,44	445348,88	121146,37	22938,286	212049,43	463941,63	103187,82
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4 [P63104,	17825,365	29065,428	11240,433	3030,8269	18496,401	29894,78	10274,228
4 [P63104,	143322,17	313643,19	111752,39	25221,599	147013,94	326021,62	100818,88
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2 [P63104,	1200,0874	2777,1282	1106,5739	261,21454	1227,8686	2887,3349	1017,3697
1 [P63104]	123377,93	283838,34	119001,46	22352,673	126273,35	294863,84	110543,5
1 [P63104]	47458,435	105218,39	44676,967	8418,0656	48656,595	109177,64	41583,277
1 [P63104]	88090,75	162855,52	72834,818	21880,126	91005,217	167934,4	67979,163
4 [P63104,	270648,98	438252,41	204835,35	63037,342	280925,22	449496,03	192341,01
1 [P63104]	144932,04	299165,94	132895,55	24769,492	149064,77	309597,04	124545,23
1 [P63104]	136913,37	291959,53	128421,58	27324,531	140618,53	302469,52	120028,6
1 [Q9BSJ8]	21208,178	42315,012	11050,093	1587,514	21838,941	43996,003	9334,7644
1 [Q9BSJ8]	16700,664	36942,648	8917,9223	1702,9898	17119,717	38549,461	7345,9864
1 [Q9BSJ8]	250244,3	353757,47	110113,27	25141,266	260800,15	362594,99	96777,993
1 [Q9BSJ8]	84318,83	150827,61	35745,685	4428,4288	87195,257	156381,69	29406,49
1 [Q9BSJ8]	203885,99	407338,75	106679,13	11169,776	209938,55	423526,96	90368,256
1 [Q9BSJ8]	455260,81	379874,82	93166,972	33297,927	480060,41	378303,63	76838,009
1 [Q9BSJ8]	15378,973	24827,867	7013,8611				
1 [Q9BSJ8]	4347,7642	2064,7039	1967,2888	157,36188	4618,8749	1889,5514	1998,7056
1 [P04792]	28719,318	31373,207	34495,707	8241,2162	30143,013	30941,24	35035,311
1 [P04792]	41928,32	56278,563	38684,638	17566,06	43774,236	56866,572	37669,176
1 [P04792]	286294,59	477605,53	284940,19	113886,76	296907,54	488419,48	274284,51
1 [P04792]	171030,94	311996,59	132475,82	46849,632	176773,74	321812,19	122400,81
1 [P04792]	52958,355	99754,547	20716,929	4937,5998	54655,915	103701,93	16200,468
1 [P04792]	35415,683	65218,984	11886,821	3563,5715	36581,687	67803,163	8788,4159
1 [P04792]	36643,71	63565,715	10433,89	3386,3818	37933,038	65986,365	7328,9195
1 [P04792]	665417,65	730793,94	609365,67	259684,94	698198,01	727266,29	603524,01
1 [P04792]	45873,348	45175,082	36430,546	15357,802	48241,43	44695,277	36007,322
1 [P04792]	526776,69	514547,89	421778,65	173964	554062,72	508589,05	417550,49
1 [P04792]	144942,95	162245,03	132273,11	56358,306	152017,19	161736,71	130787,78
1 [P04792]	1550142,7	1369213,8	1012999,7	383595,75	1633404,2	1347438,1	996656,97
1 [P04792]	377555,68	371459,66	281859,7	112393,43	397041,89	368062,39	277567,8
1 [P05388]	27531,377	38999,648	9476,0238	872,03593	28689,3	40063,446	7875,3295
1 [P05388]	18864,312	24956,902	6307,5435	916,59998	19695,515	25550,5	5288,9331
1 [P05388]	21477,699	36915,777	10932,143	1572,1476	22243,846	38151,016	9534,8392
1 [P05388]	529022,18	1046542,6	299562,98	41175,489	544964,27	1086979,8	259158,13
1 [P05388]	143301,2	47676,721	19690,63	4096,0421	152645,54	41735,116	18403,906
1 [P05388]	477185,76	708398,25	200427,66	66612,187	496581,64	728272,76	171387,57
1 [P05388]	70923,667	143003,09	30341,551	5302,9355	72996,672	148958,62	23987,79
1 [P05388]	282805,66	107607,69	32354,941	6922,3579	300952,18	97175,07	28529,75
1 [P05388]	8122,1708	22026,678	5158,4986	865,59162	8239,2859	23106,68	4212,4672
1 [P05388]	17228,233	32241,26	7790,8959	1350,9552	17785,679	33474,416	6429,2051
1 [P05388]	107404,16	121381,57	62795,397	17592,225	112598,8	122233,86	59858,319

1 [Q9Y678]	39705,674	95713,758	29749,942	3951,6992	40538,142	99888,2	26222,048
1 [Q9Y678]	33441,865	76573,039	22864,193	3539,7552	34228,405	79836,389	19953,163
1 [Q9Y678]	27967,586	54152,07	14275,165	2816,0111	28834,622	56246,496	12058,011
1 [Q9Y678]	69197,864	99611,734	28628,514	4504,1344	72077,16	102257,34	24793,216
1 [Q9Y678]	61062,114	124724,45	33673,213	6446,5971	62817,257	129736,12	28626,931
1 [Q9Y678]	114821,35	179495,84	41219,857	6501,8068	119289,76	185227,13	33537,718
1 [Q9Y678]	3906,5449	7945,3296	1964,344	257,12849	4019,444	8269,3503	1635,1109
1 [Q9Y678]	50166,176	114961,16	44463,53	11775,457	51350,574	119535,97	40622,861
1 [Q9Y678]	70424,148	44441,609	12758,15	2535,496	74566,973	43104,652	11078,856
1 [P61019_	144991,47	268274,56	76028,299	21330,415	149755,44	278070,31	65158,398
1 [P61019_	151058,98	213465,4	65176,574	16471,904	157431,83	218836	56972,568
1 [P61019_	17051,833	33003,375	8246,8542	1477,4522	17580,453	34294,046	6869,7532
1 [P61019_	21765,577	42243,156	11888,391	1581,1064	22438,704	43855,736	10245,324
1 [P61019_	10515,724	26692,23	5233,4898	1042,2014	10705,637	27991,121	4007,1516
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1 [P61019_	86870,106	164809,81	39905,699	6645,5043	89633,218	171186,93	32961,01
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1 [P06396_	57662,286	202553,58	37358,44	9404,4215	57502,219	213896,06	27768,848
1 [P06396_	43385,171	98427,172	27856,982	9377,8783	44424,011	102647,22	23785,234
1 [P06396_	67576,088	228694,08	48671,943	17601,716	67578,176	241134,07	38064,829
1 [P06396_	206763,46	276476,88	84430,45	28797,332	215820,64	282726,38	73499,692
1 [P06396_	50604,073	80521,359	19743,294	5681,7995	52544,023	83109,989	16276,442
1 [P06396_	148075,54	393654,66	101423,27	31519,013	150385,37	412474,61	84564,25
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1 [P06396_	175643,75	393865,31	136515,8	56160,882	179963,82	409815,04	121418,82
1 [P37802_	55277,357	156912,81	42661,088	9679,9678	55928,786	164580,03	36238,207
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1 [P37802_	58724,152	198106,94	53017,421	14343,698	58746,415	208519,22	44733,97
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1 [P37802_	144640,14	400237,31	127784,86	58374,669	146577,18	418954,53	111467,25
1 [P37802_	30634,509	44445,813	13457,305	4895,5953	31902,241	45620,064	11675,739
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1 [P37802_	51116,106	167197,83	47738,099	14493,455	51249,133	175790,14	40884,93
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1 [P38646_	88047,126	164767,7	70464,024	10068,608	90915,886	170076,79	65813,059
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1	[P04908_	19562,057	125967,13	53273,593	6849,4746	18304,092	133085,02	49639,635
1	[Q15365]	258603,35	426925,13	124567,97	32558,139	268200,82	440623,46	107654,32
1	[Q15365]	124180,78	246282,08	81423,736	22569,614	127916,75	255466,69	72230,889
1	[Q15365]	181586,72	268081,69	77779,823	17659,973	189000,58	275474,75	67271,073
2	[Q15365,	69293,276	141407,06	40137,354	7761,3417	71289,048	147021,58	34553,008
2	[Q15365,	147090,82	383260	119836,66	20355,901	149564,69	400710,92	105554,63
1	[Q15365]	17249,776	41322,617	12753,608	2449,5688	17616,893	43121,095	11191,383
1	[Q15365]	221591,82	527762,13	156859,82	28569,354	226369,31	550844,95	136545,81
1	[Q15365]	138250,51	338163,38	100850,85	19349,18	141042,04	353180,52	87811,756
1	[Q15365]	143203,44	324067,63	92645,827	17911,471	146650,41	337906,2	79873,429
2	[Q15365,	116293,84	227579,41	81825,787	17455,645	119861,89	235754,1	74005,072
1	[Q15365]	71997,597	168485,73	52396,027	9080,3217	73615,008	175699,73	46099,342
1	[Q15365]	550107,26	668562,38	237532,57	52776,965	575652,61	679398,65	214559,2
1	[Q15365]	549630,75	1084103,6	347712,05	67707,082	566286,2	1124682,2	307761,38
1	[Q15365]	1769,8566	4081,396	3035,0034	1444,9242	1812,0333	4197,5385	2970,5038
1	[Q14247]	176072,13	27687,062	27292,033	7948,5232	188218,98	17812,769	27699,911
1	[Q14247]	151214,81	88660,612	45131,908	13034,547	160267	84674,867	43022,329
1	[Q14247]	86765,031	55445,878	21891,848	6862,4888	91858,23	53654,856	20112,157
1	[Q14247]	144503,89	238683,42	57234,447	22662,894	149856,16	246749,75	46596,321
1	[Q14247]	106610,04	69089,151	46095,517	13751,125	112859,86	66344,444	45152,24
1	[Q14247]	2242,1346	928,62619	441,3748	188,89455	2384,5004	845,99783	415,44772
1	[Q14247]	90916,68	57366,248	31958,835	13484,206	96275,11	55139,867	30586,19
1	[Q14247]	64081,859	46760,013	26828,31	11133,807	67725,582	45558,298	25751,256
1	[P50995]	188234,76	415096,91	88028,93	20875,81	192977,54	433509,42	69320,992
1	[P50995]	19838,031	51782,57	10199,904	2609,3109	20165,849	54336,802	7798,4451
1	[P50995]	28973,175	56690,277	10175,017	1341,0662	29855,72	59056,544	7542,449
1	[P50995]	35122,748	79003,961	17314,723	5641,836	35974,953	82535,319	13725,85
1	[P50995]	85350,982	238597,22	53260,782	12734,203	86427,838	250548,98	42655,937
1	[P50995]	99615,242	192386,2	46713,228	11245,057	102711,38	199940,85	38463,998
1	[P50995]	10263,31	28740,193	6627,983	1218,3849	10391,887	30174,009	5381,1059
1	[P50995]	47556,569	137064,31	30341,033	5230,6703	48068,498	144031,77	24316,473
1	[P50995]	30731,134	82034,57	19381,479	2992,4008	31202,215	86020,654	15882,324
1	[P29692_	1759,0904	1578,0971	707,67532	407,58736	1852,7677	1569,6503	653,61368
1	[P29692_	56211,057	57000,125	23358,887	10272,062	59063,782	57231,845	21412,195
1	[P29692_	37136,563	38868,895	15165,71	8607,3702	38995,059	39128,008	13706,59
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1	[P29692_	727905,5	728332,13	307027,91	167424,61	765060	730408,84	281289,41
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1	[P29692_	295701,94	266021,12	94122,161	52934,068	311417,1	265462,48	83680,558
1	[P60660_	1358647,2	2108298,5	926742,12	489981,12	1412137,4	2160724,2	853983,58
1	[P60660_	133433,83	210747,34	96157,74	52677,414	138611,18	216025,95	89002,593
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1	[O75083_	5611,2727	13651,924	2541,1422	573,47057	5725,1505	14305,824	1901,6956
1	[O75083_	127692,66	261578,59	76882,926	15004,858	131350,93	271910,25	66734,444
1	[O75083_	59577,373	119633,71	36758,858	7457,2416	61336,561	124232,4	32220,733
1	[O75083_	122498,76	224146,63	60282,823	16952,508	126575,07	232349,54	50981,91
1	[O75083_	124389,99	276264,34	66392,733	10196,353	127487,38	288321,37	54722,582
1	[O75083_	48559,392	113128,74	32214,494	5314,775	49659,169	118054,7	27784,07
1	[O75083_	166935,51	372266,91	90267,86	13245,313	171060,61	388530,94	74626,745
1	[O75083_	238484,77	580935,94	145925,1	37044,204	243333,72	607558,19	121182,82
1	[Q8NBS9_	113084,99	243640,16	89090,428	38001,554	116080,73	253074,39	79987,552
1	[Q8NBS9_	39748,167	80468,25	30791,517	11899,16	40911,838	83386,964	27925,591
1	[Q8NBS9_	78392,056	157211,02	56783,977	23865,453	80716,532	162975,94	50890,14
1	[Q8NBS9_	143116,1	368605,34	120602,46	60026,623	145617,86	385119,39	105550,83
1	[Q8NBS9_	96474,862	192075,45	70759,805	35068,313	99366,136	199030,88	63415,271
1	[Q8NBS9_	218197,49	383492,82	108996,71	44669,067	225797,88	396792,31	92887,515
1	[Q8NBS9_	161938,48	261271,52	93565,017	37329,715	168088,82	268862,6	83850,89
1	[Q8NBS9_	2873,7988	5056,9985	2022,4032	903,4909	2974,1454	5213,7014	1843,0732
1	[Q8NBS9_	2961,7236	4886,1641	1618,6452	1152,8827	3071,8326	5036,7285	1406,8085
1	[Q8NBS9_	141277	229922,98	93472,246	42321,142	146607,55	236322,83	85401,427
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1	[P00338_	58890,805	160165,3	43019,201	7578,5768	59733,737	167850,9	36523,981
1	[P00338_	57071,516	189789,98	36539,451	8068,2136	57142,415	200174,12	27712,915
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1	[P00338_	33935,921	95909,469	25996,985	4008,0057	34344,809	100588,54	22147,398
1	[P00338_	181100,72	333714,38	141674,4	34522,354	187110,69	344327,45	131565,99
1	[P00338_	76105,64	203444,61	40992,198	9212,2082	77261,606	213566,52	31672,792
1	[P00338_	309785,47	510835,16	105426,18	26106,492	321266,85	528614,44	82263,69
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2	[P00338_	34812,434	97232,5	28104,315	4833,153	35257,597	101893,61	24308,463
2	[P00338_	20176,841	50441,992	16509,096	2888,824	20562,007	52662,856	14680,283

2 [P00338_	62821,507	131972,13	41447,689	11182,999	64553,095	137201,28	36381,52
1 [P26038_	36290,962	85322,156	22345,261	13889,896	37095,073	89123,891	18421,56
1 [P26038_	225789,39	326046,56	116468,31	64843,851	235177,17	334024,19	103568,26
1 [P26038_	327881,01	420226,81	150123,34	82578,679	342645,05	428160,96	133592,86
3 [P15311_	63120,929	155536,11	26952,613	5595,8545	64358,647	163102,01	19547,319
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1 [P26038_	195509,39	208647,41	68499,142	65152,712	205199,92	210705,26	58814,336
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1 [P00387_	304976,51	844296,25	144644,71	31629,199	308972,4	887817,97	104206,97
1 [P00387_	96443,11	189762,25	44175,915	6404,201	99364,766	197389,88	36087,266
1 [P00387_	72459,403	154720,13	28983,812	3646,7103	74390,824	161559,93	21887,049
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1 [P62701_	4335,9128	14673,147	1923,5939	214,56673	4335,2915	15509,964	1186,8457
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1 [P62701_	4244,8108	11394,796	1902,6179	328,07449	4308,0155	11975,56	1357,3535
1 [P62701_	13421,284	30159,4	8560,4502	4392,6011	13748,821	31443,891	7249,4435
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2 [Q13838_	72279,297	129756,84	41253,776	6092,8856	74741,848	134211,68	36538,902
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1 [O00148_	9164,5463	12349,118	3552,8221	559,57324	9563,8438	12639,683	3078,4168
1 [O00148_	19985,734	26410,164	7940,2832	1105,6983	20867,811	26995,88	6957,4617
1 [P23246]	125584,57	91066,203	41596,839	13144,162	132730,61	89019,352	39019,11
1 [P23246]	67218,444	92516,205	27301,149	8586,5988	70106,243	94763,462	23610,061
1 [P23246]	12146,457	29044,533	9592,6405	5810,7868	12406,476	30287,743	8368,3908
1 [P23246]	110777,16	145789,02	52638,51	27295,333	115684,66	148712,63	47002,169
1 [P23246]	283329	394303,56	65264,679	14710,694	295375,9	405733,55	46397,885

1 [P23246]	44209,97	68775,25	21063,694	7003,5769	45941,011	70787,696	18346,211
1 [P23246]	87595,984	151291,53	48590,547	12218,372	90707,52	156259,5	42916,375
1 [Q96AG4]	214053,45	366373,63	94482,529	17742,922	221712,87	379030,5	79406,128
1 [Q96AG4]	132988,29	210538,11	56216,045	11574,446	138112,37	217114,03	47660,155
1 [Q96AG4]	56911,925	95688,609	28843,975	5859,1826	58987,77	98795,459	25187,289
1 [Q96AG4]	35307,938	55444	15156,112	4047,3552	36678,243	57146,317	12888,34
1 [Q96AG4]	73079,976	119278,09	37176,77	7760,697	75822,852	122975,24	32699,384
1 [Q96AG4]	740174,76	1252832,6	268009,39	50193,286	766924,24	1297373,8	212525,7
1 [Q96AG4]	220709,76	344260,44	66508,944	12292,664	229307,21	355628,08	50782,732
1 [Q96AG4]	1166908	1946943,4	471084,39	80137,507	1209716,2	2013332,9	389145,92
1 [Q96AG4]	183104,32	311658,22	78004,103	15525,835	189691,91	322436,9	64973,165
1 [Q96AG4]	20147,898	25046,389	5954,5499	973,99066	21069,711	25576,893	4901,7081
1 [Q96AG4]	68639,139	85744,844	21415,973	3780,5055	71771,291	87549,066	17874,138
1 [Q96AG4]	17422,977	24301,293	5866,5168	1054,9821	18163,819	24948,464	4844,3685
1 [Q96AG4]	1279105,5	1861069	446274,83	84770,117	1331850,4	1914243,6	367506,97
1 [Q96AG4]	193547,84	275213,81	72930,324	12469,652	201669,77	282572,69	61844,347
1 [Q96AG4]	81715,593	176486,66	28458,573	4425,5439	83848,004	184497,64	19983,539
1 [Q96AG4]	39717,4	90076,406	15437,303	2787,198	40662,593	94262,272	11158,939
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1 [P53618]	24449,117	18583,99	5330,236	827,03605	25820,182	18343,32	4630,6529
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1 [P53618]	182443,86	334447,08	86153,975	17924,768	188499,43	346829,29	72291,014
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1 [P53618]	24502,518	35358,652	11873,223	2020,4753	25521,311	36246,218	10630,024
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1 [P25398_	164152,5	295627,34	76376,932	35587,627	169713,75	306385,71	63293,379
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1 [P25398_	73379,711	69763,36	25336,58	13633,851	77200,235	69860,926	22655,23
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1 [O43852_	53311,443	89895,508	32164,725	20273,812	55253,618	92663,093	28496,317
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1 [O43852_	118394,28	226044,8	204571,01	118819,6	122225,78	230006,35	202263,69

1	[O43852_	264412	468454,72	345179,7	201766,2	273678,6	477995,36	336060,55
1	[O43852_	530301,2	984672,63	329797,74	147092,49	547683,81	1019116,3	290977,99
1	[O43852_	186515,6	179073,73	193373,97	38496,331	196272,09	175282,37	196573,27
1	[P52272_	56058,802	127670,06	39463,078	9366,458	57392,818	133049,12	34567,524
1	[P52272_	78744,847	173323,89	57763,087	13313,865	80749,367	180322,78	51428,878
1	[P52272_	406690,72	445990,25	163342,54	39451,563	426605,3	450532,89	148279,88
1	[P52272_	37485,828	93520,713	18281,481	5175,3647	38197,588	98032,82	13915,599
1	[P52272_	44009,209	65023,719	23455,836	4814,4452	45807,882	66670,484	21250,056
1	[P52272_	254711,78	441930,13	186638,31	41252,893	263745,66	455067,95	173387,48
1	[P52272_	81705,232	105463,59	45943,525	10277,647	85373,817	107221,67	42904,011
1	[P52272_	158612,78	230584,91	97625,009	22318,845	165184,66	235795,23	90732,464
1	[P52272_	97519,783	152449,75	43980,711	11404,715	101320,62	157027,96	37917,925
1	[P52272_	24309,767	55136,871	14091,989	3656,8802	24891,19	57549,145	11759,28
1	[P52272_	15894,685	37363,305	8926,8868	2526,6945	16246,459	39055,004	7293,5764
1	[P21291_	53437,406	84393,656	30548,586	12574,773	55505,863	86763,306	27416,113
1	[P21291_	78868,644	176621,26	43138,977	10967,924	80801,861	184349,84	35540,456
1	[P21291_	130145,86	480557,88	121049,04	42290,385	129305,78	506845,37	100012,06
1	[P21291_	197337,43	739948,63	158266,82	66449,858	195804,83	781531,69	123570,18
1	[P21291_	84458,022	227780,14	69778,753	24476,888	85713,311	238389,59	60637,479
1	[P21291_	74852,368	206493,14	53892,34	21974,181	75860,539	216523,63	44865,306
1	[P21291_	84759,896	299083,44	86762,992	35168,042	84516,208	314836,03	74205,23
1	[P21291_	11039,73	33294,355	9613,1914	3743,7247	11128,5	34947,267	8221,2681
1	[P21291_	107436,85	316416,72	72648,745	30519,095	108450,51	332570,34	58149,907
1	[P13674_	82049,442	136467,08	39107,555	10626,759	85072,495	140907,9	33634,071
1	[P13674_	133457,89	547279,25	107165,82	24533,967	131415,01	579145,63	81758,696
1	[P13674_	84416,695	278446,63	50430,636	11385,945	84568,193	293740,77	37247,963
1	[P13674_	391201,22	1247410,3	288076,28	143130,6	392860,76	1313102,7	230021,38
1	[P13674_	175708,1	540755,63	104416,25	29806,578	176856,83	569500,14	79016,232
1	[P13674_	169563,92	406043,5	87321,842	27038,557	173151,43	424943,79	68812,732
1	[P13674_	134650,8	330803,25	74102,725	21525,677	137323,04	346327,54	59276,342
1	[P13674_	49842,709	142798,8	26967,69	6800,4883	50394,483	150189,66	20262,946
1	[P13674_	59953,162	64546,391	26372,765	11499,552	62916,147	65046,831	24162,587
1	[P16403_	150058,2	264838,84	80422,889	45962,91	155264,86	273899,77	69055,907
1	[P16403_	100127,07	168473,44	59101,823	36918,585	103781,76	173684,38	52179,623
1	[P16403_	149292,81	255475,13	106681,71	64655,11	154662,14	262987,79	97167,77
1	[P16403_	14077,829	29187,232	9308,6908	3847,7713	14474,18	30327,698	8140,5506
1	[P16403_	277167,92	482303,81	112772,21	72794,852	286909,58	499646,53	89860,796
1	[P16403_	122508,11	197137,09	61171,627	30138,156	127165,81	203150,32	53005,68
1	[P16403_	53651,276	90240,047	30988,675	15576,115	55609,87	93050,693	27408,733
1	[P16403_	101609,75	185307,06	53771,842	36340,856	105006,54	191944,43	45433,942
1	[P16403_	11699,135	20807,447	5696,232	4191,8051	12101,267	21545,383	4728,3657
2	[P16403_	31734,2	42786,771	51801,094	16353,276	33141,709	42517,813	52685,285
2	[P16403_	37019,338	49561,801	58886,523	18971,571	38667,803	49269,899	59820,76
1	[Q9H0U4]	124230,6	254697,73	52234,662	10534,607	127770,62	265496,65	40724,258
1	[Q9H0U4]	235985,27	519430,75	142924,68	28425,439	241972,91	541381,68	122029,38
1	[Q9H0U4]	190171,73	375802,91	103707,78	21047,732	195908,68	390436,98	88620,977
1	[Q9H0U4]	87033,013	163063,94	38684,866	9385,7868	89844,603	169331,02	31630,393

4 [Q9H0U4,	82500,889	141584,25	43163,82	7937,039	85449,268	146274,1	37821,143
4 [Q9H0U4,	160537,73	337016,25	110682,77	16852,287	164970,86	350203,5	98636,211
4 [Q9H0U4,	127991,53	191676,92	55432,544	10887,652	133159,18	197085,63	47976,939
5 [Q9H0U4,	432318,58	838045,13	159830,87	31220,876	445661,07	872467,25	121178,97
1 [Q9H0U4]	56164,867	109822,95	25321,251	4447,9591	57880,835	114223,22	20588,988
1 [Q9H0U4]	50660,488	95037,57	25374,858	4977,6477	52296,32	98602,499	21510,074
1 [Q9H0U4]	34168,844	68604,844	19510,719	4091,5451	35176,925	71292,569	16791,147
1 [Q86VP6_	76623,247	102214,27	25911,201	5546,3552	79981,483	104683,9	21667,356
1 [Q86VP6_	49829,109	88764,594	27881,297	5430,6036	51541,226	91798,916	24574,916
1 [Q86VP6_	19242,85	45905,238	11317,916	1955,9746	19654,634	47990,277	9388,2567
1 [Q86VP6_	3392,3622	7702,2661	2248,7916	387,74107	3473,5074	8030,362	1950,5812
1 [Q86VP6_	4220,866	10215,01	2923,9741	481,93093	4308,3415	10669,74	2524,8173
1 [Q86VP6_	80033,432	167365,63	42332,8	13918,264	82249,116	174305,56	35103,889
1 [Q86VP6_	6058,138	13784,33	4851,4707	782,25642	6202,9532	14345,549	4379,9026
1 [Q86VP6_	16676,124	36030,633	10268,08	1965,2775	17113,864	37522,261	8847,6105
1 [P31949]	14280,849	23547,561	7586,1321	2592,2101	14811,914	24278,992	6675,9732
1 [P31949]	14558,741	22451,383	6947,9508	2482,8988	15133,025	23097,994	6058,2651
1 [P31949]	40680,252	56946,043	17571,826	7145,7868	42408,071	58349,024	15279,842
1 [P31949]	96471,997	130832,91	41029,494	16659,849	100659,55	133843,37	35809,974
1 [P31949]	41628,321	80181,422	29265,906	8003,3109	42933,059	83006,078	26466,318
1 [P31949]	43183,347	84159,297	26226,974	7732,195	44513,053	87301,98	22958,431
1 [P31949]	64231,22	117890,72	36573,223	11236,38	66364,029	122060,38	31969,214
1 [P31949]	170248,46	329350,75	104483,43	30324,013	175543,96	341509,75	91838,469
1 [P31949]	23228,871	23062,854	14406,067	6450,5146	24421,367	22965,616	13915,312
1 [P31949]	10862,227	13482,708	7594,6141	3455,8183	11362,451	13625,607	7251,5071
1 [P31949]	5375,7129	9254,9033	3046,1599	1874,2081	5567,3419	9555,5632	2656,3641
1 [P31949]	17628,965	30878,467	10548,669	5199,0406	18246,407	31888,415	9323,902
1 [P31949]	126865,2	223793,78	69804,8	43359,675	131270,66	231387,55	60151,846
1 [P31949]	5458,4397	6847,9521	2800,7624	1056,3063	5707,5971	6958,3544	2572,2906
1 [P31949]	50587,506	84785,938	26683,836	9844,2496	52439,105	87493,105	23333,175
1 [P31949]	111624,93	203386,16	61601,146	20004,921	115362,23	210576,57	53513,421
1 [P31949]	271441,79	310385,5	118462,83	54174,304	284466,45	314135,66	107192,99
2 [P31943_	78124,053	113615,57	34631,515	10989,853	81351,428	116621,31	30161,266
2 [P31943_	13680,925	28940,758	8684,3248	3372,2869	14053,488	30106,885	7501,2373
1 [P31943_	131718,8	203424,38	59909,519	21125,366	136906,29	209393,74	51664,518
1 [P31943_	24422,341	56601,391	16369,811	5350,2574	24981,9	59050,326	14057,359
1 [P31943_	328994,79	756209,25	189476,28	42838,553	336647,48	789696,56	157489,36
1 [P31943_	192901,8	404357,72	124863,19	37799,162	198236,22	420422,82	109018,81
2 [P31943_	382942,34	603622,5	223366,62	110162,73	397792,94	620371,21	200478,9
2 [P31943_	32996,028	69696,195	22963,215	10616,885	33898,107	72435,496	20169,935
1 [P31943_	77368,924	112394,1	35629,042	13092,992	80568,602	115318,21	31220,419
1 [P05455]	5269,339	14336,717	5288,3886	854,20504	5345,5661	14978,244	4814,0611
1 [P05455]	8085,0592	12010,577	4195,1165	1584,226	8414,0283	12322,153	3746,6902
1 [P05455]	15175,614	30064,652	13575,935	2226,0586	15635,207	31066,841	12766,574
1 [P05455]	18739,658	50522,84	19094,203	3326,0759	19020,893	52757,975	17445,796
1 [P05455]	62056,603	170984,42	68712,868	24603,809	62912,394	178505,87	62882,961
1 [P05455]	53536,258	101379,02	45909,4	19034,834	55256,864	104606,21	42696,751
1 [P05455]	106384,25	288848,94	91108,173	19103,23	107925,99	302260,94	80238,945

1 [Q32P28_	81619,623	218855,77	57879,711	20331,277	82853,847	229315,95	48503,73
1 [Q32P28_	79303,899	206739,63	49846,293	18472,586	80625,876	216636,85	40638,955
1 [Q32P28_	2747,1574	10090,905	1778,6315	306,85145	2730,0621	10666,598	1301,1084
1 [Q32P28_	8356,3396	30954,088	5222,5413	827,40078	8298,6452	32732,078	3743,9211
1 [Q32P28_	3857,6676	10872,341	2105,164	416,8941	3904,2482	11429,362	1603,261
1 [Q32P28_	23472,344	64297	17827,368	5191,6166	23798,878	67375,461	15171,46
1 [Q32P28_	50317,074	138156,64	38196,241	13469,664	51010,057	144783,02	32380,674
1 [Q32P28_	25175,837	58106,078	17564,07	5152,4216	25758,296	60588,801	15265,498
1 [Q32P28_	25947,593	51542,68	13062,894	3774,1799	26723,919	53596,218	10862,629
1 [P51149]	127882,34	224736,28	62030,066	9747,1745	132336,19	232585,51	53151,197
1 [P51149]	30052,863	60202,703	15075,445	2636,8672	30941,134	62622,985	12567,01
1 [P51149]	74999,526	117547,43	37508,613	8681,8959	77918,507	120973,22	33125,284
1 [P51149]	51878,091	87857,375	28407,102	10269,503	53758,086	90672,606	24991,682
1 [P51149]	32817,764	50028,473	12317,041	1791,3688	34122,626	51547,129	10244,012
1 [P51149]	26567,524	42597,75	10473,224	2135,3081	27579,138	43979,024	8678,7106
1 [P51149]	180175,21	298316,94	90388,094	21357,327	186845,68	307813,48	78895,698
1 [P51149]	237580,47	382121,94	149779,32	30052,215	246637,39	392752,69	137663,29
1 [P62753]	548679,56	934137,94	213363,76	61777,969	568401,17	967119,85	172018,23
1 [P62753]	12667,927	24782,045	6301,0249	1479,9071	13055,091	25756,436	5259,4506
1 [P62753]	24573,835	47250,137	11548,277	2762,8792	25342,123	49096,221	9528,3886
1 [P62753]	13895,911	23766,801	6350,5328	1741,5418	14393,656	24580,16	5364,7235
1 [P62753]	111847,98	48483,657	84543,854	29383,356	118943,68	42512,427	87245,785
1 [P62753]	52936,289	28412,88	40918,425	13934,499	56177,758	25995,221	41937,75
1 [P62753]	24764,811	15882,935	19274,743	6842,1649	26225,676	14955,172	19591,591
1 [P62753]	303840,49	369367,41	109090,59	26412,843	317933,54	376076,57	94750,676
1 [P62753]	254645,32	396813,22	115980,57	21610,679	264598,11	408627,88	100668,92
1 [P62753]	19625,323	21137,457	9840,5307	4242,3358	20595,831	21262,923	9192,2146
1 [P05141_	44004,416	56168,035	18675,278	4996,3034	45989,892	57260,859	16615,714
1 [P05141_	81145,852	94686,266	30767,209	7531,4285	84995,753	96108,123	27286,478
1 [P05141_	492363,97	660537,38	217376,57	66382,763	513895,76	675063,15	192612,73
3 [P12236_	96570,831	120096,44	35224,63	5661,7981	100992,47	122426,51	30665,662
2 [P05141_	23655,432	29158,609	10034,774	2038,8202	24745,01	29663,143	9017,7687
3 [P12236_	1534354	2022952,3	622786,26	80143,885	1602181	2067120,4	548868,61
3 [P12236_	33575,348	30079,606	10741,729	2153,9959	35362,47	30003,506	9734,4223
3 [P12236_	208258,51	244153,17	73612,964	10600,074	218111,19	248065,44	64560,42
1 [P05141_	693314,99	916452,69	296674,47	49723,188	723922,5	936107,77	263765,87
1 [P05141_	142624,4	207181,19	56700,284	11565,268	148517,26	212859,12	48399,899
3 [P12236_	7931,0385	15362,886	1697,5692	176,251	8175,2609	16033,393	907,81025
3 [P12236_	41960,044	59388,574	13775,967	2230,827	43725,453	61027,67	11247,374
1 [O60716_	96554,878	144537,86	28881,721	3759,9839	100446,25	149031,59	22421,366
1 [O60716_	52647,563	104239,52	32720,545	10481,251	54234,033	108178,01	28650,769
1 [O60716_	13002,47	29627,139	6350,4472	1147,317	13309,764	30966,593	5034,7379
1 [O60716_	21087,055	26154,652	8308,5366	2284,8606	22054,441	26638,114	7321,2236
1 [O60716_	20625,654	37769,281	12999,921	2777,932	21313,22	39060,357	11662,732
3 [P12814,	35879,958	83097,82	18290,581	7126,0467	36699,564	86877,535	14469,11
2 [P35609,	42656,48	106824,2	22171,407	9194,6129	43458,616	111947,37	17145,478

3 [P12814,	70833,683	217578,55	45573,3	8896,8401	71308,003	229019,48	35771,026
3 [P12814,	243074,63	730376,31	142526,67	25091,966	245042,94	768782,33	109001,46
3 [P12814,	96885,122	270347,94	60284,765	9963,8472	98117,996	283880,03	48456,456
4 [P12814,	126786,71	229563,41	59690,657	13945,789	131056,16	237945,71	50150,778
4 [P12814,	192853,16	341273,56	109590,11	20553,168	199529,42	352780,78	97084,896
4 [P12814,	60510,765	139196,98	30069,584	4867,2396	61912,857	145519,29	23928,355
4 [P12814,	19197,787	53475,641	12686,772	3146,0887	19444,569	56125,736	10357,251
4 [P12814,	8741,7363	25503,754	5993,0766	1485,6763	8829,4678	26795,87	4877,5405
4 [P12814,	158331,16	471333,34	99320,838	24678,54	159712,15	495788,22	77907,827

1 [Q9NZN4]	171619,27	298895,72	136403,6	73630,305	177688,44	307503,13	126279,6
1 [Q9NZN4]	20451,857	79852,328	17324,909	3368,7045	20225,645	84384,763	13762,96
2 [Q9NZN4,	80168,664	195200,64	48199,829	10863,165	81799,98	204170,4	39888,134
1 [Q9NZN4]	5544,4277	16793,598	2896,7876	552,19435	5586,2167	17691,832	2096,6106
1 [Q9NZN4]	2780,4087	10982,956	1868,6076	498,96638	2746,611	11625,1	1336,0958
1 [Q9NZN4]	26605,423	39251,078	13965,129	4258,4248	27693,909	40249,189	12559,904
1 [Q9NZN4]	66723,735	187438,47	43535,711	8677,9668	67547,183	196793,18	35396,593
1 [Q9NZN4]	39891,541	102136,55	24765,058	5752,4543	40596,25	106975,51	20373,927

1 [P27797_	14894,863	41225,066	11479,83	3540,6031	15093,069	43207,168	9771,5431
1 [P27797_	53287,574	126051,76	40407,063	8662,8783	54456,7	131446,88	35711,07
1 [P27797_	34930,066	102769,75	17457,838	3749,8842	35257,924	108211,68	12525,036
1 [P27797_	122032,02	184128,48	54273,994	11343,024	126930,4	189349,68	47154,275
1 [P27797_	80832,647	207606,7	77320,801	30938,773	82264,133	216588,23	69716,747
1 [P27797_	170976,37	211688,03	74564,343	30836,299	178832,74	215347,17	66624,991
1 [P27797_	542248,25	384412,64	265998,71	133250,81	573347,59	372086,97	258990,98
1 [P27797_	38954,289	102216,31	29548,417	11381,654	39592,611	106967,51	25289,854
1 [P27797_	157373,6	320558,81	101139,92	33115,357	161925,38	332942,27	88621,271

1 [P26599]	81345,704	125768,42	40981,58	18216,721	84548,897	129338,11	35975,962
1 [P26599]	6574,499	17543,963	3841,138	617,25388	6675,2168	18406,123	3069,5601
1 [P26599]	65136,771	141070,47	38213,735	5294,6614	66838,17	146984,45	32596,858
1 [P26599]	75229,969	69012,301	38337,924	3487,2274	79208,763	68508,327	37179,115
1 [P26599]	27000,459	44012,547	14064,56	1934,1338	28015,284	45363,121	12480,231
1 [P26599]	6376,5974	13916,166	3671,1586	607,71089	6540,8343	14505,889	3105,4621
1 [P26599]	41653,853	79661,422	23352,344	7871,6122	42967,795	82634,451	20118,274
1 [P26599]	37660,507	40338,809	12523,009	3451,0604	39523,609	40766,831	10987,392
1 [P26599]	207178	499562,38	145546,06	28325,699	211512,34	521670,98	126024,67
1 [P26599]	24735,603	46523,715	14205,965	6270,5154	25532,884	48215,94	12290,896
1 [P26599]	481861,74	963157,69	285104,14	135207,18	496177,22	1000408	244464,94
1 [P26599]	302887,51	616946,63	152790,34	66825,956	311621,34	642136,93	125224,85

1 [O75947_	202011,87	207221,52	70796,256	38682,199	212204,55	208671,03	62531,667
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1 [O75947_	593643,31	265356,59	130907,13	86881,163	630927,39	244592,73	122394,57
1 [O75947_	684997,56	343270,82	174756,42	109097,39	727237,92	321514,86	164201,38
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1 [P00558]	283124,16	1042137	305189,35	80293,262	281394,26	1097701,4	263466,41
1 [P00558]	221747,92	287752,84	91194,503	33821,616	231650,08	293733,35	79925,951
1 [P00558]	29575,367	101044,66	22102,585	4005,8453	29556,312	106538,82	17625,931
1 [P00558]	69896,724	271188,25	57958,198	7996,1177	69159,708	286580,71	45940,43
1 [P00558]	62838,685	189133,27	38385,224	7683,8696	63341,653	199037,76	29770,288
1 [P00558]	48999,486	178109,08	40686,742	6191,2974	48740,654	187936,75	32966,689
1 [P00558]	15113,349	42154,805	11172,655	1995,5058	15307,181	44207,08	9450,6128
1 [P00558]	53183,534	137321,92	41496,556	9412,888	54103,741	143591,12	36173,665

6 [P60709_	13510,768	22746,746	10148,038	3039,745	14005,035	23380,125	9470,2272
6 [P60709_	409431	784178,56	290998,43	113476,5	422360,82	811510	262484,16
6 [P60709_	416,08235	762,12024	289,98635	85,621849	429,96614	787,28841	263,93553
6 [P60709_	221,99668	366,86652	164,68984	43,033489	230,26468	376,78708	154,10339
6 [P60709_	75,481362	133,56972	56,09181				
6 [P60709_	212,054	336,50269	129,03285	31,298038	220,23281	345,77762	117,93028
6 [P60709_	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
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5 [P60709_	2404345,9	6616989	1661626,9	298420,38	2437026,2	6940076,7	1384656,1
5 [P60709_	3435994,8	9739154	2255721,6	466492,01	3476542,1	10227395	1831596,3
5 [P60709_	5275789,7	15097403	3245935,8	598961,66	5334826,8	15865587	2573746,9
5 [P60709_	76825,314	159564,39	47267,741	9136,1857	78979,943	165922,79	41105,743
5 [P60709_	89164,326	241555,5	43800,138	9595,7238	90447,125	253807,39	32402,661
5 [P60709_	515509,33	1282652,7	206123,63	47308,175	525342,66	1345889,7	143709,91
5 [P60709_	245846,38	629859,33	110487,06	27615,526	250153,58	661077,72	80377,987
5 [P60709_	48015,281	122457,09	26248,995	6819,9116	48871,499	128358,46	20713,204
1 [POCG38]	26132,668	60116,32	20530,897	5663,9551	26743,001	62603,076	18326,706
4 [P60709_	146165,42	482749,5	157402,75	35841,937	146459,39	507013	139433,32
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1 [P49368]	90934,909	150270,72	43130,161	10552,323	94306,151	155121	37158,763
1 [P49368]	24746,275	39681,359	11737,424	3639,908	25689,731	40904,356	10152,58
1 [P49368]	214626,85	355200,63	90447,561	29851,474	222565,06	367059,58	75203,344
1 [P49368]	33527,154	64405,906	21023,051	5050,2797	34580,031	66749,387	18635,672
1 [P49368]	80252,374	128668,05	42076,948	13477,499	83314,996	132503,03	37186,267
1 [P49368]	144122,29	173221	56043,102	13813,397	150852,49	176105,56	49648,386
1 [P49368]	88405,141	67302,574	25681,282	9030,1036	93364,598	66234,367	23395,882
1 [P49368]	12349,921	20291,082	4662,8913	1111,1719	12809,521	20979,06	3777,6091
1 [P49368]	9984,6256	17985,811	4873,7994	1539,8063	10322,95	18632,996	4122,8795
1 [P49368]	16867,166	27836,23	6345,877	1759,3679	17492,212	28786,507	5117,1063

1 [Q02543]	64260,666	126843,28	34714,409	6428,4395	66202,111	131787,27	29628,364
1 [Q02543]	22167,092	45272,23	12869,412	2697,389	22804,794	47070,287	11073,895
1 [Q02543]	108492,73	169852,05	52891,1	15129,707	112718,44	174837,43	46341,749
1 [Q02543]	210468,74	254636,06	93199,869	34967,471	220268,48	258617,6	84027,912
1 [Q02543]	78303,027	103701,43	41816,081	14910,137	81760,92	105669,75	38349,326
1 [Q02543]	5175,8743	9449,9307	2077,2739	213,8014	5348,2549	9809,9763	1669,7473
1 [Q02543]	21975,188	38830,902	9012,3675	1481,1821	22734,91	40250,055	7350,805
1 [Q02543]	84044,537	93436,102	29079,878	4952,7885	88129,693	94627,437	25655,444
1 [Q02543]	11434,474	24319,287	4914,5491	1076,0712	11741,549	25379,99	3806,0534
1 [Q02543]	24355,13	56364,395	9146,915	1250,6542	24910,285	59031,852	6449,4531
1 [Q02543]	42213,794	80053,077	19205,986	3410,4066	43557,133	83155,255	15810,748

1	[Q15084_	63483,818	174862,42	54346,415	11300,846	64350,239	183066,36	47712,053
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1	[Q15084_	24187,742	61665,773	17117,715	3615,5588	24622,047	64510,623	14633,25
1	[Q15084_	3524,648	9106,2822	2440,764	608,05254	3585,3155	9532,2271	2063,6738
1	[Q15084_	13381,633	28421,855	8201,8565	1689,4745	13743,41	29580,752	7083,8165
1	[Q15084_	12456,4	31146,576	8497,7792	1867,1242	12692,973	32573,038	7229,6636
1	[Q15084_	72579,344	94612,883	27315,126	10644,505	75809,515	96686,775	23417,192
1	[Q15084_	128156,42	327522,63	104663,25	31712,863	130449,47	342209,28	92024,016
1	[Q15084_	18601,539	31314,754	10548,273	3751,0569	19279,899	32297,429	9360,9196
1	[Q15084_	141753,07	338917,06	115775,69	28425,939	144791,11	353289,81	103494,81
1	[Q15084_	54666,738	121890,69	30862,774	7313,9194	56018,77	127173,82	25717,245
1	[Q15084_	24692,894	55585,27	13989,923	2432,9028	25292,311	58012,108	11675,297
1	[P61224_	16994,035	38278,625	10893,76	1313,6111	17406,866	39909,632	9415,8504
1	[P61224_	166369,88	412528,78	127197,94	25079,256	169612,97	430858,89	111557,09
1	[P61224_	63245,851	146242,34	50245,241	5713,2638	64707,255	152301,03	45254,568
1	[P61224_	102521,28	222344,83	73669,25	8879,094	105201,27	231239,58	65864,977
1	[P61224_	49932,863	97782,391	31725,159	5003,4281	51461,242	101407,65	28198,775
1	[P61224_	184318	362624,88	102391,98	18028,064	189914,18	376618,19	88118,87
1	[P61224_	462632,39	805430,75	250460,92	67260,42	478924,41	832381,33	219497,03
1	[P61224_	494064,49	885835,31	294197,79	83903,62	510928,9	915810,34	261187,96
2	[P06733_	75178,424	261372,14	70051,931	18306,255	75041,712	275252,46	59154,845
2	[P06733_	25290,058	51307,195	16839,322	6793,9628	26026,347	53261,984	14823,311
2	[P06733_	6035,3187	16362,644	4812,7532	789,08505	6123,0741	17133,064	4181,9083
2	[P06733_	6702,5573	17321,297	5708,5808	1087,5093	6818,5143	18097,046	5079,2982
2	[P06733_	35539,015	83739,141	25306,876	4598,7694	36324,74	87363,96	22114,738
2	[P06733_	28947,497	81614,75	21065,29	3561,7432	29299,784	85626,305	17698,741
1	[P13929_	36394,219	106686,64	30287,085	3950,8293	36752,015	111933,28	26134,084
1	[P13929_	243199,16	556216,5	161671,07	30644,574	248929,98	580047,15	139961,58
1	[P13929_	213512,71	434841,69	132372,46	28155,145	219686,64	451790,61	115729,13
1	[P13929_	212496,42	415121,09	102411,74	20265,803	219001,25	431524,72	84909,881
1	[P13929_	51093,559	88278,008	25082,262	7329,2595	52905,693	91284	21501,951
1	[Q9NVA2_	64365,243	114516,19	34944,012	13391,223	66579,168	118460,33	30321,311
1	[Q9NVA2_	14998,408	15813,648	6016,7226	2722,1914	15746,452	15930,902	5444,3248
1	[Q9NVA2_	21933,839	29209,836	8174,0197	3307,0907	22896,698	29888,656	6948,3917
1	[Q9NVA2_	30831,495	71580,789	16473,748	4538,107	31532,511	74817,842	13308,109
1	[Q9NVA2_	59361,315	177561,22	44443,038	8264,615	59865,474	186564,08	36980,844
1	[P62424_	51944,594	107050,96	36338,283	5586,1941	53422,222	111141,05	32597,216
1	[P62424_	505191,7	833270,25	196953,67	51550,449	523926,86	861471,99	160776,86
1	[P62424_	190218,22	346232,22	111516,69	31935,676	196598,74	358244,32	98370,744
1	[P62424_	288406,02	534937,63	168316,97	32007,741	297865,15	553971,09	148428,66
1	[P62424_	397041,35	631709,69	181831,6	39002,65	412281,01	651141,15	157022,33
1	[P62424_	51930,294	105207,38	33957,598	4946,8629	53444,96	109227,75	30165,662
1	[P62424_	110201,13	229486,59	54742,991	10408,483	113270,49	239078,19	44942,381
1	[P62424_	63923,148	131861,34	29661,783	4796,774	65729,157	137392,12	23939,32
1	[P62424_	128443,14	273970,38	62960,273	11171,344	131880,49	285697,12	51118,694
1	[P62424_	22104,658	36719,539	10354,771	1928,876	22919,954	37917,941	8908,7791
1	[P62424_	37544,9	77049,047	19035,623	3477,4271	38615,257	80213,398	15798,935

1	[P62424_	137772,88	255495,69	71967,877	13058,023	142287,12	264857,35	61893,268
1	[P62424_	123807,09	223658,91	69942,13	21457,181	127994,63	231427,37	61248,627
1	[P62424_	41452,762	63644,047	26268,475	7093,0551	43098,131	65252,39	24268,545
1	[P62424_	53910,299	136681,48	24275,436	4886,3637	54885,703	143410,33	17814,051
1	[P46781_	5197863,4	9803635	2835352	570627,43	5364722,1	10166114	2451544,7
1	[P46781_	82373,621	126393,15	38839,27	7789,9619	85636,342	130014,61	34076,178
1	[P46781_	115729,69	191478,06	53360,363	10770,235	120014,16	197718,57	45739,323
1	[P46781_	61543,516	125045,63	38547,178	7604,0207	63329,686	129894,65	33820,958
1	[P46781_	341227,88	614373,75	171961,04	25859,256	352800,22	636287	147900,87
1	[P46781_	53275,783	96206,219	30420,316	6901,5301	55078,751	99535,133	26807,987
1	[P46781_	69975,231	126315,34	32834,525	6012,1254	72339,777	130914,1	27656,462
1	[P37837]	13707,018	87013,219	23459,854	2978,6454	12843,514	92349,602	19961,641
1	[P37837]	137309,03	227494,06	73889,767	22556,463	142392,46	234582,42	65250,853
1	[P37837]	27278,756	60595,211	18073,788	3540,4395	27960,051	63126,541	15737,881
1	[P37837]	15866,378	80375,781	23368,773	3680,1688	15301,442	85046,223	20237,319
1	[P37837]	9825,1824	45454,977	10877,802	2214,3776	9565,7755	48117,808	8915,8632
1	[P37837]	2902,9896	23173,68	5456,728	807,07042	2618,488	24668,119	4460,324
1	[P37837]	70520,67	277988,06	68285,051	14669,879	69689,303	293552,12	56392,878
1	[P37837]	112706,61	218214,84	66631,937	19851,32	116206,79	226360,9	58057,173
1	[P37837]	118937,5	564464	154037,8	25598,84	115506,35	597112,04	131263,72
1	[Q14764_	64977,295	112812,98	40366,51	12683,921	67275,536	116405,85	36310,606
1	[Q14764_	52086,618	60925,84	21159,714	8960,7516	54555,544	61805,523	18851,068
1	[Q14764_	118358,27	171937,67	64552,026	25297,289	123259,6	176086,29	58381,962
1	[Q14764_	31581,619	67860,266	28064,525	8344,6364	32424,221	70376,734	25885,092
1	[Q14764_	53919,689	69289,484	26618,669	7951,5931	56344,944	70545,145	24285,909
1	[Q14764_	69719,258	119627,39	46844,157	19591,028	72217,945	123255,67	42601,705
1	[P39023_	63776,558	123801,8	36221,777	7361,3577	65749,322	128484,37	31398,895
1	[P39023_	140013,37	244097,75	76754,48	17834,825	144937,43	252249,83	67547,773
1	[P39023_	17756,818	17348,493	4163,5355	1308,0626	18670,043	17472,828	3415,427
1	[P39023_	7245,116	8635,5352	2227,3505	639,09403	7584,6219	8793,8564	1865,5933
1	[P39023_	46107,053	71377,727	17509,857	5798,4527	47916,998	73592,758	14406,264
1	[P39023_	43175,165	67162,234	16542,702	5824,9478	44863,165	69257,654	13611,537
1	[P39023_	376814,66	663112,5	238820,12	74686,128	389954,63	684507,18	215090,11
1	[P39023_	323101,11	765382,5	180113,35	36542,235	330124,83	800281,79	147088,43
1	[P39023_	127911,55	207395,19	52220,395	8337,2825	132733,71	214171,39	43668,302
1	[P62258_	175922,91	184091,19	99362,564	25769,451	184745,57	184420,38	95294,734
4	[P63104,	161857,69	327951,88	117754,95	25383,247	166585,44	340101,77	106454,3
4	[P63104,	17331,97	42488,875	13986,94	3246,2065	17680,765	44335,72	12418,334
4	[P63104,	374942,26	985718,38	313352,7	67796,007	381064,95	1030651,9	276359,6
4	[P63104,	79175,538	162033,38	56059,267	13864,788	81452,618	168155,96	50248,542
4	[P63104,	40150,962	105845,82	34122,592	7792,3713	40800,761	110662,48	30165,92
4	[P63104,	181306,25	305822,41	113912,04	20782,076	187912,4	315085,45	103868,47
4	[P63104,	5050,6447	11932,093	4021,4808	976,54269	5161,9051	12436,051	3585,8903
4	[P63104,	10281,669	22831,688	7389,229	1685,6517	10538,985	23766,561	6540,1139
4	[P63104,	206607,44	445348,88	121146,37	22938,286	212049,43	463941,63	103187,82
4	[P63104,	19130,251	29969,615	11579,75	3823,6273	19876,379	30777,486	10553,591
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4 [P63104,	143322,17	313643,19	111752,39	25221,599	147013,94	326021,62	100818,88
4 [P63104,	48798,28	83598,586	26060,965	6321,984	50545,699	86343,99	22881,8
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4 [P63104,	42474,388	95235,047	35559,846	10193,587	43520,942	99007,931	32258,941
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1 [P62258_	57425,58	105426,05	47388,164	11538,793	59341,301	108680,22	44377,58
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4 [P63104,	270648,98	438252,41	204835,35	63037,342	280925,22	449496,03	192341,01
1 [P62258_	146924,01	267342,53	117625,53	29828,821	151874,44	275594,18	109765,72
4 [P35579,	29623,641	107651,21	22440,925	5349,4235	29466,369	113660,73	17534,001
4 [P35579,	137316,58	273428,63	90231,125	33820,793	141424,3	283668,09	79632,887
1 [Q7Z406_	396383,79	1529006	187983,96	58124,9	392304,62	1620146,8	108597,01
1 [Q7Z406_	67234,84	249286,28	40644,452	8354,6394	66764,783	263655,37	28550,63
1 [Q7Z406_	42267,166	132852,5	27732,85	8213,6648	42485,632	139904,55	21618,787
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1 [Q7Z406_	62586,067	126357,91	49174,387	15469,51	64426,204	130902,91	44878,635
4 [P35579,	208584,84	197051,83	60282,73	49456,609	219464,15	197611,54	51338,963
3 [P35579,	107194,22	147863	49260,952	43769,057	111795,99	151293,85	42514,311
3 [P35579,	745239,18	997033,5	386753,1	239471,32	777925,31	1016958	348046,73
3 [P35579,	9433,1273	33864,453	6362,7484	747,60718	9391,4648	35770,006	4804,086
3 [P35579,	7433,375	28744,109	5036,7686	725,12901	7356,3357	30409,862	3680,0403
3 [P35579,	40926,696	134970,06	27892,803	4947,6283	41002,92	142271,15	21802,465
3 [P35579,	12036,969	37694,543	8080,9164	1876,692	12102,303	39685,633	6382,7185
3 [P35579,	21245,044	59111,055	12949,905	4670,0311	21518,879	62073,952	10237,856
1 [P21964_	68528,888	219563,72	66826,868	13264,677	68807,687	230622,43	58408,027
1 [P21964_	13082,327	18217,579	4530,1928	3792,6561	13639,301	18697,751	3645,0521
1 [P21964_	40717,972	96188,125	26796,96	4412,2243	41611,499	100431,93	22986,438
1 [P21964_	46271,293	80210,141	22635,119	3846,0635	47906,687	82955,544	19490,794
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1 [P21964_	22925,566	74465,742	19010,615	2731,6253	22994,921	78354,523	15939,691
1 [P21964_	12309,961	26068,416	6781,7883	3380,0763	12643,924	27153,446	5618,3369
1 [Q14974]	17303,568	32825,195	9667,0833	2648,2428	17855,118	34039,791	8363,8813
1 [Q14974]	13913,689	24306,182	7757,8441	2227,2307	14402,037	25116,098	6830,7451
1 [Q14974]	10232,784	16890,131	2924,9303	143,74494	10611,329	17496,633	2145,3757
1 [Q14974]	27211,591	42880,992	14101,465	3048,4805	28266	44126,546	12540,719
1 [Q14974]	25789,688	31454,201	7196,4842	2195,91	26982,358	32098,747	5810,5694
1 [Q14974]	40661,113	69364,219	20749,676	4296,9251	42122,849	71659,348	18083,289
1 [Q14974]	197842,98	323053,81	90715,303	46794,421	205258,94	333401,64	76681,393
1 [Q14103_	291090,32	440270,94	251076,09	71500,988	302830,19	448877,97	241811,35
1 [Q14103_	244320,5	439787,13	169344,69	44872,695	252638,31	453976,15	154673,43
1 [Q14103_	1085129,5	962377,27	546058,66	266716,92	1143225,2	952731,13	521455,78
1 [Q14103_	834410,68	1357406,6	356265,33	94943,475	865780,53	1401473	299701,34
1 [Q14103_	11570,968	19172,49	6270,5618	1236,9086	11999,342	19768,39	5574,5995
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1	[Q14103_	417479,66	906015,06	402467,74	112195,46	428445,77	938978,5	375545,03
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1	[Q14103_	889999,04	1851369,1	588272,46	159233,32	914924,31	1923951,2	517656,81
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1	[Q16629_	24754,759	36231,367	9348,6821	3674,8007	25771,398	37254,953	7780,3883
2	[Q16629_	90890,683	124275,56	40253,194	13591,062	94815,274	127140,66	35492,663
2	[Q16629_	172771,56	233493,28	82496,915	16593,579	180294,43	238524,28	74488,875
1	[Q16629_	53921,896	61620,578	22508,698	11728,395	56509,384	62395,942	20148,855
1	[Q16629_	156660,41	153540,98	58628,494	28130,072	164721,04	153970,52	53029,825
1	[Q16629_	62160,169	88754,609	23623,12	8521,5498	64760,859	91141,819	19861,773
1	[Q16629_	214091,16	231448,88	92776,373	44982,757	224650,45	233358,68	84545,476
1	[Q16629_	301915,39	315972,09	113602,07	57331,595	317019,1	318387,94	101513,55
1	[POCG47_	43218,822	66436	29941,732	15381,199	44934,174	68038,252	27711,003
1	[POCG47_	132127,88	191484,02	89104,682	46230,464	137620,14	195530,2	82827,733
1	[POCG47_	226080,26	315965,09	176739,07	123820,12	235744,23	321176,04	166712,1
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1	[POCG47_	119763,05	163595,84	50826,465	29450,335	124936,23	167432,73	43888,859
1	[POCG47_	80521,477	82194,414	67252,313	41547,904	84617,973	81480,364	65968,577
1	[POCG47_	923779,67	1291714,4	622513,2	355768,08	963189,54	1316257	580031,28
1	[POCG47_	105910,9	158875,73	78979,063	44253,411	110202,51	162307,14	73914,143
1	[POCG47_	98479,966	140418,36	69603,632	36871,385	102625,06	143146,89	65214,68
1	[POCG47_	62234,248	87912,055	43723,43	24155,298	64871,282	89578,954	40941,931
1	[POCG47_	105054,51	69847,348	205445,62	154584,83	111277,74	62127,951	211089,07
1	[POCG47_	69140,463	48525,592	134722,45	96005,973	73181,011	43664,508	138490,3
1	[POCG47_	59792,264	46197,959	96855,965	66633,106	63182,971	42966,555	98998,195
1	[Q02809_	169881,85	506004,63	126573,89	25585,773	171370,34	531617,8	105215,63
1	[Q02809_	7895,781	21183,57	4463,7733	820,04243	8014,1992	22232,969	3514,9474
1	[Q02809_	25628,072	63794,094	16090,562	3092,0827	26120,085	66750,884	13420,123
1	[Q02809_	40086,034	117450,91	20740,63	6093,7746	40473,228	123634,51	15088,314
1	[Q02809_	837,18257	2299,5813	438,12305	76,414466	848,56634	2416,2709	331,93497
1	[Q02809_	9275,0627	26340,358	5890,1174	1028,3118	9383,2997	27668,762	4736,2726
1	[Q02809_	29063,47	33104,629	10884,683	4318,3413	30459,638	33553,86	9606,214
1	[Q9Y224]	5381,5859	12897,17	3754,5085	1118,9055	5495,8582	13466,035	3233,6113
1	[Q9Y224]	19517,501	37616,711	12021,563	4194,3116	20127,626	38998,13	10552,922
1	[Q9Y224]	162996,88	277379,41	77313,986	19181,105	168867,28	286715,97	66114,26
1	[Q9Y224]	16833,884	29179,051	10926,981	3422,5946	17430,625	30090,865	9910,6164
1	[Q9Y224]	13406,059	21726,275	9405,6233	2996,6415	13914,201	22308,646	8732,0018
1	[Q9Y224]	38101,82	60602,598	28926,573	9645,5701	39572,067	62095,076	27207,694
1	[Q9Y224]	99831,779	192934,42	65936,545	16972,749	102944,16	199897,35	58940,589
1	[Q9Y224]	76319,542	132224,88	30285,859	11656,961	79013,954	136976,87	24312,757
1	[P21980]	10458,8	71238,266	8751,3563	1677,3098	9689,9524	75994,501	5085,2474
1	[P21980]	4056,4153	22111,676	3377,5689	841,84862	3876,7403	23515,032	2279,6654
1	[P21980]	44086,335	221088	35360,163	8303,2994	42545,758	234843,65	24519,159
1	[P21980]	22475,268	119130,59	22993,672	4662,2677	21555,177	126496,47	17456,468
1	[P21980]	35524,796	117491,59	25401,241	5236,7744	35584,501	123817,56	20148,713
1	[P21980]	3179,2593	9911,6426	2081,0919	473,31665	3197,4354	10435,703	1631,9564
1	[P21980]	37768,787	70750,258	24371,218	8220,6404	38994,05	73223,985	21736,578

1 [P21980]	7607,3982	50378,207	10686,049	2115,7034	7081,8396	53582,709	8412,3366
1 [Q9NVI7_]	39060,201	44476,261	10688,272	1587,9868	40934,4	45205,604	8838,5357
1 [Q9NVI7_]	17988,941	21822,545	6911,4364	1823,9083	18824,6	22201,467	6090,1012
1 [Q9NVI7_]	89408,208	98082,891	28261,826	5294,1293	93780,628	99331,514	24484,069
1 [Q9NVI7_]	87792,142	94537,789	27241,288	4646,9409	92123,274	95638,31	23622,084
1 [Q9NVI7_]	122920,22	153019,89	43535,913	9795,2507	128544,12	156040,83	37508,344
1 [Q9NVI7_]	160231,91	169294,48	48672,69	17460,125	168205,86	171078,71	41792,9
1 [Q9NVI7_]	97809,078	48815,384	20468,707	8627,1727	103841,89	45836,78	18915,766
1 [P67809_]	101618,38	148309,17	95906,334	42198,633	105837,7	150618,48	92912,782
1 [P67809_]	35479,497	51107,211	31133,683	14788,395	36965,613	51935,735	29939,34
1 [P67809_]	52499,725	63776,625	38142,328	13037,133	54948,195	64308,758	36840,553
1 [P67809_]	451246,02	553207,19	336939,58	121738,35	472188,82	557891,33	325754,33
1 [P67809_]	1093907,9	1335556,3	825346,67	295799,24	1144801,5	1346192,4	799217,14
1 [P67809_]	77363,141	72147,46	45307,001	14546,527	81433,188	71535,286	44040,499
1 [P67809_]	79276,041	98023,563	63055,112	30414,726	82939,844	98790,155	60958,157
1 [P67809_]	173367,6	210427,22	136346,09	81985,054	181463,47	211841,73	131207,65
1 [P67809_]	7211,2683	10388,688	5234,0873	2192,6482	7512,5995	10592,452	4939,0982
1 [P67809_]	142103,32	208443,28	121446,67	66177,051	147972,93	212168,7	115877,67
1 [P67809_]	5037,5214	8125,1572	4281,4759	2339,4727	5229,7736	8316,9285	4037,9539
1 [P67809_]	24570,154	36302,992	20451,562	9806,3298	25579,046	36985,522	19499,731
1 [P69849_]	56983,931	94224,203	24340,947	6560,5612	59093,531	97355,293	20383,5
1 [P69849_]	155792,16	204246,42	61521,766	15623,952	162702,74	208695,65	53626,803
1 [P69849_]	5223,4818	8494,1367	1754,0856	235,03482	5419,6262	8785,0838	1377,7135
1 [P69849_]	101042,99	141362,81	43039,026	7710,2028	105336,02	144858,53	37735,657
1 [P69849_]	35075,011	48928,699	14030,545	2345,5037	36567,722	50160,161	12139,935
1 [P62081]	93866,439	211159,58	64646,216	9831,8928	96155,426	220002,16	56745,206
1 [P62081]	39114,558	83793,875	27797,224	4395,7121	40159,104	87114,696	24814,182
1 [P62081]	186645,64	425604,34	127622,86	27032,093	191073,37	443677,54	111169,77
1 [P62081]	134304,25	255071,34	60067,677	13109,234	138569,27	265005,56	49062,538
1 [P62081]	28726,297	63823,406	15962,917	2728,4398	29441,496	66589,368	13300,568
1 [P62081]	128960,37	201842,11	68495,75	49979,516	133987,92	207588,3	59782,835
1 [P62081]	66854,127	139981,8	44600,498	11309,614	68707,11	145493,55	39301,798
1 [P62081]	131576,49	224668,41	41157,294	11459,498	136285,3	232953,93	30549,179
1 [P62081]	43223,683	79540,117	18418,064	5246,1295	44650,507	82562,859	14913,242
1 [P07910_]	25058,601	38637,66	7722,3364	1938,9226	26044,467	39886,957	5954,1665
1 [P07910_]	1442010,3	1999358	592054,12	105366,22	1503650,9	2048516,8	515893,98
1 [P07910_]	1194382,7	1496909,6	360504,42	72110,287	1248772,4	1529090,2	297336,7
1 [P07910_]	822881,44	511424,49	389435,31	167141,15	871612,08	487412,21	383527,36
1 [P07910_]	265267,19	183550,3	85791,682	30533,614	280549,27	178589,38	80594,453
1 [P07910_]	253979,33	158905,12	100990,65	36059,576	268984,87	152197,56	98241,224
1 [P07910_]	68152,979	102726,38	29966,898	5223,212	70890,717	105644,72	26017,574
1 [P07910_]	12777,222	19023	5944,9476	1088,7317	13295,769	19540,659	5240,1413
1 [P07910_]	144319,95	179622,13	66050,425	10879,125	150933,39	182681,76	60193,713
1 [P07910_]	62458,925	75321,719	27038,956	6414,1256	65371,974	76502,924	24453,386
4 [P35579,	29623,641	107651,21	22440,925	5349,4235	29466,369	113660,73	17534,001
4 [P35579,	137316,58	273428,63	90231,125	33820,793	141424,3	283668,09	79632,887

4 [P35579,	208584,84	197051,83	60282,73	49456,609	219464,15	197611,54	51338,963
2 [P35580,	52654,342	133701,67	32801,122	11553,117	53608,461	139996,93	26910,529
3 [P35579,	107194,22	147863	49260,952	43769,057	111795,99	151293,85	42514,311
3 [P35579,	745239,18	997033,5	386753,1	239471,32	777925,31	1016958	348046,73
3 [P35579,	9433,1273	33864,453	6362,7484	747,60718	9391,4648	35770,006	4804,086
3 [P35579,	7433,375	28744,109	5036,7686	725,12901	7356,3357	30409,862	3680,0403
3 [P35579,	40926,696	134970,06	27892,803	4947,6283	41002,92	142271,15	21802,465
3 [P35579,	12036,969	37694,543	8080,9164	1876,692	12102,303	39685,633	6382,7185
3 [P35579,	21245,044	59111,055	12949,905	4670,0311	21518,879	62073,952	10237,856

1 [P22695_	8641,9844	9968,3297	2728,5948	483,36835	9054,13	10128,187	2334,9268
1 [P22695_	17193,981	20696,113	7005,7132	2362,237	17996,447	21032,489	6235,6547
1 [P22695_	285618,47	254228,45	82017,9	17930,583	300850,61	253752,03	72819,314
1 [P22695_	103962,44	126501,98	52580,733	18158,558	108791,77	128314,66	48490,186
1 [P22695_	24957	24594,814	10158,485	3097,6575	26238,749	24647,204	9383,397
1 [P22695_	84243,311	93496,523	36476,091	12141,285	88346,272	94441,871	33328,126

1 [P08134_	90111,691	153582,48	43320,698	15400,162	93352,403	158745,27	36954,052
1 [P08134_	9745,3576	19910,543	4734,1699	1497,1791	10024,955	20731,625	3857,2632
1 [P08134_	10886,156	24046,895	5753,4666	1839,3269	11159,996	25093,662	4694,6541
1 [P08134_	83214,314	188038,38	55284,716	13134,339	85224,14	196011,49	47877,369
1 [P08134_	153454,08	346549,72	110761,82	37625,631	157170,47	360953,37	97239,335
1 [P08134_	30693,507	68191,234	16526,217	3765,6679	31457,4	71163,741	13602,786
1 [P08134_	19535,635	47678,766	11531,943	2675,868	19930,614	49880,422	9481,5045

1 [Q16643_	111145,49	97384,358	36314,516	15726,833	117108,93	96934,485	32801,851
1 [Q16643_	228324,87	427255,22	127488,25	37858,14	235728,99	442814,02	110516,35
1 [Q16643_	288670,03	210481,35	120003,78	45985,639	305086,82	205081,9	115273,59
1 [Q16643_	85304,412	143766,14	59896,736	24242,028	88419,237	147913,44	55057,4
1 [Q16643_	65109,71	68222,688	21409,494	7311,2558	68363,185	68849,253	18769,132
1 [Q16643_	27728,879	40554,574	15730,82	7713,1306	28871,675	41529,077	14240,199

1 [P08107_	284369,53	529296,31	217531,96	32212,059	293689,86	546539,81	201895,31
2 [P08107_	118620,86	193842,93	110910,95	12827,423	123100,55	198223,87	107652,21
2 [P08107_	162411,59	218295,98	176297,73	17523,794	169572,71	219729,27	176634,71
2 [P08107_	174028,34	215875,23	160090,31	19659,598	182070,5	216900,91	159205,25
2 [P08107_	80137,071	129457,68	94351,575	9497,4909	83208,113	131668,04	93753,784
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1 [P08107_	11847,165	17337,559	6937,1355	1538,6338	12335,344	17747,379	6392,6346
4 [P11142_	292485,47	385919,53	160695,99	39658,933	305435,58	393007,4	148883,96
4 [P11142_	130441,7	604609	106496,38	64842,367	126948,73	641289,24	75827,47

1 [P39019_	509798,36	1088914,4	308934,16	67446,037	523446,94	1133670,8	265555,19
1 [P39019_	6110,7714	10534,386	3674,3147	1410,8974	6328,4421	10870,263	3278,2875
1 [P39019_	78662,981	158188,09	47925,059	18900,344	80980,357	164300,09	41480,144
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1 [P39019_	45535,518	87131,438	29167,844	9648,1824	46973,247	90267,508	25874,853
1 [P39019_	95123,578	172250,8	56011,106	18104,941	98333,627	178178,9	49418,448
1 [P39019_	74036,52	124874,72	43465,213	15318,73	76732,319	128757,01	38826,405
1 [P39019_	79512,629	146687,28	49565,85	16297,21	82139,529	151770,36	44060,502

1 [Q96D15_	71906,102	150313,11	77951,046	39932,735	73923,616	155255,89	73460,259
1 [Q96D15_	61187,624	148470	49329,184	19697,898	62451,784	154870,84	43524,737
1 [Q96D15_	529476,07	905340,75	542206,49	332514,77	548639,34	926638,87	517124,61
1 [Q96D15_	170632,74	275774,16	146066,2	95047,392	177133,44	282284,05	137185,45
1 [Q96D15_	458868,83	805391	420071,63	256837,25	474998,24	827121,52	394455,64
1 [Q96D15_	85771,957	154525,52	61772,853	31994,132	88690,62	159445,61	56099,039
1 [Q96D15_	21922,566	29705,092	12927,154	8423,7163	22877,014	30271,341	11829,976
1 [Q96D15_	36283,545	49229,02	23262,961	15066,826	37863,038	50111,107	21543,555
1 [Q96D15_	256407,58	589685,63	348332,5	217244,93	262493,49	609346,14	331457,38
1 [Q96D15_	474705,34	1071905,4	599173,79	362649,71	486369,09	1108190,1	567189,47
1 [Q6DD88]	13248,273	32392,111	7956,9142	1426,5009	13514,969	33885,35	6590,4863
1 [Q6DD88]	18101,315	59897,789	13622,038	2210,4058	18131,51	63101,507	11017,695
1 [Q6DD88]	18174,399	65522,477	13709,586	2926,8956	18089,102	69169,33	10741,407
1 [Q6DD88]	66141,67	153505,17	44968,5	8671,1451	67652,914	160132,84	38994,439
1 [Q6DD88]	16121,263	38654,141	7989,8282	1518,0377	16461,082	40464,95	6247,5725
1 [Q6DD88]	413440,29	1153203,9	308047,73	64286,746	418743,86	1209271,4	260712,35
1 [Q6DD88]	121975,39	313524,72	67493,062	12609,49	124098,57	328684,43	53550,755
1 [Q6DD88]	55654,432	139516,13	35548,382	8529,258	56702,237	145996,36	29660,044
1 [Q6DD88]	47054,385	132131,53	33981,526	5991,1779	47638,33	138618,07	28511,997
1 [P48444]	87961,728	133345,84	43056,831	8764,5259	91481,641	137031,9	38175,639
1 [P48444]	25019,248	48342,785	14384,23	2398,4772	25798,083	50156,023	12540,813
1 [P48444]	19507,733	36181,875	8335,6341	2795,2467	20145,605	37568,17	6720,0889
1 [P48444]	117134,65	180200,84	66427,648	9664,6476	121771,33	185024,96	60580,164
1 [P48444]	32589,887	58777,07	16101,524	2842,6545	33692,784	60888,455	13755,798
1 [Q14204]	11035,926	19427,627	5634,9371	1040,4367	11419,745	20098,581	4880,5786
1 [Q14204]	4095,7321	8713,3516	2210,3361	342,82231	4205,963	9078,8833	1850,8644
1 [Q14204]	55738,692	109352,91	32657,115	5590,0151	57438,683	113505,15	28488,477
1 [Q14204]	2495,1118	4777,3291	1086,1449	97,884631	2573,4998	4965,9131	883,26331
1 [Q14204]	6818,4933	14618,6	4157,0632	1034,1751	6999,8864	15220,791	3569,8852
1 [Q14204]	59884,109	91829,344	29113,13	6005,1067	62257,818	94429,209	25709,096
1 [P28331_	9929,6429	20662,209	4676,0827	755,24207	10206,377	21533,481	3781,3631
1 [P28331_	10582,795	13272,132	4209,0986	1979,589	11065,173	13525,368	3671,9877
1 [P28331_	64772,781	62395,896	28015,896	13722,605	68131,307	62364,512	25977,666
1 [P28331_	47206,014	88206,789	26262,455	7997,3133	48739,497	91416,451	22746,292
1 [P28331_	28419,093	62766,781	15546,384	3417,1679	29134,518	65481,327	12884,553
1 [P28331_	11198,449	20137,043	6549,0468	1630,0639	11579,359	20824,965	5799,5057
1 [P62937_	50135,854	103221,12	28385,359	7105,8318	51559,909	107377,73	24173,444
1 [P62937_	97274,77	119398,39	43290,147	9743,3032	101767,46	121367,2	39241,594
1 [P62937_	70201,697	154758,61	39105,451	9475,3751	71975,635	161418,41	32559,04
1 [P62937_	487520,49	963240,25	227034,51	62958,092	502206,02	1002003,5	184883,06
1 [P62937_	118411,22	204936,36	48356,153	12249,857	122597,13	212246,53	39462,393
1 [P62937_	15007,461	28167,775	7431,6698	1909,4763	15491,691	29227,833	6260,3626
1 [P62937_	15283,667	28781,291	7111,2606	1574,7811	15774,473	29883,213	5892,1355
1 [P62937_	118047,82	164602,51	48425,731	12165,467	123073,95	168703,29	41978,88
1 [P62937_	469075,28	791451,75	219883,16	40384,825	486113,6	817857,9	188493,81
1 [P62937_	33732,605	54514,293	15472,432	3002,1795	35009,246	56231,959	13328,951

1 [P62937_	154522,6	263041,31	77912,377	14588,498	160089,01	271748,65	67813,285
1 [P62937_	29172,403	44564,398	11382,417	2204,0893	30330,601	45907,895	9542,2275
1 [P62937_	230176,54	389057,25	114290,98	23943,662	238526,58	401863,71	99178,39
2 [Q99729_	244320,5	439787,13	169344,69	44872,695	252638,31	453976,15	154673,43
2 [Q99729_	1085129,5	962377,27	546058,66	266716,92	1143225,2	952731,13	521455,78
2 [Q99729_	834410,68	1357406,6	356265,33	94943,475	865780,53	1401473	299701,34
1 [Q99729_	67369,839	80274,266	51932,943	14964,926	70547,404	80734,457	50671,506
1 [Q99729_	36474,445	44371,262	26638,559	7854,5928	38174,292	44741,175	25793,36
1 [Q99729_	33455,008	50400,148	24899,111	6767,3456	34806,027	51501,267	23593,373
1 [Q99729_	20497,138	25830,518	12650,335	3423,0233	21431,65	26185,092	11978,975
1 [Q99729_	107814,6	142401,88	79583,494	29962,987	112598,12	144370,04	76181,666
1 [Q99729_	228430,17	228942,58	156276,19	58974,323	240120,41	227683,68	152677,91
1 [Q99729_	328132,71	462973,56	150098,86	92623,696	341996,62	474318,16	130549,45
1 [Q99729_	201468,36	254338,88	95293,799	58107,143	210625,31	258806,71	85296,136
1 [Q99729_	188094,05	251125,69	67153,492	55649,562	196335,39	257099,16	55192,933
1 [Q99729_	80341,356	93701,609	51615,857	31189,736	84167,61	94425,188	48835,912
1 [Q13200]	21531,135	43004,843	17112,865	3589,8087	22174,317	44524,447	15753,464
1 [Q13200]	18834,395	35590,273	13184,74	2007,6593	19439,445	36814,711	12024,717
1 [Q13200]	67250,14	103229,84	48966,371	6384,36	69924,062	105630,41	46450,553
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1 [Q13200]	13619,683	25588,814	9931,7346	2346,3133	14060,632	26449,736	9094,9264
1 [Q13200]	34434,667	65209,457	21123,223	4357,2398	35535,933	67556,123	18726,426
2 [O60506_	335867,68	703514,38	172287,36	29955,616	345137,98	732898,27	142680,33
2 [O60506_	237844,49	477782,91	130325,71	27243,137	244853,03	496688,08	110996,87
1 [O43390_	65589,134	169604,16	42486,036	8012,2591	66713,022	177636,66	35368,424
1 [O43390_	122785,51	192899,94	74817,039	18632,449	127563,13	198111,39	68492,143
1 [O43390_	113974,31	169008,75	42016,676				
2 [O60506_	142780,24	233729,7	80297,654	31711,114	148129,19	240763,45	71405,705
2 [O60506_	64709,529	109979,84	34946,124	11690,031	67045,789	113538,33	30671,676
2 [O60506_	122211,41	198839,64	65621,357	21538,504	126814,01	204862,02	58077,857
1 [P61026]	72784,953	170373,53	44155,266	7327,4856	74413,407	177955,31	37163,931
1 [P61026]	19851,68	45373,148	11840,566	2193,4191	20319,228	47359,925	9975,3714
1 [P61026]	11957,95	18426,605	5758,6466	1557,7032	12429,98	18954,795	5053,6553
1 [P61026]	268994,75	563108,25	154236,18	24459,569	276436,91	586088,34	131820,16
4 [Q9H0U4,	82500,889	141584,25	43163,82	7937,039	85449,268	146274,1	37821,143
4 [Q9H0U4,	160537,73	337016,25	110682,77	16852,287	164970,86	350203,5	98636,211
4 [Q9H0U4,	127991,53	191676,92	55432,544	10887,652	133159,18	197085,63	47976,939
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1 [P10606_	747476,09	757860,31	488622,35	170912,58	785527,62	755170,86	475458,89
1 [P10606_	522965,83	537213,75	342946,85	126007,66	549438,96	535857,52	333124,31
1 [P10606_	192438,66	333001,97	138076,32	63613,28	199280,84	342959,13	126485,29
1 [P10606_	167634,24	279757,88	119729,61	50734,194	173815,88	287621,75	110414,58
1 [P10606_	628340,26	795809,13	433133,14	194002,96	656931,24	805546,69	412086,59
1 [P10606_	325744,8	529232,5	221770,59	84285,684	338059,05	543710,81	204288,14
1 [P10606_	363527,46	416967,53	184510,45	75771,902	380959,74	421255,34	171263,26
1 [P10606_	204378,17	274521,28	95690,21	27408,787	213312,25	280400,76	85832,217
1 [P10606_	43557,609	36907,599	24743,763	9908,4332	45928,429	36290,704	24120,019

1	[P10606_	89809,344	77629,184	43150,437	16967,39	94659,674	76734,123	41293,664
1	[Q96AY3_	40749,546	74090,25	21239,836	7612,0094	42116,453	76743,079	18183,992
1	[Q96AY3_	15981,875	48058,777	11380,78	4434,6438	16111,77	50522,382	9214,4568
1	[Q96AY3_	31101,616	105093,59	25360,279	9084,936	31107,959	110710,38	20681,765
1	[Q96AY3_	22539,183	71720,203	18356,784	6990,1319	22639,154	75435,81	15215,474
1	[Q96AY3_	8922,8858	20372,482	8050,3846	4403,9035	9135,2489	21176,062	7283,5122
1	[Q96AY3_	4351,5923	12661,791	4070,345	2169,5794	4396,6864	13267,366	3542,1014
1	[Q96AY3_	36433,789	71184,695	14767,359	4404,872	37547,069	74088,661	11503,201
1	[Q07020_	53199,366	76055,164	17707,162	2917,9695	55421,507	78186,285	14470,762
1	[Q07020_	54162,009	86821,344	27036,521	6461,7109	56228,443	89451,806	23741,862
1	[Q07020_	88781,368	153455,27	33737,649	8856,2961	91922,526	159001,75	26894,766
1	[Q07020_	803901,34	1371005,8	391304,04	98996,377	832796,84	1416968,6	336494,73
1	[Q07020_	126299,74	208828,69	50159,084	9596,5223	130973,29	215889,39	41299,357
1	[Q07020_	737004,44	1218420,9	355042,59	96090,441	764319,94	1257596,9	306596,41
1	[Q07020_	87105,99	210384,75	58057,379	14191,712	88918,803	219810,16	49480,17
1	[Q07020_	86711,504	128740,88	39866,955	10150,675	90237,927	132241,41	34948,189
1	[Q07020_	46449,18	134833,13	43358,498	8072,0434	46937,39	141271,07	38382,91
1	[P62873_	44237,484	132930,6	22028,313	7677,4231	44592,985	140048,25	15480,467
1	[P62873_	60102,091	143236,5	32908,457	8762,8586	61389,689	149817,17	26580,855
1	[P62873_	52241,129	183145,83	54721,912	9037,3083	52117,398	192716,23	47698,561
1	[P62873_	33357,93	70454,469	21018,353	5435,6503	34268,642	73293,375	18248,097
2	[P62873_	38152,247	139069,52	27282,576	3207,5399	37939,525	146894,94	20966,898
2	[P62873_	25574,609	88586,367	16959,604	2455,0008	25530,748	93503,821	12887,152
2	[P62873_	29367,196	87861,477	23925,74	10411,738	29617,438	92255,37	20114,853
2	[P62873_	23165,799	87219,461	17369,396	2396,8605	22977,49	92167,492	13411,376
2	[P62873_	18228,887	34944,172	10602,696	4333,7612	18802,383	36239,605	9174,6244
1	[P08195_	152048,08	249777	59406,054	10066,468	157708,69	258178,41	48824,398
1	[P08195_	199392,45	297834,09	90562,438	25120,156	207462,14	306063,75	78977,886
1	[P08195_	45626,03	79943,281	18617,933	3306,9598	47217,938	82838,48	15191,695
1	[P08195_	53836,455	83757,266	18300,2	3487,6515	55939,563	86445,578	14621,822
1	[P08195_	7214,8676	16354,481	4021,8409	637,53313	7387,5305	17074,76	3336,6069
1	[P08195_	2307,4847	5325,6074	1171,0665	181,99526	2360,5902	5567,3121	937,922
1	[P08195_	44227,756	90668,688	24813,995	7763,4488	45492,194	94312,013	21039,381
1	[P08195_	88134,589	170578,83	49847,123	11492,187	90871,543	177016,3	43139,305
1	[P54886_	6585,686	12135,131	2558,2622	558,51273	6802,5748	12604,965	2013,8892
1	[P54886_	33969,501	55493,242	16838,153	3774,9972	35243,11	57230,131	14711,418
1	[P54886_	20047,959	47568,402	10626,433	2155,9426	20481,751	49757,843	8533,5922
1	[P54886_	223015,36	401055,44	90757,631	20419,626	230574,99	416040,71	73184,76
1	[Q86UP2_	171383,47	93800,872	39479,649	16898,704	181779,09	89126,896	36470,263
1	[Q86UP2_	161332,39	128902,51	74490,844	28530,031	170270,14	126547,34	71636,017
1	[Q86UP2_	96464,945	80299,983	28474,861	10366,715	101729,45	79669,365	25580,245
1	[Q86UP2_	187942,54	190227,91	77697,811	52367,77	197487,91	190991,36	70400,885
1	[Q86UP2_	126657,31	112904,22	37621,73	16883,258	133409,18	112667,69	33247,077
2	[P17844,	53902,28	74552,102	21720,558	7105,401	56210,075	76388,92	18715,492
2	[P17844,	63390,037	88860,469	27517,873	9369,2019	66079,838	91051,808	24025,923

2 [P17844,	39761,312	51745,656	18980,104	6204,7123	41535,346	52744,799	17154,101
1 [Q92841]	165716,42	283754,97	40853,812	12430,948	171622,93	294609,31	26655,776
1 [Q92841]	23403,618	41323,477	6493,941	2073,5139	24211,397	42933,076	4457,3066
2 [P17844,	110788,3	156870,38	41807,435	6167,5931	115451,67	161027,25	35548,635
2 [P17844,	74281,641	38555,14	21426,798	9388,3154	78835,239	36221,688	20504,58
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1 [Q92841]	355808,85	451677,94	107940,24	36994,292	371888,52	461710,44	88149,554
1 [Q99829]	38544,959	91415,039	19019,239	3076,5107	39378,976	95666,715	14931,501
1 [Q99829]	70043,986	155880,48	32608,549	4888,1055	71778,259	162849,76	25673,79
1 [Q99829]	2608,6416	5193,6001	1082,7353	245,02404	2686,289	5408,4375	848,23136
1 [Q99829]	34082,263	62468,336	13986,998	3054,151	35212,351	64848,925	11242,466
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1 [P30050]	576704,88	659469,06	336449,07	91053,945	604431,26	664686,02	320300,97
1 [P30050]	235993,09	330581,84	130141,61	35885,768	246029,77	337823,67	119321,21
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1 [P30050]	371431,09	609593,44	182485,56	50297,301	385295,46	628865,26	158542,23
1 [P30050]	137772,95	193563,27	56188,369	17275,134	143607,4	198477,24	48417,285
1 [P30050]	12002,064	21794,332	5306,2396	1510,4846	12404,648	22604,081	4363,6822
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1 [Q9Y277]	68345,307	102037,49	30570,804	4271,239	71112,136	104868,64	26752,617
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1 [P29401]	59410,295	157193,05	38276,376	9295,3799	60351,551	164761,64	31509,257
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1 [P62241_ 46278,506 78232,68 22477,734 4815,671 47956,794 80824,563 19398,589
1 [P62241_ 56069,579 94542,039 28556,599 7041,3184 58108,99 97620,256 24894,134

1 [P62241_	54576,155	88284,602	25716,343	5438,8609	56640,238	91048,457	22272,637
1 [P27695_	45221,811	73767,75	21047,345	6013,0275	46918,722	76115,937	18070,902
1 [P27695_	410197,5	373010,09	156824,87	22236,422	431929,09	371692,18	146401,56
1 [P27695_	19841,422	34354,148	8002,4028	1125,7363	20542,462	35583,261	6543,2444
1 [P27695_	51265,553	91475,828	21518,839	2912,5658	53019,144	94841,521	17651,75
1 [P27695_	69756,622	141066,03	33977,519	3702,2982	71789,251	146822,52	28098,232
1 [P21589_	5724,5168	19732,83	6122,9475	935,60836	5718,2593	20750,513	5386,1075
1 [P21589_	64986,405	143899,83	49391,964	13586,441	66623,329	149689,46	44137,727
1 [P21589_	44745,448	88373,133	21020,721	4606,5226	46094,178	91921,921	17219,233
1 [P21589_	83916,766	193543,39	57451,186	7598,1781	85860,521	201841,25	50123,602
1 [P21589_	37746,28	94673,594	29325,139	4390,0895	38459,219	98903,331	25804,579
1 [P21589_	37222,308	98160,203	33510,778	5837,2205	37825,177	102567,18	30050,12
1 [P21589_	34025,256	93422,648	22383,335	2709,3251	34491,696	98013,718	18452,012
1 [P21589_	288305,76	576812,06	229459,26	32486,851	296897,53	597223,89	211895,16
1 [P41252]	23432,178	43842,32	12479,296	5232,6091	24191,758	45458,515	10631,542
1 [P41252]	7127,1447	19410,678	4841,3576	794,67227	7228,3444	20354,777	4029,8319
1 [P41252]	21050,871	30361,582	8859,0021	2261,6862	21925,627	31166,425	7662,2256
1 [P41252]	200457,54	353559,5	102960,47	18960,953	207415,16	365781,11	89263,186
1 [P41252]	18119,098	27992,49	9062,7219	1893,136	18833,011	28787,552	8037,1776
4 [P63104,	161857,69	327951,88	117754,95	25383,247	166585,44	340101,77	106454,3
4 [P63104,	17331,97	42488,875	13986,94	3246,2065	17680,765	44335,72	12418,334
4 [P63104,	374942,26	985718,38	313352,7	67796,007	381064,95	1030651,9	276359,6
4 [P63104,	79175,538	162033,38	56059,267	13864,788	81452,618	168155,96	50248,542
4 [P63104,	40150,962	105845,82	34122,592	7792,3713	40800,761	110662,48	30165,92
4 [P63104,	181306,25	305822,41	113912,04	20782,076	187912,4	315085,45	103868,47
4 [P63104,	5050,6447	11932,093	4021,4808	976,54269	5161,9051	12436,051	3585,8903
4 [P63104,	10281,669	22831,688	7389,229	1685,6517	10538,985	23766,561	6540,1139
4 [P63104,	206607,44	445348,88	121146,37	22938,286	212049,43	463941,63	103187,82
4 [P63104,	19130,251	29969,615	11579,75	3823,6273	19876,379	30777,486	10553,591
4 [P63104,	17825,365	29065,428	11240,433	3030,8269	18496,401	29894,78	10274,228
4 [P63104,	143322,17	313643,19	111752,39	25221,599	147013,94	326021,62	100818,88
4 [P63104,	48798,28	83598,586	26060,965	6321,984	50545,699	86343,99	22881,8
4 [P63104,	28937,502	67741,461	22231,776	4448,0805	29587,833	70604,95	19758,674
4 [P63104,	42474,388	95235,047	35559,846	10193,587	43520,942	99007,931	32258,941
4 [P63104,	25250,18	45418,703	14748,901	4816,5985	26108,741	46971,76	13007,364
2 [P63104,	1200,0874	2777,1282	1106,5739	261,21454	1227,8686	2887,3349	1017,3697
4 [P63104,	270648,98	438252,41	204835,35	63037,342	280925,22	449496,03	192341,01
1 [P27348]	5559,2085	15679,184	5378,9547	744,98568	5627,6041	16406,815	4835,8149
1 [P27348]	44238,613	92049,734	30127,632	7365,888	45477,597	95630,66	26710,48
1 [P27348]	109813,35	273588,97	116957,69	23522,263	111947,35	284723,64	108886,79
1 [P27348]	55793,807	130941,3	56791,218	11616,593	57049,564	136038,06	52982,488
3 [P07900_	122186,62	232096,64	78936,665	11215,546	126081,64	240350,27	70889,882
3 [P07900_	56157,411	116752,67	44219,293	5803,8799	57736,156	121096,17	40516,83
3 [P07900_	25286,983	50557,582	18598,504	2428,8311	26040,305	52394,567	16956,374
3 [P07900_	23515,33	46398,074	16775,4	4271,9403	24228,791	48074,206	15157,331
3 [P07900_	20579,424	46136,738	9904,6325	2559,7447	21081,91	48201,169	7824,103
1 [Q58FF8_	16041,413	29395,264	7261,7422	2088,3393	16573,884	30493,353	5996,4198

1 [Q58FF8_	10212,06	21465,932	5056,6946	1339,7076	10492,181	22371,384	4118,9339
2 [P08238,	132455,66	198660,66	49185,353	13259,53	137791,85	204547,49	40713,314
2 [P08238,	108206,43	176112,91	62466,597	11872,13	112283,15	181306,87	56442,552
2 [P08238,	104732,75	169881,75	56269,022	16129,794	108688,28	174999,61	49938,855
3 [P07900_	1510868	2087383,5	782609,22	164114,37	1575716,4	2133044,9	713888,53
3 [P07900_	806877,96	1300636	504243,81	128462,82	837572,89	1337119,4	461429,19
3 [P07900_	503039,57	865610,44	317257,04	76576,656	521001,93	892645,35	287637,54

1 [Q02218_	49301,387	88435,625	25900,637	3518,7347	50981,166	91540,98	22537,892
1 [Q02218_	25100,273	44286,883	13068,214	1835,2074	25971,244	45812,667	11389,431
1 [Q02218_	59407,347	100994,98	30736,534	6855,2626	61550,754	104306,82	26870,561
1 [Q02218_	48861,747	65813,492	25891,033	11910,154	50995,667	67137,199	23532,52
1 [Q02218_	12886,892	18717,771	4434,4987	625,49403	13418,95	19252,86	3647,8125

1 [P61106_	60470,974	105455,59	22194,194	7292,7317	62589,916	109333,94	17359,911
5 [Q9H0U4,	432318,58	838045,13	159830,87	31220,876	445661,07	872467,25	121178,97
1 [P61106_	20820,632	39676,473	9196,2009	2751,8105	21478,868	41231,161	7441,7577
1 [P61106_	293807,66	597268,56	129869,88	33667,617	302293,39	622196,65	103083,28
1 [P61106_	37190,18	71878,265	14395,082	3555,9799	38342,987	74801,508	11096,984

1 [P61313]	28846,213	48009,672	13916,274	2456,2229	29908,462	49567,786	12058,566
1 [P61313]	5994,704	9360,1582	2776,9936	526,43636	6228,6364	9638,2752	2418,3678
1 [P61313]	101780,57	161843,5	48334,775	7486,0792	105690,35	166760,82	42226,386
1 [P61313]	46325,927	65153,305	19313,609	3170,4409	48286,574	66796,868	16843,801
1 [P61313]	5111,128	8495,5127	1193,7261	150,59328	5298,7626	8811,8668	776,06344
1 [P61313]	79454,027	152546,13	38814,178	5338,9224	81943,952	158448,27	32569,708
1 [P61313]	56929,063	110718,51	35189,244	5641,2779	58687,375	114822,27	31139,467

1 [P07195_	150225,06	191313,72	74606,794	11598,607	157019,6	194656,61	68702,997
1 [P07195_	7338,8578	14165,846	5688,2431	1465,0383	7568,5666	14649,114	5232,7022
1 [P07195_	10644,573	22821,074	9484,4925	2264,1748	10929,691	23664,208	8778,6845
1 [P07195_	46946,72	83356,938	32129,262	9356,7577	48569,423	86004,828	29315,185
2 [P00338_	40565,218	111711,16	31917,153	5804,5279	41117,544	117042,24	27516,338
2 [P00338_	34812,434	97232,5	28104,315	4833,153	35257,597	101893,61	24308,463
2 [P00338_	20176,841	50441,992	16509,096	2888,824	20562,007	52662,856	14680,283
2 [P00338_	62821,507	131972,13	41447,689	11182,999	64553,095	137201,28	36381,52

1 [Q13724]	19566,821	32537,092	9019,9461	2029,7456	20287,702	33605,375	7712,4086
1 [Q13724]	19822,487	30009,815	8872,4863	1653,896	20616,04	30864,117	7722,5353
1 [Q13724]	13019,639	20435,43	5439,9543	895,46749	13525,038	21067,101	4618,1659
1 [Q13724]	49054,813	45534,764	12180,449	2143,4787	51629,505	45664,375	10375,838
1 [Q13724]	7357,2955	13121,212	2757,5515	364,16039	7608,8925	13614,396	2178,931
1 [Q13724]	6297,5502	8965,1172	2768,2642	519,17508	6561,8485	9192,5982	2433,5622
1 [Q13724]	23053,555	34666,707	9019,756	1896,1282	23980,662	35683,558	7594,1345

1 [P30044_	13920,474	33484,594	8605,7762	1731,7045	14212,696	35001,569	7212,8384
1 [P30044_	13310,553	44231,738	11190,459	2592,268	13329,497	46564,67	9316,0089
1 [P30044_	137944,06	501514,03	136394,97	32672,021	137227,29	528483,94	115740,88
1 [P30044_	181042,54	630122,25	185877,36	54280,985	180709,45	663049,32	160523,83
1 [P30044_	34985,5	111257,2	26310,547	7811,4655	35140,731	117089,28	21395,613
1 [P30044_	49743,974	154261,36	39590,924	11600,058	50050,497	162168,41	32992,869
1 [P30044_	36732,951	104557,02	31194,575	6959,1537	37161,544	109582,77	27113,416

1 [P30044_	188496,8	676633,94	202464,32	44723,032	187714	712271,8	176044,71
1 [P30044_	201057,7	568547,87	165975,8	40677,289	203480,97	595911,5	143372,17
1 [P49327]	6214,135	10750,109	2860,8103	586,67346	6434,1205	11122,872	2422,5557
1 [P49327]	32292,342	32882,203	11822,447	2359,3902	33927,239	33077,25	10721,248
1 [P49327]	13111,709	12223,586	3750,3764	595,71939	13799,077	12246,424	3303,3107
1 [P49327]	10820,906	8063,6213	3620,2183	911,01523	11432,003	7903,4156	3397,4249
1 [P62906_	57340,056	82866,781	22656,127	4865,5572	59718,287	85119,848	19324,485
1 [P62906_	130000,24	176034,31	49696,183	18339,428	135645,34	180249,9	42410,126
1 [P62906_	355234,57	625800,81	175551,13	37874,897	367575,91	647623,8	150587,97
1 [P62906_	266727,91	438662,94	141353,59	33930,726	276671,18	452240,35	125021,32
1 [P62906_	104057,34	206914,17	61218,453	10975,261	107171,77	214879,34	53265,731
1 [P62906_	42387,44	65864,266	20100,076	4027,4723	44048,697	67790,189	17607,507
1 [O94925_	2345,1434	6444,8062	1308,5778	519,43656	2377,0156	6769,3639	1004,2427
1 [O94925_	18070,919	83620,391	13153,443	3098,7694	17589,015	88741,322	9039,3085
1 [O94925_	9762,2922	46885,352	8250,8707	1278,0994	9465,9246	49751,685	6033,2479
1 [O94925_	147310,43	199817,7	60213,96	9098,8629	153702,39	204493,17	52751,907
1 [P41091_	72543,183	99308,656	28466,663	8608,6588	75670,62	101723,16	24464,458
1 [P41091_	31200,777	21213,093	5352,7838	811,62011	33003,296	20752,435	4506,2317
1 [P41091_	40657,155	65373,309	16864,014	2784,9148	42201,838	67474,682	14194,191
1 [P41091_	221065,22	303266,31	87081,712	24926,906	230582,19	310664,1	74930,003
1 [P41091_	389456,91	545827,5	150116,32	25837,545	405972,96	559888,77	128526,44
1 [P41091_	452971,58	667513	178562,62	30781,684	471481,92	686355,52	151761,55
1 [P41091_	283133,87	451456,63	132127,04	26247,422	293981,98	465311,64	114639,98
1 [P53396]	9882,1481	17949,043	5386,2683	1514,0802	10214,187	18583,192	4679,408
1 [P53396]	42620,471	82443,594	23750,283	2413,8419	43944,782	85563,827	20616,517
1 [P53396]	9751,0846	22599,252	7290,8566	1077,3408	9974,9889	23552,344	6473,4366
1 [P53396]	36436,929	74994,758	24729,917	3619,1462	37475,017	77880,584	22063,887
1 [P53396]	32731,29	57593,441	18922,525	2802,3363	33871,651	59509,586	16875,276
1 [P53396]	66972,822	99459,648	36564,669	11166,682	69699,677	101978,93	33081,023
1 [O95782_	28956,986	57463,809	16298,105	2386,1019	29825,687	59694,818	14062,025
1 [O95782_	38811,022	75955,086	21484,121	3933,412	39997,954	78871,959	18490,958
1 [O95782_	35804,55	60980,555	17818,805	3083,4487	37093,53	63008,157	15470,974
1 [O95782_	22272,151	34426,102	8982,7883	2092,9861	23147,933	35474,668	7559,1735
1 [O95782_	45006,861	61625,688	16445,654	5435,3825	46946,103	63164,151	13860,819
1 [Q16891_	18972,41	17998,399	6214,7605	4422,1714	19960,829	18031,588	5458,3583
1 [Q16891_	451501,94	425180,55	106819,96	68518,377	475065,31	427042,2	87316,756
1 [Q16891_	42651,766	36783,163	13698,96	5510,314	44952,696	36571,005	12390,282
1 [Q16891_	50691,228	86127,32	30232,363	10850,827	52523,791	88820,515	27040,357
1 [Q16891_	203349,88	207240,17	64410,374	41902,996	213634,71	208813,69	55498,327
1 [Q15019]	59164,886	90496,813	21527,468	5577,4445	61510,356	93281,521	17616,43
1 [Q15019]	3349,7281	9386,7813	2050,0347	291,34458	3391,4789	9858,9222	1638,2391
1 [Q15019]	6991,2215	13052,468	4374,5092	951,59607	7218,8802	13511,169	3903,1527
1 [Q15019]	24963,349	74376,93	15398,556	2999,8425	25179,545	78246,005	12036,223
1 [Q15019]	133118,54	311962,09	63251,619	16443,697	136077,82	326425,59	48915,813

1	[P07737_	107577	272022,06	72174,41	10593,105	109554,23	284622,34	61181,055
1	[P07737_	157711,04	458582,53	135626,74	20833,518	159344,54	480878,11	118045,05
1	[P07737_	1051591,7	2719905,3	892531,2	172738,04	1069733,3	2841900,9	793322,34
1	[P07737_	416425,72	692289,63	238799,21	54364,141	431801,54	713495,67	214235,96
1	[P07737_	170950,14	223238,56	78879,399	19274,581	178559,32	227682,06	71084,564
1	[P07737_	59371,54	140052,92	43639,379	7766,283	60681,653	146077,1	38402,02
1	[P07737_	32403,91	74358,781	23500,619	4416,267	33163,413	77490,433	20734,939
1	[P07737_	79384,881	190340,56	55445,092	9820,2599	81068,632	198735,92	48048,912
1	[P07737_	46339,328	105883,99	32600,144	5660,922	47434,544	110358,64	28620,378
1	[P07737_	13554,56	28481,035	8781,8705	1807,6001	13927,936	29614,888	7701,6602
1	[P07737_	60002,501	89056,414	28018,86	7052,3503	62443,622	91462,358	24650,179
1	[P07737_	20496,957	30437,602	11183,318	3952,3434	21331,541	31208,824	10093,623
1	[P07737_	125884,6	309282,31	74325,817	14131,322	128385,82	323632,26	61124,776
1	[P07737_	37194,682	96630,492	29209,538	6122,5971	37825,64	101056,19	25485,963
1	[Q99613]	89852,97	150354,67	40110,57	7777,8711	93142,286	155377,82	34011,41
1	[Q99613]	89509,444	127540,69	33969,987	8522,1183	93260,051	130957,77	28727,64
1	[Q99613]	226706	388974,56	96040,472	30615,055	234795,21	402588,33	79184,701
1	[Q99613]	30874,354	56709,797	14584,453	2595,6389	31896,708	58813,948	12250,943
1	[Q99613]	339044,9	515655,09	179344,05	39901,237	352584,8	529564,86	161231,67
1	[Q99613]	58542,573	94264,094	24851,239	6865,9492	60764,281	97282,68	20921,101
1	[Q969G5]	44939,481	116260,75	26523,352	6528,6934	45706,707	121852,71	21392,251
1	[Q969G5]	19363,808	38286,758	9683,233	4769,0507	19946,923	39807,539	7962,5899
1	[Q969G5]	292759,16	522424,63	128652,96	58364,16	302775,99	541470,14	105227,09
1	[Q969G5]	335427,18	571793,94	165352,09	85679,916	347490,47	590893,49	140750,61
1	[Q969G5]	218412,34	366594,59	117507,24	33612,597	226396,79	378248,83	103575,48
1	[Q969G5]	118231,33	281659,44	58749,522	21137,145	120762,79	294790,71	45663,112
1	[Q969G5]	113796,09	251210,44	52807,21	21673,857	116657,29	262378,18	41058,166
1	[P16188_	89998,539	171513,75	55361,506	19500,936	92853,629	177730,44	48694,175
3	[P16188_	37369,557	75994,523	20574,852	3407,3359	38450,888	79035,677	17527,447
3	[P16188_	230598,35	256942,5	69991,154	23367,878	241788,32	260577,03	59357,386
3	[P16188_	51642,7	77292,813	28471,204	7456,6951	53732,68	79274,246	25820,521
1	[P16188_	112538,38	222125,17	69322,88	17860,297	115944,14	230507,46	60811,981
1	[P16188_	142343,73	256963,56	66069,273	19869,365	147152,92	266344,46	55148,15
2	[P31943_	78124,053	113615,57	34631,515	10989,853	81351,428	116621,31	30161,266
2	[P31943_	13680,925	28940,758	8684,3248	3372,2869	14053,488	30106,885	7501,2373
1	[P52597_	82593,661	137279,03	31505,294	8321,8453	85633,709	141996,14	25476,589
1	[P52597_	302185,84	436177,38	116999,82	38919,369	314729,19	448088,9	98710,222
1	[P52597_	190500,13	349651,25	128153,45	48828,441	196838,23	361383,65	115399,49
1	[P52597_	77082,745	129931,43	52680,87	20267,931	79895,977	133727,15	48262,195
2	[P31943_	382942,34	603622,5	223366,62	110162,73	397792,94	620371,21	200478,9
2	[P31943_	32996,028	69696,195	22963,215	10616,885	33898,107	72435,496	20169,935
1	[P27824_	279172,31	318014,81	84329,525	21188,588	292569,87	322983,06	71309,748
1	[P27824_	92677,8	230501,75	39154,65	7166,8251	94448,97	241794,75	28164,589
1	[P27824_	94518,132	164062	43264,289	8112,0123	97852,161	169783,81	36580,18
1	[P27824_	32801,573	56984,957	17701,627	5971,9659	33959,283	58888,153	15457,184
1	[P27824_	45302,949	89570,344	21470,056	3598,334	46666,545	93164,741	17676,298

1 [Q06830]	422769,57	850426,19	209360,14	45041,259	435187,89	884845,41	173300,47
1 [Q06830]	32758,387	74778,617	13410,216	2572,5267	33527,992	78247,982	9894,4204
2 [Q06830,	209172,96	363375,03	106543,03	21522,763	216551,86	375712,36	92439,885
2 [Q06830,	202379,34	374594,34	135663,36	40262,999	209044,97	387322,88	122386,65
1 [Q06830]	80843,638	155627,38	41199,499	11229,656	83369,308	161611,79	34706,893
1 [Q06830]	31476,573	47003,266	15621,461	4141,2674	32751,618	48258,424	13891,614
1 [P55769_	137904,08	163962,17	41058,767	10002,331	144374,15	166985,92	34184,313
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1 [P55769_	43947,404	50053,645	15566,052	4783,2031	46058,103	50761,139	13637,248
1 [P55769_	32785,628	42487,723	13453,719	4440,593	34250,875	43368,232	11812,887
1 [P55769_	74407,037	113131,69	37627,612	13729,596	77378,112	116238,78	33302,172
1 [P55769_	71551,471	104030,03	24288,575	5554,375	74503,139	107020,56	19798,071
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1 [P62491_	19858,741	35771,906	9692,5172	1369,8728	20531,666	37058,734	8271,9424
1 [P62491_	88645,244	122979	40171,913	10318,407	92435,38	125885,13	35621,267
1 [P62491_	106069,51	209382,19	59081,51	13960,582	109274,94	217486,83	50683,238
1 [P62491_	353097,04	542043,88	208406,91	58870,11	367104,21	556234,62	190218,83
1 [P62280_	7290,3161	13194,086	3473,7018	1399,9894	7535,9645	13674,383	2903,0228
1 [P62280_	66789,099	110925,8	27038,984	6591,0756	69250,246	114682,84	22299,566
1 [P62280_	539867,99	1077368,8	284711,6	63114,222	555922	1120070,4	240327,86
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1 [P62280_	189692,91	392809,28	119472,97	21987,594	195040,1	408325,06	104574,25
1 [P62280_	148246,14	231061,75	45493,159	12276,716	154025,05	238657,75	34832,572
1 [Q99714_	90327,222	163368,75	62305,263	12819,055	93385,536	168685,69	56972,752
1 [Q99714_	15753,068	17860,665	7544,289	788,97625	16512,669	18043,888	7054,4174
1 [Q99714_	15498,241	16829,506	6461,004	1489,3138	16260,876	16981,631	5916,5067
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1 [Q99714_	19768,715	32371,709	11479,479	1434,1042	20509,327	33334,046	10404,072
1 [Q99714_	8015,6508	11698,857	4976,2443	697,61274	8346,8076	11964,376	4647,102
1 [Q15717]	96879,224	232786,13	60015,33	11455,424	98918,372	243319,39	50371,852
1 [Q15717]	93930,893	208290,09	68375,59	18235,5	96288,546	216779,7	60583,124
1 [Q15717]	46682,346	66971,797	22345,93	6203,383	48631,627	68640,682	19877,723
1 [Q15717]	95439,789	194903,88	84327,827	23113,471	98204,302	201709,36	78408,573
1 [Q15717]	33556,748	68229,594	24357,47	7503,9949	34531,764	70769,876	21899,094

1	[O15460_	47396,842	145008,69	40756,687	14269,829	47733,247	152286,92	34692,493
1	[O15460_	228191,93	606531,31	131019,14	44750,533	231737,59	636343,5	103193,92
1	[O15460_	38025,13	129862,2	30199,109	11346,703	38002,853	136865,55	24321,412
1	[O15460_	56572,756	83161,172	30975,682	12182,392	58894,545	85218,589	27973,112
1	[O15460_	17872,129	119851,95	22154,547	5199,1492	16603,348	127595,96	16477,178
1	[Q9Y3F4]	37273,647	64967,746	18625,89	3846,984	38583,66	67195,157	16070,533
1	[Q9Y3F4]	51960,104	88847,328	28907,006	8823,1443	53825,089	91720,105	25534,108
1	[Q9Y3F4]	29730,808	52543,66	18490,721	7701,2192	30762,513	54261,445	16498,79
1	[Q9Y3F4]	60495,639	108364,38	28953,75	5259,7258	62558,245	112254,58	24570,449
1	[Q9Y3F4]	27875,602	42106,738	13804,284	2264,8569	28994,44	43257,476	12301,373
1	[P04216_	86469,753	230141,06	51126,228	13766,809	87807,729	241413,78	40819,366
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1	[P04216_	13708,408	50867,453	8868,6355	2618,2721	13612,062	53781,761	6407,3104
1	[P04216_	28962,925	148472,77	23998,572	5417,2413	27882,004	157743,2	16744,308
1	[P04216_	71593,889	400187	64572,158	14784,307	68212,679	425589,78	44993,36
1	[P04216_	7161,6482	32442,48	5682,9349	1235,2274	6985,9403	34400,893	4131,7874
1	[P04216_	329169,45	918688,25	182745,14	38003,059	333340,17	965394,2	140608,12
1	[P04216_	56057,979	126786,27	31372,265	6041,0029	57405,72	132356,12	26028,284
1	[P04216_	126745,05	298642,88	70029,609	20846,914	129534,2	312226,66	56840,663
1	[Q9P258]	54428,511	86314,742	29926,101	7942,6973	56526,942	88794,328	26829,025
1	[Q9P258]	113824,75	167883,23	49253,334	13692,556	118475,74	172489,1	42602,359
1	[Q9P258]	76696,88	126161,75	35892,438	8528,3265	79552,433	130221,74	30868,478
1	[Q9P258]	9921,1957	18300,396	3782,2262	586,79012	10247,479	19011,989	2966,2455
1	[P83731]	70312,804	126163,82	42788,611	13866,425	72711,383	130408,02	38075,311
1	[P83731]	50643,046	61238,715	18747,373	6792,4558	52999,383	62313,074	16318,904
1	[P83731]	3485,9137	6428,0449	1682,7251	432,77637	3600,8265	6666,4927	1414,586
1	[P83731]	6637,591	15985,313	3415,4184	620,50369	6776,0757	16732,428	2704,0584
1	[P83731]	38327,767	78698,938	21027,031	3851,0712	39420,54	81881,122	17834,415
1	[P83731]	197566,99	413094,09	110941,02	17804,399	203041,98	430008,81	94327,09
1	[Q92616_	19770,223	45786,098	10696,297	1885,958	20222,277	47848,154	8728,0249
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1	[Q92616_	2838,2573	2548,9817	1065,8136	518,18619	2989,2962	2538,0069	978,37228
1	[P00505_	10164,415	33009,922	10336,537	1261,8658	10196,516	34671,794	9125,3088
1	[P00505_	15503,516	38840,16	10836,524	1951,5015	15796,53	40613,019	9290,4952
1	[P00505_	28281,34	65038,602	19662,889	3491,3274	28940,662	67810,452	17188,64
1	[P00505_	45006,456	100433,47	27076,096	6039,4694	46118,872	104735,57	22967,052
1	[P49756]	567431,56	307410,4	174786,05	113302,83	601946,21	290266,69	166054,38
1	[P49756]	146753,77	165688,84	60571,381	27655,157	153838,79	167658,87	54399,855
1	[P49756]	1121330,3	730773,78	338738,89	138340,42	1186884,1	706966,35	317189,86
1	[P49756]	2659,1343	2752,2688	766,01605	578,28935	2792,6683	2778,708	639,53132
1	[P49756]	24253,372	25534,154	8417,3947	6560,6389	25462,957	25763,749	7296,3158
1	[Q16658_	62765,8	109106,07	30893,746	5974,2178	64977,777	112848,43	26592,71
1	[Q16658_	125348,71	213623,2	61784,127	10471,807	129858,03	220751,83	53522,625

1	[Q16658_	153341,16	267733	88406,831	21934,462	158728,14	276552,74	78542,607
1	[Q16658_	436667,32	731127,25	203103	29472,566	452648,72	755306,75	174447,09
1	[Q16658_	67862,357	130023,42	35688,201	6340,4295	69996,397	134961,24	30496,441
1	[Q16658_	70115,669	141043,31	37240,234	7020,9284	72176,822	146670,09	31479,911
1	[O75396_	88413,758	75594,865	36091,776	14215,218	93202,397	74853,916	33911,759
1	[O75396_	199723,36	189089,28	89967,289	34551,682	210152,53	188610,04	84502,718
1	[O75396_	42297,378	51849,289	32849,842	11544,915	44261,375	52246,889	31896,995
1	[O75396_	52311,864	76433,242	28548,778	8352,304	54468,712	78300,915	25918,559
1	[O75396_	9444,6895	15842,796	4390,7432	1659,739	9789,7181	16368,407	3724,9129
1	[O75396_	419524,03	747301,81	225695,81	62394,008	433933,52	773142,89	196419,98
3	[P35908,	405655,88	235232,8	129998,88	55128,792	430001,48	224046,3	124339,86
1	[P13647]	82762,063	71116,998	28432,804	13532,159	87233,532	70625,312	25934,15
2	[P35908,	151998,31	148126,89	28065,021	11269,572	159818,71	149406,6	21076,699
2	[P35908,	129274,52	118208,59	33781,09	16131,12	136099,1	118354,59	28815,595
1	[P13647]	37348,304	64943,219	19953,274	7381,5916	38665,079	67121,654	17352,923
1	[P59998_	33532,328	71775,57	15527,014	2245,7874	34423,738	74886,476	12376,762
1	[P59998_	32204,391	70161,773	18326,003	2677,3198	33036,305	73137,342	15476,058
1	[P59998_	12497,44	23376,781	6133,5888	2127,1817	12902,36	24255,047	5135,4541
1	[P59998_	150286,82	305373,25	72247,721	12759,867	154634,13	317923,73	59210,738
1	[P59998_	104042,12	195570,17	58006,179	9736,5441	107397,07	202731,64	50536,428
1	[P59998_	51020,548	118452,3	35096,97	7447,3724	52185,675	123554,96	30486,105
1	[P59998_	26315,26	49504,891	17341,295	4793,2077	27164,685	51233,368	15562,005
1	[P59998_	95780,193	166788,2	56419,621	11565,389	99155,329	172222,36	50472,738
1	[Q92499]	6369,8307	15350,915	3353,5656	1039,6895	6502,5515	16066,362	2657,1666
1	[Q92499]	38823,832	90423,617	26422,793	5545,6157	39704,062	94338,706	22879,354
1	[Q92499]	104596,98	220947,17	58070,28	11047,224	107446,93	230103,92	49015,821
1	[Q92499]	16241,526	32273,461	8203,3103	1456,3873	16727,24	33558,665	6866,6291
1	[Q92499]	7648,418	16415,561	5293,5985	2379,5183	7851,9121	17072,287	4631,5791
1	[P62269_	32285,091	75395,094	20966,745	3116,9128	33012,119	78699,154	17992,204
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1	[P62269_	128028,61	239317,23	61049,364	12275,654	132179,17	248357,25	51101,996
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1	[P62269_	72297,418	158177,77	44518,049	13857,15	74152,828	164803,5	38010,589
1	[P62269_	77838,174	134161,28	40117,19	11443,812	80607,073	138652,98	34822,452
1	[P62269_	40556,192	60086,613	20681,433	6363,4125	42209,589	61648,055	18481,171
1	[O75367_	178619,97	235820,63	36580,376	11187,407	186485,91	242152,8	25010,997
1	[O75367_	98671,546	128880,27	17313,816	5702,6207	103044,76	132360,63	10796,584
1	[O75367_	140245,11	131230,1	16469,913	6416,9234	147571,66	132279,57	9771,0168
1	[O75367_	28188,881	29367,221	4381,2034	1576,4132	29597,949	29783,006	2927,0128
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1	[P61247_	58683,426	108116,47	20089,273	8064,9316	60614,67	112390,11	14890,44
1	[P61247_	189251,88	285079,13	86927,649	22596,045	196860,42	293050,08	75918,856
1	[P61247_	65065,797	106711,88	30320,822	8967,2661	67495,034	110135,28	25992,972

1	[P61247_	69304,741	146039,05	39456,718	9519,0573	71201,394	152046,24	33462,285
1	[P15531_	105088,52	185312,48	69810,065	15632,95	108747,01	191204,5	63648,978
1	[P15531_	41784,828	69675,773	20693,354	5223,1307	43321,038	71926,344	17965,275
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1	[P15531_	48397,642	72627,922	22625,894	5364,5761	50349,563	74631,343	19876,687
1	[P15531_	42502,869	92796,477	29755,662	4990,7041	43600,147	96559,248	26363,701
1	[P15531_	102177,13	215458,42	66274,793	13995,582	104975,38	224064,35	58075,914
1	[P15531_	174893,01	371757,47	121096,07	25609,866	179623,93	386477,59	107422,35
1	[Q00839_	71007,916	95305,734	45990,044	11899,166	74121,676	96930,126	43483,308
1	[Q00839_	381681,86	541115,1	280141,64	59369,73	397820,94	551086,75	267749,55
1	[Q00839_	148291,05	351070,19	77296,539	10843,352	151515,76	367243,44	61979,634
1	[Q00839_	99199,669	193940,36	41720,881	8316,2971	102229,19	201807,11	33105,271
1	[Q00839_	221085,58	492972,81	155443,74	37309,398	226572,86	513349,44	136742,19
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1	[Q00839_	97567,208	191851,58	50773,869	8294,1022	100529,46	199361,53	43005,204
1	[Q00839_	28234,817	53966,945	15362,998	3086,3082	29125,841	55994,332	13232,512
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2	[P11940_	251739,07	288422,25	132021,33	33997,007	263820,52	291223,86	124003,07
2	[P11940_	12349,653	23501,988	6468,8578	1331,8468	12741,423	24388,651	5523,988
1	[Q13310_	38532,102	44264,84	16029,512	3234,5129	40376,115	44838,103	14546,786
1	[Q13310_	87797,187	122141,66	38461,507	12729,365	91542,911	125090,68	33719,89
1	[P60900]	15296,037	51482,48	17029,286	2646,3389	15306,472	54080,475	15182,652
1	[P60900]	20288,986	55017,309	14757,615	3208,8319	20582,842	57654,3	12498,887
1	[P60900]	31553,522	83941,656	22518,285	4805,2859	32045,082	87926,842	19076,987
1	[P60900]	19926,91	56781,875	18511,974	2825,423	20159,117	59461,466	16462,029
3	[P16188_	37369,557	75994,523	20574,852	3407,3359	38450,888	79035,677	17527,447
3	[P16188_	230598,35	256942,5	69991,154	23367,878	241788,32	260577,03	59357,386
3	[P16188_	51642,7	77292,813	28471,204	7456,6951	53732,68	79274,246	25820,521
1	[P30504_	17210,735	17995,861	5681,0061	1107,0251	18071,569	18157,578	5022,6906
1	[P32119_	104417,22	220105,44	58701,724	12913,983	107272,65	229186,15	49667,743
1	[P32119_	132583,12	236784,72	65714,671	25075,3	137120,16	245183,52	55746,838
1	[P32119_	155741,65	286450,13	100441,66	22497,474	160907,79	296226,11	90384,887
1	[P32119_	171519,74	308986,53	105500,07	18741,888	177345,27	319398,21	94668,557
1	[P32119_	72693,862	137620,53	37042,225	9436,9111	75014,719	142815,99	31372,448
2	[Q06830,	209172,96	363375,03	106543,03	21522,763	216551,86	375712,36	92439,885
2	[Q06830,	202379,34	374594,34	135663,36	40262,999	209044,97	387322,88	122386,65
1	[P61619_	28488,641	57028,02	17968,623	3176,5752	29333,931	59199,968	15857,366
1	[P61619_	29711,815	55750,486	17840,316	6206,6756	30672,847	57747,067	15667,088
1	[P61619_	3329,8677	4397,3667	1397,9115	287,61639	3476,9426	4492,3154	1235,8554
1	[P61619_	1527,6024	2267,668	843,7109	276,31868	1589,8263	2324,7465	764,14912
1	[P61619_	5502,0974	7192,9092	2230,0745	363,34913	5746,6347	7346,5065	1965,1832
1	[P61619_	101145,37	125350,13	40135,601	6158,4305	105787,9	127650,68	35635,729

1 [Q9Y262_	84555,974	144901,26	44005,699	6534,5576	87582,16	149698,34	38593,029
1 [Q9Y262_	18256,769	32459,541	8373,9065	1353,7095	18884,23	33625,805	7046,8463
1 [Q9Y262_	68102,279	95276,688	27357,15	4033,3777	70994,706	97685,961	23701,276
1 [Q9Y262_	89793,951	119650,68	34044,382	4881,605	93734,67	122414,55	29442,344
1 [P62851]	44808,868	88265,813	19425,409	4038,2267	46163,461	91853,553	15527,774
1 [P62851]	165031,19	320661,5	107409,49	21632,783	170138,24	332360	95890,68
1 [P62851]	75551,158	147927,8	46533,025	8605,5229	77863,208	153459,05	41036,971
1 [P62851]	44595,975	88609,531	23666,76	5297,7744	45930,529	92101,153	20031,99
1 [P62851]	837497,75	1754367,3	523664,39	115171,24	860671,24	1824607,5	455586,36
1 [P62851]	242502,64	329526,81	99081,565	19423,156	253012,45	337272,91	86566,956
1 [P62851]	177406,5	351612,5	96527,272	20937,588	182735,98	365354,56	82316,925
1 [P62851]	36457,396	63044,391	14983,595	3239,0571	37747,392	65287,651	12279,089
1 [P62851]	88668,729	155464,86	33642,92	7590,2047	91758,523	161182,25	26725,448
1 [P43243_	178002,21	207936,05	79483,355	28455,085	186450,09	210687,47	72275,715
1 [P43243_	112973,85	145594,89	52972,397	17741,523	118044,51	148350,23	47789,563
1 [P43243_	23212,442	32796,363	12340,687	5381,8206	24193,334	33546,422	11142,876
1 [P43243_	283366,62	431311,88	172111,97	59498,855	294689,92	442249,91	157597,87
1 [P43243_	476613,99	675147,94	304563,95	116323,23	496749,73	689031,35	283694,37
1 [P43243_	26920,657	31033,105	12253,303	6741,5159	28207,343	31409,009	11101,688
1 [P43243_	22237,976	28272,559	10338,023	5746,2533	23244,333	28787,339	9236,8715
1 [P43243_	41491,832	73900,563	14864,4	6124,1904	42912,352	76697,266	11376,768
1 [P43243_	12919,905	23607,975	6576,0924	1863,8326	13350,675	24463,463	5611,226
1 [P43243_	79307,719	146632,89	32338,228	8540,0282	81909,907	152281,37	25796,466
1 [Q9UBV2_	32490,642	60658,993	16194,843	4017,8845	33545,996	62924,645	13691,968
1 [Q9UBV2_	34271,695	25788,251	10894,141	7388,2393	36201,4	25320,328	9933,636
1 [Q9UBV2_	7171,3916	5761,0818	2589,4782	1819,9018	7567,5454	5682,405	2379,3349
1 [Q9UBV2_	13020,903	19710,383	5670,0932	1718,4916	13542,114	20276,625	4874,9943
1 [P13797]	57036,536	172231,72	33599,115	6819,106	57480,194	181306,91	25653,319
1 [P13797]	105554,72	261718,38	50056,036	8555,7233	107592,9	274338,66	38006,54
1 [P13797]	1004,353	5521,4482	972,79364	116,03495	958,95174	5868,2075	713,00839
1 [P13797]	3074,6794	14970,357	3130,0283	364,90793	2977,3062	15872,197	2463,2729
1 [P13797]	169092,2	153635,09	56262,305	14041,11	178047,75	153354,4	51094,379
1 [P13797]	29468,656	56688,992	9484,0518	3443,7104	30386,58	59046,464	6706,465
1 [Q9UHD8_	92060,404	195525,88	45031,367	10290,791	94542,064	203867,23	36488,731
1 [Q9UHD8_	34300,86	69711,594	21432,939	5056,7226	35295,94	72417,458	18758,327
1 [Q9UHD8_	21675,991	55277,602	13249,8	2089,9207	22063,521	57895,772	10905,291
1 [Q9UHD8_	72427,612	200177,72	48268,998	10478,422	73392,644	210036,55	39667,649
1 [P63010]	7421,6716	17345,51	3283,5286	517,06304	7587,5153	18155,897	2484,9889
2 [P63010,	6727,1165	12593,108	3629,837	544,27396	6945,0789	13055,882	3144,0546
2 [P63010,	53595,617	95128,797	27875,586	4867,582	55443,212	98433,102	24213,608
2 [P63010,	51515,546	87203,797	25741,471	4308,3625	53381,688	90074,873	22409,556
1 [P63010]	81552,979	118695,8	28052,877	7017,077	84914,796	122102,49	22927,016
1 [P63010]	14669,944	31196,971	7726,2502	1392,0781	15064,904	32511,457	6417,1587
1 [P06744_	5696,5364	11970,026	3235,0102	797,81393	5853,1518	12461,357	2743,0195

1	[P06744_	107202,67	289488,06	65115,439	10393,833	108773,11	303739,75	52511,326
1	[P06744_	61630,129	146231,92	39463,055	5643,44	62968,045	152742,09	33613,823
1	[P06744_	59502,004	142804,78	39288,278	5780,9491	60759,635	149181,65	33623,357
1	[P06744_	37748,451	92196,672	27554,548	4102,1043	38513,615	96285,225	24054,933
1	[P07602]	45998,069	125614,96	64679,241	32068,44	46665,34	130657,5	60925,733
1	[P07602]	31091,874	83198,242	40850,689	19909,719	31577,794	86562,35	38264,321
1	[P07602]	252036,19	401349,88	199634,92	99425,273	261756,56	410999,37	187361,03
1	[P07602]	103252,5	163383,53	77736,983	43440,384	107254,37	167385,27	72331,824
1	[P07602]	171782,51	276053,81	136617,03	79408,582	178354,26	282815,8	127641,89
1	[P07602]	82182,623	132771,31	63183,147	34624,103	85310,107	136132,51	58818,399
1	[P07602]	50234,778	78785,758	26392,012	10880,82	52189,587	81044,52	23335,592
1	[O43143]	166673,66	191079,19	75560,164	47421,406	174662,37	193333,02	68224,698
1	[O43143]	64303,343	96857,531	28890,55	5086,0706	66888,261	99585,78	25210,66
1	[O43143]	81982,034	129136,38	38921,95	6073,5385	85157,589	132999,41	34073,098
1	[O43143]	151331,66	237582,67	58003,732	15355,899	157201,52	245099,67	47818,257
1	[P20073_	38028,377	115466,38	25837,262	5752,3441	38312,79	121456,75	20723,222
1	[P20073_	39804,724	90657,516	21738,901	5321,8064	40747,795	94680,661	17818,795
1	[P20073_	13529,798	27416,307	7589,6511	1635,8076	13923,488	28505,069	6486,0948
1	[P20073_	14335,181	35463,156	6021,0147	1181,4926	14613,207	37195,85	4326,6384
1	[P20073_	46843,153	117728,68	19787,16	2806,6655	47712,09	123534,55	14193,288
1	[P20073_	28769,769	70108,563	16896,662	3145,554	29353,696	73344,948	13910,91
1	[P20073_	11077,807	25339,736	4433,7114	940,86118	11336,878	26520,426	3230,509
1	[Q86Y82]	53687,538	69769,492	28782,696	11733,602	56087,084	71009,052	26430,066
1	[Q86Y82]	63463,195	110587,15	37712,141	9411,5441	65698,135	114183,47	33718,099
1	[Q86Y82]	41810,695	30131,19	13847,366	4157,425	44193,84	29434,728	13009,809
1	[Q86Y82]	194171,11	167731,96	73386,133	24330,719	204647,18	166430,93	68323,234
1	[Q86Y82]	35867,545	52125,789	12606,801	5075,9824	37347,922	53609,584	10292,723
1	[Q9UKM9_	189595,5	266254,5	121807,69	53047,988	197655,6	271572	113405,8
1	[Q9UKM9_	302339,02	332354,44	198921,75	88544,673	317176,3	333296,69	191301,9
1	[Q9UKM9_	41567,149	99087,492	19227,271	5038,9212	42454,879	103754,93	14611,929
1	[Q9UKM9_	41033,9	46826,156	18919,853	7685,9063	43005,532	47352,566	17324,343
1	[Q9UKM9_	13112,066	40792,762	9045,9115	3113,3158	13189,156	42932,531	7185,5626
1	[Q9UKM9_	29888,757	80574,203	19856,813	5930,3474	30330,628	84482,184	16355,951
2	[P08107_	162411,59	218295,98	176297,73	17523,794	169572,71	219729,27	176634,71
2	[P08107_	174028,34	215875,23	160090,31	19659,598	182070,5	216900,91	159205,25
2	[P08107_	80137,071	129457,68	94351,575	9497,4909	83208,113	131668,04	93753,784
2	[P08107_	90328,131	117769,98	69489,087	9342,6908	94370,683	119201,35	67635,957
1	[P34931]	89697,41	90249,516	28584,286	3962,7993	94259,215	90841,629	25363,611
1	[P34931]	69938,842	139101,41	48074,21	10855,487	72035,899	144233,59	43129,701
1	[P34931]	266889,49	338789,53	117217,67	21364,115	278974,35	345137,57	105540,15
4	[P11142_	292485,47	385919,53	160695,99	39658,933	305435,58	393007,4	148883,96
4	[P11142_	130441,7	604609	106496,38	64842,367	126948,73	641289,24	75827,47
2	[P62136_	24589,21	40612,598	11632,64	1448,7566	25501,253	41923,097	10077,427
2	[P62136_	85548,09	123306,91	27128,566	8982,7713	89098,961	126858,94	21571,082
2	[P62136_	86532,146	108348,8	37364,388	6746,873	90482,06	110307,97	33625,31

2 [P62136_	46228,245	69404,383	14932,069	2147,5048	48087,693	71536,42	11899,812
1 [P62136_	126871,33	165379,31	40457,413	7601,9125	132513,29	169237,87	33537,335
2 [P62136_	29763,676	43796,758	11759,1	2139,216	30981,335	45028,912	9998,9878
2 [P62136_	32935,293	59928,164	17040,175	2802,0624	34039,03	62079,317	14701,963
1 [Q8NC51_	174824,47	161321,75	81543,048	32900,005	184045,36	160476,42	77121,391
1 [Q8NC51_	118120,23	81314,33	30397,307	9532,153	124929,13	79323,874	27661,162
1 [Q8NC51_	732,38977	1227,6787	495,05623	210,71978	759,26267	1263,3766	452,26668
1 [Q8NC51_	2657,1835	2216,4415	917,25172	455,06664	2802,1849	2195,163	840,53194
1 [P11279_	33531,725	77241,375	27480,41	5978,8363	34313,367	80403,435	24792,072
1 [P11279_	6073,582	12216,632	4306,8634	786,29085	6252,8386	12668,966	3886,4775
1 [P11279_	9469,6941	18535,172	6316,6791	1944,3453	9759,9339	19212,456	5629,4533
1 [P11279_	9168,9595	16395,691	4919,5962	1211,889	9482,528	16965,898	4281,4487
1 [P11279_	2498,4469	5113,3984	1821,3184	419,48649	2570,3292	5304,9262	1642,8884
1 [P11279_	212725,33	448159,44	104123,22	45618,269	218537,99	467144,49	83667,523
1 [O00469_	3579,8847	8879,166	1584,7729	270,7467	3648,8724	9311,077	1167,7688
1 [O00469_	38237,797	118140,01	26505,527	5260,8374	38480,343	124309,41	21304,653
1 [O00469_	71668,247	215083,81	63922,208	15238,486	72268,268	225678,46	55461,811
1 [O00469_	24005,61	77316,641	20640,928	3130,2976	24092,824	81312,232	17512,014
1 [O00469_	24365,043	74952,094	23688,345	3541,1935	24530,988	78636,746	20928,2
1 [P40939_	77700,649	96241,891	52951,677	12046,442	81282,444	97289,584	50946,636
1 [P40939_	36636,768	61191,039	18792,954	3141,3918	37981,995	63150,957	16508,764
1 [P40939_	42178,375	67891,844	21146,187	3705,5348	43781,645	69959,484	18628,071
1 [P40939_	15034,451	26326,744	7395,5457	1134,939	15560,159	27238,642	6366,0936
1 [P40939_	505438,13	261495,06	64927,919	11685,199	536388,69	248159,38	54505,73
1 [P40939_	28250,331	46430,082	14324,662	2782,3737	29303,711	47886,457	12580,108
1 [P16401_	193762,74	326668,31	84117,917	42036,332	200801,97	337778,18	69538,81
1 [P16401_	52361,105	63515,707	27463,085	13441,189	54798,277	64381,996	25307,745
1 [P16401_	16188,428	33501,91	12579,974	6895,5649	16646,714	34748,198	11283,424
2 [P16403_	31734,2	42786,771	51801,094	16353,276	33141,709	42517,813	52685,285
2 [P16403_	37019,338	49561,801	58886,523	18971,571	38667,803	49269,899	59820,76
2 [P62136_	24589,21	40612,598	11632,64	1448,7566	25501,253	41923,097	10077,427
2 [P62136_	85548,09	123306,91	27128,566	8982,7713	89098,961	126858,94	21571,082
2 [P62136_	86532,146	108348,8	37364,388	6746,873	90482,06	110307,97	33625,31
1 [P62140_	65515,328	96173,469	26728,714	5446,5625	68201,131	98839,925	22903,918
2 [P62136_	46228,245	69404,383	14932,069	2147,5048	48087,693	71536,42	11899,812
2 [P62136_	29763,676	43796,758	11759,1	2139,216	30981,335	45028,912	9998,9878
2 [P62136_	32935,293	59928,164	17040,175	2802,0624	34039,03	62079,317	14701,963
1 [P30153]	259310,17	450610,25	132463,35	26316,309	268455,03	465903,22	115017,79
1 [P30153]	11611,258	21992,754	7515,5276	1619,6477	11982,761	22771,689	6731,9176
1 [P30153]	31581,034	52315,402	12533,22	3638,4856	32747,527	54089,338	10257,779
1 [P30153]	1870,4938	3359,6204	1065,5907	186,97429	1934,1838	3475,1117	942,05076
1 [P30153]	890,91223	1570,8625	451,98551	69,177518	921,84171	1625,3192	391,34273
6 [P60709_	13510,768	22746,746	10148,038	3039,745	14005,035	23380,125	9470,2272
6 [P60709_	409431	784178,56	290998,43	113476,5	422360,82	811510	262484,16

6 [P60709_	416,08235	762,12024	289,98635	85,621849	429,96614	787,28841	263,93553
6 [P60709_	221,99668	366,86652	164,68984	43,033489	230,26468	376,78708	154,10339
6 [P60709_	75,481362	133,56972	56,09181				
6 [P60709_	212,054	336,50269	129,03285	31,298038	220,23281	345,77762	117,93028
6 [P60709_	514,99965	839,37134	320,27644	110,90529	534,39177	863,45299	291,02018
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5 [P60709_	89164,326	241555,5	43800,138	9595,7238	90447,125	253807,39	32402,661
5 [P60709_	515509,33	1282652,7	206123,63	47308,175	525342,66	1345889,7	143709,91
5 [P60709_	245846,38	629859,33	110487,06	27615,526	250153,58	661077,72	80377,987
5 [P60709_	48015,281	122457,09	26248,995	6819,9116	48871,499	128358,46	20713,204
4 [P60709_	146165,42	482749,5	157402,75	35841,937	146459,39	507013	139433,32
4 [P60709_	215,04315	357,79355	151,64598	78,690837	222,99499	367,86064	139,02002

1 [P12111_	5910,7328	23302,176	6235,685	958,96601	5841,3304	24590,217	5291,3195
1 [P12111_	4193,5069	11135,824	4214,9879	832,39829	4260,0556	11624,273	3847,9767
1 [P12111_	32942,002	86912,75	23078,068	5317,2391	33470,437	91029,461	19481,681
1 [P12111_	21475,875	69888,711	23791,335	4232,1739	21541,863	73348,584	21311,624
1 [P12111_	76140,291	126253,12	35054,436	9288,9222	78953,115	130383,18	29924,531

1 [P25205_	13632,534	23742,945	4793,6467	830,2203	14110,758	24621,426	3724,0455
1 [P25205_	40785,199	44915,195	17578,269	8810,7125	42779,038	45348,119	15942,419
1 [P25205_	36356,105	51541,023	14998,94	3769,3005	37885,898	52869,066	12968,04
1 [P25205_	25635,375	38172,961	10887,661	2519,673	26674,943	39245,853	9375,7953

1 [Q9Y5M8]	24562,078	43000,395	10333,552	2723,2031	25420,024	44546,237	8475,3811
1 [Q9Y5M8]	19599,009	36448,813	9188,0833	2253,5299	20238,294	37822,928	7647,8806
1 [Q9Y5M8]	38388,118	61662,871	19619,739	5048,3568	39850,298	63522,7	17293,183
1 [Q9Y5M8]	897180	636202,55	231756,16	51813,388	948498,36	622539,42	210808,23
1 [Q9Y5M8]	674618,88	489239,19	186613,36	38272,576	712981,54	479434,63	171220,05
1 [Q9Y5M8]	213574,53	174094,74	66445,355	15445,175	225311,7	172291,11	60854,795

1 [Q6P2Q9_	58561,643	89512,57	27949,515	9005,9995	60888,787	92049,443	24461,44
1 [Q6P2Q9_	24365,211	39144,02	9708,384	1714,7701	25291,373	40413,59	8076,692
1 [Q6P2Q9_	24373,357	50003,625	12494,016	2630,0482	25068,619	52052,311	10388,549
1 [Q6P2Q9_	24921,225	41476,29	8935,3699	1618,3424	25836,969	42922,286	7105,9792

1 [Q13740_	78003,447	152199,56	34617,411	15200,156	80393,241	158304,46	27631,827
1 [Q13740_	51855,957	136066,31	48536,917	14994,276	52711,712	142092,48	43608,837
1 [Q13740_	12650,528	38628,867	13576,718	3462,5026	12743,667	40477,937	12192,821
1 [Q13740_	85680,167	244605,31	81434,146	19044,733	86669,884	256105,5	72441,345

1 [Q13505]	108458,82	135408,34	37873,209	9360,6686	113412,33	138122,87	32457,05
1 [Q13505]	6894,581	15905,235	5700,1092	1526,2981	7054,8265	16555,72	5137,099
1 [Q13505]	4292,0299	5960,3317	1882,1028	741,52885	4475,3719	6103,608	1645,9566
1 [Q13505]	3679,7648	5932,165	1374,7262	260,77114	3819,1408	6128,5039	1119,6907

1 [Q16181_	49255,765	105644,07	28137,804	7847,8941	50564,008	110058,95	23726,431
1 [Q16181_	14643,527	22209,994	5317,1704	669,10125	15228,08	22884,34	4390,3629
1 [Q16181_	59361,315	177561,22	44443,038	8264,615	59865,474	186564,08	36980,844

1 [Q99497]	102526,18	214993,11	67805,787	29242,762	105360,57	223493,22	59100,026
1 [Q99497]	878,55808	1733,9825	442,11334	76,697565	905,08433	1802,6112	370,48068

1 [Q99497]	208952,36	441555,72	118750,09	37139,146	214643,69	459776,15	100220,55
1 [Q99497]	96506,374	207306,22	58979,28	17153,447	99065,229	215857,4	50547,186
1 [O15260_	21101,701	33846,684	10120,126	1661,893	21906,081	34886,4	8839,1916
1 [O15260_	40830,536	63677,283	19835,929	2986,8683	42426,096	65535,505	17497,19
1 [O15260_	3986,7016	8765,9248	2860,7631	695,9824	4088,3417	9121,6025	2534,6025
1 [O15260_	11698,563	18575,182	7293,9813	1420,2473	12149,647	19081,99	6708,0215
1 [O15260_	25297,914	38612,008	14917,078	3764,4219	26306,256	39611,212	13645,875
1 [O15260_	15123,797	16393,432	6432,2086	1604,4044	15868,72	16535,428	5906,2852
1 [O15260_	41211,117	65332,852	19018,33	3326,6874	42798,088	67326,01	16500,182
2 [P19105_	116914,2	238599,77	49041,86	16403,466	120269,22	248679,95	37986,542
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1 [O60568_	8290,9833	21810,998	6344,9918	1807,3584	8425,6917	22824,727	5466,2459
1 [O60568_	12864,093	30235,895	9016,2716	2648,2949	13150,022	31546,831	7811,4419
1 [O60568_	32413,921	64495,121	18479,052	2728,4537	33382,803	66998,57	15981,959
1 [O60568_	10667,749	12130,159	5445,2172	2455,7519	11181,592	12246,567	5055,3086
1 [O60568_	5401,7217	7900,0552	2204,5357	541,98666	5623,7976	8117,5429	1887,0139
1 [P46777_	599655,77	796424,25	195641,6	36622,673	626008,2	815700,75	162364,28
1 [P46777_	113774,15	208040	59447,282	12918,076	117565,44	215534,59	51215,124
1 [P46777_	250277,38	281527,78	72838,014	28363,845	262363,17	285787,34	60757,3
1 [P46777_	1662,5017	4645,71	1302,2405	306,3548	1683,686	4869,7981	1114,3872
1 [P12277_	2094,5991	1343,1604	735,00174	109,89168	2217,588	1293,5892	710,63336
1 [P12277_	7461,9932	7236,4266	2982,6333	515,86723	7847,7142	7244,3822	2771,311
1 [P12277_	89227,133	79060,888	36784,354	6634,594	94000,575	78521,658	34778,142
1 [P12277_	163429,75	78397,761	44195,668	7884,0679	173584,54	72841,708	42871,149
1 [P50914_	172967,75	317380,81	96435,243	23589,327	178711,74	328667,45	84166,29
1 [P50914_	80856,436	158530,33	50110,621	11479,988	83326,414	164457,65	44142,45
1 [P50914_	150368,15	278692,13	92001,365	22881,731	155307,18	288462,52	81716,29
1 [P50914_	39674,344	81272,445	26845,333	7472,4187	40812,881	84387,212	23806,887
1 [P50914_	240364,59	536940,63	143386,51	22360,825	246292,9	559998,81	121737,29
1 [P50914_	88997,464	180880,09	37798,576	9228,59	91567,731	188477,68	29605,952
1 [P50914_	191963,77	252986,22	48716,672	9938,9482	200433,1	259450,04	37150,156
1 [P50914_	210225,9	312551,31	84491,28	16164,224	218758,46	321464,82	71934,363
1 [P62495_	17803,766	28435,654	9895,4505	1876,5094	18485,908	29259,288	8909,8035
1 [P62495_	23264,048	40293,176	12724,604	1747,6922	24087,892	41627,125	11261,031
1 [P62495_	12280,895	21289,301	6725,3832	1240,8967	12715,393	21994,797	5938,558
1 [P62495_	26685,564	36305,813	12620,795	3430,6452	27842,247	37106,335	11322,214
1 [P42704_	8989,9539	17027,92	3347,3638	665,19121	9275,994	17710,998	2568,9319
1 [P42704_	120736,43	190497,94	62790,344	12530,315	125409,83	196035,95	55911,77
1 [P42704_	18698,524	29372,393	8511,5389	1297,302	19424,314	30258,818	7385,132
1 [O00203]	34656,884	83067,313	17790,16	3342,8621	35388,453	86937,846	14092,069
1 [O00203]	9124,3469	18982,598	4589,1605	1026,1612	9378,9089	19773,495	3776,2252

1	[O00203]	70900,458	106269,17	27098,375	6970,403	73758,785	109389,7	22634,617
1	[P51659_	265992,68	374006,38	112217,16	47244,024	277252,89	383399,63	96894,473
1	[P51659_	5043,6465	11075,837	2987,4547	548,14558	5172,1301	11545,087	2539,6246
1	[P51659_	46338,003	90122,781	23261,858	4379,4035	47765,682	93637,623	19545,378
1	[P51659_	28064,775	60082,324	17041,275	4224,4509	28813,221	62556,154	14625,63
2	[P35637_	268922,37	332224,94	108109,06	43861,726	281289,19	338217,92	95134,472
1	[P35637_	401813,16	335807,15	247800,32	128042,21	423796,21	329117,64	242306,49
1	[P35637_	574080,13	508087,27	398158,41	194235,85	604908,06	499369,63	391629,23
1	[P35637_	231351,42	229393,06	153142,62	78260,505	243240,99	228090,01	148439,49
1	[P35637_	424528,47	420221,4	253478,04	153061,43	446343,28	418667,78	242286,98
1	[P35637_	1261231,8	1070942,8	647779,74	372001,97	1329786,7	1055506,5	620433,53
1	[P35637_	3212950,5	2872480	1641514,3	883460,4	3384487,4	2844979,6	1565204,8
1	[P52907_	39156,137	72686,484	22373,396	4705,0799	40438,792	75290,955	19615,951
1	[P52907_	41742,32	59190,66	16141,345	4001,9235	43497,764	60751,482	13736,672
1	[P52907_	67410,027	74591,313	22375,114	8178,9249	70693,549	75550,38	19392,588
1	[P52907_	24177,587	44484,727	15234,805	3059,171	24979,02	46015,135	13662,769
1	[P60866_	43992,962	84992,414	25508,06	6969,3736	45362,819	88173,417	22165,857
1	[P60866_	122446,74	228976,55	59645,358	12579,035	126415,15	237589,31	50190,183
1	[P60866_	71495,619	104763,04	29846,556	10513,438	74431,066	107636,75	25541,053
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1	[P60866_	260633,48	444513,91	115926,82	25085,626	269994,28	459770,11	97585,869
1	[P60866_	81368,713	139701,94	35166,594	8082,7613	84270,553	144572,35	29292,013
1	[Q9UBG0_	31244,946	46791,906	15949,76	4342,1858	32508,003	48034,285	14249,882
1	[Q9UBG0_	20564,107	55252,422	14193,401	4998,3864	20872,423	57909,404	11798,665
1	[Q9UBG0_	29683,501	55398,883	20529,535	6524,6625	30651,772	57282,011	18578,285
1	[Q9UBG0_	6513,2033	22643,125	5540,9388	2357,54	6501,0425	23862,852	4521,5323
1	[Q9UBG0_	6029,4562	20371,988	5110,0634	1897,188	6030,8484	21454,486	4212,76
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1	[Q9UBG0_	12177,575	24542,992	7480,9638	3322,0928	12535,191	25491,608	6467,803
1	[Q9UBG0_	1091,7901	3291,5065	909,68938	289,32644	1100,5685	3456,1906	772,32309
1	[Q96AE4_	69929,893	155270,69	68712,168	20274,879	71692,227	161031,52	64029,905
1	[Q96AE4_	31275,814	72819,82	36026,605	10924,026	31994,9	75495,446	34070,693
1	[Q96AE4_	51655,466	138068,22	77403,309	23126,702	52472,302	143333,61	74305,401
1	[Q96AE4_	147564,24	277438,94	140967,7	40363,559	152359,05	285704,13	133905,73
1	[Q9UMS4_	28349,285	42263,023	13000,714	2338,6748	29498,479	43422,184	11421,749
1	[Q9UMS4_	94019,111	120303,3	33173,48	4445,582	98250,587	122878,6	28487,283
1	[Q9UMS4_	87490,923	107726,39	27514,452	5044,1626	91517,151	109893,57	23102,211
1	[Q9UMS4_	103858,06	131273,32	29061,88	7934,3344	108562,24	134234,86	23247,99
1	[Q9UMS4_	45997,787	59635,246	14606,309	2799,5993	48050,222	61010,263	12110,179
1	[P16615_	132161,14	243627,47	70686,142	18262,661	136523,94	252438,54	60994,386
1	[P16615_	65031,316	93905,344	31978,972	14414,349	67734,209	96252,73	28322,558
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1	[P61604_	587620,06	583775,17	380212,02	129755,17	617789,3	580825	370476,19

1 [P61604_	429237,19	442206,25	273798,61	89995,135	450933,39	441441,31	265625,84
1 [P61604_	97788,188	79495,821	58008,339	20486,879	103184,58	77761,502	57083,141
1 [P61604_	1638068,6	1538321,2	980584,03	352487,41	1724030,8	1525535,5	952898,71
1 [P61604_	320972,7	456490,22	167662,16	49393,994	334469,96	467192,76	151759,84
1 [P61604_	68752,794	82495,219	50765,328	16261,245	71981,832	83083,368	49222,546
1 [P61604_	845585,71	918807,38	447055,96	149848,69	887243,16	924104,88	421894,47
1 [P48047_	75310,058	127153,77	27608,091	4747,9621	78038,757	131649,18	22024,543
1 [P48047_	97037,648	114815,3	35639,837	5747,1724	101606,74	116679,25	31430,21
1 [P48047_	38244,338	41906,41	13313,644	2234,2072	40116,471	42396,922	11799,624
1 [P48047_	103215,8	144345,41	33254,312	5105,5027	107595,48	148258,25	27105,665
1 [P61158_	41054,589	55241,125	22697,418	6877,5505	42849,389	56317,541	20929,383
1 [P61158_	81297,352	103939,27	43056,557	10561,905	84967,344	105694,86	39866,109
1 [P61158_	71258,261	96421,109	41270,726	11665,166	74363,111	98271,806	38330,623
1 [P61158_	29733,172	55982,203	17601,352	4110,8698	30690,625	58003,274	15485,479
1 [P61158_	89339,951	138076,3	41134,961	5605,6135	92856,62	142115,08	35952,711
1 [P61158_	53380,824	92852,367	28860,672	4085,6356	55262,436	95955,933	25448,295
1 [P99999_	82455,525	129251,66	57579,999	9488,9836	85674,833	132489,78	54065,598
1 [P99999_	10290,772	15812,938	7553,8872	1140,1398	10699,626	16179,658	7165,7372
1 [P99999_	88242,635	119544,31	50702,906	11803,234	92084,24	121859,98	47135,177
1 [P99999_	85602,027	123075,3	51300,624	11401,074	89177,343	125822,4	47580,743
1 [P15259_	19435,363	42045,801	14440,066	2785,7639	19945,974	43708,472	12957,202
1 [P15259_	29412,013	62919,898	20184,973	3619,4155	30198,893	65433,193	17876,508
1 [P15259_	119892,62	277820,31	83795,631	16168,003	122642,76	289725,48	73155,493
1 [P15259_	35347,96	56005,645	18046,972	4091,2436	36710,956	57656,705	15973,97
1 [P15259_	34193,123	47538,633	19961,864	4913,8705	35655,777	48523,216	18516,32
1 [P15259_	106008,1	199853,98	59268,694	12273,032	109413,9	207193	51534,041
4 [Q9H0U4,	82500,889	141584,25	43163,82	7937,039	85449,268	146274,1	37821,143
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4 [Q9H0U4,	127991,53	191676,92	55432,544	10887,652	133159,18	197085,63	47976,939
5 [Q9H0U4,	432318,58	838045,13	159830,87	31220,876	445661,07	872467,25	121178,97
1 [P61006_	28615,547	65039,516	14664,339	3411,2998	29295,779	67952,162	11795,3
1 [P26640]	22446,647	63583,328	17115,962	2894,2591	22713,94	66692,49	14544,099
1 [P26640]	11909,079	25105,395	5049,9823	816,72296	12233,655	26194,396	3916,6203
1 [P26640]	87408,155	190864,14	49764,711	12453,803	89656,797	198975,35	41781,551
1 [P40429_	323066,86	657634,56	176708,16	50034,517	332400,42	684019,99	149343,2
1 [P40429_	42241,114	72445,758	20531,288	6763,6696	43750,684	74894,71	17557,034
1 [P40429_	656503,17	1020984,4	261615,7	49992,465	682182,34	1052491,1	219528,52
1 [P40429_	669632,42	888701,69	307904,62	52704,711	699131,85	907278,54	277407,34
1 [P40429_	193540,38	325490,31	105632,05	25566,507	200602,79	335819,1	93550,023
1 [P40429_	56162,428	108863,35	25257,477	4079,8283	57898,793	113188,92	20594,01
1 [P40429_	936231,03	1169072,8	479849,71	161924,47	979084,1	1187582,7	441781,54
1 [Q02818_	58573,492	120481,07	44816,456	22348,841	60247,061	124953,59	40226,052
1 [Q02818_	26727,947	57819,277	25677,089	13940,565	27433,924	59919,163	23666,058
1 [Q02818_	26730,572	58137,922	23816,204	11415,318	27428,706	60322,929	21746,413

1 [Q02818_	38763,266	67029,18	33032,891	19387,61	40145,865	68863,255	30833,772
1 [P08648_	25193,709	50541,172	25563,972	6066,5234	25945,118	52157,8	24321,336
1 [P08648_	64875,625	127357,19	51105,58	11969,71	66861,015	131773,11	47057,609
1 [P08648_	54749,707	87682,776	33793,087	8473,1138	56844,453	90126,255	30899,295
1 [P08648_	58594,985	98564,044	34058,787	9592,8554	60734,036	101625,82	30485,517
1 [Q92520_	6181,4769	14225,287	3130,8837	909,50997	6324,6232	14869,765	2490,12
1 [Q92520_	15615,745	38156,117	8667,7029	2671,0596	15930,163	39937,501	6959,1759
1 [Q92520_	23720,948	48997,641	14760,206	4238,7114	24392,127	50934,187	12825,992
1 [Q92520_	8633,0641	17975,645	6194,5499	1641,2901	8874,7859	18665,27	5543,3014
1 [Q92520_	11463,787	20833,828	6867,5393	1909,4007	11849,11	21550,4	6089,6035
1 [Q92520_	10428,867	17614,328	4781,2345	1965,0427	10807,214	18206,574	4027,6735
1 [P62879_	23313,58	62244,456	12890,984	4016,1869	23669,555	65328,386	10015,928
1 [P62879_	153993,98	261248,56	60672,451	10150,424	159549,61	270403,8	49497,442
2 [P62873_	38152,247	139069,52	27282,576	3207,5399	37939,525	146894,94	20966,898
2 [P62873_	25574,609	88586,367	16959,604	2455,0008	25530,748	93503,821	12887,152
2 [P62873_	29367,196	87861,477	23925,74	10411,738	29617,438	92255,37	20114,853
2 [P62873_	23165,799	87219,461	17369,396	2396,8605	22977,49	92167,492	13411,376
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1 [O95302_	84826,402	320232,53	76916,544	21676,018	84126,917	337990,9	62876,995
1 [O95302_	33388,287	88604,969	26386,336	7008,8673	33914,748	92721,933	22879,17
1 [O95302_	92298,676	266624,13	80672,507	26422,079	93293,169	279492,7	69979,026
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1 [O95302_	19367,216	59344,547	13062,874	3701,1907	19500,41	62441,816	10384,863
2 [P08107_	118620,86	193842,93	110910,95	12827,423	123100,55	198223,87	107652,21
2 [P11142_	76678,125	60244,932	23163,883	4409,0132	80940,122	59438,633	21287,158
2 [P11142_	29083,632	38917,437	14464,057	2434,8216	30358,705	39714,497	13200,931
4 [P11142_	292485,47	385919,53	160695,99	39658,933	305435,58	393007,4	148883,96
4 [P11142_	130441,7	604609	106496,38	64842,367	126948,73	641289,24	75827,47
1 [P38919_	88495,771	175556,91	53229,348	10913,386	91154,071	182260,32	46515,818
1 [P38919_	89597,713	112845,15	29791,203	7415,1421	93667,69	115214,88	25151,812
1 [P38919_	62599,256	100141,63	26752,681	7524,9513	64989,091	103311,19	22596,173
2 [P60842,	49742,966	82555,5	28240,77	4802,3916	51582,472	85086,245	25365,38
1 [P18206_	3908,1687	12823,742	3357,0146	1431,9697	3917,2826	13493,477	2793,2787
1 [P18206_	3602,8972	11252,211	2984,7375	1226,6869	3623,4699	11827,54	2494,7361
1 [P18206_	9418,5718	27601,043	7940,4383	2841,4042	9511,4124	28955,214	6795,9093
1 [P18206_	11017,517	30930,912	8617,3177	3144,3423	11154,811	32428,103	7314,6623
1 [P18206_	5353,4759	16990,648	4664,5973	1906,4337	5378,3664	17859,815	3934,8223
1 [P18206_	5899,3545	14268,242	4077,0262	1643,8475	6021,7969	14903,613	3477,0561
1 [P18206_	1007,1599	2409,4392	897,50407	255,94997	1028,7627	2509,2555	813,80845
1 [P18206_	2992,1939	8198,9824	2320,1772	1021,3046	3033,7937	8590,1576	1969,7444
1 [P18206_	60062,204	146201,06	55313,371	16529,622	61297,646	152297,18	50258,413
1 [P18206_	57734,923	112777,16	38025,063	11714,858	59509,05	116903,9	33816,188
1 [P46459]	45512,399	67054,886	20534,645	5049,1528	47374,185	68863,363	17965,094

1 [P46459]	13483,078	28524,359	6252,7332	1202,684	13848,729	29748,077	4994,1834
1 [P46459]	59182,899	122203,45	30425,115	6117,8526	60854,301	127238,06	25283,715
1 [Q99584]	86813,742	71117,372	33861,224	23091,036	91581,461	70193,905	31388,917
1 [Q99584]	294866,31	261666,14	109986,61	67872,508	310624,8	260300,94	100428,07
1 [Q99584]	1141500,6	950025,61	456506,51	267210,25	1203877,7	938704,35	425566,18
1 [Q99584]	466165,25	321997,21	130677,84	76777,57	493020,15	313890,13	118979,39
1 [Q99584]	2335769,5	1958731,4	840614,8	515140,44	2463029,8	1939771,6	770318,57
1 [Q99584]	700822,31	581155,85	265569,43	167043,23	739154,44	574513,32	245399,76
1 [Q99584]	139422,63	209815,48	73403,983	19386,773	145038,26	215368,51	65934,699
1 [Q96N66]	102841,83	184254,34	71722,734	17199,583	106361,93	190142,99	65707,426
1 [Q96N66]	34298,362	44742,496	16762,453	3485,6377	35826,63	45599,834	15292,519
1 [Q96N66]	12802,726	24509,461	7504,4857	1400,6874	13206,263	25414,415	6578,9772
1 [P61160]	59257,14	88547,533	24075,993	3939,8587	61652,8	91087,296	20556,806
1 [P61160]	29550,032	23325,191	8997,5543	1687,6629	31190,233	23020,828	8273,9034
1 [P61160]	166675,07	291151,13	104084,17	31255,454	172532,65	300491,41	93671,379
1 [Q13492_	4502,0647	14543,104	2854,1418	1580,9145	4516,838	15329,062	2140,7738
1 [Q13492_	35388,887	80716,75	24535,478	4435,0627	36228,192	84134,037	21471,374
1 [Q13492_	49044,238	40559,934	39079,612	9608,4372	51742,341	39421,543	39399,085
1 [P12109]	61919,571	64437,863	24192,834	4576,8934	65025,617	64873,588	22116,696
1 [P12109]	46529,759	92921,703	30399,498	7758,3578	47915,758	96417,881	26937,614
1 [P12109]	56279,847	96723,414	36174,474	17204,249	58292,462	99718,233	32549,673
1 [P08708_	141998,07	221041,58	46846,222	10752,956	147541,58	228188,65	36956,207
1 [P08708_	74686,051	122600,24	33708,813	6079,1993	77471,398	126573,25	28828,797
1 [P08708_	54228,661	75235,578	26812,415	12110,846	56548,62	76942,401	23956,706
1 [P08708_	47562,455	74607,602	27434,337	13404,991	49414,559	76668,627	24600,995
1 [P08708_	21271,081	29827,951	11074,985	5787,6823	22174,627	30504,976	9935,4356
1 [P08708_	42652,33	63802,539	23261,745	11804,357	44379,023	65445,685	20810,926
1 [P08708_	9013,674	13633,695	5428,4989	2567,073	9375,6745	13976,383	4939,2375
1 [P08708_	21132,784	32677,367	12035,906	5362,5596	21965,747	33560,162	10818,885
1 [P08708_	18578,958	27181,682	10046,729	4872,0037	19344,142	27851,283	9020,8468
1 [P08708_	449213,08	771513,56	217374,48	44505,675	465242,69	797669,54	186784,66
1 [P08708_	342109,55	615265,5	162722,37	34780,018	353720,45	637495,42	137487,95
1 [P32969]	242707,4	474489,28	158430,37	29173,974	250156,22	491910,58	141465,66
1 [P32969]	94397,714	167320,63	60040,116	12346,74	97663,836	172768,25	54314,153
1 [P32969]	40651,001	93396,922	21523,289	5306,833	41596,244	97592,572	17422,223
1 [P32969]	49175,62	58657,703	19678,541	6875,6191	51481,956	59588,608	17474,711
1 [P32969]	126510,29	167286,28	51127,882	22749,738	132092,02	170977,97	44289,713
1 [Q14444_	258861,23	229707,31	132245,86	52551,788	272718,72	227349,9	127004,65
1 [Q14444_	344313,28	360786,5	149263,99	45170,18	361541,28	362933,86	137894,76
1 [Q14444_	103772,95	85814,63	44342,755	17495,494	109457,31	84647,666	42083,126
1 [Q14444_	85561,25	66683,192	38070,998	16208,719	90336,452	65346,396	36497,561
1 [Q14444_	117529,32	97414,232	60209,496	25936,571	123968,81	95788,071	58169,394
1 [P51571_	139970,17	277998,06	43572,914	7495,3618	144141,53	289941,16	30116,393

1 [P51571_	66608,484	105199,14	28877,286	5269,5598	69180,787	108449,18	24687,407
1 [P51571_	21989,872	42393,594	7370,6526	1746,3576	22673,064	44150,41	5351,3707
1 [P60891_	20379,533	42958,746	10221,817	2959,9068	20936,045	44771,188	8341,1577
1 [P60891_	68379,53	142047,7	33218,197	6957,715	70291,051	147995,79	27076,665
1 [P60891_	8882,516	22944,908	3853,1168	845,10944	9034,012	24092,352	2749,4206
1 [P61803_	145201,56	226776,86	76135,768	37493,062	150872,14	233235,77	67086,232
1 [P61803_	43121,957	62367,285	22203,24	5940,3075	44912,763	63898,627	20008,338
1 [P61803_	40312,429	67044,523	21214,472	5117,4807	41799,094	69161,183	18689,502
1 [P61803_	37465,189	58772,969	16248,942	3471,3039	38920,585	60569,02	13894,968
2 [P19105_	116914,2	238599,77	49041,86	16403,466	120269,22	248679,95	37986,542
2 [P19105_	47988,246	111627,84	36296,691	19281,909	49081,561	116340,66	31679,369
2 [P19105_	140544,32	354530,38	104463,69	51089,084	143152,21	370602,07	89357,619
1 [P24844_	46662,138	77043,759	25780,553	10084,482	48395,796	79410,09	22809,99
1 [Q01105_	987918,5	1051065,5	884761,23	342168,28	1037302	1043748,9	878419,07
1 [Q01105_	35611,305	39287,129	33420,187	10370,113	37362,352	39085,547	33313,486
1 [Q01105_	121842,95	183298,23	89350,764	29699,002	126768,03	187332,03	84286,807
1 [Q01105_	54360,849	82531,258	43953,064	20685,981	56544,653	84260,249	41653,706
1 [Q01105_	58146,895	102727,66	56758,804	22135,917	60178,703	105418,38	54202,653
1 [Q01105_	392673,5	436392,78	292559,01	86776,602	411864,38	436881,15	286321,26
1 [P62829]	190572,84	376785,06	105044,68	30200,575	196318,51	391430,91	89610,94
1 [P62829]	17139,913	32156,438	8305,6757	1753,356	17693,128	33371,824	6972,6886
1 [P62829]	204258,94	417545,84	104035,53	15669,246	210117,46	434614,44	86703,255
1 [P62829]	42924,295	83478,484	20545,499	3885,9375	44246,258	86766,452	17030,513
1 [P62829]	12725,113	22185,291	6294,063	1276,9039	13172,188	22948,254	5417,7465
1 [P62829]	178646,24	200194,08	43295,659	14008,452	187283,71	203454,27	34293,889
1 [P62829]	79144,379	145277,95	35921,142	8871,9473	81766,177	150712,26	29732,496
1 [P47897_	36901,553	50076,95	11415,003	2190,101	38499,91	51368,837	9255,6508
1 [P47897_	15922,439	25868,352	8965,1051	1804,759	16523,174	26636,28	8060,903
1 [P47897_	11770,525	17167,197	4581,9917	820,95151	12255,31	17644,434	3890,802
1 [Q5SSJ5_	14358,397	18413,518	5487,6647	6667,237	15003,983	18797,735	4544,8575
1 [Q5SSJ5_	12167,142	16491,402	4421,7246	7015,8876	12694,976	16895,802	3491,9778
1 [Q5SSJ5_	39623,127	84094,688	19438,596	5764,7054	40692,57	87678,443	15712,404
1 [P31930_	93458,822	133214,98	37624,612	8520,2905	97375,298	136716,63	32336,356
1 [P31930_	117895,04	160241,2	41908,278	9296,9924	122999,63	164213,04	35328,779
1 [P31930_	174431,56	255438,5	84348,183	26344,995	181604,14	262063,48	74742,934
1 [P09211_	4542,5014	16299,165	5066,521	790,32249	4523,9038	17151,31	4457,5986
1 [P09211_	32677,667	102756,99	21767,497	3603,3397	32845,805	108201,57	17182,331
1 [P09211_	15741,961	31711,127	8031,8647	1495,5699	16203,543	32988,663	6713,1107
1 [P49591]	27838,277	59044,266	18516,643	3348,098	28593,608	61401,369	16318,895
1 [P49591]	93083,009	100049,36	30141,645	10101,212	97679,942	101161,65	26192,78
1 [P49591]	16127,768	28954,342	9043,9234	2037,2424	16677,1	29953,846	7949,7174

1 [Q13151]	63781,747	128144,71	49341,981	29927,809	65669,955	132754,39	44329,681
1 [Q13151]	7760,0266	13980,213	7046,3027	2372,9853	8025,0308	14377,981	6671,7277
1 [Q13151]	10578,368	15308,933	7404,546	2703,4561	11018,73	15622,159	6967,9324
1 [Q13151]	25740,064	68984,172	16113,8	4248,5897	26128,69	72348,993	13081,745
1 [Q13151]	33011,16	46471,555	15626,275	4522,2342	34408,527	47586,364	13914,683
1 [O00567]	110990,65	152698,86	34850,336	6328,9465	115753,76	156734,31	28282,175
1 [O00567]	100914,27	97356,951	29141,35	8353,6556	106134,33	97787,11	25361,857
1 [O00567]	166543,3	211932,23	58475,621	10941,699	174063,79	216410,31	50090,171
1 [Q9Y6C9_	270764,64	369555,72	111360,34	19089,797	282464,87	378310,43	97459,37
1 [Q9Y6C9_	275922,63	378686,91	110309,7	18625,33	287798,78	387878,51	95800,227
1 [Q9Y6C9_	36511,675	44535,453	12799,829	2250,6672	38201,789	45363,48	11082,753
1 [Q9Y6C9_	309844,68	364303,63	105508,57	21886,27	324478,12	370340,13	91392,768
1 [Q9H299]	71671,638	132390	71233,683	36815,102	74052,906	136129,33	67424,764
1 [Q9H299]	52415,929	95872,758	33014,19	12518,04	54165,57	99146,846	29385,443
1 [Q9H299]	128583,69	198876,31	113253,02	55688,405	133676,55	202959,5	108042,23
1 [Q9H299]	4146,2082	7897,6007	4024,1732	1973,5419	4278,7725	8136,1493	3788,4146
1 [P06756_	9523,7609	40751,082	9264,3319	2426,9415	9342,5768	43108,718	7448,4764
1 [P06756_	61522,195	54359,962	29454,935	8401,1676	64819,388	53844,135	28242,196
1 [P06756_	29199,095	76900,367	16679,319	4766,13	29668,002	80660,76	13196,368
1 [Q9NSD9]	19447,642	34108,344	11412,988	3891,8002	20127,692	35232,892	10120,844
1 [Q9NSD9]	15458,803	22335,26	5797,2466	824,44218	16099,892	22952,211	4895,6022
1 [Q9NSD9]	104929,99	177897,05	54062,128	10005,111	108726,2	183714,48	47335,85
1 [O43175_	6845,9081	15374,388	4674,2273	983,10999	7013,3806	16018,59	4084,848
1 [O43175_	27878,104	55155,551	17094,933	3162,4542	28718,933	57244,72	15026,938
1 [O43175_	15657,905	31280,514	9772,7609	1569,0596	16123,785	32472,503	8615,5944
1 [O43175_	40130,746	81860,203	25104,469	3854,9597	41288,533	85048,63	22048,313
1 [O43175_	17286,18	29549,502	9854,2434	1518,367	17906,966	30496,549	8812,6948
1 [O43175_	50202,019	72511,563	22699,056	4308,5819	52286,887	74388,197	20010,802
1 [O75694_	16607,875	21461,25	7119,2509	1318,3102	17351,628	21892,31	6356,1936
1 [O75694_	5868,1564	6806,2212	2026,8269	345,63653	6147,323	6912,1299	1770,3805
1 [O75694_	28266,77	39759,297	12663,043	2726,2312	29463,565	40734,22	11191,67
1 [P60953_	116950,8	135331,94	25091,82				
1 [P60953_	14255,02	32606,297	7684,3884	1979,4883	14589,69	34061,552	6260,8441
1 [P60953_	11508,644	28992,236	6161,8232	1353,9222	11721,501	30382,098	4858,4381
1 [P60953_	8974,5606	24288,629	5922,4831	1224,2779	9105,1756	25470,838	4886,3744
1 [P60953_	5944,8819	13416,68	3617,6013	1126,4783	6088,6133	13995,731	3054,8461
1 [P60953_	109433,52	332351,13	67501,004	12001,249	110245,95	349816,64	52429,836
1 [P33993_	14030,984	26110,371	5920,7155	1572,0856	14487,871	27116,719	4766,4533
1 [P33993_	9878,4867	19650,898	4275,0758	1195,5678	10172,988	20457,526	3390,4459
1 [P33993_	7341,3311	11496,277	2822,0422	938,09325	7626,7194	11858,374	2322,0184
1 [P33993_	21228,553	37448,68	7074,8159	1894,4225	21962,76	38867,554	5323,4087
1 [P33993_	11935,108	21140,975	5551,1401	1768,3641	12347,044	21894,778	4656,3944

1 [Q15233]	100902,73	130824,91	35762,829	8843,8223	105407,29	133721,67	30467,091
1 [Q15233]	226562,16	279478,47	77754,94	16479,52	236981,38	284921,68	66669,453
1 [Q15233]	11229,558	25128,781	3980,6365	1168,2904	11503,834	26297,65	2744,4564
1 [Q15286]	82500,889	141584,25	43163,82	7937,039	85449,268	146274,1	37821,143
1 [Q15286]	160537,73	337016,25	110682,77	16852,287	164970,86	350203,5	98636,211
1 [Q15286]	127991,53	191676,92	55432,544	10887,652	133159,18	197085,63	47976,939
5 [Q9H0U4,	432318,58	838045,13	159830,87	31220,876	445661,07	872467,25	121178,97
1 [Q15286]	15687,773	31950,809	6743,0855	1630,6885	16139,458	33292,792	5301,1528
1 [P52292_	31050,996	16240,841	6570,3504	1586,6504	32950,283	15352,203	6087,8459
1 [P52292_	55882,418	31351,852	13494,926	1904,018	59256,032	29868,275	12672,46
1 [P52292_	27641,082	16641,113	6462,5544	965,38962	29285,283	16004,968	5969,2524
1 [P30041_	11360,509	18768,953	5332,6815	2170,401	11781,734	19376,533	4545,7561
1 [P30041_	36172,106	92665,039	28146,481	4316,1734	36813,673	96872,314	24654,311
1 [P30041_	68812,25	186228,16	39294,665	5481,0068	69809,907	195489,75	31031,292
1 [P36542_	382447,97	535741,31	152364,87	35314,135	398675,58	549370,16	131145,46
1 [P36542_	223940,7	330240,66	96636,654	23905,902	233092,18	339305,8	83664,443
1 [P36542_	32004,998	42683,684	13539,267	2625,0727	33409,685	43626,416	11970,617
1 [P36542_	74162,028	100056,72	38564,774	8749,9325	77396,892	102100,8	35318,901
1 [P36542_	218055,36	258093,17	81448,573	17544,361	228321,6	262245,73	71892,542
1 [A1LOT0]	50168,739	72633,742	19514,407	5389,8673	52246,52	74625,737	16518,095
1 [A1LOT0]	24125,172	44083,781	11092,2	1518,8543	24928,766	45719,354	9280,3707
1 [A1LOT0]	1724,6604	3385,1191	593,51159	159,98318	1776,9597	3527,2318	431,73879
1 [P05023_	54539,278	98169,406	32349,327	8154,346	56392,62	101512,86	28719,912
1 [P05023_	133773,81	250530,77	80251,443	17969,281	138111,02	259481,95	70920,172
1 [P05023_	117044,46	217966,14	57183,326	16752,721	120857,37	226121,72	48009,774
1 [P29590_	23245,847	32724,445	11196,812	3023,6406	24229,971	33503,183	10013,873
1 [P29590_	102894,26	154089,16	54272,061	17073,898	107054,89	158124,18	48694,003
1 [P29590_	1049,7653	3493,6604	710,69184	190,08655	1051,0363	3683,6384	549,45522
1 [P30086_	48123,13	95133,82	26038,214	10705,667	49573,931	98847,726	21969,898
1 [P30086_	64790,389	128724,89	40027,798	15794,812	66733,08	133615,66	34848,55
1 [P30086_	232108,44	521455,94	137549,78	34142,625	237768,93	543991,31	115851,35
1 [P30086_	29326,927	60153,164	15588,451	4637,047	30164,124	62599,497	13036,635
1 [P06748_	190027,65	235360,81	75698,142	27413,373	198753,01	239665,55	66592,603
1 [P06748_	44532,922	34284,829	27385,689	21465,511	47032,218	33312,663	26634,118
1 [P06748_	40327,629	30207,221	24283,3	20002,105	42608,624	29276,437	23587,995
1 [P06748_	4576943,5	3272604,4	1647632,2	656031,58	4838460,5	3190069,4	1559350,9
1 [P02768_	49455,274	109717,38	28920,717	27274,351	50690,856	114424,61	23487,971
1 [P02768_	348101,97	767241,75	217414,08	271209,51	356915,5	799540,15	177165,71
1 [P02768_	68463,116	154932,38	36665,139	50417,749	70105,931	161804,73	28145,319
4 [P63104,	161857,69	327951,88	117754,95	25383,247	166585,44	340101,77	106454,3
4 [P63104,	17331,97	42488,875	13986,94	3246,2065	17680,765	44335,72	12418,334

4 [P63104,	374942,26	985718,38	313352,7	67796,007	381064,95	1030651,9	276359,6
4 [P63104,	79175,538	162033,38	56059,267	13864,788	81452,618	168155,96	50248,542
4 [P63104,	40150,962	105845,82	34122,592	7792,3713	40800,761	110662,48	30165,92
4 [P63104,	181306,25	305822,41	113912,04	20782,076	187912,4	315085,45	103868,47
4 [P63104,	5050,6447	11932,093	4021,4808	976,54269	5161,9051	12436,051	3585,8903
4 [P63104,	10281,669	22831,688	7389,229	1685,6517	10538,985	23766,561	6540,1139
4 [P63104,	206607,44	445348,88	121146,37	22938,286	212049,43	463941,63	103187,82
4 [P63104,	19130,251	29969,615	11579,75	3823,6273	19876,379	30777,486	10553,591
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4 [P63104,	28937,502	67741,461	22231,776	4448,0805	29587,833	70604,95	19758,674
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1 [P31947_	109813,35	273588,97	116957,69	23522,263	111947,35	284723,64	108886,79
1 [P31947_	55793,807	130941,3	56791,218	11616,593	57049,564	136038,06	52982,488
1 [Q13247_	345363,82	326768,4	106166,1	52779,55	363370,69	327522,99	93089,353
2 [Q13247_	381935,69	393521	149404,96	74351,121	401179,31	395896,69	134862,51
2 [Q13247_	210235,88	225681,17	85063,435	37487,733	220635,54	227622,85	76883,896
1 [Q13247_	132101,28	133952,91	53490,948	29580,139	138804,59	134543,95	48569,562
1 [P62910]	9812,3837	18066,441	3855,4548	634,00557	10135,876	18763,861	3057,2678
1 [P62910]	29024,406	45045,207	13377,664	2859,0648	30162,864	46372,104	11639,082
1 [P62910]	125486,24	234251,86	61142,309	19330,887	129561,91	243046,56	51200,694
1 [P17813_	231598,28	470262,72	155254,68	60501,319	238332,9	488162,45	136925,43
1 [P17813_	86948,594	217655,28	44750,085	12162,905	88585,282	228103,87	34759,329
1 [P17813_	76041,736	200152,48	46582,575	13197,953	77267,39	209834,47	37736,045
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1 [P36871_	32651,863	121007,12	26144,162	5512,2036	32428,912	127773,51	20722,446
1 [P36871_	8560,3709	24338,064	5469,3858	1198,5894	8659,7002	25565,281	4394,6772
1 [P36871_	28710,21	73873,492	18179,366	2999,4492	29209,784	77373,589	15074,538
1 [Q9NYL9]	221972,59	311498,56	131700,79	95763,289	231406,75	318067,02	119556,12
1 [Q9NYL9]	94897,642	102341,86	51558,161	33885,685	99590,169	102833,21	48155,507
1 [Q9NYL9]	70779,97	98008,313	40602,488	7826,8989	73815,746	100037,4	37678,012
1 [Q13263_	11659,507	48702,063	12212,373	2750,3528	11463,766	51465,032	10140,047
1 [Q13263_	34773,878	102561,44	33128,175	7671,0639	35105,009	107489,57	29288,404
1 [Q13263_	244231,26	518414,19	222582,73	95215,318	250887,7	537191,3	205232,93
1 [P46977]	63807,192	107842,71	34465,643	8531,8781	66123,856	111302,37	30417,008
1 [P46977]	86735,17	144948,22	40571,319	7774,1265	89915,61	149721,92	34831,508
1 [P46977]	299885,53	630320,94	122030,1	26593,83	308095,46	657761,78	92933,833
1 [Q15185]	30087,123	32234,204	14530,188	4721,0621	31578,313	32430,486	13579,153
1 [Q15185]	59241,172	97307,977	37258,714	11163,606	61455,958	100124,64	33949,745
1 [Q15185]	40728,257	73585,164	22136,028	6194,7889	42105,059	76169,542	19243,287

1 [P51114_	2967,1239	4199,2998	1328,4326	314,60722	3092,1945	4303,7359	1171,1341
1 [P51114_	107450,19	164411,89	63980,12	27479,685	111724,53	168671,2	58109,912
1 [P08729_	196026,93	349824,5	229115,34	58922,012	202825,75	357948,7	223975,5
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2 [P08670_	35412,555	21975,646	12709,714	7563,6802	37507,775	21070,942	12118,523
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1 [Q9UNX3_	85302,088	193497,69	47249,598	8402,5583	87340,356	202034,53	39078,412
1 [Q9UNX3_	98093,641	201843,06	44879,28	10041,699	100875,5	210311,14	35961,865
1 [Q9UNX3_	170112,57	347755,41	138562,01	22608,216	175024,89	360290,81	127854,97
1 [Q9UNX3_	116217,18	193159,52	57571,996	8411,6821	120503,48	199366,64	50287,616
1 [P50402]	224464,57	226024,61	105610,29	59443,446	235898,25	226426,77	98121,772
1 [P50402]	179551,75	194260,64	90414,7	36582,199	188412,39	195465,63	84557,238
1 [P50402]	127729,9	156089,5	63019,096	23161,644	133647,94	158421,49	57790,114
1 [P50402]	160923,5	127228,46	56968,862	31245,832	169856,36	125333,76	52700,072
1 [P43304_	40656,168	51607,164	14841,392	3310,1168	42495,189	52671,768	12819,783
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1 [P43304_	23119,755	45101,41	11376,856	2065,7145	23829,013	46873,38	9501,2113
1 [Q13283_	58896,926	89614,539	26463,814	9468,6896	61245,15	92186,489	22831,6
1 [Q13283_	96627,016	123982,33	36006,992	15142,107	100969,7	126596,73	30866,71
1 [P18085_	12956,971	44550,492	8361,4949	2069,4692	12941,694	47023,042	6264,2038
1 [P18085_	221251,98	518352,22	116771,06	29995,836	226181,21	542002,73	93766,637
1 [P18085_	81806,956	245440,63	58417,601	10824,914	82484,025	257998,52	47887,702
1 [P18085_	37376,313	100327,63	25769,584	4178,5876	37938,768	105148,93	21632,261
1 [P18085_	36245,696	96437,188	30572,553	4886,3684	36813,111	100863,37	27021,352
1 [P14923]	11979,654	36465,012	10283,668	1815,0198	12068,678	38289,87	8838,0557
1 [P14923]	13741,779	39818,48	8349,9186	2325,9865	13884,859	41862,522	6527,801
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1 [P49411_	242933,09	174718,5	84730,239	29667,579	256790,22	170506,27	79988,174
1 [P49411_	58661,904	113842,53	35638,183	10861,82	60478,6	118072,76	31212,637
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1 [Q92688_	88161,561	208768,72	48888,424	11067,825	90079,474	218294,01	39813,859
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1 [P63092_	81491,867	181279,7	39541,836	10139,761	83512,269	189330,79	31414,227
2 [P04899_	87286,601	244996,64	51514,799	13852,042	88364,738	257394,54	40338,362
2 [P04899_	129117,43	410965,47	132249,33	34135,535	129705,22	431380,11	116662,84
2 [P04899_	127461,61	187987,69	67415,211	24081,68	132677,88	192749,13	60568,494
1 [P63092_	18686,688	43669,723	12446,816	2030,2155	19107,029	45574,554	10738,346
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1 [P31942_	88413,622	149730,14	99197,738	36665,884	91650,304	152886	96600,835
1 [P31942_	214862,45	307889,6	135682,41	42181,417	223863,1	314481	126374,42
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1 [P23528_	9225,38	19875,814	5995,2925	1946,7911	9468,9581	20686,439	5200,942
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1 [P14866]	144791,13	290252,85	66836,352	20415,874	149062,57	302119,28	53943,9
1 [P14866]	68768,71	139616,64	34161,404	9935,6963	70761,173	145315,33	28114,166
1 [P14866]	20589,426	41834,16	11136,217	3547,8116	21185,851	43513,664	9371,4073
1 [P55010]	68968,232	108442,45	32781,197	6551,7342	71643,904	111675,75	28654,631
1 [P55010]	35474,609	61711,18	18414,675	6839,2016	36724,419	63799,8	15907,752
1 [P55010]	25497,345	35746,469	11861,929	2456,0416	26579,69	36602,223	10577
1 [P55010]	18206,924	23640,89	7982,8551	1921,0187	19019,966	24116,857	7133,1674
1 [Q9Y4L1_	21855,274	49642,621	14906,926	5815,5693	22377,86	51745,178	12874,789
1 [Q9Y4L1_	52278,941	124489,89	33528,181	8166,6424	53404,296	130046,99	28397,967
1 [Q9Y4L1_	1070229,7	1299879,3	685003,5	264026,38	1120088,2	1313707,4	651174,74
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2 [P34932,	56258,644	79074,867	22043,665	5885,0558	58639,782	81113,162	18846,91
1 [P34932]	23263,021	56148,695	15142,885	1856,8518	23747,75	58674,189	12908,985
1 [P34932]	35144,763	68991,625	26374,938	4018,4063	36219,485	71425,698	24183,964
5 [P68363,	4815,985	9767,1973	3636,2349	502,92132	4956,5462	10125,096	3320,887
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1 [Q9H853]	59621,132	80387,5	21936,591	3292,2784	62217,009	82319,773	18768,503
1 [Q9H853]	442962,46	578032,5	161938,25	21413,039	462660,98	590882,69	139610,5
1 [Q9H853]	101665,65	144591,16	42640,658	7197,605	105934,06	148318,58	37133,344
1 [O75390_	60826,192	137980,58	32588,198	5942,5249	62278,828	144103,99	26675,44
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1 [O15400_	68130,329	79876,055	28673,061	13522,327	71356,417	81009,537	25643,908
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1	[Q03252_	365539,47	333303,25	135150,25	67953,68	384882,59	332360,65	123364,01
1	[Q03252_	313452,69	290246,19	159668,53	93463,194	329972,32	288381,92	151267,07
1	[Q03252_	1796583,5	1600603,8	762305,89	544388,45	1892521,4	1589831,6	705393,29
1	[P20591_	3091,263	18279,82	3149,103	9274,8745	2923,9702	19446,962	1899,5466
1	[P20591_	27312,386	52778,105	15164,667	5724,2879	28162,148	54776,002	12975,157
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1	[P17931_	153964,77	447493,25	69109,605	15223,293	155522,9	471293,96	47129,938
1	[P17931_	34943,75	84368,922	15051,315	4427,1457	35666,318	88414,445	11009,744
1	[O95470]	10124,253	21863,85	5249,0161	1113,4465	10389,606	22800,478	4312,1742
1	[O95470]	2066,2751	4918,8486	701,8665	48,761385	2110,3852	5158,5113	461,29726
1	[P55084_	17295,013	27867,516	6135,5101	1200,2287	17950,172	28799,758	4912,788
1	[P55084_	39593,908	69181,648	17048,728	3404,0655	40980,061	71649,858	14135,218
1	[P55084_	54074,921	73640,852	25415,06	6696,825	56417,151	75273,863	22777,598
1	[Q16531]	16828,752	41038,719	9981,6419	1822,2367	17169,757	42930,972	8241,9668
1	[Q16531]	17541,892	43915,742	12713,646	2115,5959	17874,39	45904,525	11006,291
1	[Q16531]	42369,972	98424,805	25867,483	3719,2981	43334,24	102772,55	21879,832
1	[Q15005_	283924,92	460396,13	148029,36	30697,662	294648,4	474402,26	131079,35
1	[Q15005_	478289,64	862529,38	266737,69	51175,704	494497,14	892525,08	234336,02
1	[Q15005_	53127,197	100142,34	29148,816	9281,5443	54834,044	103837,67	25094,277
1	[Q15005_	132878,88	236209,47	69116,728	20582,294	137451,87	244432,13	59649,197
1	[Q96FQ6]	96345,806	135461,16	40590,352	9526,6599	100424,57	138863	35363,5
1	[Q96FQ6]	68999,744	76055,477	25980,735	5082,0212	72369,034	76913,067	23333,068
1	[Q96FQ6]	65613,226	69097,477	21111,096	4401,4268	68884,117	69771,09	18520,262
1	[Q96FQ6]	6003,7859	11176,915	3284,1504	814,44429	6199,6737	11583,579	2843,7385
1	[Q96FQ6]	64547,628	111944,45	31324,491	8952,6971	66827,663	115787,38	26760,272
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1	[Q02952_	19757,827	20377,039	14212,569	6735,5279	20757,054	20292,001	13851,566
1	[Q02952_	14655,363	14098,172	13045,856	6075,0017	15419,984	13872,769	12992,676
1	[P16070_	143751,64	285284,5	65366,808	39781,521	148053,66	296871,02	51820,799
1	[P16070_	237061,91	494661,81	137216,58	88816,119	243655,49	514758,58	114760,24
1	[P16070_	65435,702	144087,67	46996,952	10246,52	67099,53	149940,65	41685,029
1	[P16070_	15308,319	21918,707	6485,9027	4914,3295	15947,907	22490,441	5487,7553
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1	[P54727]	301208,79	378565,5	225463,81	92869,281	314988,8	382421,3	216979,19
1	[P54727]	160639,28	202319,44	109180,14	47189,956	167972,13	204767,88	103848,02
1	[P54727]	21301,545	30553,557	18450,192	10486,006	22196,44	31048,723	17652,39
1	[P54727]	64646,632	86617,914	59377,199	33181,339	67495,851	87522,173	57536,492
1	[P54727]	63537,386	83360,328	56141,074	32459,981	66374,339	84179,042	54268,748
1	[P54727]	1662,8138	2023,9509	1193,8012	353,19019	1740,2696	2041,5724	1153,7685
1	[P54727]	2244,0736	3027,1838	1863,3975	646,13576	2342,4143	3066,5093	1804,3046

1	[Q8NBJ5_	162663,44	251239,78	66720,716	9982,5631	169064,47	258845,46	56652,566
1	[Q8NBJ5_	168595,92	308019,69	104137,13	18108,216	174230,04	318584,1	93278,58
1	[Q8NBJ5_	13397,855	26316,736	7103,819	1222,523	13805,319	27341,494	6045,6251
1	[Q0ZGT2_	400670,11	591892,37	385540,67	185153,76	417158,03	601332,87	373086,75
1	[Q0ZGT2_	255695,97	234974,6	153750,12	69643,167	269225,35	232547,23	149163,95
1	[Q0ZGT2_	15030,591	13167,709	4753,7756	5269,3307	15836,974	13112,492	4130,7904
1	[P14868]	108085,1	125772,34	36352,833	7175,5718	113217,62	127787,74	31491,642
1	[P14868]	47297,698	68724,086	20234,367	15284,572	49252,406	70564,541	17101,023
1	[P14868]	32296,086	48623,668	12898,714	7272,6271	33593,777	50045,359	10719,858
1	[P14868]	27233,179	42556,332	11152,45	1769,875	28294,227	43869,818	9431,3092
1	[P56134_	21371,805	35962,402	9126,2284	1706,7269	22149,615	37186,592	7636,5745
1	[P56134_	27614,88	52251,031	11916,835	1951,2542	28495,748	54291,912	9663,3143
1	[P56134_	26107,601	46089,574	12540,721	2201,7828	27012,301	47712,782	10696,499
1	[P56134_	40523,437	68247,5	19340,599	2689,4844	41998,311	70507,282	16698,473
1	[P56134_	5270,6179	8978,6045	2396,6439	452,59617	5460,1748	9284,5712	2032,9148
1	[P56134_	25728,085	38592,293	14325,685	5095,6215	26767,549	39581,99	12951,698
1	[P56134_	99043,541	166115,39	58053,533	10577,783	102670,02	171234,74	52324,821
1	[P40227_	36054,733	53796,5	14741,723	5688,5234	37514,122	55333,118	12470,763
1	[P40227_	136467,71	177551,39	68585,729	11039,777	142559,81	180862,92	63038,419
1	[P40227_	20629,6	28562,215	10624,241	1935,858	21513,705	29192,482	9690,4841
1	[P40227_	181075,03	197562,19	65968,226	16970,273	189959,16	199722,75	58809,468
1	[P40227_	213583,3	241495,86	74719,626	16286,285	223878,56	244821,69	65678,228
1	[Q9BWM7_	10146,68	17179,4	4746,135	1100,1478	10513,958	17755,729	4052,9722
1	[Q9BWM7_	15395,781	34361,922	7021,2064	811,12369	15774,754	35906,403	5490,637
1	[Q14566]	28907,129	48592,848	12142,711	2897,7511	29960,107	50251,37	10089,343
1	[Q14566]	29946,721	70658,992	19379,034	8234,1226	30605,456	73785,177	16340,175
1	[Q14566]	23435,677	38942,477	9498,4772	3941,5639	24298,849	40262,366	7764,8787
1	[Q07021_	202710,06	102580,8	55475,429	17219,507	215191,24	96097,341	53241,263
1	[Q07021_	214070,78	113825,83	70325,985	18885,95	227140,96	107038,76	68540,552
1	[Q07021_	223076,75	120650,17	89910,628	27653,381	236663,74	113203,43	88909,151
1	[Q07021_	56281,686	69704,836	27956,898	9353,1796	58869,568	70800,324	25648,633
1	[P35268_	241050,16	382313,19	170364,81	32462,303	250366,97	392071,67	159779,93
1	[P35268_	126597,38	189241,63	82363,462	15150,17	131733,93	193672,07	77017,128
1	[P35268_	174049,14	275031,19	94498,497	47658,769	180779,65	282925,27	83598,582
1	[P35268_	166459,73	271081,47	68891,443	13678,171	172710,27	279965	57642,913
1	[Q15758]	32674,501	81872,203	15642,256	3091,041	33287,1	85842,786	11853,178
1	[Q15758]	19716,519	47690,332	11241,639	2068,8602	20124,137	49890,678	9193,7821
1	[Q15758]	9051,3112	20765,748	5069,8637	966,19106	9262,6006	21688,51	4189,9566
1	[Q01813]	13129,91	21465,883	5824,2563	1450,2805	13621,389	22160,725	4947,0518
1	[Q01813]	10598,089	15968,277	5052,8781	944,99525	11024,203	16408,897	4464,7202
1	[Q01813]	12170,007	24041,047	8135,8932	1885,3868	12538,287	24928,405	7267,2632
1	[Q01813]	6075,1838	6301,0474	2751,7009	1026,3542	6380,6277	6329,9706	2554,537

1	[P07996_	22618,812	135851,52	22298,734	5671,1901	21349,453	144570,15	15651,991
1	[P07996_	44401,765	155498,27	48057,548	16458,286	44301,094	163571,09	41842,919
1	[P07996_	35079,608	86308,117	27221,166	9437,1692	35778,161	90106,928	23817,077
1	[P30533_	244293,14	224758,97	106961,86	58546,241	257187,81	223753,48	99724,243
1	[P30533_	245813,92	212824,85	106506,33	62573,374	259074,55	210782,4	99782,259
1	[P30533_	414012,28	301242,07	166504,17	102160,47	437567,13	293637,11	157749,56
1	[P30533_	112612,07	191129,75	55261,944	12984,221	116679,94	197479,68	47713,744
1	[P50991_	90125,919	144479,5	37382,608	7128,3928	93559,413	149103,02	31449,439
1	[P50991_	455690,06	531412,88	367057,62	194840,18	477441,29	533108,27	356445,3
1	[P50991_	337540,86	430759,75	172418,86	107170,5	352790,99	438205,18	155982,78
1	[P50991_	88059,614	147974,97	37759,535	6974,5568	91268,94	152997,73	31648,849
1	[P50991_	167038,33	296224,49	73642,78	10262,785	172793,65	306930,1	61401,383
1	[P34897_	145839,2	155458,95	54377,951	11557,59	153073,96	156865,17	49023,878
1	[P34897_	237368,68	327698	85815,382	12638,115	247538,24	336052,98	72638,705
1	[P34897_	101806,96	177643,69	53180,386	10049,297	105382,36	183668,24	46392,801
1	[Q16555]	60352,71	161873,63	40809,539	11672,955	61263,148	169675,49	33860,286
1	[Q16555]	35355,108	109561,08	26269,055	8248,2504	35573,455	115235,24	21435,026
1	[P61769_	20867,785	25690,17	14218,066	9630,2953	21833,081	25960,438	13413,027
1	[P61769_	19128,263	24795,785	12815,135	6473,7084	19986,173	25149,952	12085,968
1	[P61769_	273002,09	409365,13	222914,66	121983,26	284080,32	417572,18	211069,48
1	[Q9UBQ0]	6724,701	11676,129	3383,1649	754,17572	6962,0269	12073,657	2924,0855
1	[Q9UBQ0]	128339,97	296148,75	77665,088	22492,92	131302,87	309184,12	65167,13
1	[Q9UBQ0]	61707,568	138431,48	40496,893	8113,1477	63219,3	144279,03	35095,252
1	[P49755_	95602,421	160829,2	40122,704	9735,0673	99082,22	166325,25	33314,99
1	[P49755_	402325,82	838156,81	166584,17	44648,646	413502,75	874281,25	127842,79
1	[P49755_	62020,639	116728,56	33516,048	9440,97	64016,7	121044,58	28812,795
1	[P22087]	25991,847	31160,914	7187,0951	1633,1662	27205,422	31769,284	5842,7165
1	[P22087]	49441,833	69259,734	18063,131	3543,9975	51538,634	71074,426	15233,625
1	[P22087]	261849,66	288832,13	93184,174	33063,855	274627,92	292281,52	82098,172
1	[Q8N556]	97470,132	142142,22	37753,285	11665,984	101484,79	146099,98	31805,6
1	[Q8N556]	12132,624	31360,178	7360,5258	1800,5007	12340,477	32861,204	5991,2146
1	[Q8N556]	9081,1668	17901,459	4715,6946	1306,3863	9355,913	18604,478	3966,0603
1	[Q14554_	11846,943	26551,113	6025,1998	1075,4565	12136,6	27728,302	4870,9736
1	[Q14554_	19755,905	47028,094	11980,273	2972,7426	20181,067	49149,15	9992,4305
1	[Q14554_	22240,101	55632,488	14370,81	9253,9374	22661,466	58208,385	11786,066
1	[P12270_	7721,7441	6780,737	1596,7072	710,42618	8135,131	6780,6248	1294,3724
1	[P12270_	7492,0974	9094,0645	2700,6533	1006,4462	7839,9054	9258,1241	2333,4291
1	[P12270_	266956,06	236915,91	73861,408	51469,748	281206,04	236512,64	63586,076
1	[Q9HDC9_	30450,334	82517,82	21780,032	2961,1096	30892,289	86482,733	18443,914

1 [Q9HDC9_	40922,56	99876,219	24039,094	6113,5247	41749,861	104492,13	19712,582
1 [Q9HDC9_	47415,06	126420,01	40900,959	8760,8609	48152,21	132202,48	36209,606
1 [P24539_	112089,5	197036,3	42425,568	7348,6685	115984,47	204307,38	33738,878
1 [P24539_	288502,23	401007,06	127615,14	28870,171	300819,1	410626,73	112712,42
1 [P24539_	113081,7	144498,98	44542,863	8628,1597	118178,31	147430,94	39147,195
1 [P38159_	227295,97	303846,47	227036,49	92665,168	237340,67	306372,46	223098,96
1 [P38159_	188700,92	264216,94	184600,87	77858,195	196780,51	267398,29	180258,88
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1 [P38159_	55278,941	100026,83	29942,025	13603,586	57144,26	103551,16	25774,35
1 [P38159_	81434,864	98190,961	83115,269	36963,326	85263,984	98184,749	82328,678
1 [P38159_	133137,34	122786,53	43974,572	20487,3	140149,29	122723,81	39362,864
1 [P20618_	26585,542	74842,969	20212,537	3593,7858	26912,057	78490,194	17182,633
1 [P20618_	60122,648	79774,281	23376,152	3236,5905	62768,869	81578,844	20363,053
1 [P07099]	38512,245	77855,211	22358,987	4148,6258	39637,331	80914,972	19311,031
1 [P07099]	197392,91	339571,72	75586,632	11769,342	204411,92	351753,87	60857,605
1 [P07099]	35407,915	77617,648	23550,947	3728,2342	36314,536	80817,281	20626,179
1 [Q9UKV3]	140175,95	107535,55	63070,75	24551,481	148036,46	105185,26	60738,604
1 [Q9UKV3]	11898,928	16514,848	5378,0821	1920,6605	12407,514	16906,1	4742,5699
1 [Q9UKV3]	141172,4	147486,89	42787,471	20837,913	148233,65	148929,41	36584,104
1 [Q9UKV3]	73788,102	70500,593	20673,058	12837,976	77619,3	70782,188	17610,105
1 [P37108_	344299,99	537086	188893,49	54852,36	357765,37	552071,31	169609,75
1 [P37108_	74088,286	131578,73	40264,293	7343,8584	76641,785	136096,66	35308,959
1 [P37108_	64343,583	96066,875	29931,114	6657,1958	66949,057	98695,853	26314,303
2 [Q70UQ0,	100059,95	188119,17	66301,828	15052,938	103292,5	194669,68	59709,215
1 [Q70UQ0]	139735,99	295592,28	104454,54	34576,135	143551,61	306991,92	93621,689
1 [Q70UQ0]	63988,025	84542,531	37275,56	5779,6739	66820,102	86032,94	34978,51
1 [Q70UQ0]	69691,095	143468,28	51315,281	15197,974	71678,512	148861,86	46177,64
2 [Q70UQ0,	37475,813	71100,383	12745,739	3446,7413	38664,909	73996,578	9368,2359
1 [Q9NVD7]	13224,559	46297,266	12742,247	2152,6627	13193,921	48750,704	10885,534
1 [Q9NVD7]	5988,0946	15833,557	4018,5413	582,57312	6083,2916	16590,307	3365,1789
1 [P13987_	9840,3458	35913,297	7105,4529	2483,8167	9784,5706	37933,317	5407,8601
1 [P13987_	63436,837	188122,88	45845,518	16899,108	64009,506	197668,56	37490,043
1 [P13987_	15662,168	85491,875	14569,219	4367,7889	14966,898	90870,418	10396,743
1 [P13987_	150305,72	746186,13	133401,47	40633,788	145224,42	792063,16	97391,904
1 [P13987_	36028,226	129837,17	25785,572	7419,9345	35859,349	137107,85	19723,94
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1 [Q99439_	88449,979	170500,05	35057,727	6585,1049	91201,904	177389,43	27387,237
1 [Q99439_	75175,094	160962,78	40628,131	14527,265	77176,125	167754,6	33617,223
1 [Q99439_	56056,846	106701,18	31456,153	16842,668	57835,97	110662,15	26867,157
1 [Q9Y5X1]	28976,591	53289,121	11918,095	4128,0148	29933,556	55326,884	9509,9546
1 [Q9Y5X1]	18004,231	26297,928	5935,8474	3339,1902	18744,223	27066,25	4700,83

1	[O75380_	336047,78	257834,8	163589,2	84253,795	354899,08	251807,29	157888,73
1	[O75380_	140432,64	115583,78	71156,838	34058,8	148143,98	113601,68	68573,381
1	[O75380_	53723,241	55873,449	32782,923	13526,071	56426,445	55868,56	31512,103
1	[O75380_	259335,25	250403,7	150629,4	61915,35	272794,21	249079,81	145200,06
1	[P09669_	398376,7	472911,19	147288,88	40794,908	417101,81	480659,77	129248,82
1	[P09669_	100247,08	125799,93	31177,539	6824,1204	104809,26	128484,18	25906,057
1	[P09669_	419527,06	469370,6	114442,61	43311,558	439835,49	476554,36	93918,169
1	[P09669_	447013,94	374729,42	124895,05	29467,357	471348,56	372241,94	111561,19
1	[Q9Y2D5]	82845,211	78183,361	32957,87	11718,426	87173,818	78105,253	30471,282
1	[Q9Y2D5]	13527,279	12346,225	6915,9426	2581,5471	14244,076	12250,255	6628,8674
1	[Q13641_	148464,34	267135,16	112632,12	26063,024	153527,33	275433,17	104551,18
1	[Q13641_	11272,755	20526,438	9696,4547	2677,2275	11652,695	21139,027	9129,3344
1	[Q13641_	6451,7372	12209,614	5056,1059	2155,889	6658,9495	12613,325	4637,3613
1	[P09525_	194897,21	294492,66	61732,04	23715,336	202695,25	303675,03	48104,395
1	[P09525_	4361,3698	15634,694	1711,8494	344,38221	4341,7957	16553,79	894,52384
1	[P09661_	228076,55	390262,22	108277,62	22131,924	236245,07	403493,39	92687,777
1	[P09661_	87877,052	92913,859	38919,269	30595,693	92256,621	93506,022	35210,561
1	[Q6IAA8_	420960,06	471686,38	151093,76	51678,165	441345,89	477778,23	132993,59
1	[Q6IAA8_	197838	213702,69	72365,299	25927,257	207590,89	215883,36	64378,298
1	[Q6IAA8_	40356,994	67416,75	17043,282	3579,2663	41836,201	69695,248	14229,545
1	[P62888_	54327,046	93989,688	35439,203	6351,0682	56256,837	96911,367	32386,364
1	[P62888_	19493,643	41543,66	14673,431	2438,2311	20019,404	43154,767	13254,604
1	[P62888_	360835,53	545307	205932,89	66204,875	375330,21	559348,22	187044,79
1	[P62888_	30455,219	39597,524	24816,393	13390,12	31821,428	40028,563	23867,231
1	[P07093_	20656,776	49741,25	19088,187	6394,7233	21093,325	51792,604	17356,896
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1	[O75534_	24035,377	56806,164	15241,515	3351,5277	24561,855	59332,271	12912,358
1	[O75534_	66890,973	142582,55	46328,136	7230,1801	68691,882	148243,37	41186,001
1	[O75534_	222732,18	446400,06	143089,19	21834,853	229331,01	463339,04	126887,41
1	[O75534_	55279,341	106967,84	30541,689	5676,0191	56996,008	111026,89	26344,161
1	[Q10713_	31009,298	74508,769	28046,048	4231,3749	31667,727	77593,847	25639,83
1	[Q10713_	11282,414	27011,279	10679,113	1426,8834	11524,387	28110,492	9852,2874
1	[Q10713_	9515,3308	24542,193	9323,812	975,39722	9681,772	25599,985	8555,1409
1	[Q92598_	65268,113	62891,656	25486,011	13990,782	68650,153	62950,501	23205,174
2	[P34932_	56258,644	79074,867	22043,665	5885,0558	58639,782	81113,162	18846,91
1	[Q92598_	5511,7269	7912,917	3593,3643	415,79773	5742,3719	8079,3893	3391,4274
1	[O00231_	35957,875	77762,969	26237,354	7561,2088	36902,833	80852,985	23353,512
1	[O00231_	54217,924	103562,11	33108,707	13618,378	55932,666	107334,48	28977,746
1	[O00231_	32572,642	61915,986	17892,58	3767,6443	33608,015	64222,007	15460,028

1 [P30049_	527544,06	367226,43	206479,34	78646,525	557911,84	356377,78	198097,98
1 [P30049_	355935,97	208702,89	188542,05	38746,357	377296,22	196655,78	189792,47
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1 [P30049_	196179,05	300266,56	82851,021	25323,641	203959,3	309145,59	70491,106
1 [P30049_	480721,5	345622,28	224859,64	93085,272	508181,47	335431,5	218561,56
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1 [P62913_	40291,346	87697,703	24811,503	4100,1483	41335,151	91352,969	21368,749
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1 [P62913_	33719,398	45779,868	15896,461	4554,9966	35182,979	46785,444	14247,814
1 [P62913_	128143,73	151367,54	58532,733	10200,925	134190,28	153437,62	53790,966
1 [P62913_	59291,684	94517,359	28064,422	7400,5745	61564,156	97404,51	24353,235
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1 [Q15436]	76898,229	136251,88	37316,936	8761,8903	79552,5	141061,02	31786,835
1 [Q15436]	6402,38	14247,856	3310,8718	617,36823	6561,1227	14874,182	2696,0095
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1 [Q53GQ0]	2285,8361	5633,2002	1096,4313	230,70454	2330,7213	5903,3472	836,60865
1 [Q53GQ0]	25519,916	53488,041	16051,987	2773,2194	26225,478	55627,505	14015,085
1 [Q53GQ0]	10957,935	22405,031	7008,5146	1146,5366	11273,043	23274,907	6179,0313
1 [Q53FA7]	3378,0952	10074,016	2500,9645	318,70493	3407,4237	10584,78	2082,4482
1 [Q53FA7]	879416,92	1225652	253378,91	136528,67	916802,97	1259645	194843,77
1 [P04632]	21079,062	39639,738	11999,958	3591,1239	21758,566	41084,338	10435,512
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1 [P41250]	7895,9015	24629,844	6322,3383	869,5531	7941,4955	25895,011	5311,2742
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1	[P09874_	11429,776	9303,8428	2060,2426	585,30145	12057,228	9254,6952	1652,9661
1	[P09874_	11722,601	11330,987	2828,3553	743,67564	12328,162	11400,686	2353,3771
1	[Q92791]	12803,341	32868,719	7739,5331	2527,8467	13027,5	34435,736	6278,8298
1	[Q92791]	8526,9249	23906,736	4891,9615	997,49365	8632,7313	25120,21	3805,9013
1	[Q92791]	5597,2717	15350,402	3315,4043	802,93037	5674,1502	16116,176	2625,117
1	[P62917_	84980,473	180691,38	49148,389	9333,6511	87271,818	188161,72	41862,186
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1	[P24534_	255257,92	350525,88	112459,11	41455,476	266246,94	358712,91	98809,7
1	[P24534_	54262,059	37548,649	19231,696	7436,3481	57389,134	36479,77	18251,27
1	[P24534_	241404,73	157694,5	92122,856	36433,814	255521,84	151978	88705,53
1	[P24534_	643552,06	467359,55	200972,61	51607,378	680148,86	457317,88	187428,32
1	[Q93008_	27765,699	48545,512	15420,333	2588,0123	28739,321	50166,604	13642,984
1	[Q93008_	5644,6095	11053,436	3545,8319	569,53129	5817,3634	11464,54	3143,8124
1	[Q14019_	6371,8189	21903,059	4245,8529	1146,0207	6364,5088	23114,23	3219,9492
1	[Q14019_	20022,853	62207,352	14028,917	3367,2175	20142,554	65460,775	11270,22
1	[Q14019_	10861,858	33004,369	9380,0338	2654,8108	10943,857	34652,701	8033,7596
1	[O76094_	65390,693	94866,688	20048,637	3527,2992	68091,263	97652,522	15852,674
1	[O76094_	39746,307	63258,141	16709,166	3767,0324	41270,499	65253,331	14111,217
1	[Q13423_	331058,8	461655,25	94833,094	26035,032	345127,15	474484,87	73831,762
1	[Q13423_	77176,265	144279,22	39248,557	7079,2762	79679,443	149650,59	33460,21
1	[O14602_	31730,108	43309,488	22373,852	9397,9168	33107,153	44034,956	21179,47
1	[O14602_	14479,12	14970,392	9019,1427	2195,4871	15209,69	14955,739	8759,1629
1	[P46063_	106646,86	165851,36	35651,474	6347,7517	110814,04	171190,72	28345,199
1	[P46063_	3476,0544	4411,1665	933,09624	131,58574	3633,0982	4512,9461	740,07014
1	[P46063_	9803,6011	13171,838	3967,6742	931,87989	10231,673	13474,244	3461,4625
1	[P54136_	74607,044	98344,188	30778,7	7914,9799	77905,839	100474,97	27052,016
1	[P54136_	77530,362	95011,539	36029,536	16165,531	81115,354	96520,915	32571,361
1	[Q6NYC8]	42643,063	23786,671	17779,326	6624,4143	45225,172	22402,19	17533,665
1	[Q6NYC8]	20001,57	5981,6761	5475,2458	1740,807	21322,033	5010,3407	5503,3847
1	[Q9Y4P3]	86833,551	166366,4	39131,833	7211,126	89560,083	172895,71	32006,881
1	[Q9Y4P3]	53247,385	90079,922	26580,219	5991,9293	55177,431	93044,27	23071,159

1	[O94874_	104286,05	207645,09	58199,306	15762,072	107399,34	215753,13	49755,477
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1	[P28066]	35249,651	97862,469	30835,348	5552,4542	35714,635	102457,84	27188,818
1	[P28066]	35106,337	97458,555	31462,473	5858,902	35570,044	102010,44	27876,957
1	[P28066]	24971,383	70964	26104,735	4691,1317	25268,368	74212,582	23729,649
1	[P28066]	30933,624	92221,094	31962,543	6156,2069	31208,614	96603,009	28714,826
2	[P11940_	31153,08	41044,496	14949,826	3105,5064	32532,321	41864,567	13570,845
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1	[P54920]	12912,855	22750,273	7141,333	1978,6276	13361,903	23519,223	6268,4352
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1	[P09622_	99777,684	128728,46	43106,719	14443,178	104250,69	131292,13	38280,34
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1	[Q15043_	71816,665	147790,68	28869,18	10167,4	73850,39	154121,56	21900,028
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1	[O75131_	39257,734	86971,734	13401,947	2786,928	40235,09	91004,186	9148,3008
1	[O75131_	38005,526	76269,398	12785,7	3086,7431	39121,892	79544,476	9115,182
1	[O75131_	21479,703	37250,516	7223,4005	1911,9851	22236,412	38632,718	5495,4188
1	[O14776_	29736,891	29898,604	14618,86	4637,3586	31253	29927,235	13819,205
1	[O14776_	87752,336	60916,099	38088,904	18111,959	92809,768	58977,774	36786,52
1	[P98179]	10731,755	14303,661	6877,942	2655,3958	11204,456	14543,671	6462,388
1	[P98179]	62618,936	176846,05	33166,17	20608,529	63366,551	185952,43	24320,023
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1	[P18621_	43747,089	63492,301	18855,654	5648,7316	45556,748	65182,387	16339,214
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1 [Q04837_	115148,75	195041,97	77692,753	30654,124	119330,28	200820,52	70938,481
1 [Q04837_	48416,988	92959,266	37118,459	9429,9312	49942,887	96120,895	34120,732
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1 [P61221]	31063,004	50903,695	14770,441	3508,4428	32223,829	52525,006	12763,647
1 [P61221]	85856,575	128974,88	38289,277	9172,6528	89315,176	132599,5	33271,517
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1 [Q6UVK1_	6224,296	15642,477	4801,4781	1289,687	6341,1687	16343,663	4191,9441
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1 [P08574_	27100,456	33898,607	9788,6534	1832,6773	28337,013	34571,379	8479,2185
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4 [Q9H0U4,	82500,889	141584,25	43163,82	7937,039	85449,268	146274,1	37821,143
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1 [Q9UJZ1]	166825,27	79249,165	52710,276	13123,185	177212,62	73270,294	51792,183
1 [Q9UJZ1]	90507,164	49569,613	29290,468	7728,3276	96001,788	46830,128	28423,999
1 [Q9UJZ1]	99202,438	61372,432	43365,438	14804,534	105080,94	58569,995	42615,054
2 [Q13247_	381935,69	393521	149404,96	74351,121	401179,31	395896,69	134862,51
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1 [Q13243_	465605,81	292881,33	147413,72	64722,767	493056,58	281932,97	139329,25
3 [P16188_	37369,557	75994,523	20574,852	3407,3359	38450,888	79035,677	17527,447
1 [P10321_	193126,53	274154,59	109775,41	32241,863	201264,43	280265,5	100838,66
1 [Q03135_	120562,39	337392,88	84010,54	27351,917	122081,33	354021,91	69304,89
1 [Q03135_	377160,11	1182822,8	276999,13	86971,386	379185,48	1244583,2	224367,56
1 [Q03135_	39242,266	83328,867	19937,63	6430,0971	40300,955	86859,505	16268,298
1 [Q9NX63]	28341,393	17612,425	8760,0612	5874,41	30016,797	16936,084	8180,5391
1 [Q9NX63]	102949,55	66294,704	30512,832	19888,058	108984,8	64065,624	28225,861
1 [P42766_	42743,676	86153,406	33287,552	19500,483	44003,273	89257,48	29953,393

1	[P42766_	105299,79	212595,81	57178,062	32111,805	108379,26	221072,45	47649,774
1	[P42766_	144018,33	289428,97	103874,62	14930,266	148275,53	300076,93	94221,438
1	[P42766_	537799,31	904169,75	232734,04	38949,426	557390,99	934811,43	195714,27
1	[P42766_	330741,85	504699,25	140410,21	24388,788	343892,03	519518,75	120512,35
1	[Q15008_	195383,79	278264,63	83109,257	32932,053	203579,33	285425,46	71770,714
1	[Q15008_	8938,2666	14935,204	5031,8	1206,594	9266,6095	15399,491	4490,7932
1	[Q9Y265]	43978,362	60254,191	24141,571	7309,6534	45877,693	61499,251	22171,145
1	[Q9Y265]	20747,916	23516,492	8270,0038	1524,4843	21747,444	23811,342	7471,4154
1	[Q9Y265]	31015,873	34860,578	13129,433	2362,823	32516,869	35252,968	12010,932
1	[O75531]	15293,178	14905,884	6150,2736	1778,3485	16082,114	14927,138	5684,525
1	[O75531]	384980,53	359660,66	147395,95	40387,128	405170,4	359188,48	136209,31
1	[O75531]	2424,795	3483,8623	922,08667	309,11492	2525,7803	3578,6947	775,10319
1	[P49257_	67378,518	157754,88	42504,494	14447,494	68886,241	164725,27	35829,625
1	[P49257_	295209,02	558597,81	125731,95	30268,868	304624,08	580473	101101,59
1	[P49257_	107213,24	204143,19	47099,544	11449,835	110606,16	212143,26	38172,259
1	[P49257_	100777,23	159717,94	40709,583	9938,962	104655,24	164776,58	34014,341
1	[O75368]	96210,444	123809,92	54235,827	19894,054	100538,46	125847,22	50354,26
1	[O75368]	49342,993	71708,195	31249,973	11566,939	51388,52	73299,591	28977,997
1	[O75368]	39528,037	79902,586	45468,062	20696,19	40697,375	82316,212	43427,127
1	[O75368]	18346,639	31653,262	14757,092	6135,442	19002,009	32543,372	13781,751
1	[P49773_	246418,58	411452,88	137777,04	39426,184	255476,35	424261,1	122538,82
1	[P49773_	220344	291674,31	99613,863	34066,917	230065,89	297785,42	88767,178
1	[P33176_	106163,26	132575,54	39405,633	14924,222	111012,69	135160,87	34039,753
1	[P33176_CHAIN_0]							
1	[Q15293_	400958,9	601163,06	405433,24	256293,38	417281,06	610698,27	390937,59
1	[Q15293_	175278,87	342152,28	251480,52	120908,73	180757,27	350271,37	245885,53
1	[P30084_	112390,63	486380,09	156139,96	26218,237	110165,07	513123,32	138217,87
1	[P30084_	38013,783	70479,656	21143,493	4434,305	39260,499	73019,914	18431,435
1	[P30084_	20214,566	50082,227	14606,127	2855,278	20608,961	52333,548	12648,793
1	[P17301_	36150,156	76916,867	28306,827	5958,6448	37128,526	79859,457	25708,571
1	[P17301_	17946,853	37327,32	14739,782	2875,7738	18451,448	38697,161	13560,082
1	[O14737_	58972,672	45211,997	21447,17	7752,5429	62276,972	44385,241	20173,17
1	[O14737_	21844,588	14438,455	7180,3099	3616,4254	23117,666	13972,22	6754,9107
1	[O14737_	88178,313	69451,479	30614,812	15802,436	93078,368	68411,372	28300,571
1	[Q14344]	87286,601	244996,64	51514,799	13852,042	88364,738	257394,54	40338,362
1	[Q14344]	129117,43	410965,47	132249,33	34135,535	129705,22	431380,11	116662,84
1	[Q14344]	127461,61	187987,69	67415,211	24081,68	132677,88	192749,13	60568,494
1	[Q14344]	23596,96	43425,023	12316,744	2737,7375	24377,317	45002,037	10589,087
1	[O14653]	8815,1928	14101,675	4838,9219	1478,9087	9152,4216	14513,352	4321,0022

1 [O14653]	192812,31	169570,55	65305,823	18602,46	203145,51	168763,94	59732,485
1 [P22102]	26806,239	26680,554	9777,6458	1489,0297	28176,582	26794,259	8918,0808
1 [P22102]	124549,3	168552,53	67955,021	13128,794	129972,99	171922,98	62794,533
1 [Q13895]	16275,51	17822,127	5334,4742	1101,3801	17072,268	18040,697	4657,9511
1 [Q13895]	10444,306	11650,468	4869,5166	2084,4183	10951,937	11761,261	4478,3923
1 [Q16666_	45456,96	93269,866	26527,627	7045,3026	46755,46	96987,565	22765,141
1 [Q16666_	11617,792	35603,445	9396,8899	5603,7859	11698,586	37411,901	7768,7178
1 [Q10567_	12445,198	29506,883	5684,5752	754,11432	12714,376	30893,679	4339,2039
2 [P63010,	6727,1165	12593,108	3629,837	544,27396	6945,0789	13055,882	3144,0546
2 [P63010,	53595,617	95128,797	27875,586	4867,582	55443,212	98433,102	24213,608
2 [P63010,	51515,546	87203,797	25741,471	4308,3625	53381,688	90074,873	22409,556
1 [P14927_	117735,11	89166,507	36806,331	11936,29	124351,62	87622,223	34002,428
1 [P14927_	72299,555	69049,747	25404,878	7217,6204	76057,422	69155,321	23047,324
1 [P14927_	237603,03	243843,25	98647,467	29345,706	249599,05	245055,24	90843,065
1 [Q13177_	78717,973	99684,328	33649,997	10188,09	82286,903	101568,17	29979,044
1 [Q13177_	41030,371	47914,129	21656,212	8062,7071	42980,138	48439,286	20196,912
1 [P62249_	390557,04	798256,13	188641,38	31914,618	401754,87	831216,51	154603,86
1 [P62249_	287594,48	561810,5	129107,54	32062,836	296392,42	584318,71	104464,1
1 [P62249_	58805,188	116305,62	29737,617	4787,316	60575,551	120913,92	24954,772
1 [P62249_	41884,13	84273,211	23393,631	4095,9901	43115,688	87598,775	20047,231
1 [P62249_	131456,8	326211,81	87136,003	13581,474	134005,29	341147,56	73964,775
1 [O43294]	4204,3124	12391,142	2850,8983	813,33257	4243,7967	13023,648	2300,0469
1 [O43294]	9478,5232	20071,293	5154,3524	1872,4788	9735,654	20908,698	4284,6776
1 [AOFGR8_	22548,679	50041,004	11108,725	1546,9218	23110,387	52253,509	8934,6627
1 [AOFGR8_	29128,8	51474,977	14295,023	3828,5091	30137,268	53280,651	12199,251
1 [AOFGR8_	61669,27	107114,38	31495,765	7610,9517	63845,171	110747,87	27291,009
1 [Q9Y512]	75444,153	86842,789	24690,578	7266,586	79046,588	88196,351	21202,757
1 [Q9Y512]	14817,694	5334,3009	6715,5264	924,13522	15778,248	4600,7487	6909,6463
1 [Q8WUM4.	7717,474	17465,984	5206,7197	1187,9322	7903,3431	18204,999	4525,7618
1 [Q8WUM4.	19520,193	34990,629	11358,726	4276,5688	20186,497	36183,061	9992,4265
1 [P09496_	147101,45	124565,52	90914,719	47018,27	155114,46	122240,61	88814,527
1 [P09496_	107856,11	185445,64	86135,634	22302,401	111722,25	190644,43	80984,776
1 [P63000]	196960,73	355774,84	121266,15	20728,439	203629,85	367803,54	108813,76
1 [P63000]	182026,62	400616,09	79243,73	14742,957	186626,2	418547,5	60966,29
1 [P68402]	14124,08	40851,65	9243,6106	2208,5355	14273,17	42925,107	7435,916
1 [P68402]	4217,0498	11930,306	2777,3526	739,58573	4267,3069	12527,461	2251,6924
1 [O15145_	117351,78	191404,34	59270,722	10304,167	121758,87	197344,02	52147,9

1	[O15145_	14112,627	25055,082	7313,2396	2574,504	14598,977	25926,798	6290,7117
1	[O15145_	112092,32	195052,42	55963,459	13612,055	116038,81	201726,99	48206,268
1	[P26368_	79092,512	132674,2	34729,383	10175,991	81980,534	137141,31	29151,285
1	[P26368_	108851,1	179650,34	37653,822	6818,4195	112882,44	185889,72	29655,879
1	[P26368_	68850,591	129554,26	35345,363	6683,2988	71065,902	134402,77	30141,224
1	[P26368_	36758,589	63414,824	14005,774	2515,8566	38061,767	65700,115	11232,506
1	[P26368_	21931,151	40982,473	9375,4133	2150,3879	22641,703	42565,121	7583,8155
1	[O43684_	72178,988	127895,48	40539,192	12939,783	74673,784	132232,27	35584,402
1	[O43684_	32990,506	66583,664	15489,618	3297,6344	33954,261	69314,693	12604,112
1	[P13073_	137051,19	169264,72	44465,032	10432,221	143347,92	172657,12	37521,956
1	[P13073_	104783,33	148845,31	42755,803	11803,342	109185,71	152712,24	36806,246
1	[P62995_	107907,36	122885,88	45618,093	14584,828	113094,99	124382,72	41350,528
1	[P62995_	329947,12	383332,63	117786,56	43614,722	345632,33	389220,14	102590,8
1	[P26373_	158465,17	247763,06	58202,751	10874,181	164632,01	255633,84	47621,065
1	[P26373_	10034,572	21275,939	5299,535	1455,1003	10306,105	22169,628	4387,4006
1	[P26373_	203202,05	285691,28	72403,375	17393,724	211796,22	293292,83	60443,206
1	[P26373_	42923,181	88971,188	27456,085	5665,7666	44131,52	92475,523	24083,442
1	[O75844]	178853,32	301353	89710,939	13885,038	185362,64	311197,18	78301,42
1	[O75844]	61834,59	71787,578	21558,527	4522,6928	64774,914	72902,71	18830,21
1	[Q9UKM7]	3201,7616	13602,355	3285,4755	601,74544	3143,058	14381,557	2703,7791
1	[Q9UKM7]	26714,225	95886,813	26317,449	4504,0092	26601,92	101013,53	22463,235
1	[P29992]	51597,252	100563,48	17402,717	3255,9284	53176,943	104769,35	12643,647
1	[P29992]	125515,01	226220,19	48763,236	17667,287	129757,32	234770,69	38391,651
1	[P62750_	87347,665	152851,47	63043,547	13832,578	90417,056	157492,07	58357,795
1	[P62750_	321159,81	408471,03	158326,03	47950,509	335696,1	415618,19	144644,46
1	[P62750_	267155,88	427643,91	161294,13	56681,511	277379,53	439670,18	146237,7
1	[P42224_	7859,9831	24795,375	4881,7844	3843,694	7898,4842	26123,421	3617,4989
1	[P42224_	45504,88	159394,56	43057,151	42774,676	45396,892	167876,98	35074,716
1	[P30837_	3056,6215	25343,82	6910,5294	1034,5109	2737,5407	26955,21	5889,2914
1	[P30837_	5895,598	55793,934	16021,652	2313,175	5133,4354	59368,248	13835,164
1	[P30837_	58840,168	231540,66	68273,114	12251,952	58162,455	244128,27	59275,641
1	[Q9H930_	17130,971	39321,09	8259,6281	4611,66	17529,592	41112,96	6366,5659
1	[Q9H930_	6105,6836	18372,852	3553,6634	2146,2736	6154,5243	19340,89	2642,4448
1	[Q9H930_	13573,096	36036,008	8673,3279	5287,29	13785,435	37778,015	6977,7013
1	[Q9UHX1_	6456,9887	8452,0127	2855,6475	545,1071	6743,8875	8625,4235	2558,0385
1	[Q9UHX1_	31488,739	45946,566	12607,36	2384,5175	32785,427	47213,636	10776,79
1	[Q9NP72_	38102,585	69663,063	20619,498	7415,4272	39372,909	72149,897	17786,563
1	[Q9NP72_	56119,463	107381,63	31773,66	5779,0182	57888,746	111380,43	27646,113

1 [Q9UJS0]	9858,1514	9556,7472	3062,3011	518,97335	10367,241	9595,411	2720,304
1 [Q9UJS0]	17011,416	21222,223	8809,8113	1675,1025	17790,554	21553,732	8181,2125
1 [Q9UL25_	79258,21	122968,91	30210,168	7070,2351	82363,791	126794	24992,523
1 [Q9UL25_	46032,064	71279,844	19470,741	3748,1465	47839,966	73427,81	16617,778
1 [Q9UL25_	47548,477	77174,797	21091,2	4046,5059	49340,375	79645,884	18000,384
1 [O75915]	555539,3	826291,56	369153,38	109289,4	578173,55	845160,34	344712,69
1 [O75915]	237125,54	368522,34	124719,52	35010,276	246425,55	378906,21	111212,49
1 [O75915]	626421,22	893001,31	311028,41	91537,796	652707,42	914580,51	278784,68
1 [O75915]	25049,342	47372,113	12881,755	4224,1574	25850,226	49154,79	10898,488
1 [P62244_	6793,8708	15078,646	3886,4066	534,97378	6963,4297	15727,913	3271,3279
1 [P62244_	12522,483	26959,732	7169,3573	1174,9475	12852,918	28089,578	6078,3406
1 [P62244_	21380,598	38043,117	17499,558	14411,008	22119,69	39164,737	16004,012
1 [P62244_	75678,215	167407,17	44361,468	6884,6511	77579,609	174560,42	37589,07
1 [Q9POL0_	499187,83	500238,69	142863,54	56219,063	524608,21	503904,98	122295,17
1 [Q9POL0_	181834,69	174983,82	51212,51	17979,237	191249,21	175766,25	44199,363
1 [Q9POL0_	355598	334229,93	101998,95	39980,23	374181,53	335062,89	88705,22
1 [Q9POL0_	43980,359	28800,878	9870,1486	5844,8985	46546,303	27989,029	8726,0834
1 [P14314_	17258,025	27603,344	9542,4001	4327,7471	17918,37	28407,035	8472,4209
1 [P14314_	143531,15	205036,44	82125,196	39962,752	149551,88	209666,94	74758,712
1 [P14314_	682772,2	910976,5	272036,09	114565,82	712719,3	931676,79	234682,03
1 [P14314_	310972,95	443822,56	108762,92	50436,565	323981,72	456056,46	88869,864
1 [P62899]	152748,03	257748,7	104889,87	24794,3	158317,23	265272,94	96819,628
1 [P62899]	12486,198	27478,734	8368,9145	1500,3009	12803,633	28613,646	7328,11
1 [P62899]	182411,3	354200,31	93920,5	17496,489	188045,2	367914,77	79501,271
1 [P62899]	18900,968	26037,883	8947,9775	3044,937	19713,292	26630,598	7982,8637
1 [P62899]	23549,218	52600,297	16251,569	3011,8041	24131,563	54787,702	14271,187
1 [P46776_	54364,878	93152,391	24027,987	5250,8638	56308,038	96374,231	20163,175
1 [P46776_	147388,32	292210,53	78853,547	17604,25	151813,16	303678,3	66926,094
1 [P46776_	244444,53	472614,06	123894,77	27734,974	252036,91	490893,67	104353,57
1 [P46776_	89463,116	166949,88	44516,517	10038,695	92370,601	173184,6	37667,493
1 [P51572_	266129,7	332872,81	94579,03	36457,036	278272,09	339532,4	80801,634
1 [P51572_	35277,675	46331,648	17249,031	6751,3207	36842,876	47238,85	15582,367
1 [P51572_	514248,03	716561,94	249156,13	102059,42	536178,15	733159,13	222032,16
1 [P51572_	53884,456	72216,711	25259,419	9187,9807	56243,403	73753,375	22587,924
1 [O75340]	62778,477	128898,38	37575,858	6593,1441	64570,509	134008,6	32584,604
1 [O75340]	27712,552	59544,199	16296,863	2664,5524	28446,63	62021,145	13921,161
1 [Q969H8_	150840,61	344458,94	94146,143	26873,212	154402,39	359397,74	79884,95
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1	[Q01844_	214638,47	247750,25	118822,67	52945,788	224903,9	250088,26	111340,97
1	[Q01844_	268695,06	259350,53	101194,11	85670,991	282606,26	259754,78	90269,835
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1	[Q9UJ70_	1813,9397	3971,2732	1288,0551	124,9329	1860,5473	4132,1269	1147,8788
1	[Q9UJ70_	32938,713	88968,539	27840,494	3949,7572	33425,826	93095,446	24558,632
1	[P12004]	194162,8	261434,81	104261,67	28485,311	202645,29	266638,94	95817,578
1	[P12004]	216848,33	306425,38	98922,466	28453,397	226000,32	313961,6	87366,109
1	[P12004]	341134,39	530028,13	152733,06	33648,202	354499,41	545817,16	131902,1
1	[P12004]	26004,657	42950,84	12750,326	2371,6383	26969,477	44322,469	11105,091
1	[P35221_	8082,2123	23001,773	6237,1727	1558,741	8176,1857	24127,6	5288,2729
1	[P35221_	135380,72	196112,94	60059,823	22972,375	140989,99	201259,15	52194,287
1	[P35221_	299186,85	424855,75	122209,78	51114,836	311759,97	435885,24	104489,9
1	[P16152_	74557,199	154985,05	45574,008	10254,07	76645,194	161176,22	39502,349
1	[P16152_	36217,641	71853,836	26154,69	4491,2244	37308,268	74456,08	23754,243
1	[A2RRP1_	14378,8	28460,705	6685,9278	1356,1165	14810,828	29608,295	5460,4181
1	[A2RRP1_	3656,5605	8705,041	2033,7473	478,85105	3735,1182	9103,6181	1654,2094
1	[Q14498_	79738,201	94306,777	25512,046	7634,3542	83491,141	95958,209	21628,713
1	[Q14498_	157873,3	177493,17	48782,315	11614,286	165500,79	180079,35	41664,458
1	[Q14498_	74095,581	84795,289	23932,124	7625,5766	77644,053	86095,382	20490,206
1	[Q14498_	46312,998	57011,363	18292,602	5435,0133	48446,942	58037,261	16135,866
1	[Q99805_	24078,496	50918,629	8206,6619	1425,2414	24730,036	53198,069	5755,4949
1	[Q99805_	266671,75	303882,38	85438,385	17588,53	279470,26	308477,85	73499,048
1	[Q9Y2W2]	12888,531	13916,882	10054,686	2403,9963	13527,452	13885,594	9929,7501
1	[Q9Y2W2]	19807,471	16010,617	6493,5454	2473,4287	20899,124	15821,989	5964,7653
1	[P35613_	134651,45	215460,06	74002,901	16887,95	139801,43	221748,93	66341,222
1	[P35613_	1048157,3	760286,19	379320,3	127050,84	1107815,5	742182,8	359607,7
1	[P35613_	400203,97	343693,89	166086,42	52863,698	421848,96	340370,72	156838,95
1	[O75489_	46588,981	84273,281	21971,168	4213,9372	48159,621	87345,469	18512,849
1	[O75489_	27817,001	45605,445	14199,506	2637,1761	28856,7	47027,388	12500,473
1	[Q9BXP5_	15182,851	27072,264	6983,6924	1254,52	15703,003	28047,797	5871,377
1	[Q9BXP5_	40235,766	53521,07	14171,788	3867,4223	42002,859	54787,542	11956,449
1	[Q8N163]	5331,4852	14402,182	2614,0344	678,61068	5409,0738	15131,64	1930,1188
1	[Q8N163]	29099,782	50375,578	10279,497	3575,9526	30127,183	52225,15	7940,782
1	[O94905]	95320,081	127297,69	28962,094	7941,4698	99492,594	130487,59	23368,256
1	[O94905]	11016,86	14765,01	4348,3244	891,08426	11498,632	15105,427	3779,6287
1	[O43747_	11434,768	27715,807	8869,0336	1505,1612	11671,451	28920,43	7852,0954
1	[O43747_	20685,91	48718,258	11656,59	1798,2115	21141,77	50925,708	9592,7251

1 [P84103]	46629,643	70287,047	20586,101	7849,6231	48502,757	72282,196	17706,053
2 [Q16629_	90890,683	124275,56	40253,194	13591,062	94815,274	127140,66	35492,663
2 [Q16629_	172771,56	233493,28	82496,915	16593,579	180294,43	238524,28	74488,875
1 [O00629_	261401,42	423776,13	154484,24	19463,693	271288,07	436071,64	140715,59
1 [O00629_	7141,0204	9709,1035	2670,8772	546,70016	7450,2282	9945,6358	2283,4331
1 [O94826_	20993,799	30413,145	8771,2274	2029,9488	21863,267	31228,545	7574,2479
1 [O94826_	115977,35	179827,92	61355,939	14038,321	120535,11	184861,18	54936,244
1 [P60903_	287064,03	704300,25	189106,73	57752,999	292801,32	736314,8	159526,04
1 [P60903_	410365,51	1140155,6	304248,92	94163,372	415724,59	1195503,4	256106,46
1 [P60903_	611306,7	1518103,3	281481,97	68502,709	623053,61	1591660,5	210065,81
1 [P60903_	671513,36	1563805,5	387830,15	109447,61	686697,8	1633752,1	320451,74
1 [P60903_	29992,979	80153,766	41936,396	11308,338	30465,624	83306,952	39990,09
1 [P60903_	106831,61	211993,19	73160,437	27008,097	110045,04	219804,92	65165,52
1 [P10301_	18103,278	69933,641	13228,398	2542,2369	17917,774	73953,817	9971,672
1 [P10301_	25335,407	85100,594	15464,167	2948,6076	25348,174	89802,683	11461,541
1 [P11387_	37379,96	48792,895	14460,557	4649,7929	39042,425	49853,307	12516,311
1 [P11387_	35419,371	41248,141	10809,688	2405,2788	37099,88	41946,968	9124,4066
1 [Q96CW1]	40475,403	82889,156	23288,88	3780,5878	41634,823	86196,881	20029,414
1 [Q96CW1]	42346,242	80898,023	20467,884	3090,822	43681,817	84018,47	17136,18
1 [Q96CW1]	44714,168	72340,141	21099,642	3628,272	46405,105	74604,099	18315,81
1 [Q9HBRO_	103008,68	184308,9	113980,71	37229,087	106566,82	188825,95	110468,73
1 [Q9HBRO_	23506,454	31906,443	16671,23	7701,4296	24530,492	32426,652	15772,965
1 [Q16698_	27615,118	88776,516	18495,988	2783,3335	27715,621	93529,571	14523,286
1 [Q16698_	65132,5	116839	34869,866	7666,887	67351,95	120921,5	30348,804
2 [P35637_	268922,37	332224,94	108109,06	43861,726	281289,19	338217,92	95134,472
1 [Q92804]	137571,08	178112,22	69719,478	42633,666	143731,47	181368,51	62867,603
1 [P23634_	12115,193	43171,602	8677,3356	2049,5879	12068,909	45577,065	6688,2628
1 [P23634_	11152,568	34984,824	7599,0785	1852,4441	11211,888	36830,812	6026,0592
1 [P23634_	19450,811	70939,82	16342,84	5163,5138	19343,07	74854,416	13162,521
1 [P26639]	20623,518	34349,355	10419,244	2165,4443	21382,734	35450,185	9109,3875
1 [P26639]	30221,84	59358,387	18478,43	2467,8324	31142,653	61589,957	16299,965
1 [O15144]	168525,28	181607,77	63411,814	27822,766	176843,52	183374,7	56527,912
1 [O15144]	40237,58	63116,176	20262,549	4369,4741	41802,612	64953,678	17931,289
1 [O15144]	35455,332	63982,445	18195,994	4365,9602	36654,829	66260,746	15640,972
1 [Q9P0K7_	38614,09	33195,618	17342,854	14618,955	40702,608	32837,044	16143,129
1 [Q9P0K7_	12826,297	17462,059	6028,5826	3449,2639	13381,966	17849,38	5323,0673
1 [P39687]	81133,016	262749	72524,008	37901,138	81398,552	276284,63	60904,105
2 [Q92688_	57120,541	95549,539	34421,3	11107,917	59218,023	98452,331	30991,753

1 [P63173]	52298,851	102784,35	21235,278	8763,0535	53883,983	107000,4	16411,084
1 [P63173]	36677,439	65470,609	13317,553	4508,6997	37930,139	67948,448	10279,056
1 [P63173]	42318,134	82871,297	17536,858	6349,2252	43607,386	86247,275	13711,531
1 [P63173]	38490,938	73655,023	18088,802	7182,8288	39701,944	76518,819	14823,292
1 [Q9H0S4_	9768,7936	11310,945	2966,4303	403,9232	10233,682	11498,871	2515,58
1 [Q9H0S4_	18054,056	24774,164	8220,7072	2093,7391	18831,859	25342,952	7313,8169
1 [Q9Y3I0]	29108,9	52151,918	15130,083	4811,1279	30101,923	53986,221	13017,581
1 [Q9Y3I0]	25479,632	56742,234	20217,024	4720,937	26115,055	59010,308	18231,521
1 [P63167]	96783,344	101365,27	30902,002	8071,4338	101619,92	102322,3	27026,981
1 [P63167]	80331,732	95513,156	27647,014	5247,6382	84103,036	97153,704	23964,801
1 [P63167]	176869,03	180859,63	46713,059	9480,6154	185795,62	182572,75	39345,417
1 [Q12797]	41982,52	78669,211	19145,86	3634,2869	43338,834	81677,278	15819,502
1 [Q12797]	19239,375	49858,969	14402,022	2112,7186	19567,964	52160,946	12472,56
1 [Q9Y3U8_	87706,638	123904,22	37206,835	12323,313	91407,15	127040,74	32275,989
1 [Q9Y3U8_	65732,008	136512	32862,261	9706,095	67570,876	142197,42	26904,72
1 [Q9Y3U8_	121933,82	251596,95	62073,747	13683,829	125380,8	261975,52	51396,443
1 [Q8TAQ2_	7385,8535	16391,186	5005,1175	2049,0346	7570,7122	17071,954	4335,4482
1 [Q8TAQ2_	45754,944	49231,871	15613,179	5647,6229	48013,946	49757,142	13703,071
1 [P26196]	144868,7	199858,63	60004,472	15972,45	151083,17	204701,1	52223,345
1 [P26196]	37224,73	55129,242	15448,801	3053,0172	38740,508	56674,626	13268,982
1 [P26196]	25290,097	39438,23	13017,237	2472,0669	26278,905	40565,401	11600,295
1 [P16949]	207731,8	203728,18	113142,51	64564,629	218440,05	203166,85	107358,14
1 [P16949]	634041,88	631343,12	224492,16	99462,868	666443,76	634288,04	200833,27
1 [P16949]	187437,31	164687,58	106053,09	62614,098	197513,05	162520,88	102118,93
1 [P36957_	102969,79	149192,2	39732,429	5011,1685	107231,75	153298,89	33811,168
1 [P36957_	113108,18	148130,89	48566,819	17629,041	118131,24	151223,55	42884,357
1 [Q02880_	18867,079	41206,184	13224,908	4514,3135	19353,868	42877,549	11620,534
1 [Q02880_	44631,305	35009,44	9535,588	2413,2185	47110,72	34663,484	8138,4481
1 [P42892_	4370,2052	10512,925	3186,1939	797,6343	4462,2409	10973,577	2776,5348
1 [P42892_	23621,575	37343,848	13484,518	3663,6856	24535,093	38394,614	12177,709
1 [P05161_	136827,55	266028,66	81209,738	26062,472	141053,11	275997,33	70673,268
1 [P05161_	84322,32	262223,56	82875,669	30571,603	84836,325	275176,97	72433,729
1 [P05161_	58633,398	162898,92	49578,414	16744,792	59403,194	170609,23	43045,37
1 [Q15417]	47770,555	111530,77	43006,82	5749,6594	48854,607	116029,26	39513,864
1 [Q15417]	23753,938	54358,082	18387,366	2906,4945	24314,694	56603,983	16475,892
1 [Q15417]	79129,637	132179,73	40397,861	8624,7262	82034,625	136420,81	35368,698
1 [Q15417]	9278,0866	27146,977	11011,357	1448,7757	9372,5144	28373,889	10199,062
1 [Q15417]	17885,718	47671,066	19762,718	3253,266	18166,933	49710,487	18341,96

1	[P49821_	19491,013	36938,363	11826,809	2802,1393	20113,676	38273,153	10443,649
1	[P49821_	23574,154	53408,145	14703,71	2966,4828	24139,95	55708,821	12553,034
1	[P25786]	45146,982	120558,62	37093,73	7052,0168	45843,69	126139,08	32523,572
1	[P25786]	84375,635	175366,03	48293,014	14858,629	86737,091	182477,3	41021,373
1	[O95816]	88141,363	96137,07	28854,288	11314,793	92464,388	97292,605	24979,958
1	[O95816]	122194,34	124031,2	41941,374	16132,744	128387,46	124829,76	37264,681
1	[Q7L014]	68194,122	81422,195	23081,435	4816,3437	71388,04	82854,798	19888,435
1	[Q7L014]	85806,531	52032,144	30337,613	11869,991	90909,217	49756,078	29220,552
1	[Q7L014]	40573,75	28048,064	16046,872	5626,758	42913,665	27192,54	15445,551
1	[P46939]	4784,6618	12024,07	2607,2489	748,22121	4873,8141	12598,116	2062,7802
1	[P46939]	11352,262	20741,101	4373,316	959,91038	11729,912	21537,985	3442,8547
1	[Q13425]	10959,792	23191,293	5868,9117	1592,1398	11257,408	24161,054	4881,7934
1	[Q13425]	19266,256	41505,719	9953,4913	2573,5013	19773,357	43281,276	8154,3683
1	[Q13425]	38251,093	75596,516	17509,308	3720,7217	39402,702	78649,104	14229,198
1	[P28370_	23103,612	30341,793	8318,533	2054,7324	24126,789	31031,846	7091,6623
1	[P28370_	36435,104	49872,172	14657,051	3927,8422	38006,234	51072,646	12693,041
1	[Q8WUJ3_	3056,1603	46036,52	5161,0317	1697,9712	2291,4071	49362,026	2720,7484
1	[Q8WUJ3_	16388,176	85710,414	13383,247	3403,2066	15739,917	91098,473	9145,5979
1	[Q9H3N1_	45707,937	46916,078	14796,919	2619,7962	48012,776	47284,676	13092,227
1	[Q9H3N1_	199764,54	284412,34	89715,669	26892,645	208148,89	291571,22	78799,021
1	[P62318]	60267,665	91981,32	25418,593	4110,5958	62663,454	94688,279	21792,965
1	[P62318]	112345,68	204326,22	64734,012	12215,613	116116,92	211442,81	57176,283
1	[P62318]	47799,301	108948,51	28935,101	5800,5374	48931,83	113694,46	24473,811
2	[P08727,	69830,796	120016,22	50761,353	10716,736	72331,754	123539,66	47190,712
4	[P13645,	451944,03	446936,27	141966,96	75470,67	475094,64	449374,46	123652,5
4	[P13645,	91560,734	80761,94	29345,135	15175,245	96461,444	80453,357	26277,709
1	[P13473_	40884,143	80000,953	20465,649	4885,9132	42133,319	83143,093	17108,517
1	[P13473_	27828,088	53179,035	24150,309	7498,5648	28712,29	54885,35	22577,409
1	[Q99733_	148126,52	70422,565	26707,012	9125,1915	157335,44	65769,121	24394,745
1	[Q99733_	146909,56	72835,758	25236,838	7223,4867	155977,77	68500,294	22741,744
1	[P46783]	47223,719	79559,403	22974,584	5018,955	48942,133	82181,309	19847,425
1	[P46783]	5397,5611	11333,368	3321,4431	908,0292	5546,3022	11789,966	2869,6583
1	[P46783]	1153,0468	2326,4485	614,11777	172,85141	1186,7927	2419,4983	516,62705
1	[P46783]	7009,3688	14362,843	4150,3049	1236,1109	7210,0445	14932,663	3569,6078
1	[P02042_	1040089,7	314421,84	559305,2	40103,779	1108859,1	255271,05	584638,9
1	[P02042_	34821,578	14222,506	31407,09	3600,8173	37052,709	12127,605	32945,871

1 [Q13242]	46443,25	26231,493	8518,7298	2689,3702	49241,513	25100,198	7561,7683
1 [Q13242]	161984,14	142991,08	58344,86	19932,12	170655,98	142244,21	53722,391
1 [Q13242]	139789,09	123569,96	47105,056	21738,891	147266,92	123045,34	42651,038
1 [Q6P1M0]	2970,4137	4858,6709	1026,1376	204,11055	3081,3634	5025,4795	809,64025
1 [Q6P1M0]	167761,38	222124,59	95050,277	43695,52	175174,38	226163,03	87554,725
1 [P17655_	177656,99	292223,34	97802,283	39234,526	184281,08	301155,73	86494,984
1 [P17655_	25851,627	50026,563	13032,657	3310,5896	26653,569	51965,667	10941,492
1 [P23526_	40952,05	79547,625	21662,545	3813,0939	42216,648	82610,11	18474,64
1 [P23526_	35493,781	77161,516	18602,663	3045,7072	36413,218	80479,389	15340,379
1 [P61353]	28518,906	53557,02	15826,988	3295,1509	29439,564	55518,497	13749,68
1 [P61353]	567589,15	1066021,9	215222,39	51904,018	585845,47	1108300	166505,01
1 [P48735_	18863,151	70780,945	17830,393	3767,6532	18717,321	74671,71	14837,692
1 [P48735_	19360,391	60143,961	17824,264	2931,0569	19478,991	63151,193	15510,876
1 [Q8TCS8_	106352,39	141679,08	41966,391	7811,619	111021,62	144896,91	36561,453
1 [Q8TCS8_	15831,937	20018,889	6441,8022	1120,1074	16550,163	20405,744	5719,3646
1 [Q08945_	94371,18	79181,842	16930,02	4548,7723	99500,974	78967,902	13430,225
1 [Q08945_	139493,84	79386,444	29275,532	13706,481	147888	75918,199	26416,5
1 [O43854_	50901,532	242399,69	44385,541	7017,4193	49401,481	257135,48	33041,081
1 [O43854_	37547,708	169277,38	33667,229	4561,6022	36646,5	179353,93	25975,401
1 [O43854_	70084,912	259371,33	58170,927	9430,6156	69615,471	273798,83	46822,868
1 [O00410_	10689,539	23224,84	6999,4017	1042,7665	10967,635	24177,731	6123,731
1 [O00410_	105651,49	148010,52	53551,88	20578,414	110141,47	151407,29	48136,578
1 [Q12841_	55027,052	84561,563	56474,947	19874,293	57223,461	86004,707	55087,475
1 [Q12841_	13213,803	33210,512	19238,054	6394,5815	13467,679	34406,915	18507,552
1 [Q00325_	18588,953	25233,045	8435,1482	1327,6774	19395,695	25797,416	7551,4133
1 [Q00325_	96937,425	156596,05	44093,156	8923,788	100607,2	161539,22	37894,871
1 [Q00325_	87734,245	131698,22	37255,279	6487,4893	91269,382	135454,35	32108,876
1 [Q86UX6]	108281,29	132483,31	57569,613	12575,538	113297,48	134337,17	53762,243
1 [Q86UX6]	1072,0028	3332,4197	726,86993	263,22512	1078,3547	3507,5601	573,54763
1 [P41223]	53572,213	100247,81	26082,123	4393,8905	55306,998	104021,61	21988,055
1 [P41223]	11382,679	16670,588	4487,8053	866,61413	11850,043	17135,805	3816,6094
1 [P20908_	21353,995	102779,02	34309,011	13613,47	20711,385	108541,9	30275,086
1 [P20908_	78733,082	133046,11	44871,117	11407,368	81593,673	137237,43	40025,77
1 [P52943]	85585,144	150289,13	45894,82	13284,21	88571,155	155392,43	40017,45
1 [P52943]	57106,422	162068,06	34492,088	17037,512	57773,991	170298,08	26791,297
1 [Q9BVK6_	165737,23	323331,78	72393,786	15168,875	170815,39	336332,74	58200,676

1	[Q9BVK6_	203772,14	386949,44	83228,477	20168,755	210239,31	402274	65891,59
1	[Q9BVK6_	224581,99	404894,5	78423,86	18573,959	232164,43	420486,87	59717,047
1	[Q9BVK6_	180427	331816,91	70796,035	17516,04	186383,42	344614,56	55881,998
1	[Q9BVK6_	239586,13	495440,94	128201,76	45097,254	246339,76	515722,15	106868,47
1	[Q12904]	323310,16	297047,51	143106,74	62198,744	340385,51	295630,46	134335,56
1	[Q12904]	269778,56	248228,44	127903,03	51299,621	284024,34	246799,84	121265,21
1	[Q12904]	69667,176	101335,09	27018,458	5577,9712	72542,324	104141,26	22904,918
1	[P07942]	33707,218	42571,773	19969,64	2602,7053	35241,467	43188,751	18923,965
1	[P07942]	60519,982	73579,852	31558,769	6073,561	63333,244	74598,416	29450,932
1	[Q07666_	80740,212	145172,98	47844,756	10362,981	83487,269	150111,14	42551,354
1	[Q07666_	280443,2	292039,28	80924,729	26650,244	294488,37	294957,83	68969,886
2	[P08727,	69830,796	120016,22	50761,353	10716,736	72331,754	123539,66	47190,712
1	[P05783_	46687,727	71971,336	28937,679	7028,2562	48534,246	73826,806	26657,396
1	[P37235_	645562,25	1214494,8	271427,72	88503,463	666300,05	1261886,1	216748,78
1	[P37235_	32970,06	79667,391	20162,592	7758,2525	33654,274	83297,074	16666,434
1	[P37235_	30537,914	73772,922	16965,162	7437,1621	31170,928	77188,927	13580,749
1	[P55265_	49913,445	35802,629	19271,392	4702,1802	52763,808	34868,871	18511,487
1	[P55265_	30269,52	55332,914	18248,221	6715,3858	31280,086	57247,437	16111,612
1	[Q9Y2H6_	83601,775	94876,188	44308,401	8292,367	87633,803	95718,173	41866,795
1	[Q9Y2H6_	59652,041	71327,539	22864,407	4296,029	62445,366	72502,394	20274,755
1	[Q9P035]	199599,54	255089,98	67905,858	14427,545	208587,84	260615,2	57559,741
1	[Q9P035]	22729,997	28913,109	8335,1519	1868,266	23756,876	29511,947	7203,4889
1	[Q9NSK0_	22571,318	47380,594	12489,715	1852,2312	23192,701	49333,896	10573,482
1	[Q9NSK0_	20164,164	59232,746	21695,919	6008,6926	20362,907	61991,009	19614,79
1	[Q04637_	143372,94	221280,88	74094,644	20803,021	149028,2	227478,58	65931,823
1	[Q04637_	92510,453	131165,72	44283,21	8900,7478	96406,706	134347,88	39632,144
1	[P36776_	50308,107	81960,75	31214,323	7727,8299	52203,134	84312,138	28486,662
1	[P36776_	63157,493	112337,21	46052,013	10830,538	65338,117	115823,14	42555,688
1	[P36776_	31140,611	53541,609	15842,55	4146,2956	32251,067	55334,634	13734,395
1	[Q13561_	126400,89	181939,34	55958,895	20930,853	131663,06	186654,56	48698,518
1	[Q13561_	85463,109	84419,394	30888,329	11557,183	89845,61	84741,104	27870,349
1	[P11413_	14447,94	33239,129	12527,39	2084,6027	14786,08	34575,834	11447,579
1	[P11413_	75444,107	185686,16	57829,077	20288,777	76944,549	193884,62	50447,347
1	[P11413_	25718,825	62853,957	20262,124	6502,9698	26240,267	65595,204	17834,235
1	[Q9Y6M1_	49412,479	68968,883	28962,038	9748,8201	51520,405	70410,233	26751,696
1	[Q9Y6M1_	57012,075	75375,391	25163,334	6084,6276	59529,141	76968,365	22431,477
1	[O95573]	200115,62	389896,88	114685,07	23912,156	206275,49	404671,49	99512,214

1 [O95573]	7177,0209	14714,197	5360,5446	1984,9034	7383,0415	15262,419	4823,0703
1 [Q06323]	19746,87	49824,535	17003,076	5402,2856	20114,535	52007,853	15141,977
1 [Q06323]	36253,979	89447,109	27437,365	8170,6961	36970,115	93415,273	23917,038
1 [Q06323]	53251,351	139715,28	41356,791	11209,197	54124,949	146176,76	35800,693
1 [Q13557_	200662,24	485253,78	94782,042	18641,7	204800,4	508274,52	72485,467
1 [Q13557_	53024,79	95587,342	28183,977	7976,4841	54821,468	98955,388	24383,986
1 [Q9BS26_	111677,7	245587,48	73367,989	17469,783	114519,86	255772,42	63777,012
1 [Q9BS26_	103042,32	186468,73	52388,103	9471,8288	106516,9	193146,97	45030,489
1 [Q96AC1_	22875,221	47823,594	15597,564	4884,7773	23511,039	49692,952	13772,051
1 [Q96AC1_	5813,5109	12051,14	3776,8337	996,40426	5977,1856	12524,002	3314,7518
1 [O15042_	46891,114	48646,008	23965,05	12150,497	49250,164	48782,733	22477,589
1 [O15042_	106548,75	66256,205	33248,527	14157,729	112846,71	63705,004	31434,279
1 [Q6NUQ4]	31760,188	101803,87	19641,412	4033,7449	31881,126	107299,53	14924,445
1 [Q6NUQ4]	65268,94	143462,13	35962,021	8386,0393	66927,049	149632,89	29887,838
1 [P56385_	138696,48	186389,25	62816,756	13052,88	144756,07	190454,12	56191,397
1 [P56385_	11930,388	13929,83	5295,4469	1114,0179	12496,728	14114,554	4844,4464
1 [Q14534]	1881,0293	6205,5991	869,02117	256,65725	1884,218	6554,7351	554,77041
1 [Q14534]	79325,507	193970	72299,426	27248,772	80937,793	202117,29	65276,28
1 [P78357_	593169,69	84195,722		5623,3933			
1 [P78357_	7954,3388	18199,834	4615,2919	1131,221	8141,1801	19001,7	3845,5822
1 [Q16851_	47900,791	83657,445	32432,754	5870,4595	49586,196	86258,075	29776,42
1 [Q16851_	5467,1912	13668,895	4044,0618	508,48499	5571,2614	14284,599	3526,0537
1 [Q12849]	47649,602	65477,723	33644,968	7767,1009	49708,155	66599,484	32102,146
1 [Q12849]	59895,093	96211,492	44699,352	13729,868	62185,475	98658,101	41940,329
1 [Q8TF01]	95123,446	196753,47	65482,303	19278,846	97813,234	204337,22	58113,167
1 [Q8TF01]	127474,37	145260,5	49488,722	17014,449	133597,88	147178,7	44100,027
1 [Q07157_	33192,871	50610,234	12395,471	6893,9027	34512,372	52150,166	10073,986
1 [Q07157_	9545,0114	31853,197	7248,0081	1345,8731	9555,207	33561,986	5855,8864
1 [O60762_	166967,51	219536,8	68283,173	15713,418	174361,59	224280,04	60015,006
1 [O60762_	7499,7081	11938,302	4604,7258	1642,3126	7788,1925	12268,089	4190,0079
1 [Q99459]	61578,763	72427,219	24650,547	5863,6367	64488,847	73509,935	22071,97
1 [Q99459]	66886,211	43163,476	17274,772	8709,2714	70803,703	41804,323	15761,712

<i>i117</i>	<i>i(116/114)</i>	<i>i(117/115)</i>	<i>N116</i>	<i>N114</i>	<i>N(116/114)</i>	<i>N117</i>	<i>N115</i>	<i>N(117/115)</i>
6902,5896	0,3185235	0,0992131	30822,67	40312,22	0,7645987	99198,351	69573,396	1,4258087
18019,486	0,3797616	0,0893591	113663,04	124685,57	0,9115974	258961,26	201652,55	1,2841953
9660,2279	0,4217094	0,0786384	68149,498	67322,041	1,012291	138828,86	122843,6	1,1301269
34836,741	0,2567364	0,1151469	158595,93	257343,07	0,6162821	500645,04	302541,75	1,6547965
57889,74	0,2803585	0,1100778	305524,94	453984,31	0,6729857	831943,82	525898,4	1,5819478
1637,7836	0,4440934	0,037894	15291,284	14344,241	1,0660226	23536,882	43220,118	0,5445816
56,553625	0,0728594	0,1410283	713,33361	4078,6381	0,174895	812,74227	401,00912	2,0267426
234,06469	0,3382798	0,1441254	980,42956	1207,3921	0,8120225	3363,7855	1624,0353	2,0712515
15422,938	0,4334964	0,135197	85648,688	82308,2	1,0405851	221645,81	114077,55	1,9429398
45776,947	0,3954209	0,1358807	224274,96	236281,18	0,9491867	657868,7	336890,72	1,9527659
21857,898	0,370705	0,1197184	117011,41	131494,53	0,8898576	314123,77	182577,6	1,7204946
29687,69	0,3921019	0,0564724	329371,8	349941,45	0,9412197	426647,11	525702,93	0,8115745
449386,55	0,4349097	0,1368247	2549043,5	2441665	1,0439776	6458214,5	3284397,5	1,9663316
62877,3	0,3707371	0,0771828	483228,45	542993,24	0,8899346	903620,94	814654,28	1,1092079
47560,028	0,4092093	0,109767	283227,96	288335,81	0,9822851	683493,68	433281,7	1,577481
19705,952	0,3830486	0,2115634	77717,442	84522,535	0,9194878	283197,77	93144,414	3,040416
17902,031	0,3700617	0,2168283	62635,316	70510,381	0,8883134	257273,3	82563,157	3,1160788
19695,268	0,3633992	0,2036447	71587,702	82065,834	0,8723204	283044,22	96713,882	2,9266142
412,15805	0,2398539	0,1797172	1739,4451	3021,147	0,5757565	5923,1971	2293,3699	2,5827483
450,61349	0,4768713	0,2175659	1795,8279	1568,814	1,1447042	6475,8471	2071,1582	3,1266791
7888,4024	0,5067982	0,0636627	63534,241	52225,271	1,2165421	113365,64	123909,33	0,914908
9625,4204	0,4887689	0,0758341	64684,931	55132,476	1,1732637	138328,64	126927,35	1,0898253
8687,5556	0,4524288	0,1029357	60771,905	55957,793	1,0860311	124850,42	84397,901	1,4793071
23280,743	0,4061454	0,0610228	199317,17	204442,46	0,9749304	334571,73	381508,89	0,8769697
68270,747	0,4767501	0,1099626	482875,19	421941,32	1,1444131	981131,13	620853,98	1,5802929
68018,687	0,5428377	0,0843827	545117,43	418338,62	1,3030531	977508,73	806073,63	1,2126792
55598,158	0,3995783	0,200759	224320,61	233870,4	0,9591663	799011,09	276939,82	2,8851433
58115,972	0,4250873	0,1965575	271265,01	265841,99	1,0203994	835195,04	295669,03	2,8247634
63395,784	0,2699056	0,0945561	300784,33	464249,27	0,647894	911072,16	670456,97	1,3588824
132582,85	0,2847037	0,0889393	692307,05	1013009,6	0,6834161	1905371,9	1490711	1,2781632
9320,7431	0,2194705	0,0806766	57699,727	109523,06	0,5268272	133950,07	115532,11	1,1594186
41557,214	0,4388865	0,186432	141742,66	134541,52	1,0535235	597226,17	222908,19	2,6792473
44707,706	0,321186	0,0994297	226663,03	293989,63	0,7709899	642502,45	449641,34	1,4289221
11589,503	0,398666	0,1226772	58754,409	61395,87	0,9569766	166554,82	94471,526	1,7630161
49512,864	0,6026377	0,0482717	538972,09	372578,59	1,4465997	711558,24	1025711,3	0,6937218
61833,359								
48358,145	0,3000845	0,122438	174671,16	242485,4	0,7203368	694963,57	394960,17	1,7595789
44972	0,3334691	0,1045487	197983,21	247332,2	0,8004749	646300,67	430153,7	1,5024877
66253,551	0,494095	0,1275172	349605,5	294764,87	1,1860487	952141,64	519565,46	1,832573
32120,615	0,3929211	0,1599459	120485,36	127742,92	0,9431862	461611,1	200821,79	2,2986107
26724,617	0,6294292	0,1913714	171972,43	113820,34	1,5109112	384064,25	139647,88	2,7502333
39505,331	0,3513304	0,3612316	113907,96	135066,06	0,8433499	567738,18	109362,88	5,1913245
34876,761	0,3173894	0,395895	86672,342	113761,71	0,7618763	501220,18	88095,978	5,6894786
84870,953	0,3877253	0,1454928	436117,77	468584,12	0,9307139	1219695,7	583334,32	2,0909033
162544,41	0,2976745	0,1544545	623980,23	873246,93	0,7145519	2335954,8	1052377,5	2,2196927
113362,17	0,3213798	0,1027808	723713,9	938115,33	0,7714551	1629148	1102950,4	1,4770819
56275,318	0,3310927	0,1130509	332135,35	417901,04	0,7947703	808742,67	497787,5	1,6246745
42747,335	0,3739493	0,0885198	326124,11	363310,61	0,8976454	614329,61	482912,56	1,2721343
37077,497	0,4166602	0,3069689	105236,43	105218,48	1,0001706	532847,35	120785,83	4,4115054
22743,666	0,2665133	0,1186563	133768,57	209094,77	0,6397509	326853,29	191676,91	1,7052304
24198,094	0,4062034	0,102008	183126,77	187808,94	0,9750695	347755,14	237217,63	1,4659751

100021,13	0,2792717	0,0669088	642810,77	958879,75	0,6703768	1437421,6	1494886,6	0,9615589
78522,006	0,2606172	0,0565473	554350,33	886113,22	0,6255976	1128453,8	1388606,8	0,8126518
53377,043	0,2868819	0,0678712	380463,26	552481,2	0,6886447	767091,04	786445,56	0,9753899
76963,732	0,2913377	0,0691988	521798,38	746129,15	0,6993406	1106059,6	1112212,5	0,9944679

5901,9938

8300,5661	0,3303822	0,0727539	36823,456	46431,829	0,793065	119288,92	114091,08	1,0455587
7085,5615	0,3668767	0,0287236	75860,742	86140,015	0,8806678	101827,87	246680,68	0,4127922
64279,677	0,2880785	0,172024	229170,84	331402,96	0,6915172	923774,75	373666,88	2,4721879
45891,951	0,2972885	0,0694296	258246,84	361880,16	0,7136253	659521,44	660985,04	0,9977857
38241,925	0,3845238	0,0743157	248624,71	269357,44	0,9230289	549581,55	514587,39	1,0680043
92200,353	0,2562907	0,184936	348603,13	566638,98	0,6152121	1325027,8	498552,68	2,6577488
4324,6068	0,2819755	0,0792301	23741,288	35075,26	0,6768671	62149,698	54582,877	1,1386299
4212,0896	0,3403399	0,0797769	25563,015	31290,111	0,8169678	60532,694	52798,347	1,1464884
5237,2469	0,2501738	0,0680917	28999,752	48290,355	0,6005289	75265,413	76914,636	0,9785578
2871,4769	0,4916467	0,075567	23309,09	19750,591	1,1801718	41266,508	37999,092	1,0859867

6445,9728

128,86016

1885,0507

8930,7863

2618,43

590,5154	0,5204839	0,0439777	6038,903	4833,4658	1,2493939	8486,4025	13427,617	0,6320111
462,82489	0,4932043	0,0407014	4509,0275	3808,5877	1,1839106	6651,3394	11371,226	0,5849272
50,694461	0,4200206	0,0357412	527,18722	522,88018	1,0082372	728,53917	1418,3749	0,5136436
147,57495	0,4901039	0,0413838	1561,1473	1326,9777	1,1764684	2120,8261	3566,0111	0,5947334
15185,794	0,4483911	0,1107434	93868,701	87211,104	1,0763389	218237,77	137126,01	1,5915126
30180,256	0,2976629	0,1210265	126777,27	177429	0,7145239	433725,87	249368,94	1,7392938
35348,631	0,6118863	0,0846324	398868,72	271560,86	1,4688005	508001,51	417672,62	1,2162672
4512,9652	0,2341412	0,0924621	17260,092	30709,536	0,5620434	64856,631	48808,816	1,3287893
20777,098	0,2916809	0,120657	120283,08	171792,59	0,7001645	298591,4	172199,63	1,733984
49500,992	0,2030767	0,0685616	254866,08	522829,15	0,4874749	711387,62	721992,86	0,9853112
7055,4508	0,3574086	0,1071342	38110,539	44420,966	0,8579403	101395,15	65856,212	1,5396444
1798,0997	0,3608627	0,0345002	20598,246	23779,14	0,8662317	25840,813	52118,588	0,495808
1071,1279	0,4107642	0,0342155	9090,5073	9219,4176	0,9860175	15393,37	31305,328	0,4917173
87035,546	0,2894006	0,0606463	543857,19	782876,65	0,6946908	1250803,4	1435134	0,8715586
4413,4337	0,3781627	0,1591703	17497,743	19275,747	0,9077595	63426,246	27727,752	2,2874644
191964,12	0,4298101	0,1875713	840030,12	814190,74	1,0317363	2758750,7	1023419,3	2,6956212
16672,597	0,3423312	0,0591424	110335,9	134269,8	0,8217477	239604,88	281905,8	0,8499466
27465,425	0,3919365	0,1231724	115577,99	122847,79	0,9408227	394710,54	222983,54	1,7701331
8027,4689	0,2698474	0,0957191	38210,625	58989,389	0,6477542	115364,19	83864,843	1,3755966
22360,19	0,298321	0,1044358	100706,73	140631,51	0,7161036	321342,29	214104,59	1,500866
2095,4847	0,1416907	0,0406211	11782,746	34642,813	0,3401209	30114,586	51586,101	0,5837733
11982,66	0,2747811	0,0717022	73983,066	112163,98	0,6595974	172204,95	167117,05	1,0304451
3274,2858	0,3533788	0,0591016	27373,628	32270,06	0,848267	47055,347	55400,99	0,8493593
13422,703	0,4452545	0,0596684	105396,83	98611,402	1,0688098	192900,07	224954,93	0,8575054
5298,6672	0,4471722	0,0560786	43780,174	40785,95	1,0734131	76148,095	94486,519	0,8059149
1969,0663	0,2209771	0,0345163	13553,818	25551,849	0,5304437	28297,804	57047,413	0,4960401
3661,8756	0,2567881	0,0845451	19157,777	31079,794	0,6164062	52625,469	43312,712	1,2150121
25770,695	0,3575175	0,0992389	125318,23	146024,2	0,8582018	370355,27	259683,28	1,4261806
44774,033	0,370988	0,0975093	226621,22	254477,07	0,8905369	643455,65	459176,92	1,401324
16364,877	0,5417846	0,0728597	130720,58	100513,69	1,3005251	235182,58	224608,16	1,0470794
27046,219	0,2550092	0,1385113	98806,999	161413,46	0,6121361	388686,06	195263,61	1,9905709
29551,775	0,410005	0,1529409	165505,87	168163,68	0,9841951	424693,85	193223,5	2,197941

871425,55	0,5881848	0,3802344	2946239,1	2086710,2	1,4119062	12523413	2291811,4	5,4644167
485015,52	0,5636145	0,3920037	1668554,5	1233292,6	1,3529267	6970244,9	1237273	5,6335547
40756,77	0,382728	0,2368609	235827,84	256692,23	0,9187182	585722,83	172070,51	3,40397
252980,31	0,5911911	0,3512169	907240,93	639297,04	1,4191227	3635625,3	720296,4	5,0474017
175455,43	0,4338821	0,1224056	884876,22	849608,24	1,0415109	2521501,3	1433393,3	1,7591134
169731,73	0,4168014	0,1274963	933018,97	932543,7	1,0005097	2439245,1	1331267,7	1,8322724
78879,452	0,3768783	0,1143324	287429,51	317715,31	0,9046763	1133590,7	689913,56	1,643091
35672,946	0,2054263	0,1451336	180091,53	365212,19	0,4931148	512662,3	245793,82	2,0857412
1500,5362	0,2152799	0,1095925	6319,6344	12229,152	0,516768	21564,474	13691,955	1,5749741
32132,788	0,4030292	0,1245763	173854,96	179704,31	0,9674502	461786,06	257936,67	1,7903079
3915,4996	0,3073292	0,107776	19565,568	26521,405	0,7377274	56270,346	36329,974	1,5488683
5015,3278	0,2411027	0,1023003	23632,207	40832,887	0,5787542	72076,174	49025,524	1,4701765
71959,406	0,2615394	0,0979556	354636,96	564878,14	0,6278114	1034141,5	734612,37	1,4077377
56120,812	0,5074914	0,0887196	407059,92	334146,98	1,2182062	806522,24	632563,77	1,2750054
56509,672	0,5745998	0,0990089	402772,62	292013,17	1,3792961	812110,61	570753,43	1,4228747
19426,362	0,608062	0,0698402	265913,94	182180,21	1,4596203	279179,73	278154,41	1,0036862
72408,085	0,5368609	0,0581242	586302,6	454954,49	1,288706	1040589,6	1245746,8	0,8353138
84800,916	0,4720858	0,0484833	750705,13	662455,02	1,1332168	1218689,1	1749074,2	0,6967624
28303,202	0,5540489	0,0473155	306842,19	230714,51	1,3299649	406750,38	598180,08	0,6799798
29262,559	0,5508235	0,082447	232448,75	175801,55	1,3222225	420537,48	354925,54	1,1848611
63187,298	0,5392562	0,0560161	565098,89	436553,23	1,2944559	908075,97	1128019,9	0,8050177
3816,7925	0,3048926	0,046036	30213,69	41282,389	0,7318784	54851,808	82908,921	0,6615912
13298,361	0,438717	0,0444402	149754,54	142201,28	1,0531167	191113,12	299241,44	0,6386586
2506,846	0,3178584	0,0784059	11614,331	15221,887	0,763002	36026,332	31972,667	1,1267853
3814,0644	0,2754714	0,0790523	21285,925	32190,221	0,6612544	54812,602	48247,362	1,1360746
230859,26	0,5506653	0,2038482	1009772	763912,39	1,3218427	3317719,7	1132505,9	2,9295386
31563,499	0,3764611	0,1300302	135244,57	149660,67	0,9036748	453604,69	242739,75	1,8686873
186716,09	0,247514	0,1096283	859669,16	1446903,3	0,5941441	2683330,3	1703174,3	1,5754878
58227,627	0,2133106	0,0994678	261518,33	510737,3	0,5120408	836799,65	585391,77	1,4294694
68503,974	0,3178417	0,129627	321959,51	421986,32	0,762962	984482,88	528470,04	1,8628925
29368,039	0,2846064	0,0866402	159521,47	233497,63	0,6831824	422053,35	338965,5	1,2451219
10288,974	0,270425	0,0753381	67438,58	103889	0,6491407	147864,69	136570,71	1,0826969
27016,223	0,2512137	0,0907413	125095,17	207446,07	0,603025	388254,97	297727,94	1,3040596
13161,893	0,2771595	0,0975483	64201,652	96499,33	0,6653067	189151,92	134926,98	1,4018836
2675,315	0,2401824	0,0801314	13967,422	24226,077	0,5765449	38447,431	33386,608	1,1515824
8594,2003	0,2742295	0,0853978	44186,175	67124,359	0,6582733	123508,79	100637,24	1,2272672

81009,523	0,3413556	0,4487376	275807,21	336594,1	0,819406	1164202,4	180527,6	6,4488883
249257,95	0,2404424	0,5790271	889261,72	1540730	0,5771691	3582130,7	430477,16	8,3213025
57814,486	0,2810161	0,5005614	204434,61	303061,75	0,6745642	830862,32	115499,29	7,1936573
57256,794	0,2562299	0,2868056	234364,97	381040,23	0,6150662	822847,63	199636,26	4,1217344
20821,388	0,2750239	0,1100174	101197,77	153288,08	0,6601803	299227,89	189255,36	1,5810801
12388,888	0,2680765	0,1257515	49146,578	76373,456	0,6435034	178042,93	98518,815	1,8071972
12100,408	0,3182246	0,2877623	32865,985	43024,998	0,7638812	173897,12	42050,003	4,1354842
1764,3503	0,225597	0,0588247	11276,458	20823,193	0,5415336	25355,793	29993,367	0,84538
3589,6754	0,3924089	0,0572598	29291,171	31096,091	0,9419567	51587,868	62690,99	0,8228913
89045,832	0,3149624	0,37834	379479,32	501923,32	0,7560504	1279693,6	235359,28	5,437192
33424,317	0,2667814	0,3780702	95925,511	149791,26	0,6403946	480346,85	88407,707	5,4333142
6348,5852	0,2478677	0,0569462	37521,193	63061,542	0,5949933	91236,655	111484	0,8183834
27608,154	0,2950267	0,0838438	136462,76	192690,68	0,708196	396761,73	329280,73	1,2049345
70802,844	0,3214307	0,2462222	360721,22	467511,49	0,7715772	1017520,3	287556,67	3,5385038
43038,004	0,4009466	0,1215349	246508,94	256126,24	0,9624509	618506,86	354120,67	1,7465992

1759,9774	0,3336686	0,0546995	14593,407	18220,037	0,8009538	25292,95	32175,377	0,7860965
15139,641	0,4019006	0,0715179	106315,08	110200,63	0,9647411	217574,5	211690,2	1,0277967
64782,438	0,336518	0,0957825	348337,33	431220,77	0,8077935	931000,01	676349,65	1,376507
67713,947	0,2693967	0,4820697	219666,61	339687,58	0,6466725	973129,25	140465,06	6,9279095
37494,217	0,2832343	0,4818547	116329,93	171101,39	0,6798889	538836,11	77812,287	6,9248204
17917,016	0,2974661	0,3852118	63211,946	88525,764	0,7140514	257488,64	46512,118	5,5359475
23802,835	0,3467203	0,4320718	73955,735	88858,816	0,8322836	342074,81	55089,994	6,2093818
8681,702	0,2923783	0,0940752	32651,591	46522,935	0,7018386	124766,29	92284,705	1,3519715
4729,7973	0,6423501	0,0593948	67802,007	43972,249	1,5419272	67972,763	79633,186	0,8535733
20548,049	0,3435003	0,288342	76765,722	93099,673	0,8245542	295299,69	71262,775	4,1438141
30272,154	0,2943326	0,3666209	118217,04	167320,69	0,7065297	435046,55	82570,735	5,2687741
5062,1876	0,3213923	0,1162899	24740,397	32068,533	0,7714852	72749,604	43530,758	1,671223
7933,6786	0,2630504	0,0557269	60251,999	95420,236	0,6314384	114016,32	142367,23	0,8008607
5574,3907	0,2206546	0,0525573	47504,613	89687,235	0,5296697	80110,567	106063,05	0,7553108
9514,0193	0,3230366	0,0930279	62805,592	80994,317	0,7754321	136727,68	102270,59	1,3369208
4299,6253	0,2524824	0,0748684	27337,516	45106,164	0,6060705	61790,685	57429,093	1,0759474
1961,6712	0,2747198	0,0417931	17827,399	27033,733	0,6594502	28191,528	46937,681	0,6006161
3440,7422	0,3311647	0,0455571	33972,205	42735,379	0,7949433	49447,522	75525,886	0,6547096
16410,569	0,3272769	0,0836712	89791,872	114295,62	0,7856108	235839,23	196131,6	1,202454
47009,217	0,2856348	0,3778211	153332,44	223630,41	0,6856511	675577,88	124421,91	5,4297341
23313,493	0,285966	0,073366	167930,39	244637,39	0,6864461	335042,38	317769,63	1,0543562
13707,729	0,2443212	0,0700609	116322,12	198339,47	0,58648	196996,22	195654,48	1,0068577
2617,8293	0,2063252	0,0769553	12775,653	25795,193	0,4952726	37621,293	34017,551	1,1059377
22906,814	0,1666247	0,0594729	120705,56	301783,78	0,3999737	329197,92	385164,13	0,8546952
25416,694	0,1670338	0,0557508	149107,24	371879,64	0,4009556	365267,86	455897,89	0,8012054
5180,2501	0,3235241	0,3869919	22351,009	28780,506	0,7766023	74446,301	13385,94	5,5615296
14004,304	0,1622408	0,1914626	101125,54	259662,17	0,3894504	201258,35	73143,823	2,7515427
4878,6895	0,371872	0,0731611	27219,13	30492,197	0,8926589	70112,521	66684,242	1,0514106
1028,2774	0,4031885	0,0866563	8225,6489	8499,0426	0,9678324	14777,559	11866,157	1,2453534
864,8742	0,3540466	0,0348032	10350,375	12178,774	0,84987	12429,262	24850,387	0,5001637
1024,7714	0,3356813	0,0299696	13765,348	17083,153	0,805785	14727,173	34193,73	0,4306981
349,43255	0,3383423	0,0405217	3787,246	4663,1044	0,8121727	5021,7578	8623,3537	0,5823439
8192,8878	0,3223084	0,073722	46513,194	60119,104	0,7736841	117741,46	111132,24	1,0594716
145240,86	0,3416164	0,1738036	792947,17	966971,17	0,8200319	2087282,4	835660,94	2,4977623
287231,78	0,3421605	0,2946321	1615206,2	1966555	0,8213379	4127859,4	974882,77	4,234211
40972,098	0,3199694	0,2441574	197822,63	257558,21	0,7680696	588817,35	167810,2	3,5088293
5862,1444	0,2640073	0,0758245	28844,996	45515,838	0,6337354	84245,927	77312,031	1,0896872
2853,5499	0,2367266	0,0710476	10422,819	18341,974	0,5682496	41008,877	40163,925	1,0210376
4282,8542	0,2643337	0,0501272	33626,692	52995,562	0,634519	61549,665	85439,801	0,7203863
36314,422	0,3509851	0,0733904	272945,06	323962,28	0,8425211	521881,05	494811,37	1,0547071
25814,138	0,2190231	0,2471618	126529,37	240662,98	0,5257534	370979,6	104442,25	3,552007
11291,443	0,2258254	0,1200098	91120,666	168093,9	0,5420819	162271,35	94087,643	1,7246829
34894,869	0,4376388	0,1954455	217871,98	207392,71	1,0505286	501480,41	178540,16	2,8087821
86756,145	0,2347339	0,2607277	356957,64	633503,05	0,5634663	1246788,1	332746,21	3,7469641
125209,02	0,3378824	0,3080385	597387,47	736543,59	0,8110687	1799401,2	406472,02	4,426876
36673,021	0,3404144	0,3164735	187370,17	229298,14	0,8171465	527034,56	115880,22	4,5480978
31413,031	0,31039	0,2851904	129242,96	173463,13	0,7450746	451442,29	110147,58	4,0985223
441527,29	0,2806686	0,520188	1201108,5	1782774,3	0,67373	6345267,7	848784,08	7,4757148
162521,87	0,3070617	0,425329	420600,48	570626,68	0,7370852	2335630,9	382108,6	6,1124792
19775,513	0,2728634	0,090307	97399,099	148702,28	0,654994	284197,44	218981,07	1,2978174
9251,6849	0,3550396	0,166079	56185,931	65926,305	0,8522536	132957,62	55706,54	2,3867506
10292,622	0,2237001	0,4214774	28512,553	53097,954	0,5369803	147917,11	24420,343	6,0571268

70480,187	0,2864571	0,282152	307801,78	447630,31	0,687625	1012883,4	249795,13	4,0548564
35541,656	0,2523406	0,2225309	133934,41	221112,37	0,6057301	510775,51	159715,58	3,1980318
4655,2998	0,2255357	0,0451376	35004,638	64657,409	0,5413863	66902,147	103135,7	0,6486808
27663,949	0,2718412	0,0706516	211028,82	323395,82	0,6525404	397563,57	391554,71	1,0153461
17334,131	0,2929254	0,1802634	92799,303	131976,2	0,7031518	249111,9	96160,035	2,590597
54758,424	0,2662009	0,3150385	201523,14	315372,2	0,639001	786943,12	173815	4,5274752
4090,4377	0,3177837	0,0487522	43137,941	56550,414	0,7628227	58784,412	83902,593	0,7006269
10047,434	0,3993908	0,1531167	58306,337	60817,096	0,9587162	144393,47	65619,467	2,200467
1763,4212	0,4056739	0,0526922	15398,785	15813,11	0,9737987	25342,442	33466,475	0,7572486
2004,3663	0,3752771	0,0349453	26638,905	29571,424	0,9008327	28805,107	57357,245	0,5022052
11700,008	0,3065738	0,0822641	71469,853	97117,126	0,735914	168142,92	142224,91	1,1822325
9462,2155	0,7148809	0,1450687	69112,262	40274,423	1,7160336	135983,19	65225,776	2,0848076
26169,138	0,2564848	0,0653794	151268,83	245694,65	0,6156782	376081,37	400265,95	0,9395787
32922,793	0,4836035	0,0971707	251722,73	216840,76	1,1608644	473139,35	338814,13	1,396457
20553,779	0,2699265	0,0599209	140713,63	217169,36	0,6479442	295382,03	343014,93	0,8611346
34213,707	0,3546924	0,0794216	251338,84	295199,55	0,8514201	491691,3	430785,84	1,1413822
107752	0,3204699	0,4893217	379500,53	493324,88	0,769271	1548523,2	220206,87	7,0321294
15079,465	0,3776293	0,2555642	66057,648	72872,786	0,906479	216709,69	59004,609	3,6727587
14644,087	0,3660639	0,099572	99690,734	113450,33	0,878717	210452,8	147070,39	1,4309665

14139,815
20667,584
3043,4763

60253,591	0,2405909	0,2340089	129519,49	224266,21	0,5775257	865915,15	257484,15	3,3629843
52839,216	0,3417803	0,0360208	472774,43	576255,29	0,8204253	759361,83	1466909,7	0,5176609
29361,544	0,2331992	0,2055596	67325,453	120270,8	0,5597822	421960	142837,17	2,9541331
40323,218	0,2817008	0,1777964	109561,75	162023,82	0,6762077	579492,18	226794,3	2,5551444
22850,513	0,3829381	0,1282136	116091,7	126293,35	0,9192226	328388,81	178222,2	1,8425809
102344,03	0,4168032	0,161972	474723,76	474479,96	1,0005138	1470804,3	631862,41	2,3277288
20552,033	0,417185	0,1733839	96096,281	95959,029	1,0014303	295356,95	118534,85	2,4917308
248323,49	0,3100414	0,2054004	685681,64	921320,64	0,7442378	3568701,3	1208972,7	2,9518462
28984,891	0,3191532	0,1615361	103882,44	135597,25	0,7661102	416547,06	179432,91	2,3214641
39300,682	0,2679881	0,1758658	117501,7	182657,13	0,6432911	564797,14	223469,72	2,5273989
71546,623	0,2587128	0,2363446	203159,15	327134,6	0,6210262	1028209,3	302721,67	3,3965501
27725,536	0,3781793	0,2268057	95947,993	105692,97	0,9077992	398448,64	122243,54	3,2594658
122,11047	0,2531793	0,2120804	355,77083	585,39645	0,6077434	1754,8715	575,77458	3,0478447
118954,32	0,3393682	0,1888194	306576,77	376336,19	0,8146354	1709513,9	629990,07	2,7135569
142593,1	0,3408174	0,1968883	346899,67	424023,66	0,818114	2049231	724233,53	2,8295169

4857,9051
32554,516

77710,043	0,2878484	0,2374772	180542,97	261291,14	0,6909647	1116784,9	327231,54	3,4128279
56088,964	0,2768181	0,0346197	260681,34	392304,62	0,664487	806064,54	1620146,8	0,4975256
7448,3189	0,4276301	0,0282502	68534,266	66764,783	1,0265032	107041,12	263655,37	0,4059888
7732,4629	0,5088494	0,0552696	51894,746	42485,632	1,2214658	111124,61	139904,55	0,7942888
10079,695	0,4582685	0,03577	82273,978	74791,185	1,1000491	144857,11	281791,61	0,5140576
14508,343	0,6965898	0,1108329	107728,77	64426,204	1,6721266	208502	130902,91	1,5927989
207292,29	0,2351681	0,2283485	514578,56	911551,5	0,5645085	2979034,6	907789,07	3,2816374
117817,32	0,3387918	0,2871302	260111,54	319841,44	0,8132515	1693173,8	410327,2	4,126399
18459,591	0,2533551	0,2448946	41673,698	68523,616	0,6081655	265286,09	75377,699	3,5194241

50754,755

35638,008	0,2842812	0,2214187	93747,024	137378,01	0,682402	512160,19	160953,03	3,1820475
103813,78	0,340526	0,2337614	305711,62	373998,26	0,8174145	1491926,4	444101,51	3,3594266

9853,2824	0,2202806	0,1483814	26494,791	50106,288	0,5287718	141603,29	66405,108	2,1324156
14701,185	0,4385306	0,0911288	99819,499	94825,129	1,0526693	211273,36	161323,19	1,3096279
7404,9658	0,4259684	0,1257328	43034,181	42086,627	1,0225144	106418,09	58894,447	1,8069291
49974,638	0,2874959	0,2241127	118937,02	172342,87	0,6901186	718194,47	222988,9	3,2207633
97166,737	0,2966039	0,240982	213447,53	299793,51	0,7119818	1396400,6	403211,56	3,4631958
54276,039	0,2414552	0,2191303	126049,25	217476,12	0,5796004	780010,68	247688,42	3,1491609
350475,95	0,1994271	0,1592927	872196,37	1821956,5	0,4787142	5036752,7	2200200,5	2,2892244
282597,72	0,1807739	0,135624	828896,45	1910172,5	0,433938	4061262,4	2083684,9	1,949077
181577,8	0,2762703	0,2027938	555948,66	838317,28	0,6631721	2609487,1	895381,22	2,9143866
21727,045	0,5773066	0,0493649	227799,92	164382,27	1,3857938	312243,25	440131,32	0,709432
33843,162	0,4819833	0,0763586	188846,61	163224,42	1,1569752	486366,14	443213,64	1,0973628
16086,192	0,4515688	0,1097561	76298,246	70387,991	1,0839668	231177,55	146563,14	1,5773239
21498,274	0,4346463	0,1370606	86544,285	82948,84	1,0433453	308955,55	156852,29	1,969723
3848,1035	0,2834916	0,1509838	13856,099	20361,453	0,6805064	55301,784	25486,86	2,1698155
2785,5567	0,4654321	0,0251188	32405,382	29004,722	1,117245	40031,735	110895,45	0,3609863
3227,4367	0,3971101	0,0192877	44231,363	46401	0,9532416	46382,071	167331,75	0,2771863
5652,8437	0,4355876	0,0362428	59040,95	56465,832	1,0456049	81238,03	155971,33	0,5208523
4347,8933	0,4988885	0,0325249	53937,782	45039,913	1,1975552	62484,353	133678,78	0,4674216
410791,2	0,2652749	0,1828871	1146332,8	1800207	0,6367784	5903553,8	2246147	2,6283026
43273,043	0,3185049	0,1509026	177672,87	232387,62	0,764554	621884,65	286761,49	2,1686477

45073,059
241217

228522,84	0,2510012	0,1539436	762944,94	1266267	0,6025151	3284142,7	1484458,5	2,2123507
16272,518	0,2279156	0,135966	44256,158	80892,377	0,5470992	233855,27	119680,79	1,9539917
8234,9267	0,5275251	0,1172134	36849,238	29100,022	1,2662959	118345,61	70255,853	1,6844946
100027,87	0,1962588	0,1355127	317632,31	674222,69	0,4711089	1437518,4	738144,01	1,9474769
60077,401	0,1354742	0,0906534	202746,04	623452,82	0,3251987	863383,09	662715,39	1,3027962
73716,609	0,1619316	0,1309122	217010,64	558286,84	0,3887081	1059394,6	563099,41	1,8813633
195756,67	0,3126373	0,2112068	559198,75	745132,19	0,7504692	2813254,1	926848,36	3,0352906
50198,329	0,2590444	0,1386236	178219,42	286608,3	0,6218223	721409,17	362119,58	1,9921849
882,03647	0,3191375	0,0329341	5542,1037	7234,4382	0,7660724	12675,904	26781,873	0,4733016
940,93839	0,3003593	0,0312119	4584,8131	6358,9947	0,7209965	13522,394	30146,769	0,448552

8498,2945
53951,131

277367,74	0,2941711	0,2653863	645185,59	913676,93	0,7061419	3986101,5	1045147,3	3,8139134
31198,752	0,2107884	0,1256818	106530,59	210540,47	0,5059863	448362,85	248235,95	1,8061963
48147,712	0,2293479	0,1624579	110350,99	200442,27	0,5505375	691939,39	296370,31	2,3347122
27878,33	0,3780029	0,2439603	74556,799	82167,501	0,9073758	400644,48	114274,03	3,5059975
47341,389	0,1781509	0,1714994	119650,94	279792,56	0,4276416	680351,57	276044,01	2,4646489
131214,51	0,1417975	0,1451089	327413,51	961913,1	0,3403774	1885707,2	904248,83	2,0853853
14302,264	0,2683638	0,1518946	51321,599	79668,054	0,644193	205540,4	94159,107	2,1829051
719983,44	0,2487308	0,2254613	1533562,2	2568501,4	0,5970649	10347011	3193379,7	3,2401443
8726,4442	0,2722755	0,2100209	20603,012	31523,185	0,6535828	125409,29	41550,365	3,0182476
24191,178	0,3375191	0,1532503	86953,416	107323,84	0,8101967	347655,75	157854,05	2,2023872
158375,85	0,3052949	0,2988828	367014,67	500808,7	0,732844	2276047,7	529892,89	4,2952977
64489,578	0,3010001	0,322984	156508,12	216609,84	0,7225347	926791,27	199668,03	4,6416607
7866,4239	0,3787566	0,0621476	52198,744	57412,668	0,9091851	113049,79	126576,56	0,8931337
43726,289	0,5919777	0,0688029	268412,52	188888,45	1,4210108	628398,33	635529,49	0,9887792
36200,74	0,6496619	0,0656799	284819,69	182637,75	1,5594787	520247,32	551169,1	0,9438978
1965,7829	0,4450028	0,0582084	11730,479	10981,482	1,0682054	28250,618	33771,449	0,8365237
6059,0235	0,4923279	0,0547956	42038,18	35571,106	1,1818069	87075,312	110575,09	0,7874767
11094,423	0,4693941	0,0746099	90333,12	80171,003	1,1267555	159439,95	148699,1	1,0722321

11927,557	0,4445401	0,0510767	136197,43	127633,87	1,0670947	171413,06	233522,31	0,7340329
7075,2461	0,4190485	0,0622847	59430,273	59081,477	1,0059036	101679,63	113595,16	0,8951053
4942,314	0,3814382	0,066726	36684,392	40064,989	0,9156222	71026,879	74068,816	0,9589309
18375,762	0,5562027	0,238988	70639,304	52907,988	1,3351349	264081,37	76889,906	3,4345388
31570,366	0,4376265	0,0596424	221993,07	211321,52	1,0504991	453703,38	529327,4	0,8571319
153359,59	0,3161857	0,1673192	536158,48	706413,37	0,7589869	2203958,1	916569,15	2,4045738
187883,9	0,2531188	0,1591839	642349,86	1057195	0,6075983	2700113,2	1180294,7	2,2876601
27868,266	0,2542425	0,1859374	84174,319	137923,86	0,6102955	400499,85	149879,85	2,6721394
58129,126	0,2182701	0,2120849	138571,87	264477,47	0,5239458	835384,07	274084,22	3,0479102
26562,591	0,2434108	0,1719512	83067,953	142167,9	0,5842947	381735,75	154477,5	2,4711414
16111,952	0,2955196	0,1075602	81799,613	115311,55	0,7093792	231547,74	149794,76	1,5457666
5206,4672	0,2396365	0,2074646	14786,915	25705,882	0,5752347	74823,073	25095,689	2,981511
116749,01	0,185108	0,2408898	271503,55	611024,08	0,4443418	1677821	484657,28	3,461871
29775,92	0,3328284	0,167673	111239,71	139234,66	0,7989369	427915,08	177583,24	2,4096591

553,01814
584,79836
4204,3018
1694,0224
4506,4179

17183,827	0,3516164	0,0521165	152266,44	180402,7	0,8440364	246951,85	329719,76	0,748975
82895,635	0,2889759	0,184467	274328,57	395473,4	0,6936713	1191308	449379,17	2,6510085
72936,438	0,247879	0,190573	208963,4	351186,93	0,5950204	1048182,6	382721,84	2,7387583
8376,1866	0,3468239	0,1095007	25761,517	30943,568	0,8325322	120375,68	76494,35	1,5736545
28129,094	0,2854787	0,1410427	54665,893	79772,029	0,6852765	404248,25	199436,77	2,0269495
10160,997	0,3653039	0,1134744	43918,84	50084,631	0,8768926	146025,5	89544,399	1,6307609
19536,565	0,4295372	0,0370708	156705,63	151981,84	1,0310812	280763,47	527006,43	0,5327515
19222,674	0,3531166	0,0507885	152356,95	179743,01	0,8476377	276252,49	378485,14	0,7298899
4703,8312	0,3189522	0,1536634	20396,261	26639,915	0,7656279	67599,601	30611,272	2,2083238
9821,3303	0,4536483	0,121297	46311,329	42528,087	1,0889587	141144,1	80969,281	1,7431808
643,43236	0,326492	0,0190374	6393,4584	8157,7666	0,7837266	9246,8816	33798,406	0,2735893
268,68908	0,6413412	0,0171168	4651,3722	3021,3419	1,5395054	3861,3789	15697,358	0,2459891
2637,9504	0,6680757	0,0305442	32777,522	20438,941	1,60368	37910,457	86364,971	0,4389564
1183,6117	0,7247082	0,0460335	7322,0664	4208,9953	1,7396233	17009,895	25711,98	0,6615552
10967,959	0,5312231	0,0367146	103679,85	81306,524	1,2751726	157622,51	298735,65	0,5276321
66402,929	0,4501425	0,0213392	826354,27	764758,34	1,080543	954288,38	3111776,6	0,3066699
3752,5061	0,5130325	0,0377998	31721,236	25758,061	1,2315071	53927,938	99273,194	0,5432276
65530,591	0,4659676	0,0227211	775428,46	693256,49	1,1185304	941751,85	2884125,8	0,3265294
2533,0187	0,3306072	0,03116	28183,857	35513,712	0,7936049	36402,465	81290,731	0,4478058
4031,1552	0,4263271	0,0273605	47886,003	46792,212	1,0233755	57932,453	147334,74	0,3932029
9087,5791	0,4700147	0,0273171	99690,957	88359,294	1,1282453	130599,23	332670,25	0,3925786
2806,4626	0,4725493	0,0304316	28626,854	25236,807	1,1343294	40332,177	92221,894	0,4373384
18845,011	0,556922	0,0225387	273167,24	204334,73	1,3368615	270825,03	836117,6	0,3239078
8464,2121	0,4223866	0,1253022	46947,162	46302,793	1,0139164	121640,71	67550,372	1,8007408

90063,686	0,3194533	0,1568891	569334,53	742451,5	0,7668306	1294321,4	574059,57	2,2546813
11759,563	0,2336852	0,2469684	60060,535	107069,55	0,5609488	168998,78	47615,657	3,5492271
55471,981	0,2788331	0,359984	164987,97	246499,39	0,6693241	797197,77	154095,69	5,1733942
277,82826	0,3613697	0,2467597	1204,9523	1389,076	0,8674488	3992,7197	1125,9061	3,546228
132,17044	0,3348067	0,2567026	540,42613	672,43472	0,8036856	1899,445	514,87759	3,6891196
71,356498	0,3278832	0,2450709	340,01496	432,00304	0,7870661	1025,477	291,16676	3,5219577
321222,49	0,2722731	0,1750759	1579268,2	2416345,8	0,6535771	4616345,9	1834761,1	2,5160474
153009,18	0,2726705	0,1584611	712760,07	1088963	0,654531	2198922,3	965594,4	2,2772732

19,37371	0,3121864	0,2371865	94,544578	126,16259	0,7493868	278,42305	81,681345	3,4086492
3594,7384	0,3305617	0,2163068	16129,557	20327,214	0,7934957	51660,63	16618,701	3,108584
79007,705	0,405426	0,3003684	294198,67	302299,24	0,9732035	1135433,9	263036,03	4,3166477
62000,407	0,2811598	0,4477894	182732,34	270751,02	0,6749092	891018,96	138458,86	6,4352614
402713,03	0,316495	0,4391438	1220524,2	1606524,7	0,7597295	5787461,1	917041,41	6,3110139
165049,34	0,2611751	0,3223959	810212,6	1292335,4	0,6269368	2371953,7	511946,19	4,6332089
276357,95	0,2863272	0,3106617	1498649	2180445,5	0,6873132	3971589,5	889578,38	4,4645751
223858,52	0,2841032	0,316204	1186115,2	1739236,6	0,6819746	3217110,8	707955,91	4,5442248
85618,518	0,2793097	0,2667844	443007,95	660744,24	0,6704681	1230439	320927,69	3,8340071
182094,25	0,3296331	0,2092587	1013078,7	1280325,1	0,7912668	2616909,1	870187,42	3,0072937
99623,774	0,3351069	0,2632529	520784,81	647415,16	0,8044063	1431711,1	378433,78	3,783254
7918,8832	0,1641085	0,3727767	27883,207	70781,462	0,3939337	113803,69	21242,966	5,3572409
112185,22	0,1618768	0,3565855	357132,87	919079,57	0,3885767	1612233,8	314609,55	5,1245547
54717,838	0,1753822	0,3136054	188518,8	447792,81	0,4209956	786359,84	174479,89	4,5068796
94595,893	0,1663741	0,3348075	325938,81	816128,23	0,3993721	1359454,5	282538,16	4,8115785
82269,578	0,1786267	0,3179502	302716,68	705989	0,4287839	1182310,8	258749,9	4,569319
51374,455	0,1782451	0,3111574	169759,65	396757,1	0,427868	738311,49	165107,59	4,4716992
6143,1777	0,1843595	0,3906662	22659,487	51202,652	0,4425452	88284,707	15724,877	5,6143337
22384,046	0,2184501	0,2127019	99619,735	189976,99	0,5243779	321685,13	105236,7	3,056777
1292000,2	0,1771117	0,3143982	4623943,4	10876100	0,4251472	18567566	4109438,7	4,518273
3406484,5	0,1570355	0,3543358	11036888	29279037	0,3769553	48955199	9613719,3	5,0922226
216712,35	0,2969352	0,1363751	1288465	1807668,8	0,7127771	3114412	1589090,6	1,9598707
90963,148	0,2477207	0,2433647	377201,58	634335,56	0,5946405	1307247,7	373772,92	3,4974382
234,29935	0,3347413	0,2178533	1071,8276	1333,9008	0,8035288	3367,158	1075,4913	3,1308092
329949,51	0,2548215	0,3230777	1257545	2055869,1	0,6116853	4741763,5	1021270	4,6430068
103029,42	0,1851151	0,2160974	335741,24	755563,08	0,444359	1480654,2	476773,14	3,1055739
141,14764	0,3947577	0,2173368	713,35197	752,80276	0,9475948	2028,458	649,44199	3,123386
412,74727	0,3560057	0,2565063	2047,7681	2396,2482	0,8545726	5931,6649	1609,1115	3,6862983
263234,89	0,2674897	0,362003	1046560,4	1629915,6	0,6420948	3782995,8	727162,19	5,2024099
88759,298	0,2065334	0,2140874	377990,12	762426,64	0,4957724	1275575,8	414593,74	3,0766885
504,7806	0,3432972	0,3013492	2120,8443	2573,6324	0,8240665	7254,2925	1675,0687	4,3307432
247,7278	0,3754361	0,310076	959,68093	1064,8754	0,9012143	3560,1406	798,92601	4,4561581
703,89968	0,3192103	0,2454553	3138,3112	4095,6892	0,7662474	10115,868	2867,7304	3,5274824
130143,69	0,5698033	0,6990979	215486,16	157544,17	1,3677825	1870318,3	186159,46	10,046861
72487,399	0,4006441	0,311738	231961,92	241193,65	0,9617248	1041729,4	232526,66	4,4800428
32158,398	0,1788407	0,2959144	94115,553	219231,47	0,4292976	462154,09	108674,66	4,2526387
880112,35	0,2287722	0,4798478	2842689,3	5176473,6	0,5491556	12648252	1834149	6,8959785
454493,48	0,1887494	0,486688	1220872,4	2694589,5	0,4530829	6531607,1	933849,7	6,9942809
117682,09	0,2909119	0,4989689	371676,57	532245,01	0,6983186	1691230,4	235850,54	7,1707718
1439855,7	0,2843082	0,4590793	4694685,5	6878996,3	0,6824666	20692424	3136398,4	6,5975114
9360,0404	0,264206	0,4249671	33427,812	52707,591	0,6342125	134514,82	22025,328	6,1072787
137048,63	0,3062392	0,4776849	479986,33	652944,14	0,7351109	1969550,3	286901,73	6,8648953
79425,152	0,246144	0,466056	278814,57	471882,77	0,5908556	1141433,1	170419,78	6,6977736
41401,571	0,2606797	0,4884578	151435,17	242006,78	0,6257476	594989,38	84759,761	7,0197152
2500,6428	0,2626047	0,4408159	9423,3743	14948,993	0,6303685	35937,185	5672,7598	6,3350443
9941,3901	0,2380305	0,4717921	34752,579	60822,224	0,5713796	142869,5	21071,55	6,7802084
91253,246	0,2455547	0,4657592	339642,1	576210,64	0,5894409	1311416,7	195923,68	6,6935081
9687,1737	0,2827515	0,4682229	35304,805	52015,979	0,67873	139216,11	20689,237	6,7289146
24631,97	0,2444266	0,4758804	89524,687	152581,67	0,5867329	353990,46	51760,841	6,8389626
37554,902	0,3064444	0,4866085	139587,96	189759,8	0,7356034	539708,22	77176,834	6,9931376
4244,8908	0,2868711	0,4669612	15686,549	22779,724	0,6886189	61004,086	9090,4567	6,7107834
105583,48	0,275904	0,4916777	372966,3	563144,1	0,6622928	1517359,1	214741,23	7,0659888

201375,56	0,2470344	0,4453836	742603,46	1252297,4	0,5929929	2894004,3	452139,65	6,4006869
70060,923	0,2380463	0,3767429	269755,13	472080,72	0,5714174	1006858,1	185964,83	5,4142392
539525,93	0,2259574	0,4773377	1871529,7	3450468,3	0,5423987	7753623,8	1130281,4	6,8599055
13423,81	0,291131	0,2504353	61783,825	88408,537	0,6988446	192915,98	53601,918	3,5990499
21399,448	0,310865	0,4059009	80634,41	108057,89	0,7462149	307535,3	52720,876	5,8332738
13045,627	0,269711	0,340263	51587,73	79681,172	0,6474268	187481,03	38339,838	4,8899798
540,02707	0,2357196	0,3293137	1913,6628	3382,0309	0,5658325	7760,8258	1639,8559	4,7326265
372299,98	0,3104809	0,4064842	1406215,7	1886796,3	0,7452928	5350389,7	915902,71	5,8416572
7042,5841	0,3203945	0,1703167	38245,406	49728,131	0,76909	101210,24	41349,921	2,4476525
667,33894	0,2542052	0,332352	2553,4461	4184,5643	0,610206	9590,4474	2007,9282	4,77629
474,76587	0,2426328	0,3194769	1799,5216	3089,6945	0,582427	6822,9454	1486,0724	4,5912604
344812,85	0,2714285	0,4691847	1250860,1	1919823	0,6515497	4955367,1	734919,19	6,7427375
1203,0725	0,3575659	0,189439	5640,9368	6572,0831	0,8583179	17289,571	6350,7118	2,7224619
1562015,4	0,2746329	0,4774711	5519676,5	8372766,5	0,6592417	22448003	3271434,8	6,861822
260047,3	0,2363924	0,4624589	979154,12	1725541,9	0,5674473	3737186,3	562314,39	6,6460799
133,70752	0,2798696	0,2066772	672,89931	1001,6184	0,671812	1921,5347	646,93895	2,9701947
2088,9334	0,1426109	0,1443285	14292,021	41749,282	0,3423297	30020,435	14473,468	2,0741701
40125,446	0,2310878	0,4081026	146977,34	264960,63	0,5547139	576649,97	98321,947	5,8649161
30232,158	0,2798107	0,4212152	113153,88	168466,32	0,6716706	434471,75	71773,657	6,0533595
5109,8411	0,2638232	0,3424816	19143,947	30229,182	0,6332936	73434,442	14920,044	4,9218649
74402,819	0,2634131	0,3636184	333183,8	526931,84	0,6323091	1069256,2	204617,87	5,2256249
25312,296	0,2287304	0,3113214	112586,61	205055,2	0,5490552	363767,54	81306,001	4,4740553
290733,79	0,2695447	0,3401464	1357298,3	2097743,7	0,6470277	4178187,4	854731,36	4,8883047
79075,13	0,2311512	0,3456102	313530,24	565055,65	0,5548661	1136402,9	228798,63	4,9668255
47187,205	0,2615085	0,3461372	203207,08	323713,56	0,6277373	678135,77	136325,14	4,9744
130989,04	0,254086	0,3476742	548230,88	898857,3	0,6099198	1882467	376758,06	4,9964878
1011,2246	0,2321289	0,2676016	4909,5842	8810,9646	0,557213	14532,49	3778,8439	3,8457503
894,78839	0,2432985	0,2862852	3997,9431	6845,4988	0,5840251	12859,164	3125,514	4,1142559
883,60214	0,2117415	0,2918511	4768,813	9382,3619	0,5082743	12698,405	3027,5784	4,1942446
1604,647	0,1745527	0,3155636	5778,4963	13791,017	0,4190044	23060,669	5085,0198	4,5350206
2578,1737	0,3374864	0,2264786	13665,068	16867,997	0,810118	37051,397	11383,742	3,2547644

7579,1722

14439,705

52578,488	0,2768865	0,4202303	192131,29	289070,84	0,6646512	755614,86	125118,28	6,0392042
60758,606	0,2586715	0,3863316	220848,81	355675,92	0,6209271	873172,81	157270,6	5,5520409
2480594,5	0,2635997	0,388357	9309414,1	14712460	0,6327571	35649067	6387408,3	5,5811474
2354751,6	0,3046216	0,5416738	6306005,5	8623856,4	0,731228	33840557	4347176,1	7,7844918
2424275,1	0,28437	0,5424177	6332033,9	9276143,1	0,6826149	34839691	4469387,9	7,7951818
94882,727	0,1542957	0,2657498	244377,05	659803,29	0,3703786	1363576,7	357037,83	3,8191377
2549242,7	0,3515394	0,3869145	7860428,8	9314942,3	0,8438516	36635623	6588646,7	5,560417
51362,102	0,2351426	0,1946215	187954,34	332988,33	0,5644472	738133,96	263907,64	2,7969405
111281,48	0,257185	0,4311062	270913,88	438827,25	0,6173588	1599246	258130,09	6,195504
43408,16	0,2378106	0,4746031	118105,41	206893,35	0,5708516	623826,44	91462,017	6,8206066
28841,466	0,256202	0,4215757	78837,102	128190,56	0,6149993	414485,87	68413,49	6,0585401
21015,961	0,2899026	0,4274916	73356,454	105412,99	0,6958958	302024,14	49161,112	6,143558
174659,23	0,1689142	0,2384733	574673,12	1417302,5	0,4054696	2510059	732405,84	3,4271423
67785,954	0,1408391	0,1767929	245376,32	725800,41	0,3380769	974164,08	383420,12	2,5407224
111627,94	0,2104504	0,2692872	395794,4	783479,86	0,505175	1604225,2	414531,23	3,8699742
36638,514	0,3136627	0,3551653	107052,52	142181,1	0,7529307	526538,65	103159,04	5,1041446
21077,733	0,279347	0,3530495	67293,924	100355,18	0,6705576	302911,87	59701,916	5,0737379
219804,53	0,2890711	0,4333751	617316,62	889633,79	0,6938997	3158850,3	507192,29	6,2281118
225646,49	0,3064589	0,4342608	595993,38	810171,84	0,7356382	3242806,1	519610,6	6,2408391

68016,911	0,3826162	0,445726	201649,49	219554,19	0,9184498	977483,21	152598,02	6,4056087
348627,09	0,3807396	0,393516	1139844,9	1247169,8	0,9139452	5010182,3	885928,58	5,6552892
25625,531	0,363803	0,4638243	73058,771	83659,258	0,8732897	368269,1	55248,357	6,6657023
10142,095	0,4203003	0,1732847	66847,545	66257,287	1,0089086	145753,87	58528,526	2,4903048
247607,57	0,3981394	0,4128034	818017,04	855923,9	0,9557123	3558412,7	599819,56	5,9324719
59327,92	0,2929545	0,4629918	169086,28	240445,17	0,7032218	852612,17	128140,32	6,6537383
367693,23	0,3709691	0,3178156	1178351,7	1323259,6	0,8904917	5284185,3	1156939	4,5673846
36764,195	0,285842	0,3645404	126189,69	183910,18	0,6861485	528344,83	100850,8	5,2388759
43142,868	0,6958041	1,2618372	35190,041	21068,845	1,6702406	620013,88	34190,519	18,134088
97301,101	0,2423397	0,1913617	436859,53	750974,45	0,5817236	1398331,5	508467,07	2,7500926
16074,667	0,2572086	0,3409444	58356,375	94517,195	0,6174154	231011,92	47147,476	4,8997727
2314,7187	0,2950007	0,3060008	8759,3893	12369,688	0,7081334	33265,237	7564,4205	4,3975922
508,1995	0,2853715	0,2580726	2741,4727	4002,039	0,685019	7303,426	1969,2113	3,7088076
1866,2684	0,2901107	0,2805498	10284,538	14768,25	0,6963952	26820,478	6652,1817	4,0318318
15171,345	0,3083634	0,2942075	71538,465	96646,195	0,7402098	218030,12	51566,826	4,2281083
246644,56	0,2884132	0,1755106	1239731,5	1790690,3	0,6923204	3544573,1	1405297,1	2,5222944
82026,276	0,2887614	0,1280715	527342,78	760784,7	0,6931564	1178814,3	640472,28	1,8405392
24765,762	0,2639056	0,2477713	130798,54	206472,5	0,6334914	355913,2	99954,132	3,5607653
61963,127	0,235615	0,2940745	286367,32	506323,84	0,5655813	890483,19	210705,51	4,2261979
6886,0912	0,2737117	0,2964184	34899,653	53117,262	0,6570303	98961,25	23230,988	4,2598813
343324,23	0,2509125	0,2606261	1696803,2	2817195,9	0,6023022	4933974	1317305,7	3,7455043
2536,1287	0,3360772	0,2867597	10542,703	13068,353	0,8067354	36447,16	8844,0912	4,1210746
4459,4558	0,2842488	0,3820657	15595,392	22856,281	0,6823242	64087,638	11671,959	5,4907351
14158,639	0,2789623	0,3847503	49746,433	74288,973	0,6696341	203476,33	36799,554	5,5293152
14423,792	0,2429221	0,2745123	62591,997	107339,52	0,5831217	207286,9	52543,334	3,9450657
104464,67	0,2452697	0,2268898	507044,9	861212,73	0,5887569	1501280,5	460420,28	3,2606741
533422,73	0,2538316	0,3139011	2105775,8	3456005,3	0,6093092	7665913,5	1699333,8	4,5111287
211,10736	0,2295308	0,1343022	1436,3348	2606,8897	0,5509764	3033,8616	1571,8834	1,9300806
37736,772	0,294496	0,618917	103812,8	146851,84	0,706922	542321,9	60972,261	8,8945676
65480,424	0,2576212	0,6067149	175456,27	283723,45	0,618406	941030,9	107926,19	8,7192081
1830414,2	0,2755775	0,6326013	5131537,4	7757319,3	0,6615091	26305209	2893472	9,0912266
1376611,8	0,305184	0,5735616	4237526,4	5784404,3	0,7325778	19783534	2400111,3	8,2427569
114053,43	0,4108393	0,4180721	419454,95	425325,31	0,9861979	1639082,2	272808,05	6,0081886
127020,33	0,2859891	0,3564077	444583,2	647607,04	0,6865015	1825431,9	356390,5	5,1219993
13653,429	0,2147203	0,2551151	49330,182	95707,836	0,5154247	196215,88	53518,7	3,666305
241994,67	0,2960687	0,4140519	681602,78	959062,28	0,7106971	3477748,7	584454,91	5,950414
1033226,6	0,3580972	0,4645209	3362944,4	3912250,3	0,8595934	14848684	2224284,2	6,6757135
124132,82	0,2737607	0,5216777	315111,87	479514,29	0,657148	1783934,9	237949,24	7,4971238
25855,263	0,2938601	0,4706314	73547,376	104264,01	0,7053956	371570,61	54937,399	6,7635276
395167,01	0,262545	0,4085645	1096241,9	1739444,7	0,6302252	5679015,8	967208,33	5,8715538
1760537	0,2848459	0,371006	5987336,4	8756523	0,6837573	25300992	4745306,1	5,3317935
106435,19	0,4108286	0,2537682	569134,49	577114,68	0,9861723	1529599,2	419418,93	3,6469484
193683,41	0,6729128	0,3096464	702032,36	434616,54	1,6152914	2783458,9	625498,6	4,4499843
28338,793	0,3551278	0,1528173	231893,64	272027,06	0,8524653	407261,87	185442,26	2,1961653
30,21643	0,4926965	0,1991615	145,65271	123,15358	1,1826917	434,24572	151,71824	2,8621853
64822,731	0,6786231	0,3922356	218568,93	134173,81	1,6289985	931579,07	165264,79	5,6368877
124630,34	0,6206534	0,3198674	566778,71	380427,88	1,4898453	1791084,9	389631,23	4,596872
4230,8925	0,8213486	0,194207	18292,35	9277,9052	1,9716034	60802,913	21785,473	2,7909843
16529,307	0,6105498	0,1719991	71611,058	48861,514	1,4655923	237545,62	96101,136	2,4718295
6375,2	0,4946033	0,2477329	22871,997	19264,378	1,1872689	91619,141	25734,164	3,5602143
9695,117	0,9534911	0,1950348	40994,103	17910,706	2,2888045	139330,26	49709,668	2,8028806

43571,332	0,7754759	0,1629078	204825,66	110033,27	1,8614885	626171,42	267460,1	2,3411769
131330,59	0,8550169	0,3809113	544289,24	265193,55	2,0524226	1887375,5	344779,98	5,4741446
3392,9727	0,8246373	0,1249694	24592,258	12423,482	1,979498	48761,018	27150,43	1,7959575
32553,525	0,8596257	0,1378435	250193,25	121247,87	2,0634858	467832,53	236162,88	1,9809741
1513,4478	0,6942772	0,1261829	12078,907	7247,741	1,6665754	21750,029	11994,083	1,8133966
5967,2267	0,6218882	0,0974965	45851,735	30715,059	1,4928096	85756,083	61204,519	1,4011397
23075,349	0,2678227	0,0739878	135614,74	210944,15	0,6428941	331619,97	311880,25	1,0632926
38591,315	0,3379748	0,1042832	202086,03	249092,1	0,8112904	554602,7	370062,53	1,4986729
81680,463	0,6083478	0,2167421	308608,13	211331,07	1,4603065	1173844,6	376855,58	3,1148393
28270,37	0,5381741	0,2756355	98474,832	76227,268	1,2918583	406278,55	102564,33	3,961207
80744,687	0,4893693	0,2836068	263017,61	223900,99	1,174705	1160396,4	284706,46	4,0757641
68928,61	0,5512222	0,2891987	229581,13	173507,18	1,3231794	990585,4	238343,44	4,1561262
168544,15	0,6463665	0,3219992	596316,54	384331,46	1,5515684	2422178,1	523430,28	4,6275085
40457,192	0,486268	0,2528562	149972,87	128482,79	1,1672604	581417,55	160000,77	3,6338423
28073,152	0,4436179	0,1934897	106286,79	99810,942	1,0648812	403444,3	145088,59	2,7806756
28990,655	0,5632027	0,2507388	115207,16	85216,302	1,3519381	416629,89	115620,94	3,603412
34690,133	0,3806043	0,1972538	164581,97	180142,61	0,9136204	498538,11	175865,48	2,8347695
31440,898	0,589569	0,2661628	109893,02	77650,343	1,415229	451842,77	118126,55	3,8250737
17024,058	0,5750585	0,2641071	61131,323	44285,312	1,3803972	244655,79	64458,914	3,7955307
60882,401	0,516704	0,2833744	206352,76	166370,53	1,2403204	874951,89	214847,92	4,0724244
73412,612	0,5217562	0,1153408	435424,8	347659,01	1,2524479	1055025,8	636484,59	1,6575826
172120,6	0,4923515	0,2624279	626788,51	530339,19	1,1818635	2473576	655877,79	3,7713977
50223,566	0,4772417	0,1164765	236523,38	206463,66	1,1455933	721771,86	431190,52	1,6739048
9541,9233	0,3798783	0,0563164	60390,721	66226,777	0,9118777	137128,69	169434,33	0,8093324
309258,73	0,5649358	0,3939056	1100960	811858,53	1,3560984	4444412,5	785108,67	5,6608883
121586,59	0,5128281	0,3765401	421622,34	342499,34	1,2310165	1747342,6	322904,73	5,4113255
24748,692	0,559825	0,4534858	79950,597	59494,575	1,34383	355667,88	54574,345	6,5171259
1613844	0,6068922	0,4517748	5366934,6	3684025,8	1,4568124	23192841	3572231	6,4925368
22548,596	0,3678559	0,168922	123728,85	140120,35	0,8830184	324049,9	133485,25	2,4276083
23823,564	0,5846067	0,4545417	78172,827	55705,738	1,4033173	342372,71	52412,279	6,5322996
1642307,5	0,5912332	0,4526716	5478446,4	3860171,1	1,4192237	23601896	3628033,1	6,5054246
185171,51	0,5314141	0,3337686	687304,19	538795,36	1,2756312	2661132,9	554790,13	4,7966478
305583,47	0,5059702	0,4237807	949065,65	781410,5	1,2145545	4391594,7	721088,68	6,0902284
140384,56	0,5204475	0,3578169	406437,6	325330,56	1,2493065	2017491,7	392336,32	5,1422506
69844,026	0,4722754	0,2851689	220384,05	194398,43	1,133672	1003741	244921,62	4,0982131
2187594,5	0,5939499	0,3002162	7655351,5	5369369,4	1,425745	31438312	7286730,8	4,3144605
161946	0,6463763	0,364248	479040,66	308741,4	1,5515919	2327355	444603,68	5,2346732
258447,01	0,4856295	0,3637828	765969,14	657073,73	1,1657278	3714188,3	710443,2	5,2279877
23020,818	0,5436491	0,354009	64309,128	49278,999	1,3050007	330836,3	65028,905	5,0875269
475618,81	0,5105213	0,2872012	1667089,1	1360356,8	1,2254792	6835203,1	1656047,4	4,12742
423116,66	0,5594172	0,2883248	1553957,7	1157207,7	1,3428512	6080685,2	1467499,9	4,1435676
22993,024	0,5225247	0,2159618	92058,333	73394,613	1,2542928	330436,87	106468,04	3,1036251
48221,12	0,4876641	0,2642944	178367,82	152371,46	1,1706117	692994,35	182452,27	3,7982227
15860,745	0,9154996	0,5147659	51389,646	23384,356	2,1976079	227937,6	30811,567	7,3977932
424755,82	0,5195592	0,2614335	1698897,6	1362197,5	1,2471743	6104241,9	1624718,7	3,757107
6913,5226	0,5140487	0,2554629	26802,321	21720,815	1,2339464	99355,471	27062,724	3,6713034
4171301,2	0,4839784	0,2830191	14333230	12337468	1,1617643	59946517	14738584	4,0673187
706112,86	0,4749765	0,2993529	2398326,3	2103507,7	1,1401557	10147674	2358797,4	4,3020542
1792449,3	0,4862804	0,3067011	6036020,8	5170968,5	1,1672902	25759609	5844286,9	4,4076565
4235295	0,4785056	0,2947885	14554215	12670966	1,1486271	60866183	14367233	4,2364583
142913,24	0,4781662	0,2443962	579061,36	504491,23	1,1478125	2053831,7	584760,41	3,5122619
716333,13	0,4349823	0,282319	2384244,5	2283427,2	1,0441517	10294552	2537318,3	4,0572567

31914,495	0,5092311	0,256579	121591,78	99471,181	1,222382	458648,92	124384,69	3,6873423
26519,137	0,4578502	0,2852675	89840,755	81744,379	1,099045	381111,27	92962,335	4,099631
971324,74	0,5210766	0,2973479	3510502,9	2806568,9	1,2508166	13959082	3266626,7	4,2732405
24209,764	0,5603041	0,2937825	87945,629	65388,055	1,34498	347922,85	82407,097	4,2220011
3338228,8	0,537731	0,2943592	12123204	9392047,7	1,2907945	47974283	11340664	4,2302887
28671,11	0,4565887	0,2732577	101267,25	92395,708	1,0960169	412037,65	104923,35	3,927035
91817,383	0,5000496	0,2866922	321828,46	268113,89	1,2003423	1319524	320264,69	4,1201046
130876,16	0,6103214	0,3880543	394819,2	269493,07	1,465044	1880844,7	337262,52	5,5767974
231779,02	0,6158855	0,3910355	739248,44	500032,64	1,4784004	3330937,9	592731,47	5,6196407
318704,41	0,5636988	0,3802984	964631,21	712889,33	1,353129	4580158,1	838037,72	5,4653365
4966139,9	0,5971925	0,3547455	16682255	11637196	1,4335288	71369285	13999164	5,0981104
1195127,1	0,3847807	0,3269459	3791648,6	4105090,3	0,9236456	17175385	3655427,6	4,6985981
5806150,1	0,5467359	0,3762551	18174664	13848308	1,3124105	83441223	15431418	5,4072299
4795057,4	0,5841075	0,3851037	14860639	10598701	1,4021189	68910628	12451341	5,5343941
1498856,2	0,5419656	0,3540423	4388018,7	3372909,2	1,3009596	21540331	4233550,8	5,0880058
840988,85	0,358452	0,2950959	3020682,4	3510605,6	0,8604448	12086001	2849883,3	4,2408759
2351387,8	0,5952742	0,3310247	7757571,1	5428959,6	1,4289241	33792216	7103360,1	4,7572156
228578,26	0,7386997	0,4678954	754077,53	425261,43	1,7732093	3284939,1	488524,28	6,7242084
930948,65	0,9379159	0,2464033	4076419,5	1810601,6	2,2514171	13378830	3778149,7	3,5411063
286259,95	1,2231677	0,3201831	918246,61	312738,45	2,9361488	4113893	894050,72	4,601409
93,707614	0,371272	0,1130155	688,6538	772,71019	0,8912187	1346,6889	829,15686	1,6241666
31907,624	0,7521042	0,8723305	54949,481	30436,415	1,8053861	458550,18	36577,447	12,536419
147918,69	0,5450405	0,5535584	249582,8	190762,85	1,3083407	2125765,9	267214,25	7,9552865
52111,859	0,5538625	0,2793531	136357,96	102562	1,3295174	748908,85	186544,75	4,0146337
50442,074	0,5080334	0,3106767	149138,3	122293,92	1,2195071	724912,08	162361,94	4,4647908
81086,517	0,3312836	0,1544453	320870,14	403494,2	0,7952286	1165308,9	525017,65	2,2195613
112936,05	0,440189	0,2629353	392504,25	371460,89	1,0566503	1623024,1	429520,25	3,7786906
78830,733	0,4439652	0,2577655	278144,59	260993,44	1,0657149	1132890,6	305823,42	3,7043944
29830,187	0,4295656	0,3276197	87392,133	84752,156	1,0311494	428694,95	91051,274	4,7082807
16211,489	0,4053329	0,2784284	52561,686	54021,348	0,9729799	232978,22	58224,995	4,0013437
151032,82	0,4358345	0,3677185	549263,88	525009,78	1,0461974	2170519,7	410729,48	5,2845481
365276,04	1,0570012	0,430444	1077839,7	424802,08	2,537275	5249447,4	848602,9	6,185988
50495,857	0,6063234	0,2243684	213248,43	146517,47	1,4554471	725685	225057,8	3,2244383
84359,358	0,6121109	0,3039919	341758,87	232593,52	1,4693396	1212343,4	277505,29	4,3687219
222852,88	0,4165363	0,2894501	663337,14	663421,34	0,9998731	3202658,7	769918,04	4,1597398
229827,99	0,5318335	0,4039292	781315,98	612010,6	1,276638	3302899,1	568980,85	5,804939
39423,491	0,8526741	0,2262577	153724,23	75104,709	2,0467988	566562,04	174241,51	3,2515905
67991,634	0,492604	0,1657458	251360,23	212572,24	1,1824697	977119,94	410216,22	2,3819632
55792,511	0,6863036	0,3754595	178126	108123,22	1,6474353	801804,16	148597,93	5,3957963
168668,33	0,8171462	0,4035259	547845,44	279296,95	1,961516	2423962,7	417986,32	5,7991436
581872,85	0,7695188	0,3251489	2027354,7	1097535,1	1,8471889	8362198,9	1789558,1	4,672773
876896,31	0,4966603	0,2725642	2815508,9	2361594,9	1,1922065	12602034	3217210,2	3,9170688

4429,798	0,3734618	0,1826052	17487,548	19507,005	0,8964753	63661,42	24258,887	2,6242515
16520,662	0,2523392	0,1680451	88111,074	145463,4	0,6057268	237421,4	98310,895	2,415006
1169,1041	0,3040266	0,1643038	5804,0038	7952,8717	0,7297997	16801,404	7115,5016	2,3612396
135100,33	0,2695306	0,1850187	463887,92	716989,75	0,6469938	1941551,1	730198,19	2,6589371
14471,588	0,3514958	0,1743843	54275,999	64327,345	0,8437469	207973,78	82986,774	2,5061075
5774,7343	0,3044272	0,116188	26758,867	36617,791	0,7307614	82989,741	49701,648	1,6697583
14923,243	0,2690212	0,1657237	57016,713	88292,468	0,645771	214464,6	90048,95	2,3816446
1512,2761	0,3212146	0,0818603	10902,749	14139,976	0,7710586	21733,191	18473,868	1,1764289
3166,761	0,4752043	0,0710123	22245,136	19501,258	1,1407026	45510,089	44594,554	1,0205302

3498,9262	0,48263	0,1104798	20889,796	18031,333	1,1585275	50283,695	31670,285	1,5877247
19560,59	0,689895	0,1968885	117476,64	70937,589	1,6560562	281108,74	99348,566	2,8295198
6669,9739	0,4372205	0,0637701	60944,661	58068,837	1,0495244	95855,389	104594,03	0,9164518
30845,421	0,4458507	0,1355003	138080,53	129018,18	1,0702409	443285,07	227640,94	1,9472994
7715,0691	0,3380156	0,0826209	57668,524	71073,89	0,8113883	110874,64	93379,126	1,18736
14139,203	0,3407458	0,0866271	76427,749	93439,065	0,8179422	203197,02	163219,08	1,2449342
43404,103	0,3530943	0,1973366	178182,78	210224,34	0,847584	623768,14	219949,56	2,83596
17187,898	0,2825282	0,0906632	99577,236	146827,09	0,6781939	247010,36	189579,57	1,3029376
50772,307	0,3049626	0,1091033	293519,64	400957,64	0,7320465	729657,91	465359,89	1,5679433
18014,264	0,3935601	0,0887654	158833,2	168127,28	0,94472	258886,22	202942,38	1,2756636
32608,173	0,3646558	0,0798709	309670,25	353772,67	0,8753368	468617,89	408261,2	1,1478384
5468,707	0,3489364	0,1562106	21701,438	25908,97	0,8376033	78591,767	35008,553	2,2449305
13479,774	0,271923	0,1458698	55294,309	84711,511	0,6527367	193720,24	92409,635	2,0963208
73128,081	0,4400449	0,1348985	383582,97	363136,83	1,0563042	1050936,7	542096,99	1,9386508
3145,3167	0,2669029	0,1911609	10154,598	15849,567	0,6406862	45201,91	16453,77	2,7472068
7671,7173	0,3988322	0,1994971	33865,964	35373,755	0,9573754	110251,62	38455,281	2,8670086
12429,312	0,4222983	0,1929957	56048,695	55290,955	1,0137046	178623,87	64402,033	2,7735751
12303,535	0,317407	0,1318987	60302,448	79145,52	0,7619187	176816,31	93280,15	1,8955405
54336,834	0,3531571	0,133942	291308,03	343631,13	0,8477347	780884,36	405674,21	1,9249051
6285,522	0,413122	0,0597883	49178,286	49591,011	0,9916774	90330,362	105129,62	0,8592285
1351,6265	0,3258997	0,0811079	7981,885	10203,036	0,7823049	19424,466	16664,539	1,1656168
1417,426	0,3814022	0,0805754	9175,865	10022,4	0,9155357	20370,083	17591,297	1,1579637
5882,5732	0,3352791	0,0914081	28534,486	35454,517	0,8048195	84539,513	64355,041	1,3136424
1731,2129	0,3692759	0,0845429	9770,5449	11022,388	0,8864272	24879,571	20477,331	1,2149811
4821,224	0,3734401	0,1174515	24454,276	27279,835	0,8964232	69286,673	41048,654	1,6879158
95303,766	0,4747151	0,2915915	336238,23	295067,89	1,1395284	1369627,5	326839,98	4,1905139
16110,435	0,4662486	0,0633079	134010,69	119737,4	1,119205	231525,95	254477,47	0,9098092
43139,008	0,311336	0,213906	187790,15	251276,26	0,7473454	619958,41	201672,74	3,0740814
53370,817	0,4967172	0,1568977	252211,8	211526,17	1,1923432	767001,56	340163,05	2,2548056
7397,2018	0,5458567	0,15147	32573,536	24859,603	1,3102999	106306,51	48836,083	2,1768026
22461,328	0,2029615	0,1665946	78535,143	161197,49	0,4871983	322795,76	134826,25	2,3941612
80622,88	0,3465621	0,1525793	446721,85	536987,38	0,8319038	1158645,8	528399,74	2,1927449
53009,614	0,3921926	0,1764982	273759,42	290788,74	0,9414375	761810,65	300340,82	2,5364872
4370,1786	0,2842395	0,1365724	27399,76	40157,829	0,6823018	62804,619	31998,993	1,9627061
22605,629	0,4070078	0,1441144	103115,81	105543,25	0,9770005	324869,55	156858,88	2,0710944
27615,166	0,2604007	0,2052476	90837,267	145321,49	0,625078	396862,5	134545,64	2,9496497
12985,133	0,3173855	0,1903219	60428,225	79315,987	0,7618669	186611,66	68227,203	2,7351504
24089,392	0,303526	0,1514919	101796,68	139715,83	0,728598	346192,96	159014,38	2,1771173
100803,15	0,3584474	0,2265318	403405,5	468839,59	0,8604339	1448660,1	444984,52	3,2555291
30410,974	0,4587922	0,1952758	183130,9	166285,18	1,1013062	437041,55	155733,47	2,8063431
15245,24	0,2026216	0,1094256	76522,15	157329,22	0,4863823	219092,07	139320,58	1,5725751
13701,427	0,3622575	0,1182953	65299,022	75092,608	0,8695799	196905,66	115823,91	1,7000432
7599,695	0,327959	0,064443	51800,602	65799,585	0,7872482	109216,58	117928,95	0,9261218
61833,359								
49687,9	0,3464852	0,1205974	232448,43	279479,43	0,8317193	714073,7	412014,51	1,7331275
27060,142	0,5001091	0,1107163	152286,67	126854,27	1,2004852	388886,15	244409,69	1,5911241
49132,043	0,3180096	0,1057979	208612,55	273280,21	0,763365	706085,39	464395,05	1,5204413
13121,392	0,5478068	0,2280257	57287,037	43564,913	1,3149811	188569,87	57543,471	3,2769986
31361,02								
26089,833	0,4046078	0,1118912	116862,34	120322,9	0,9712394	374941,67	233171,37	1,608009
8967,1585	0,2936902	0,042984	61016,13	86549,22	0,7049876	128868,64	208616,14	0,6177309

9241,827	0,4723452	0,0566975	73791,852	65081,399	1,1338394	132815,95	163002,27	0,8148104
20417,175	0,3575066	0,1929419	75497,263	87974,139	0,8581756	293418,88	105820,34	2,7728023
817,49767	0,4220123	0,0273357	12140,497	11984,483	1,013018	11748,405	29905,901	0,3928457
3290,8091	0,5432222	0,5197936	7831,3316	6005,7327	1,303976	47292,807	6330,9924	7,4700464
6037,3358	0,3548323	0,0800092	35785,212	42013,449	0,8517561	86763,634	75457,981	1,1498271

6445,9728

128,86016

1885,0507

8930,7863

2618,43

306,87315

1803,4293

5027,7937	0,5834295	0,1576059	19304,827	13784,325	1,4004913	72255,323	31901,058	2,264982
15123,307	0,5389672	0,1401595	82531,89	63792,172	1,293762	217339,76	107900,66	2,0142579
16245,486	0,4219764	0,1238844	100765,83	99479,381	1,0129318	233466,79	131134,25	1,7803647
14110,869	0,3819973	0,0740584	122781,79	133900,32	0,9169641	202789,83	190536,94	1,0643071
14104,964	0,4540377	0,2286379	61462,526	56393,156	1,0898933	202704,97	61691,287	3,2857957
8756,2327	0,4399379	0,0553157	59484,236	56327,23	1,0560476	125837,39	158295,56	0,7949521
6452,167	0,447929	0,056315	44548,674	41431,772	1,0752297	92725,248	114572,89	0,8093123
15092,877	0,3931635	0,0617322	115470,43	122350,43	0,9437681	216902,44	244489,68	0,887164
9045,8624	0,2781218	0,0911257	72768,704	108997,75	0,6676166	129999,71	99268,009	1,3095831
76096,072	0,4113105	0,1625042	296421,69	300225,88	0,9873289	1093590,3	468271,38	2,3353771
11778,695	0,4602247	0,0977368	58730,825	53162,344	1,1047448	169273,74	120514,47	1,4045926
22972,423	0,4064848	0,1280941	119526,2	122497,35	0,9757451	330140,81	179340,24	1,8408629
1722,6097	0,3461181	0,0756078	7745,137	9322,0774	0,8308381	24755,933	22783,497	1,086573
10541,301	0,3515652	0,0788956	47241,643	55979,239	0,8439136	151490,93	133610,69	1,1338234
3754,0371	0,3250347	0,0675902	44012,715	56410,043	0,7802284	53949,939	55541,163	0,9713506
44126,247	0,4390465	0,0602123	331636,45	314673,16	1,0539076	634146,2	732844,28	0,8653219

11263,913	0,66458	0,0597857	88320,029	55363,03	1,5952889	161875,71	188404,8	0,859191
21615,647	0,4244144	0,058835	148704,81	145963,02	1,0187842	310642,34	367394,06	0,845529
10758,313	0,5892466	0,0751791	46747,02	33049,491	1,4144551	154609,64	143102,46	1,0804122
516,68178	0,8868916	0,0688806	3540,4317	1663,0052	2,128936	7425,3264	7501,123	0,9898953
769,89723	0,5911781	0,0881575	4743,4409	3342,5897	1,4190916	11064,331	8733,2044	1,2669268
654,26468	0,6756194	0,0533228	4609,031	2841,9437	1,6217883	9402,5549	12269,884	0,7663117
1167,0142	0,931229	0,0444541	10507,411	4700,5335	2,2353656	16771,37	26252,146	0,6388571
1663,1123	0,6227971	0,0604786	13959,204	9337,3152	1,4949912	23900,885	27499,197	0,8691484
7526,7653	0,6696869	0,0483963	77806,212	48400,559	1,6075478	108168,49	155523,47	0,6955124
7945,4617	0,5136678	0,0422428	82678,765	67053,206	1,2330322	114185,65	188090,11	0,6070795
4574,7044	0,4733417	0,03809	33769,313	29720,452	1,1362315	65743,897	120102,35	0,5473989
2602,064	0,510111	0,0315028	22528,884	18398,52	1,2244943	37394,727	82597,951	0,4527319
5178,3128	0,4558378	0,1011639	28927,698	26436,957	1,0942144	74418,461	51187,354	1,4538447
9017,5808	0,6644436	0,1474014	25032,851	15694,958	1,5949614	129593,27	61177,028	2,1183322
20368,656	0,5570799	0,1256391	88216,756	65969,249	1,3372406	292721,6	162120,37	1,8055819
22804,58	0,9451667	0,1050428	163781,43	72187,864	2,2688222	327728,7	217097,9	1,5095894
16161,205	0,7884069	0,089964	104899,04	55427,975	1,8925288	232255,58	179640,89	1,2928881
212,94903	0,5795692	0,0378519	2958,8521	2126,7964	1,3912249	3060,3287	5625,8478	0,5439764
13481,23	0,734403	0,1592205	48922,047	27750,965	1,7628954	193741,18	84670,172	2,2881869
32049,167	1,0081983	0,0533541	297528,38	122939,19	2,4201264	460584,32	600688,03	0,7667613
14423,243	0,4446787	0,0518929	133547,75	125111,77	1,0674276	207279,01	277942,56	0,745762
11001,794	0,3531808	0,0587347	90041,459	106207,06	0,8477916	158108,75	187313,38	0,8440868
14864,752	0,709711	0,0630877	132632,92	77853,423	1,7036234	213624,01	235620,56	0,9066442

14565,285	1,3543461	0,1116653	101916,13	31348,818	3,2510357	209320,32	130437	1,6047619
11810,11	0,7508098	0,0730825	73617,06	40846,651	1,802279	169725,2	161599,7	1,0502816
11720,736	0,8520618	0,1217082	58131,559	28421,618	2,045329	168440,8	96301,917	1,7490908
22341,922	0,7724674	0,1100644	127356,54	68682,963	1,8542669	321079,76	202989,46	1,5817558
13470,455	0,7479468	0,1035039	79572,434	44320,013	1,7954064	193586,32	130144,45	1,4874727
27074,98	0,9684635	0,0662789	230786,25	99273,792	2,324745	389099,39	408500,47	0,9525066
29053,017	0,5658501	0,0344265	581137,62	427844,09	1,358293	417526,1	843915,08	0,494749
62316,035	0,5713702	0,2123097	154787,92	112856,73	1,3715436	895554,89	293514,84	3,05114
7968,8159	0,7081773	0,0579167	58474,461	34397,918	1,6999418	114521,28	137590,98	0,8323313
11298,37	0,5691891	0,0721677	83627,793	61207,13	1,366308	162370,9	156557,16	1,0371349
2003,5946	0,7317234	0,163741	6259,221	3563,5372	1,7564629	28794,017	12236,365	2,3531513
4884,3606	0,5950543	0,0755325	22093,066	15467,045	1,428396	70194,02	64665,67	1,0854913
9659,2059	0,3826286	0,1531371	40034,21	43587,479	0,9184796	138814,18	63075,544	2,2007607
8597,5422	0,9908312	0,0735426	56431,118	23726,131	2,3784374	123556,82	116905,56	1,0568943
2178,4902	0,3571757	0,0546109	24845,859	28978,776	0,8573813	31307,472	39891,136	0,7848228
3005,4872	0,4164672	0,0622066	24636,756	24643,967	0,9997074	43192,395	48314,579	0,8939826
1701,7438	0,6705715	0,0735066	14322,078	8897,5184	1,6096711	24456,065	23150,913	1,0563758
3734,2563	0,9697661	0,0660715	28343,814	12175,849	2,3278717	53665,666	56518,452	0,9495247
851,29723	0,5522727	0,0590943	8671,2382	6540,8689	1,3257013	12234,145	14405,739	0,8492549
2441,055	1,0225612	0,0657985	18629,616	7589,6636	2,4546037	35080,838	37098,961	0,9456016
3410,061	0,9616666	0,0724526	22464,66	9731,5772	2,3084295	49006,597	47066,124	1,0412287
22670,907	1,177552	0,2969826	696498,06	246404,01	2,8266507	325807,67	76337,493	4,2679901
2955,0425	0,467623	0,0669406	58511,842	52126,175	1,122504	42467,445	44144,228	0,9620158
7915,8563	0,5452705	0,0848465	36472,529	27865,176	1,3088928	113760,19	93296,184	1,2193445

194111,84	0,3112943	0,2327254	551786,03	738426,78	0,7472454	2789616	834081,12	3,344538
32712,532	0,3712706	0,2000285	80344,623	90151,758	0,8912153	470117,65	163539,38	2,874645
234909,28	0,3946063	0,2200995	575533,54	607595,52	0,9472314	3375923,3	1067286,7	3,1630894
59321,556	0,2444347	0,3453096	103313,17	176076,28	0,5867524	852520,7	171792,36	4,9625065
40345,944	0,2817408	0,347528	72195,991	106750,82	0,6763039	579818,79	116094,09	4,9943867
67684,686	0,3827259	0,3980273	142542,77	155154,82	0,9187131	972708,74	170050,34	5,7201223
22228,006	0,3492147	0,2416743	51552,978	61499,159	0,8382713	319442,65	91975,038	3,4731451
60068,314	0,5141264	0,1747617	219788,35	178091,29	1,2341331	863252,5	343715,48	2,5115322
409936,66	0,195034	0,1723528	1029134,8	2198214	0,4681686	5891273,1	2378473,5	2,4769135
16535,98	0,2534755	0,3686204	27095,847	44532,252	0,6084544	237641,54	44859,106	5,2975094
1349657,8	0,2465508	0,322438	2893620,6	4889259,5	0,5918321	19396175	4185790,8	4,6338136
31073,262	0,3273781	0,2367119	82631,579	105148,82	0,7858536	446559,4	131270,38	3,4018291
47130,176	0,4608093	0,2174053	159340,14	144049,54	1,1061481	677316,2	216784,9	3,1243698
183266	0,3513171	0,2507171	368094,2	436483,26	0,843318	2633748,5	730967,33	3,6031001
270250,47	0,3618017	0,2582615	541008,19	622932,71	0,8684857	3883817,9	1046421,9	3,7115221
73575,7	0,2500606	0,2486362	172000,21	286544,26	0,600257	1057369,6	295917,12	3,5731949
26234,601	0,2918804	0,1872921	77433,703	110517,99	0,7006434	377022,15	140073,16	2,6916087
10963,828	0,6956904	0,0875583	85085,307	50950,273	1,6699676	157563,14	125217,45	1,2583161
14035,628	0,2737947	0,1237096	63804,175	97080,491	0,6572296	201708,53	113456,28	1,7778525
207780,08	0,2035211	0,1630345	561890,81	1150139,3	0,4885415	2986044,8	1274454,4	2,3429985
54862,431	0,3573898	0,4102074	85367,898	99508,554	0,8578951	788437,82	133743,16	5,8951638
72191,216	0,2352491	0,3483239	104267,78	184641,84	0,5647029	1037472,9	207253,14	5,0058246
7658,3311	0,4825621	0,0795762	63094,754	54468,821	1,1583646	110059,25	96238,912	1,1436044
428691,94	0,2773335	0,2549878	1065250,4	1600137,7	0,6657242	6160808,7	1681225	3,664476
57413,187	0,5598965	0,1364343	303254,85	225635,78	1,3440016	825095,2	420811,95	1,9607219
9672,7341	0,2203424	0,2141419	23407,195	44254,683	0,5289202	139008,59	45169,748	3,0774711
19317,725	0,421659	0,1984271	74461,655	73566,349	1,01217	277618,48	97354,26	2,8516316

491466,23	0,2637051	0,2991638	1036344,5	1637169,1	0,6330101	7062949,2	1642799,6	4,2993371
5746,6704	0,3052278	0,0832203	39774,467	54286,051	0,732683	82586,429	69053,712	1,1959738
77361,973	0,2709735	0,2028935	174832,96	268784,57	0,6504576	1111782,8	381293,41	2,9158195
95054,217	0,2808985	0,1971778	223405,27	331323,26	0,6742819	1366041,2	482073,73	2,8336768
20106,481	0,3552617	0,1814067	59060,505	69255,895	0,8527867	288953,84	110836,51	2,6070277
20650,833	0,3581629	0,1526093	77096,295	89672,818	0,859751	296776,82	135318,34	2,1931751
20829,898	0,3323357	0,1490276	71110,521	89138,385	0,7977542	299350,2	139772,04	2,141703
29941,674	0,4249354	0,1137565	181993,49	178418,89	1,0200348	430297,16	263208,52	1,6348147
16819,434	0,3045863	0,2798661	40591,626	55518,019	0,7311433	241715,1	60098,155	4,0220053
100326,9	0,2903082	0,2489992	264316,12	379290,71	0,6968695	1441815,9	402920,59	3,5784121
244535,67	0,3145391	0,3115268	497776,48	659276,5	0,7550345	3514265,8	784958,65	4,4770076
36589,4	0,2908598	0,0412605	365120,4	522950,28	0,6981933	525832,81	886790,05	0,592962
318,90042	0,3146935	0,0446033	3197,3822	4232,6727	0,755405	4582,975	7149,7113	0,6410014
5401,3615	0,3364269	0,0545336	49601,436	61420,24	0,8075748	77623,933	99046,449	0,7837124
2572,5372	0,3917323	0,0740057	20277,211	21563,875	0,9403324	36970,393	34761,335	1,0635493
21183,797	0,2329823	0,291539	37539,412	67123,176	0,5592616	304436,14	72661,965	4,1897592
191671,45	0,2664385	0,2671238	465812,2	728319,16	0,6395715	2754544,7	717537,98	3,8388834
116785,88	0,2366358	0,2635249	255383,7	449594,19	0,5680316	1678350,8	443168,32	3,7871633
104835,89	0,2651809	0,1327624	418333,43	657185,87	0,6365527	1506615,3	789650,58	1,9079519
187751,55	0,2630863	0,1190676	687706,37	1088962,1	0,6315246	2698211,2	1576848,9	1,7111413
89842,534	0,2164628	0,0784311	359689,79	692233,88	0,5196073	1291143,1	1145497	1,1271467
86201,048	0,3328306	0,3053905	211199,2	264348,53	0,7989422	1238810,7	282264,97	4,388822
12582,484	0,1932137	0,2773266	26912,678	58026,577	0,4637992	180825,13	45370,642	3,9855097
14755,476	0,2387081	0,2079258	39752,126	69374,692	0,5730062	212053,59	70965,11	2,9881387
940,23893	0,2325881	0,1390196	1584,9743	2838,8516	0,5583153	13512,342	6763,3548	1,9978757
2217,8378	0,3007302	0,1461222	4208,4328	5829,7685	0,7218868	31872,944	15177,968	2,0999481
3139,8566	0,3175338	0,1427557	6939,0155	9103,6548	0,762223	45123,441	21994,617	2,0515675
2105,3357	0,2703276	0,1414366	3903,083	6014,8577	0,648907	30256,157	14885,365	2,032611
1143,7529	0,357234	0,1304526	3410,057	3976,6446	0,8575212	16437,077	8767,5726	1,8747581
321,25276	0,3461329	0,1312872	867,6089	1044,2128	0,8308737	4616,7809	2446,9472	1,8867513

18950,759	0,3685997	0,0408314	187242,49	211620,32	0,8848039	272344,75	464121,93	0,5867957
4827,9985	0,3998344	0,0320121	60243,414	62767,868	0,9597811	69384,031	150817,79	0,460052
20983,42	0,3932391	0,0717964	153561,6	162679,89	0,9439495	301556,49	292262,69	1,0317995
14821,535	0,4520216	0,0383664	170832,78	157441,77	1,0850537	213002,94	386315,44	0,5513705
3754,9188	0,4279013	0,0231095	55156,856	53698,712	1,0271542	53962,611	162483,68	0,332111
247,73806	0,4604716	0,0461021	2908,268	2631,1129	1,1053376	3560,288	5373,6848	0,6625413
18813,304	0,3942662	0,0300995	300600,97	317620,67	0,946415	270369,36	625037,84	0,4325648
644,4408	0,4567571	0,0399333	7914,1097	7218,1297	1,0964211	9261,3741	16137,913	0,5738892
9878,7561	0,3350613	0,1088536	62290,235	77446,827	0,8042968	141969,37	90752,659	1,564355
13811,651	0,4736896	0,0527085	134036,07	117878,8	1,1370668	198489,72	262038,39	0,7574833
582,91886	0,5037874	0,0347489	9804,3742	8107,3792	1,2093149	8377,2312	16775,175	0,4993826
1935,0945	0,5135679	0,0545729	21438,13	17389,895	1,2327923	27809,59	35458,907	0,7842766
1007,1958	0,5087698	0,0408408	13950,452	11422,861	1,2212748	14474,591	24661,496	0,5869308
4795,5745	0,4681946	0,0387533	63894,88	56852,239	1,1238762	68918,06	123746,35	0,55693
8020,4642	0,5119758	0,0390935	107020,48	87081,394	1,2289706	115263,53	205160,86	0,5618202
32969,803	0,4942968	0,109619	211485,9	178238,51	1,1865331	473814,94	300767,13	1,5753548
1669,1809	0,5398744	0,0237101	36025,505	27798,75	1,2959397	23988,097	70399,445	0,3407427
5000,7937	0,4894585	0,0416363	62825,37	53472,081	1,1749191	71867,302	120106,64	0,5983625
26672,624	0,4810041	0,0340197	412767,81	357490,89	1,1546247	383317,06	784033,72	0,4889038
48779,745	0,5157311	0,0367925	737697,89	595885,97	1,237985	701022,45	1325807,4	0,5287514
21608,535	0,5101489	0,0426456	294406,98	240413,62	1,2245853	310540,13	506700,77	0,6128669

6845,3073	0,6005542	0,0507221	78739,826	54619,806	1,4415984	98375,137	134957,08	0,7289365
39103,803	0,5818268	0,1301215	160567,75	114966,83	1,3966442	561967,75	300517,55	1,8699998
2105,1405	0,5590974	0,0548247	22610,132	16847,037	1,3420836	30253,352	38397,664	0,7878956
1794,7318	0,481724	0,044604	19798,249	17121,29	1,1563527	25792,413	40236,99	0,6410125
537,617	0,4662501	0,01998	12905,964	11531,332	1,1192084	7726,1901	26907,769	0,287136
11187,68	0,4790988	0,0248252	227556,51	197866,42	1,1500512	160780,15	450657,67	0,3567678
9870,623	0,479326	0,0463158	110437,43	95982,753	1,1505966	141852,49	213115,87	0,6656121
10953,451	0,5092275	0,0495277	116254,56	95105,604	1,2223734	157414,01	221157,98	0,7117718
11731,825	0,3204328	0,0803053	79069,091	102796,36	0,7691818	168600,15	146090,31	1,1540817
4828,0645	0,510973	0,0601375	54892,922	44753,43	1,2265635	69384,98	80283,753	0,8642468
14031,506	0,529742	0,3178303	43752,328	34406,83	1,2716175	201649,28	44147,791	4,5675962
2665,1042	0,4518878	0,032953	38381,731	35383,587	1,0847326	38300,689	80875,922	0,4735734
390,97681	0,5047954	0,0215487	9061,3783	7478,023	1,2117345	5618,7978	18143,857	0,3096805
462,65316	0,5096829	0,0210168	10519,406	8598,0323	1,2234667	6648,8715	22013,442	0,3020369
715,72524	0,5076459	0,0504259	7620,073	6253,2554	1,218577	10285,816	14193,614	0,7246791
8759,2317	0,3235845	0,041878	77827,932	100197,22	0,7767474	125880,49	209160,75	0,6018361
219,42541	0,7124727	0,0808045	13162,885	7696,4564	1,7102526	3153,4019	2715,5113	1,1612553
1592,6481	0,7668873	0,2460702	21914,028	11904,155	1,8408722	22888,232	6472,3326	3,5363188

35891,303
8655,134
8613,8591
11048,516
6794,1812
40515,288

2569,7117	0,1708726	0,1689384	10931,752	26651,72	0,4101706	36929,786	15210,94	2,4278437
12502,366	0,2723697	0,1139872	75718,889	115811,96	0,6538089	179673,75	109682,2	1,6381304
5542,8718	0,2660588	0,093143	36496,653	57145,672	0,63866	79657,603	59509,26	1,3385749
187,99201	0,2466799	0,2173538	964,29159	1628,4803	0,592142	2701,6669	864,91261	3,1236299
1101,3686	0,0801205	0,3324365	1818,4216	9454,9402	0,192325	15827,966	3313,0196	4,7775045

17783,242

18785,054	0,2280361	0,1445569	91572,088	167289,05	0,5473884	269963,37	129949,18	2,0774534
15005,989	0,2056068	0,1651284	87651,14	177593,9	0,4935481	215653,75	90874,691	2,3730892
19015,717	0,2063724	0,1087834	169406,55	341968,77	0,495386	273278,28	174803,46	1,5633459
13588,1	0,2333753	0,2061732	57706,86	103010,27	0,5602049	195277,02	65906,238	2,962952
44996,089	0,3630043	0,1831385	229402,37	263265,57	0,8713725	646646,85	245694,32	2,6319162
86387,688	0,3190298	0,1857775	416656,56	544070,18	0,765814	1241492,9	465006,09	2,6698423
9123,5319	0,1687355	0,2865294	20995,25	51834,924	0,4050406	131115,91	31841,525	4,1177647
11035,681	0,2095355	0,3656893	23569,563	46859,951	0,5029788	158595,75	30177,753	5,2553862
59622,652	0,2281237	0,2536432	205434,16	375154,57	0,5475987	856847,81	235065,02	3,6451523
14728,743	0,1794251	0,1215231	86755,402	201428,61	0,4307005	211669,4	121201,17	1,7464303
8582,7243	0,3412783	0,0828162	57069,009	69662,59	0,8192203	123343,87	103635,87	1,1901657
17404,215	0,2708264	0,1618982	77495,367	119204,48	0,6501045	250119,09	107500,96	2,3266684
36731,665	0,2875481	0,1533673	202566,27	293470,53	0,690244	527877,33	239501,3	2,2040688
22592,266	0,1386896	0,1638206	77889,276	233960,06	0,332917	324677,5	137908,59	2,354295
22880,034	0,3300623	0,0977336	186220,12	235038,28	0,792297	328813,06	234106,1	1,4045472
13749,259	0,2692007	0,059242	112654,68	174333,54	0,646202	197593,06	232086,14	0,8513781
6307,0599	0,2390402	0,155732	33586,181	58532,563	0,5738034	90639,888	40499,435	2,2380532
19680,326	0,3284964	0,0971287	150331,52	190645,84	0,7885382	282829,49	202621,21	1,3958533
51205,029	0,1833958	0,2429938	195419,42	443901,14	0,4402319	735876,64	210725,64	3,4921078
15245,189	0,2416602	0,2156785	62032,566	106935,67	0,5800924	219091,34	70684,792	3,0995541
51657,774	0,3260454	0,2160555	225436,58	288040,98	0,7826545	742383,12	239094,92	3,1049724

2137,2981	0,1877771	0,1688905	7571,7174	16798,085	0,4507489	30715,494	12654,936	2,4271552
2134,5312	0,2495574	0,2085635	7907,1015	13199,417	0,5990493	30675,731	10234,443	2,9973032
35805,423	0,3144663	0,2550124	139961,64	185414,16	0,7548595	514566,14	140406,57	3,6648295
124200,43	0,300797	0,2681994	528759,6	732306,16	0,7220472	1784906,6	463089,84	3,854342
6215,4435	0,2191292	0,1728971	89559,244	170262,18	0,5260079	89323,251	35948,796	2,4847356

6936,1598

20368,006	0,3541052	0,0385635	138808,41	163301,95	0,8500107	292712,27	528168,06	0,5542029
10426,098	0,4168154	0,0373879	79928,908	79885,521	1,0005431	149835,33	278863,17	0,5373077

7741,6851

21345,641

8264,6163

10815,369	0,2864955	0,0746	60004,335	87251,474	0,6877172	155429,6	144978,22	1,0720893
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4626,9429

19068,798

11074,322

12522,787

386,19696	0,2672792	0,0325515	3051,8063	4756,6344	0,6415894	5550,1056	11864,178	0,4678036
1927,5941	0,3853046	0,0172594	26883,778	29066,587	0,9249031	27701,8	111683,93	0,2480375

17410,1

4018,7211

1491,6322

9313,1908

2107,1595

5701,2671

11140,346	0,4686675	0,0643777	82428,876	73269,365	1,1250115	160099,9	173046,64	0,9251835
4228,2414	0,3047243	0,0309124	35676,721	48773,701	0,7314745	60764,814	136781,35	0,4442478
1917,0016	0,3293012	0,0292965	18899,971	23909,788	0,79047	27549,573	65434,603	0,4210245
32763,46	0,3469125	0,0286078	412953,59	495894,37	0,8327451	470849,55	1145263,2	0,4111278
19641,382	0,4254938	0,0627806	152731,16	149534,84	1,0213751	282269,82	312857,69	0,9022307
22289,433	0,2845548	0,1065036	82115,041	120216,7	0,6830585	320325,43	209283,47	1,5305816
7217,4368	0,3764399	0,0997117	34284,188	37940,769	0,9036239	103723,08	72383,056	1,4329745
3087,9402	0,332312	0,0420108	30438,332	38157,751	0,7976972	44377,342	73503,442	0,6037451
6535,3404	0,3284949	0,0728685	38340,664	48622,686	0,7885345	93920,547	89686,796	1,047206
1490,4006	0,3123664	0,0365349	10963,764	14621,883	0,7498189	21418,815	40793,898	0,5250495
4439,7521	0,4096854	0,0672199	26943,368	27397,402	0,9834278	63804,472	66048,165	0,9660294
13689,138	0,4039532	0,0463661	106131,48	109451,33	0,9696682	196729,05	295240,48	0,6663349

2636,7624

5228,0846	0,4290067	0,0280206	57817,619	56144,095	1,0298077	75133,74	186579,96	0,4026892
8236,898	0,4913996	0,0294796	91697,436	77737,455	1,1795786	118373,94	279409,77	0,4236571
776,29525	0,3334296	0,0466078	4175,1501	5216,4603	0,8003799	11156,278	16655,913	0,6698088

2865,7024

1353,5842

22573,889

7269,5651	0,4334513	0,0538506	56633,223	54430,069	1,0404768	104472,22	134995,19	0,7738959
4120,1526	0,2936903	0,0264023	34687,561	49203,059	0,7049879	59211,451	156052,7	0,3794324
49285,641	0,3888112	0,0644757	345644,9	370338,89	0,9333206	708292,77	764406,05	0,9265923
1483,9206	0,3945296	0,0652701	9069,7137	9576,8323	0,9470473	21325,689	22735,089	0,9380077

7021,931

32993,042

1199,7639

1319,472

714,06047
3525,2251
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594,29436
1085,8766
182,15072

96226,853	0,3407675	0,2070775	438318,63	535845,67	0,8179942	1382893,3	464689,94	2,9759485
343568,59	0,581856	0,1407394	2627228,3	1881006,3	1,3967142	4937485,7	2441168	2,0225915
28575,305	0,2830314	0,1936018	177486,82	261239,88	0,6794017	410660,83	147598,31	2,7822867
5489,7027	0,3297702	0,2032435	32079,818	40525,501	0,7915958	78893,501	27010,465	2,9208494
107688	0,3312566	0,3104277	305063,1	383648,12	0,7951638	1547603,6	346902,09	4,4612115
13975,926	0,2684494	0,147583	67462,101	104690,03	0,6443985	200850,53	94698,741	2,1209419
197796,71	0,3482381	0,4478313	619872	741538,4	0,8359271	2842571,9	441676,82	6,4358639
29985,704	0,3642825	0,3881537	102919,7	117697,74	0,8744407	430929,92	77252,14	5,5782263
9962,1461	0,2023941	0,0568802	89731,002	184693,88	0,4858364	143167,78	175142,46	0,8174362
3415,5667	0,088818	0,1343135	7526,1922	35300,595	0,213203	49085,721	25429,802	1,930244
2828,6694	0,0946061	0,1151535	7228,3778	31829,476	0,227097	40651,314	24564,336	1,6548916
9909,6997	0,5553091	0,4562246	29807,698	22361,532	1,33299	142414,07	21721,098	6,5564858
16149,47	0,2214143	0,1093345	124572,54	234382,19	0,5314932	232086,92	147707,05	1,571265
17394,791	0,1902156	0,1146716	143172,87	313561,33	0,4566024	249983,65	151692,23	1,6479661
41417,802	0,3374442	0,2124753	175738,23	216956,31	0,8100167	595222,64	194929,96	3,0535206
13515,006	0,2387582	0,1498924	74637,237	130228,24	0,5731263	194226,56	90164,705	2,1541308
15574,646	0,172209	0,1561772	59638,84	144271,72	0,4133786	223826,03	99724,183	2,2444509
24974,735	0,1712263	0,2285332	126414,8	307563,97	0,4110195	358916,39	109282,76	3,2842911
60626,709	0,2809585	0,3200046	172451,31	255700,94	0,6744258	871277,29	189455,77	4,5988428
64658,629	0,2813007	0,3436774	180918,98	267929,89	0,6752475	929220,74	188137,59	4,9390489
29957,102	0,2312337	0,2057807	122399,54	220514,19	0,5550642	430518,87	145577,77	2,9573119
39310,446	0,2293089	0,1865145	157293,86	285758,27	0,5504438	564937,46	210763,43	2,6804339
31797,999	0,2645513	0,219954	124176,24	195540,41	0,6350413	456974,74	144566,59	3,1609983
55492,599	0,3117014	0,2812483	216872,44	289850,18	0,7482225	797494,08	197308,19	4,0418701
147337,44	0,2859095	0,3438464	482719,5	703354,48	0,6863104	2117412,8	428497,91	4,9414775
67974,713	0,3386266	0,3570099	232066,43	285495,4	0,8128552	976876,76	190400,07	5,1306533
58491,438	0,3476504	0,1848169	418690,29	501716,21	0,8345162	840590,93	316483,18	2,6560367
17027,079	0,2700119	0,1296383	116749,37	180127,33	0,6481491	244699,2	131342,96	1,8630554
13917,176	0,3772293	0,1271422	90368,372	99797,336	0,9055189	200006,22	109461,48	1,8271836
7200,5891	0,3101736	0,1833183	51718,253	69461,943	0,7445552	103480,96	39279,162	2,6345001
7030,365	0,327962	0,1246871	41288,564	52446,211	0,7872554	101034,63	56384,075	1,7919002
31949,185	0,2275281	0,1066953	133593,97	244601,87	0,5461691	459147,46	299443,13	1,5333378
283708,67	0,2566367	0,1702755	1256266,4	2039251,8	0,6160428	4077228,1	1666174,4	2,4470597
21160,512	0,2752276	0,085864	256949,09	388922,48	0,6606692	304101,51	246442,31	1,2339663
542814,27	0,2502098	0,1885998	2168796,5	3610958	0,6006153	7800881,1	2878127,8	2,7104012
298770,86	0,2909499	0,1942269	1283903,1	1838323,5	0,6984098	4293689,6	1538256,5	2,7912702
135964,3	0,2526625	0,1503615	623659,26	1028287,6	0,6065028	1953967,3	904249,56	2,1608717
309207,52	0,2451542	0,168016	1360962	2312675,2	0,5884795	4443676,7	1840346	2,4145876
136905,43	0,2909286	0,2170904	686074,72	982410,28	0,6983587	1967492,5	630637,83	3,1198453
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196763,79	0,4651219	0,1774939	1503644,3	1346747,6	1,1165004	2827727,6	1108566,8	2,5507959
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5286,1392	0,1919396	0,1118494	27942,939	60647,846	0,4607408	75968,053	47261,233	1,6074073
10457,457	0,2071363	0,1427792	57793,739	116233,82	0,4972197	150285,98	73242,167	2,0519052

24214,876 0,1641619 0,2064376 85677,603 217421,65 0,394062 347996,31 117298,79 2,966751

2668,5791 0,6739673 0,355719 7144,2872 4415,9895 1,6178225 38350,628 7501,9304 5,1121013
1230,2376 0,8387729 0,0989093 7818,5757 3883,2128 2,0134296 17679,965 12438,033 1,4214438
9104,4681 0,6826008 0,0831971 64593,451 39421,182 1,6385468 130841,94 109432,48 1,1956409
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96671,69 0,9111329 0,4065875 284129,98 129910,2 2,1871261 1389286,2 237763,54 5,8431422
5868,5329 0,4739854 0,2844393 16902,585 14855,802 1,1377767 84337,737 20631,935 4,0877279
33647,326 0,8685349 0,2464776 123232,25 59107,832 2,0848717 483551,75 136512,73 3,5421734
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24714,116 0,7347216 0,3171658 74592,722 42294,277 1,7636599 355170,99 77921,757 4,5580464
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986,68472 0,4848184 0,072967 7682,8665 6601,6449 1,1637806 14179,823 13522,338 1,0486222
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8697,6638 0,606364 0,0305491 139043,88 95527,056 1,4555445 124995,68 284710,88 0,4390267
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10917,139 0,2918802 0,0325101 191348,4 273104,02 0,7006429 156892,16 335807,57 0,4672085
11613,326 0,388264 0,035432 178484,09 191505,09 0,9320071 166897,18 327763,57 0,5091999

14182,988	0,409405	0,0307472	195592,76	199024,97	0,9827549	203826,27	461277,49	0,4418734
6788,6533	0,3363866	0,0235115	109334,01	135401,82	0,8074781	97560,952	288737,97	0,3378875
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14837,077	0,42307	0,0442116	144005,64	141799,68	1,0155569	213226,29	335592,11	0,6353734
7099,0501	0,3407377	0,0369334	88850,265	108629,18	0,8179226	102021,72	192212,08	0,5307768
49595,734	0,3065563	0,0269013	760010,03	1032802	0,735872	712749,18	1843618,3	0,3866034
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2751,3944	0,3004469	0,0355518	31926,666	44268,399	0,7212067	39540,781	77391,201	0,5109209
52580,113	0,2956732	0,0271141	791752,87	1115541,3	0,7097477	755638,21	1939218,1	0,3896613
4379,8626	0,3542779	0,0348977	61126,254	71877,282	0,8504252	62943,789	125505,69	0,5015214
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17171,188	0,4877863	0,0558343	159597,13	136302,38	1,1709049	246770,22	307538,49	0,8024043
10893,246	0,4096319	0,0662517	84941,713	86384,372	0,9832995	156548,78	164422,16	0,9521149
10036,085	0,4132711	0,0496256	98648,873	99440,885	0,9920354	144230,37	202235,98	0,7131786
4689,1054	0,4435104	0,0587254	39051,72	36681,267	1,064623	67387,973	79847,951	0,8439537
5224,241	0,4920835	0,0458009	61114,447	51738,398	1,1812203	75078,502	114064,04	0,6582136
37840,761	0,4360362	0,0286069	573171,03	547607,84	1,0466816	543816,35	1322786,5	0,4111142
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9370,8292	0,4815053	0,0486846	84007,756	72681,892	1,1558279	134669,86	192480,46	0,6996547
18596,583	0,4095311	0,0668773	125145,94	127302,76	0,9830575	267254,82	278070,07	0,961106
3339,346	0,4401083	0,0811248	21463,217	20316,232	1,0564566	47990,339	41163,05	1,1658597
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35294,707	0,2706386	0,0313923	357611,03	550464,3	0,6496534	507226,55	1124312,3	0,4511438
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22666,534	0,3523612	0,0914669	158355,84	187220,72	0,8458243	325744,82	247811,28	1,3144874
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7741,6851								
21345,641								
8264,6163								
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4626,9429								
19068,798								
11074,322								
12522,787								
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17410,1								
4018,7211								
1491,6322								
9313,1908								
2107,1595								

5701,2671

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1097,994

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8935,4218
17408,417
1360,5239

1861,5722	0,3739672	0,0305373	24604,118	27408,311	0,8976882	26752,987	60960,681	0,4388564
3250,4219	0,4287974	0,0214694	54392,489	52843,884	1,0293053	46712,395	151397,73	0,3085409
5862,8863	0,4556894	0,0336498	71052,081	64955,488	1,093858	84256,589	174232,22	0,4835879
18,15436	0,3890748	0,0252475	293,72413	314,4955	0,9339534	260,89955	719,05435	0,362837
3505,4189	0,2720854	0,0253572	47576,668	72844,502	0,6531264	50377,003	138241,74	0,3644124
15,887094	0,4287763	0,0440518	147,31698	143,12978	1,0292546	228,31627	360,64594	0,633076
37,465406	0,378497	0,0380936	437,60691	481,64788	0,9085619	538,42205	983,50795	0,5474506
6846,2444	0,2948846	0,0417244	58708,266	82938,305	0,7078547	98388,604	164082,55	0,5996287
712,00281	0,4481701	0,0640263	5684,5055	5283,9379	1,0758085	10232,32	11120,471	0,9201337
10172,731	0,4119895	0,073274	97221,073	98306,489	0,9889589	146194,14	138831,42	1,0530335
99,559933	0,367749	0,0462058	916,99797	1038,783	0,8827618	1430,7936	2154,7057	0,664032

237,91609	0,3102558	0,0625656	1321,3464	1774,209	0,7447524	3419,1348	3802,6659	0,8991415
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5916,9912	0,5330855	0,0587869	48046,182	37546,544	1,2796433	85034,14	100651,49	0,8448374
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12335,908	0,5004489	0,0330656	134884,4	112281,94	1,2013009	177281,54	373073,61	0,4751919
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9736,6817	0,4814734	0,0426498	92671,238	80182,681	1,1557513	139927,6	228293,77	0,6129278
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8337,7373	0,5142578	0,0350245	91985,87	74515,763	1,2344485	119823,12	238054,39	0,5033434
13,16279	0,2355915	0,0585866	44,643854	78,942331	0,5655249	189,16481	224,67237	0,8419585
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45178,98	0,5180483	0,0389167	517482,78	416134,33	1,2435474	649275,22	1160914	0,5592793
14249,898	0,4375959	0,1140476	77337,365	73624,788	1,0504256	204787,84	124946,91	1,6389989
10690,297	0,4315026	0,0336124	151069,79	145848,55	1,035799	153632,18	318046,33	0,4830497
6860,0376	0,6203342	0,103327	40609,728	27271,705	1,4890791	98586,829	66391,52	1,484931
19756,826	0,4734136	0,0261574	315131,31	277305,69	1,1364041	283928,89	755305,16	0,3759128

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23513,076	0,4208091	0,0640994	208478,73	206388,07	1,0101297	337910,63	366821,91	0,9211844

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2018,4193	0,2856581	0,0326373	11881,616	17327,536	0,6857072	29007,065	61843,919	0,4690367
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44330,165	0,4413298	0,0488401	375712,67	354650,46	1,0593886	637076,74	907659,7	0,7018894
629814,82	0,4446508	0,0364142	7637184,6	7155205,4	1,0673606	9051181,5	17295867	0,5233147
83568,36	0,3966703	0,038618	900817	946051,63	0,9521859	1200975,9	2163973,7	0,5549864
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3760,5606	0,3908119	0,0424218	36784,902	39211,164	0,9381232	54043,69	88646,858	0,6096515
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5991,631	0,3884597	0,0313556	74480,528	79873,87	0,9324768	86106,802	191086,22	0,4506175
81,746229	0,5454444	0,0491028	908,43725	693,82894	1,3093101	1174,7897	1664,7989	0,7056646
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137,39065	0,3762926	0,0498359	1379,1139	1526,8009	0,9032703	1974,4656	2756,8607	0,7162007
7948,7045	0,3776213	0,0510773	57372,383	63292,799	0,9064599	114232,25	155621,07	0,734041
40899,611	0,4884058	0,0484997	387949,42	330904,15	1,1723921	587775,63	843296,65	0,6969975
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5714,4252	0,3953852	0,0446867	47172,5	49702,288	0,9491012	82123,027	127877,58	0,6422003
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45265,485	0,5171094	0,1213868	223164,86	179784,11	1,2412935	650518,39	372902,91	1,7444712
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12520,309	0,4179187	0,0532777	113624,25	113262,75	1,0031916	179931,61	235000,98	0,7656632
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61212,738	0,5844184	0,3152121	272065,14	193935,34	1,4028652	879699,22	194195,42	4,529969
51575,159	0,6297659	0,2988578	256305,54	169545,7	1,5117195	741195,85	172574,27	4,2949382
1142,6278	0,2940391	0,0341008	9611,8188	13617,847	0,7058251	16420,908	33507,39	0,4900683
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3139,8304	0,4361535	0,0892854	20196,882	19290,917	1,0469633	45123,065	35166,223	1,2831365
12816,872	0,5089798	0,0699249	80543,677	65923,279	1,221779	184193,57	183294,81	1,0049034

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31832,333	0,352277	0,1355169	139626,76	165117,19	0,8456222	457468,16	234895,71	1,9475373
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10837,383	0,2607828	0,0419153	66829,333	106756,93	0,6259953	155745,97	258554,51	0,6023719
31236,7	0,1658237	0,0348343	215984	542603,85	0,398051	448908,21	896721,79	0,5006104
22274,247	0,2096455	0,0410795	159366,93	316679,98	0,5032428	320107,19	542223,17	0,5903606
17952,415	0,2438639	0,0547316	112122,37	191537,02	0,5853822	257997,37	328008,27	0,7865575
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32460,18	0,2410799	0,0362958	289481,86	500228,33	0,5786995	466491,06	894324,1	0,521613
61,095266	0,2936273	0,05414	453,74692	643,76183	0,7048366	878,01101	1128,4676	0,7780561
21,171702	0,213929	0,037205	181,66471	353,76012	0,5135251	304,26232	569,0552	0,5346798
4856,119	0,3407598	0,0393202	34106,118	41695,756	0,8179758	69788,155	123501,75	0,5650783
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2641,259	0,3132239	0,0278152	19479,611	25907,969	0,7518772	37958,006	94957,359	0,3997374
96,454972	0,3794547	0,0298571	1127,7436	1238,1077	0,9108607	1386,1717	3230,5497	0,4290823
38841,938	0,3330316	0,025325	496508,57	621082,44	0,7994246	558204,45	1533737	0,3639506
1251,4962	0,2928796	0,0173983	14679,724	20880,296	0,703042	17985,475	71932,261	0,2500335
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17203,518	0,7033552	0,1203829	235042,31	139212,84	1,6883666	247234,83	142906,64	1,7300444

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13153,39	0,2675501	0,0271881	118799,57	184977	0,6422397	189029,73	483792,49	0,3907248
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9255,3169	0,3824242	0,0406992	84909,132	92494,717	0,917989	133009,82	227407,89	0,5848953
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10523,645	0,3298895	0,0442059	102122,36	128961,56	0,7918822	151237,19	238059,62	0,6352912
24058,214	0,2709495	0,0422408	149406,42	229714,73	0,6503998	345744,9	569548,84	0,6070505
5236,0457	0,3326585	0,0352356	46917,111	58754,428	0,7985289	75248,15	148600,94	0,5063774
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8034,1089
52157,758
108278,77

7330,1124	0,4819328	0,0914761	62606,255	54117,683	1,1568539	105342,36	80131,488	1,3146188
1268,7314	0,238389	0,0830748	7830,4713	13683,894	0,57224	18233,166	15272,166	1,1938821
5460,0081	0,3211216	0,0502813	60552,236	78554,048	0,7708353	78466,754	108589,21	0,7226018
2079,1924	0,3629969	0,047554	25152,222	28865,649	0,8713548	29880,446	43722,762	0,6834071
1315,7424	0,3496961	0,0497182	16304,58	19423,467	0,8394268	18908,77	26463,984	0,7145096
11443,795	0,3972585	0,0682151	106462,63	111643,13	0,9535977	164460,83	167760,43	0,9803315
6181,7547	0,3805647	0,0676238	58751,219	64312,641	0,9135252	88839,104	91413,909	0,9718336
7435,5161	0,4816078	0,0455731	125517,33	108572,06	1,1560739	106857,13	163155,71	0,6549396
36321,016	0,2407082	0,091086	311880,67	539766,01	0,5778072	521975,83	398755,25	1,309013
82837,322	0,4636357	0,179045	480262,41	431528,66	1,1129328	1190470	462662,02	2,5730878
27680,1	0,3607961	0,0945136	191139,48	220697,03	0,8660718	397795,68	292869,11	1,3582712
5427,6399	0,3938058	0,1102231	40674,589	43027,786	0,9453098	78001,584	49242,311	1,5840358
13001,162	0,3964762	0,1208606	87078,788	91496,23	0,95172	186842,03	107571,51	1,73691
19453,205	0,4436599	0,1612903	83343,605	78258,242	1,0649818	279565,49	120609,85	2,3179325
87645,607	0,3739784	0,13409	479462,92	534092,41	0,8977153	1259570,7	653632,83	1,927031
174497,69	0,3979046	0,1366302	1014259,9	1061886,9	0,9551487	2507737,6	1277153	1,9635374
283,43029	0,4175466	0,0508747	3550,1341	3541,9937	1,0022983	4073,2275	5571,1464	0,7311291
7231,1879	0,4787328	0,0589286	86420,043	75201,975	1,1491725	103920,7	122711,04	0,8468732
2895,9914	0,4558811	0,0553082	37700,767	34451,371	1,0943183	41618,811	52360,958	0,7948443
1597,1475	0,435188	0,0649882	16679,662	15966,816	1,0446455	22952,893	24575,963	0,933957
4247,6006	0,3747896	0,0580918	36731,751	40828,364	0,8996626	61043,029	73118,703	0,8348484
4694,851	0,4128746	0,0816223	33997,75	34303,62	0,9910834	67470,545	57519,223	1,1730086
29176,738	0,4823541	0,1101939	183885,49	158814,24	1,1578653	419304,13	264776,46	1,5836156
137791,68	0,3801821	0,1095614	943970,95	1034367,5	0,912607	1980228,9	1257666	1,5745268
30391,593	0,3997565	0,110553	210105,29	218952,24	0,9595942	436763,03	274905,19	1,5887769
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53899,61	0,3850672	0,1034282	401841,53	434736,63	0,9243333	774600,95	521130,49	1,4863858
25934,682	0,3968321	0,1031481	195927,14	205681,71	0,9525744	372711,96	251431,44	1,4823602
71749,406	0,3698865	0,10345	491087,11	553092,71	0,8878929	1031123,6	693565,88	1,4866988
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9669,4668 0,3498537 0,0569168 71199,282 84780,718 0,8398051 138961,64 169887,86 0,817961
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28456,254 0,4984561 0,0950945 154357,82 129005,92 1,1965174 408949,92 299241,77 1,3666204

5920,685 0,2829176 0,1712733 77431,247 114015,6 0,6791285 85087,224 34568,637 2,4613995
12804,943 0,3939222 0,1548717 85861,401 90802,004 0,9455893 184022,13 82680,952 2,2256895
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11051,186 0,3907447 0,3235091 55064,908 58706,984 0,9379618 158818,57 34160,353 4,6492075
26185,165 0,3561871 0,2905452 138551,54 162047,03 0,8550082 376311,69 90124,251 4,1754764
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512,97651 0,157165 0,1042156 3743,8001 9923,4983 0,3772662 7372,0772 4922,2605 1,4977016

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8636,8253	0,2455783	0,0678496	75632,318	128299,64	0,5894975	124121,36	127293,76	0,9750781
10127,431	0,2861076	0,0780387	78087,811	113700,35	0,686786	145543,13	129774,52	1,1215077
17912,986	0,4570037	0,1651321	152445,26	138963,96	1,097013	257430,73	108476,7	2,3731431
28746,951	0,3305133	0,3175888	155796,41	196370,59	0,7933796	413127,58	90516,27	4,5641251
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7967,2443	0,5439579	0,3808871	46264,261	35431,395	1,305742	114498,69	20917,599	5,4737971
5331,6482	0,5435763	0,2377494	33925,518	26000,035	1,3048258	76622,071	22425,495	3,4167394
7873,3771	0,2449794	0,2340749	68109,357	115820,43	0,5880599	113149,71	33636,144	3,3639323
7514,0335	0,4604481	0,1617521	73626,623	66613,485	1,1052811	107985,52	46454,009	2,3245684
9996,8721	0,4291932	0,0827855	105371,15	102276,74	1,0302553	143666,84	120756,34	1,1897251
9744,6025	0,4881844	0,0728975	110523,34	94314,396	1,1718607	140041,43	133675,41	1,047623
36845,374	0,3827656	0,158606	240113,45	261331,36	0,9188084	529511,46	232307,59	2,279355
25477,126	0,3536428	0,1543864	168837,07	198889,06	0,8489007	366136,34	165021,79	2,2187152
6156,9572	0,3917446	0,2793153	33236,321	35344,178	0,940362	88482,734	22043,034	4,0140904
15875,357	0,4255574	0,1227333	143798,89	140768,44	1,0215279	228147,59	129348,39	1,7638225

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844,70203	0,322973	0,04636	7733,0243	9974,4988	0,7752795	12139,364	18220,479	0,6662484
17119,129	0,2867207	0,0390666	162003,32	235381,73	0,6882578	246022,06	438203,26	0,5614337
8031,4679	0,3245731	0,0376839	112977,83	145006,9	0,7791204	115421,66	213127,1	0,5415626
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767,88141	0,1780691	0,0489085	6883,4762	16103,754	0,4274454	11035,361	15700,361	0,7028731
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1109,8286	0,2665647	0,0264876	15486,372	24202,204	0,6398745	15949,545	41899,928	0,3806581
598,85969	0,2673939	0,0342925	5453,8551	8496,8913	0,6418648	8606,3199	17463,3	0,4928232
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6598,5172	0,2405412	0,0546076	58270,999	100918,52	0,5774064	94828,471	120835,14	0,7847756
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1119,1592	0,2454487	0,0416244	10060,631	17075,461	0,5891865	16083,637	26887,087	0,5981919
12126,292	0,5525682	0,1147974	87445,294	65926,272	1,3264104	174269,11	105632,08	1,6497745
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4215,902	0,5768966	0,153987	25845,413	18663,514	1,3848096	60587,482	27378,298	2,2129748
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23469,774	0,6180928	0,0671356	276084,68	186078,64	1,4836989	337288,33	349587,48	0,9648181
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3034,4619
7561,2625
124658,54
44191,051
18760,343
161317,28
16575,779
66678,7
17769,521
27086,077

2676,3105	0,5504495	0,0666251	32125,832	24313,351	1,3213247	38461,737	40169,702	0,9574813
4341,892	0,5422675	0,0655854	51229,486	39356,308	1,3016842	62398,107	66202,144	0,9425391
6708,783	0,3583955	0,0868516	40100,8	46612,08	0,8603092	96413,122	77244,191	1,2481602
4352,4713	0,4178578	0,1028794	25247,729	25171,07	1,0030455	62550,144	42306,537	1,4784983
5077,5142	0,3772096	0,0787632	35461,024	39163,043	0,9054716	72969,866	64465,537	1,1319206
1857,2315	0,5190187	0,0244125	50896,038	40851,58	1,2458768	26690,606	76076,937	0,350837
4998,3539	0,2935107	0,0889142	42626,986	60501,846	0,7045568	71832,239	56215,502	1,2778013
20924,054	0,3969975	0,0710131	203519,25	213562,81	0,9529714	300703,32	294650,81	1,0205413
7061,9852	0,3124434	0,1157427	40237,515	53649,75	0,7500038	101489,05	61014,497	1,6633597
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15969,352	0,5190193	0,0431569	273575,58	219584,53	1,2458782	229498,41	370030,49	0,6202149
18615,352	0,3811053	0,0699034	155387,96	169855,78	0,9148229	267524,55	266301,08	1,0045943
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2194,4926	0,538269	0,0328051	55085,907	42633,311	1,2920861	31537,446	66894,883	0,4714478
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8534,4657	0,4073777	0,0312242	184586,44	188760,22	0,9778885	122650,33	273328,68	0,4487284
5151,4272	0,4372418	0,0944113	33123,675	31559,114	1,0495756	74032,083	54563,667	1,3568018
3023,0211	0,3243067	0,0572277	33014,782	42409,235	0,778481	43444,378	52824,475	0,822429
3970,4023	0,3235428	0,0327613	78558,64	101150,98	0,7766473	57059,363	121191,82	0,4708186

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2670,4973	0,7804172	0,0357023	14917,176	7962,835	1,8733499	38378,195	74798,982	0,5130845
2963,2688	0,6731858	0,0522134	13739,2	8502,2602	1,6159467	42585,667	56753,046	0,7503679
2336,8022	0,6859391	0,0394876	8847,3668	5373,2423	1,6465602	33582,603	59178,181	0,5674829
1418,7457	1,0276516	0,0390387	5297,9954	2147,7	2,4668228	20389,049	36342,011	0,5610325
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17558,346	0,5192257	0,0593627	161597,02	129653,76	1,2463736	252334,13	295780,64	0,8531124
8745,3479	0,6189911	0,0440962	52259,105	35171,066	1,485855	125680,96	198324,14	0,6337149
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6282,8924	0,4573503	0,0544009	37451,36	34113,52	1,0978451	90292,571	115492,34	0,7818057
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2268,2488	0,0954598	0,0943044	112302,26	490090,14	0,2291461	32597,41	24052,427	1,3552649

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2838,5418	0,482536	0,04905	21595,45	18644,06	1,1583019	40793,192	57870,399	0,704906
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22634,361	0,5130973	0,1224078	152887,58	124131,03	1,2316628	325282,45	184909,43	1,7591448
25914,88	0,7192803	0,1139473	139974,16	81069,531	1,726594	372427,38	227428,67	1,6375569
36806,089	0,5196509	0,2145926	178337,57	142968,08	1,2473943	528946,89	171516,11	3,0839488
47180,79	0,4493341	0,1750676	277734,26	257494,55	1,0786025	678043,57	269500,37	2,5159281
67524,326	0,676258	0,1873072	375219,04	231142,79	1,6233214	970404,18	360500,39	2,6918256
100636,37	0,4348823	0,2128155	479708,88	459530,13	1,0439117	1446263,2	472880,85	3,0584094

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7439,1659	0,9079002	0,1967958	44407,789	20376,471	2,179366	106909,58	37801,443	2,828188
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18010,507	0,5823701	0,168189	86579,615	61933,339	1,3979485	258832,23	107084,9	2,4170749
16666,141	0,5951867	0,1589474	83852,338	58690,781	1,428714	239512,1	104853,2	2,2842613

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1022,2771	0,509055	0,0439185	12725,514	10414,023	1,2219595	14691,327	23276,703	0,6311601
3945,0126	0,3561408	0,03671	38627,665	45183,996	0,8548971	56694,482	107464,15	0,5275665
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19152,386	0,6507109	0,1365495	108599,56	69526,108	1,5619968	275242,36	140259,68	1,9623769
3024,8099	0,542408	0,0238945	54978,873	42225,777	1,3020216	43470,085	126590,26	0,343392
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22657,647	0,711959	0,0518274	266811,68	156119,74	1,7090195	325617,09	437174,86	0,7448212
18483,998	0,4848515	0,0927154	155065,12	133233,45	1,1638603	265636,84	199362,81	1,3324293
2965,9831	0,7110925	0,0264978	62733,475	36752,015	1,7069398	42624,674	111933,28	0,3808043
26120,034	0,5622528	0,0450309	335970,31	248929,98	1,3496579	375375,69	580047,15	0,6471469
24658,65	0,5267918	0,0545798	277801,61	219686,64	1,2645357	354373,88	451790,61	0,7843764
17570,25	0,3877141	0,0407167	203821,64	219001,25	0,9306871	252505,2	431524,72	0,5851466
6833,8414	0,4064204	0,0748635	51614,289	52905,693	0,9755904	98210,358	91284	1,075877
17633,94	0,6122997	0,039972	250470,9	170412,38	1,4697928	253420,51	441157,58	0,5744444
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42313,035	0,4832573	0,0613418	362842,04	312785,88	1,1600333	608088,2	689791,15	0,8815541

11623,886	0,282545	0,0220286	167443,56	246881,61	0,6782342	167048,94	527671,48	0,3165775
27718,232	0,397214	0,0749106	158844,95	166593,02	0,953491	398343,67	370017,51	1,0765536

3713,9681	0,4950452	0,0200399	92749,88	78050,636	1,1883296	53374,1	185328,49	0,2879973
8650,3198	0,3466182	0,0749003	71735,745	86216,868	0,8320384	124315,29	115491,12	1,0764057
13675,633	0,5222721	0,0225286	285436,51	227677,76	1,2536864	196534,96	607033,55	0,3237629
4186,4474	0,8731369	0,0473571	56699,517	27052,345	2,0959187	60164,186	88401,741	0,6805769
19903,4	0,8297218	0,0569408	249629,16	125334,54	1,9917029	286035,33	349545,45	0,8183065
7331,0701	0,8166421	0,0424572	107582,17	54880,296	1,9603059	105356,12	172669,59	0,6101602
9140,3754	0,3279777	0,0585874	105672,77	134222,93	0,787293	131357,97	156012,55	0,8419706
4213,8771	0,7054298	0,049806	48565,651	28680,276	1,6933467	60558,383	84605,782	0,7157712
13710,556	0,3409274	0,1208234	73005,36	89207,364	0,8183782	197036,86	113476	1,7363747
14919,915	0,6208311	0,064134	197340,19	132418,91	1,490272	214416,77	232636,49	0,9216816
22171,253	0,5586398	0,058425	314975,99	234884,04	1,3409851	318627,05	379482,19	0,8396364
9821,6509	0,4374023	0,0851943	90601,361	86290,228	1,0499608	141148,7	115285,36	1,224342
6533,2782	0,9344184	0,0839653	50350,685	22447,705	2,2430215	93890,91	77809,26	1,2066804
6144,0751	0,4447419	0,0798308	46670,971	43716,637	1,0675792	88297,603	76963,741	1,1472624
2346,0363	0,4313531	0,027984	28401,895	27429,781	1,0354401	33715,308	83834,838	0,4021635
4677,4339	0,8563206	0,0338959	86575,382	42117,826	2,055552	67220,24	137994,29	0,4871233
1362,8739	0,6379434	0,0259097	32718,611	21365,874	1,5313491	19586,104	52600,819	0,3723536
4793,5872	0,8862321	0,0392573	76995,822	36193,251	2,127353	68889,5	122106,74	0,5641744
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5818,2665	0,4195014	0,0670261	57986,987	57584,432	1,0069907	83615,349	86805,934	0,9632446
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1243,9397	0,4403504	0,069001	11891,778	11250,099	1,0570377	17876,88	18027,841	0,9916262
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18564,242	0,3553595	0,1113179	88264,324	103472,57	0,8530215	266790,05	166767,75	1,5997701
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36051,178	0,2188293	0,2019773	115738,47	220333,36	0,525288	518097,93	178491,28	2,9026513
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18340,132 0,3273506 0,150249 131709,3 167614,35 0,7857877 263569,32 122064,93 2,1592551

20309,866 0,3857734 0,2106041 133746,13 144429,82 0,9260285 291876,72 96436,233 3,0266292

14669,888 0,4949424 0,2631523 87146,964 73350,92 1,1880828 210823,59 55746,75 3,7818095

32453,661 0,4076038 0,1451708 242914,16 248269,01 0,9784313 466397,37 223554,95 2,0862761

2205,5126 0,6983496 0,3759125 12816,268 7645,3368 1,676351 31695,816 5867,0906 5,4023056

19536,104 0,7713062 0,353748 116736,31 63050,29 1,8514794 280756,85 55226,044 5,0837761

3502,4929 0,3710217 0,0825642 26929,795 30237,203 0,8906179 50334,952 42421,433 1,1865453

53549,169

35891,303

8655,134

8613,8591

11048,516

6794,1812

40515,288

948,21564 0,2281167 0,0835313 6533,6905 11931,895 0,547582 13626,977 11351,623 1,200443

216,2652	0,1961144	0,081046	1417,0604	3010,1414	0,4707621	3107,986	2668,4265	1,1647261
17783,242								
11038,59								
15956,955								
1545,8075	0,3572955	0,0759234	12357,172	14407,861	0,8576687	22215,077	20360,082	1,0911094
34534,753	0,2024698	0,082917	240716,79	495283,78	0,4860179	496305,12	416497,9	1,1916149
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106651	0,8485708	0,250823	827614,46	406301,01	2,036949	1532700,7	425204,18	3,6046228
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2500,6602	0,4334655	0,1543525	26747,515	25706,136	1,0405109	35937,435	16200,969	2,2182275
3703,9923	0,4722914	0,1618035	38047,727	33560,358	1,1337104	53230,736	22891,918	2,325307
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21617,469	0,4476682	0,1152699	168064,68	156396,9	1,0746037	310668,51	187537,88	1,656564
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2175,2047	0,4904073	0,1104488	18085,14	15362,889	1,1771966	31260,256	19694,227	1,5872801
3892,8092	0,5343761	0,1004123	36215,694	28233,042	1,2827415	55944,257	38768,234	1,4430438
3978,4205	0,5390631	0,1159243	32507,955	25122,217	1,2939923	57174,594	34319,127	1,6659688
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3946,0701	0,5265583	0,1117619	29252,083	23142,925	1,2639752	56709,68	35307,822	1,6061506
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2783,8292	1,1288236	0,1327983	36671,998	13533,696	2,709681	40006,908	20962,84	1,9084679
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6081,0965	0,7689705	0,0807185	50980,577	27618,685	1,8458727	87392,526	75337,124	1,1600194
3910,6488	0,8185679	0,0720291	36792,372	18724,534	1,9649286	56200,635	54292,615	1,0351433
8855,8907	0,5868162	0,0696008	73935,098	52487,577	1,4086209	127269,59	127238,28	1,000246
1452,8437	0,5163884	0,0407956	16957,406	13680,152	1,2395627	20879,076	35612,717	0,5862815
6897,7121	0,6159148	0,0561395	74973,693	50710,304	1,4784706	99128,256	122867,36	0,8067908
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55526,102	0,4498173	0,1109033	367438,29	340295,5	1,0797624	797975,55	500671,16	1,5938117
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28471,087								
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4144,4171	0,4228151	0,0705461	32924,812	32439,991	1,0149452	59560,16	58747,665	1,0138303
4189,9359	0,5774928	0,0691888	36775,826	26529,176	1,3862408	60214,319	60558,022	0,9943244
7122,8238	0,4840157	0,0451208	77700,726	66876,498	1,161854	102363,38	157861,2	0,6484391
15839,972	0,4980227	0,0410977	187600,81	156925,51	1,1954769	227639,08	385422,76	0,5906218
78739,237	0,5112811	0,0945853	478474,96	389858,87	1,227303	1131575,7	832467,61	1,3593029
3828,7998	0,6017033	0,0634391	35813,473	24795,451	1,4443566	55024,368	60353,945	0,9116946
7610,0043	0,5843687	0,0721671	64358,917	45880,666	1,4027459	109364,73	105449,83	1,0371257
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26594,8	0,4767924	0,0413936	283384,98	247602,72	1,1445148	382198,64	642486,18	0,5948745
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2849,6681	0,4842116	0,0434804	32565,85	28017,874	1,1623241	40953,091	65539,176	0,6248643
1320,0869	0,4171036	0,0398149	15337,295	15318,377	1,001235	18971,205	33155,589	0,5721872
2367,7732	0,5210356	0,0323811	37169,899	29718,844	1,2507182	34027,692	73122,129	0,4653542
2984,8807	0,4403317	0,0365613	38899,509	36802,054	1,0569929	42896,255	81640,341	0,5254296
569,77231	0,6044955	0,0440137	7011,6958	4832,1226	1,4510592	8188,2999	12945,333	0,6325291

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2262,7963 0,4065653 0,0202307 36191,313 37083,61 0,9759382 32519,051 111849,4 0,2907396
13601,716 0,3018624 0,0190045 175771,88 242576,24 0,7246047 195472,7 715709,26 0,2731175
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1150,3175 0,2097923 0,0185677 15201 30184,953 0,5035953 16531,419 61952,473 0,2668403
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52065,499 0,5645656 0,0243308 935324,21 690169,39 1,3552096 748242,6 2139897,4 0,3496628
7278,9937 0,5609758 0,0286762 109573,43 81370,88 1,3465926 104607,72 253833,92 0,4121109
359,11455 0,4705276 0,0160782 6486,1925 5742,6546 1,1294763 5160,8994 22335,455 0,2310631
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357,06195 0,3231012 0,0204874 3733,3587 4813,5902 0,7755872 5131,4012 17428,357 0,2944283
5732,8832 0,2272285 0,0316256 37937,626 69552,9 0,54545 82388,291 181273,78 0,4544965
1479,8307 0,0937125 0,0256893 3690,2757 16404,732 0,2249519 21266,912 57604,945 0,3691855
21480,202 0,356458 0,0503056 152755,02 178523,34 0,8556585 308695,83 426994,46 0,7229504
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21890,729 0,4433511 0,0295434 259276,88 243626,18 1,0642407 314595,58 740968,75 0,4245733
8004,6001 0,4720314 0,0383373 96464,458 85134,262 1,1330862 115035,54 208794,27 0,5509516
24172,72 0,5612431 0,0748683 232034,98 172230,63 1,3472341 347390,49 322869,95 1,0759456
4780,7487 0,2231272 0,0212954 42706,302 79734,687 0,5356051 68704,995 224496,46 0,3060404
1428,2843 0,2559092 0,0284227 12482,39 20319,818 0,6142963 20526,13 50251,48 0,4084682
40883,51 0,4534807 0,0493123 341748,32 313946,42 1,0885562 587544,24 829072,85 0,7086762
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4176,2703 0,3482493 0,0614782 34100,243 40792,01 0,835954 60017,928 67930,921 0,8835141
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3190,3349 0,4176243 0,0979984 21919,722 21865,388 1,0024849 45848,874 32554,96 1,408353
2569,6946 1,1142917 0,048656 16762,511 6266,8326 2,6747979 36929,541 52813,517 0,6992441
6604,8617 1,8520829 0,1057047 25730,475 5787,5574 4,4458263 94919,651 62484,108 1,5191007

45558,211	0,9071754	0,1074862	167295,3	76824,614	2,1776263	654725,21	423851,67	1,5447036
13097,093	1,9869759	0,0891507	65824,491	13800,755	4,7696296	188220,67	146909,58	1,2812008
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6320,8402	0,4378437	0,0525033	80782,795	76861,29	1,0510206	90837,926	120389,47	0,7545338
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64350,568	0,3700267	0,0639016	705964,18	794799,51	0,8882293	924793,53	1007025,1	0,918342
17185,721	0,3709705	0,065097	182195,33	204600,08	0,8904949	246979,08	264001,64	0,935521
59582,897	0,28678	0,2325138	237923,14	345617,52	0,6884001	856276,49	256255,3	3,3414976
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17708,121	0,3118852	0,0527406	163090,49	217842,08	0,7486638	254486,58	335758,7	0,7579449
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27836,783	0,263811	0,1683914	191401,1	302245,22	0,6332643	400047,39	165310,05	2,4199823
78918,879	0,2755693	0,1865506	591217,95	893767,9	0,6614894	1134157,3	423042,77	2,6809519
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567,26661	0,4584787	0,0727562	7103,7381	6454,6948	1,1005537	8152,2901	7796,8198	1,0455917
44478,721	0,2511338	0,1069125	374710,5	621582,21	0,6028334	639211,66	416029,01	1,5364594
7804,8474	0,3245083	0,1220505	62594,154	80355,549	0,7789649	112164,86	63947,688	1,7540096
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37454,811	0,6959776	0,0900984	250649,96	150030,76	1,6706571	538269,79	415709,99	1,2948204
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4909,9581	0,3028415	0,0362036	40403,364	55578,921	0,7269548	70561,887	135620,64	0,5202887
12160,726	0,5689392	0,0594584	102615,83	75137,444	1,3657083	174763,97	204524,84	0,8544878
13173,909	0,5499982	0,0524055	125978,19	95420,577	1,3202414	189324,6	251384,04	0,753129
37801,689	0,4907839	0,0629577	273004,33	231732,62	1,1781006	543254,85	600430,32	0,9047758
3326,4163	0,6086363	0,0237983	71214,515	48743,712	1,460999	47804,524	139775,62	0,342009
313676,79	0,5382323	0,059478	2903254,5	2247104,7	1,2919979	4507905,3	5273826,2	0,8547694
16915,843	0,4996104	0,0715854	133397,74	111230,77	1,1992881	243100,6	236303,11	1,028766
19710,142	0,5091282	0,0748539	151936,55	124320,59	1,2221351	283257,98	263314,9	1,0757385
22255,607	0,4257408	0,0914811	145454,63	142327,96	1,0219681	319839,31	243280,81	1,3146919
18052,758	0,4198991	0,0609201	149083,29	147908,1	1,0079454	259439,41	296335,02	0,8754936
13687,874	0,4771101	0,0618309	118288,82	103284	1,1452773	196710,89	221376,05	0,8885825
2118,7462	0,4663958	0,0594988	14030,479	12532,156	1,1195582	30448,88	35609,905	0,8550677
9317,1307								
64256,955								
11953,731								
49150,089								
32949,205								
6587,4442	0,3987509	0,0582451	57702,508	60283,848	0,9571802	94669,339	113098,64	0,8370511

2897,3277	0,4337091	0,0526996	21027,39	20197,367	1,0410956	41638,015	54978,147	0,7573557
29196,328	0,49645	0,0525907	263077,45	220757,78	1,1917018	419585,66	555161,8	0,7557899
2124,8806	0,5894752	0,0471773	21876,622	15460,469	1,4150038	30537,04	45040,342	0,6779931
2275,7291	0,7338808	0,0316059	42858,019	24328,453	1,7616418	32704,911	72003,209	0,4542146
9188,9384	0,3725678	0,0764685	62208,233	69558,542	0,8943292	132055,88	120166,34	1,0989423
26067,369	0,5832172	0,0843642	209081,91	149346,17	1,3999818	374618,82	308986,16	1,212413
9113,0151	0,6740487	0,0250414	164670,85	101773,19	1,618018	130964,77	363918,1	0,3598743

3339,0173	0,4210754	0,0358927	27326,068	27034,925	1,0107691	47985,615	93027,813	0,5158201
15875,911	0,617217	0,0686828	149061,54	100608,72	1,4815966	228155,56	231148,26	0,9870529
4090,4577	0,3944652	0,0538937	30866,564	32597,742	0,9468927	58784,699	75898,689	0,7745154
6293,6748	0,3751452	0,030197	48253,778	53584,576	0,9005162	90447,527	208420,51	0,4339665
31527,089	0,5108303	0,0675116	170070,34	138694,69	1,226221	453081,45	466987,62	0,9702215
24637,783	0,5327091	0,0715119	145518,12	113798,06	1,2787399	354074	344527,17	1,0277099
43983,123	0,6788558	0,0707211	273779,66	168008,62	1,6295572	632089,34	621923,32	1,0163461
45125,406	0,4308917	0,0653824	397217,89	384033,08	1,0343325	648505,29	690176,46	0,9396224
121628,87	0,6720337	0,0716118	867291,42	537628,08	1,613181	1747950,2	1698447,2	1,029146
83765,518	0,7380448	0,072232	740372,48	417902,98	1,7716372	1203809,3	1159673,5	1,0380588
114494,68	0,7109112	0,0648537	947467,97	555209,81	1,7065044	1645423,6	1765429	0,9320248
50260,305	0,5696618	0,0993143	293040,23	214297,97	1,3674429	722299,84	506072,99	1,4272642
13422,549	0,412164	0,0745939	73156,523	73941,95	0,9893778	192897,85	179941,57	1,0720027
19864,676	0,6016596	0,0695375	141341,7	97864,99	1,4442519	285478,82	285668,53	0,9993359

4827,287	0,1842573	0,0274454	37047,769	83761,679	0,4422997	69373,806	175886,94	0,3944227
2458,7214	0,495074	0,0376217	35499,788	29871,951	1,1883987	35334,725	65353,758	0,5406686
3768,6616	0,4870308	0,0649664	33443,679	28606,555	1,1690915	54160,111	58009,429	0,9336432
1291,0989	0,4087818	0,0233225	22140,249	22563,107	0,9812589	18554,613	55358,552	0,3351716
1614,1276	0,3807775	0,0252242	27370,257	29944,39	0,9140362	23196,916	63991,267	0,3625013
2496,0679	0,3617965	0,0227993	43076,879	49600,705	0,8684731	35871,438	109480,2	0,3276523
75562,173	0,3964534	0,1260348	391815,29	411715,5	0,9516652	1085917,5	599534,06	1,8112691
92533,68	0,4166211	0,1131375	498438,99	498400,8	1,0000766	1329818,1	817887,25	1,6259186
9333,8642	0,3939088	0,0553378	76463,861	80866,463	0,9455571	134138,63	168670,76	0,795269
3610,0538	0,1807676	0,0544383	16929,543	39015,081	0,433923	51880,73	66314,579	0,7823427
7013,6115	0,4864433	0,0769883	58097,82	49754,861	1,1676813	100793,87	91099,733	1,1064123
7070,4294	0,3525387	0,0493127	66531,056	78618,653	0,8462503	101610,41	143379,35	0,7086823
5131,6965	0,5402187	0,0524405	55111,272	42499,001	1,2967663	73748,529	97857,465	0,7536321
19290,231	0,4877079	0,0299749	321581,37	274687,59	1,1707168	277223,36	643545,27	0,4307752
17488,135	0,4558461	0,043503	207877,42	189975,23	1,0942343	251325,11	401998,4	0,6251893
4376,0176	0,4333301	0,0456849	54089,984	52000,304	1,0401859	62888,532	95786,942	0,656546

6929,802	0,2987959	0,0965347	38132,115	53164,795	0,7172437	99589,425	71785,619	1,3873172
36037,814	0,3972305	0,0456204	327981,47	343965,31	0,9535307	517905,87	789950,1	0,6556185
33965,374	0,4464634	0,1302309	143061,58	133488,88	1,0717116	488122,47	260808,9	1,8715714
12682,894	0,3067363	0,03139	139899,92	190002,92	0,7363041	182268,14	404041,97	0,4511119
2494,2087	0,3817671	0,0371407	32067,349	34992,298	0,9164116	35844,72	67155,713	0,5337553
7701,1685	0,4143994	0,0460759	79884,456	80306,575	0,9947437	110674,87	167140,97	0,6621648
57493,587	0,3206858	0,0569946	498627,73	647745,86	0,7697891	826250,63	1008754,8	0,8190798
565,02978	0,3273818	0,0216685	7973,2275	10145,828	0,7858627	8120,1441	26076,073	0,3114021
4945,6357	0,3779459	0,0355348	63391,418	69872,892	0,9072391	71074,617	139177,07	0,5106776
3011,1214	0,4623816	0,0373002	43291,356	39003,951	1,1099223	43273,365	80726,642	0,5360481
1989,8772	0,3158823	0,0410659	22117,699	29169,074	0,7582585	28596,882	48455,739	0,590165
13610,884	0,3838403	0,0598492	107991,84	117205,58	0,9213882	195604,45	227419,62	0,8601037

28596,344	0,4087919	0,1329632	123764,75	126125,41	0,9812833	410963,19	215069,61	1,910838
3106,7421	0,4696766	0,0356331	45491,043	40349,197	1,1274337	44647,547	87186,938	0,5120899
25996,719	0,7303463	0,1144726	155523,25	88710,379	1,7531574	373603,5	227100	1,6451057

1966,4593	0,7802555	0,2248995	8800,1654	4698,529	1,8729618	28260,338	8743,7264	3,2320703
178918,79	0,4356653	0,1849428	593080,09	567111,36	1,0457912	2571273,9	967427,75	2,657846
218698,59	0,3689483	0,1747154	724592,09	818155,79	0,8856407	3142956,5	1251741,6	2,5108669
4003,5566	0,3661431	0,0521312	28767,738	32731,268	0,8789069	57535,829	76797,648	0,7491874
26801,166	0,3412697	0,0562987	223337,42	272628,76	0,8191998	385164,36	476052,77	0,8090791
5265,4289	0,3650789	0,0605212	49171,928	56109,762	0,8763525	75670,421	87001,456	0,8697604
1371,8839	0,980345	0,3144116	8160,2545	3467,6295	2,353266	19715,589	4363,3379	4,518465
2346,8678	1,0378293	0,3320324	13283,443	5332,0309	2,4912539	33727,257	7068,1891	4,7716971
34161,579	0,6548614	0,1360362	316348,74	201244,78	1,5719599	490942,17	251121,18	1,9550011
48379,142	0,6342981	0,1045514	451654,08	296633,66	1,5225989	695265,32	462730,81	1,5025265
20234,376	0,5799452	0,0866219	203897,36	146464,58	1,3921275	290791,84	233594,29	1,2448585
17743,472	0,6634972	0,1199765	142870,48	89703,906	1,5926896	254994,61	147891,27	1,7242033
49635,176	0,501908	0,2017211	428120,56	355344,73	1,2048035	713316	246058,39	2,8989704
24804,234	0,7225077	0,1915128	184636,61	106459,21	1,7343413	356466,09	129517,34	2,7522654
25124,071	0,7725565	0,1943605	190832,58	102903,52	1,8544807	361062,52	129265,32	2,7931893
49812,581	0,5074816	0,1034781	425612,21	349382,94	1,2181826	715865,52	481382,7	1,4871027
197499,61	0,8769153	0,2801404	1459771	693481,72	2,1049884	2838302,3	705002,28	4,0259476
108818,87	0,5844878	0,259963	687933,82	490319,48	1,4030318	1563855,4	418593,62	3,7359753
56386,989	0,8416773	0,2365042	428212,52	211944,26	2,0204016	810347,51	238418,58	3,3988437
50456,025	0,7983022	0,366589	450179,98	234923,68	1,9162818	725112,57	137636,49	5,2683165
59771,843	0,7021683	0,2138364	550832,81	326803,38	1,6855175	858991,86	279521,39	3,073081
152216,97	0,2738491	0,2305101	1159522,9	1763907,7	0,6573603	2187537,4	660348,28	3,3127025

3691,8342	0,3609125	0,0342737	46081,697	53190,554	0,8663511	53056,01	107716,12	0,492554
11868,907	0,3059817	0,0241959	233074,26	317326,81	0,7344928	170570,18	490532,91	0,3477242
6920,3756	0,4038146	0,0458486	84452,905	87124,531	0,9693355	99453,957	150939,62	0,658899
124,01835	0,3106329	0,0200248	1945,4554	2609,0463	0,7456577	1782,2899	6193,2469	0,2877796
1664,4034	0,294856	0,0211094	24930,826	35223,67	0,7077862	23919,439	78846,721	0,3033663
1872,8836	0,292821	0,0195929	29747,026	42320,354	0,7029012	26915,545	95589,845	0,2815733
1121,3004	0,2946163	0,0334903	13643,373	19291,808	0,7072107	16114,409	33481,377	0,4812947
1599,8132	0,4773446	0,0529187	20364,518	17772,562	1,1458403	22991,202	30231,546	0,7605037
1429,441	0,4379754	0,0327517	24447,238	23253,484	1,0513365	20542,752	43644,757	0,4706809
1792,7808	0,5014938	0,0442889	31202,98	25920,207	1,2038091	25764,374	40479,201	0,6364842
6252,7359	0,3698642	0,0505944	72009,72	81106,703	0,8878393	89859,187	123585,62	0,7271007
8839,0752	0,4642002	0,0404448	113509,97	101867,72	1,1142879	127027,93	218546,42	0,5812401
688,92348	0,4423223	0,0549349	7479,9218	7044,7595	1,0617711	9900,6427	12540,733	0,7894788
10431,779	0,3723248	0,0400079	150312,8	168182,95	0,8937458	149916,97	260743,22	0,5749602
4118,2609	0,3085569	0,0537604	42279,754	57082,787	0,7406743	59184,264	76603,971	0,7726005
9139,5645	0,2518555	0,0506969	95040,49	157204,56	0,6045657	131346,32	180278,58	0,7285742

4673,2903	0,2954377	0,0221497	132362,02	186640,3	0,7091824	67160,691	210986,21	0,3183179
11023,246	0,322306	0,0713627	104349,84	134874,98	0,7736783	158417,04	154467,99	1,0255655
1965,3546	0,2464047	0,0392921	34962,301	59109,731	0,5914813	28244,463	50019,134	0,5646732
2412,8587	0,3015947	0,0544968	30862,205	42629,591	0,723962	34675,625	44275,236	0,7831833
3594,8275	0,3132572	0,0465034	53558,658	71225,666	0,7519573	51661,91	77302,45	0,6683088
3435,4207	0,2602545	0,0503438	44707,031	71562,505	0,624727	49371,046	68239,153	0,7235003
160,50838	0,1875902	0,0101296	5760,2216	12791,955	0,4503003	2306,6947	15845,437	0,1455747
264,19074	0,1809087	0,0152734	6295,1575	14496,23	0,4342617	3796,7324	17297,425	0,219497

990,66584	0,2479496	0,0559394	8785,5238	14760,876	0,5951899	14237,036	17709,625	0,8039152
734,28613	0,2064249	0,0287308	10949,328	22097,001	0,495512	10552,557	25557,425	0,412896
11402,333	0,2182322	0,0547553	115791,45	221037,34	0,5238547	163864,97	208241,71	0,7868979
73992,857	0,3495982	0,1346282	409206,8	487620,12	0,8391918	1063364,6	549608,88	1,934766
91901,228	0,2381531	0,0986302	567046,17	991904,93	0,5716739	1320729	931775,79	1,4174322
1110,0079	0,3118626	0,0607541	13398,536	17897,895	0,7486096	15952,122	18270,501	0,8731081
23913,564	0,2832193	0,0562918	260530,11	383215,51	0,6798527	343666,11	424814,21	0,8089798
9037,1164	0,3737286	0,0559675	123255,6	137390,99	0,8971156	129874,02	161470,7	0,8043194
11481,781	0,3495206	0,0449535	214343,31	255473,02	0,8390057	165006,72	255414,77	0,6460344
2876,3265	0,3420059	0,0669902	37098,112	45188,318	0,8209669	41336,202	42936,529	0,9627281
16785,297	0,3634838	0,0475744	309692,5	354938,86	0,8725235	241224,51	352822,09	0,6837001
3181,1401	0,2979388	0,0657136	39303,458	54955,556	0,7151862	45716,734	48409,138	0,9443823
2432,9233	0,3881843	0,0508671	41105,662	44113,515	0,9318156	34963,976	47829,061	0,7310195
3473,4274	0,2639817	0,0378488	49200,988	77643,992	0,6336741	49917,247	91771,046	0,5439324

96794,452	0,3699984	0,0771806	1090511,3	1227830	0,8881615	1391050,4	1254130,1	1,1091755
43401,203	0,4486146	0,1240179	305263,42	283471,4	1,0768755	623726,45	349959,25	1,7822831
3830,7033	0,1971476	0,0740197	37810,913	79897,56	0,4732424	55051,723	51752,49	1,0637502
8733,5625	0,5417828	0,0773472	96285,357	74035,998	1,3005208	125511,59	112913,69	1,111571
24560,787	0,4783092	0,0705199	264779,96	230613,27	1,1481558	352967,46	348281,59	1,0134543
9818,7272	0,2680079	0,0624825	77451,001	120389,15	0,6433387	141106,69	157143,72	0,8979467
16073,815	0,4916515	0,0839669	167952,42	142310,46	1,1801832	230999,67	191430,33	1,2067036
15738,453	0,4087925	0,0783103	131896,32	134411,89	0,9812846	226180,12	200975,4	1,125412
23876,701	0,2938178	0,1111998	138840,82	196855,24	0,705294	343136,35	214718,9	1,5980724
1277,8586	0,4530194	0,0282958	38180,485	35110,142	1,0874489	18364,335	45160,639	0,4066447
569,64193	0,447394	0,042965	10033,365	9342,5283	1,0739454	8186,4262	13258,292	0,6174571
2606,3614	0,5005607	0,100903	23263,066	19360,57	1,2015693	37456,486	25830,377	1,4500944
1384,9801	0,4610877	0,0261887	42462,015	38364,102	1,1068164	19903,797	52884,556	0,3763631
2809,8249	0,4065343	0,017321	120121,33	123092,29	0,9758639	40380,496	162220,98	0,2489228
1589,2025	0,4757932	0,0400251	32607,129	28549,747	1,1421162	22838,714	39705,131	0,5752081
13395,144	0,4221372	0,047827	196718,54	194133,12	1,0133178	192504,02	280074,68	0,687331
4721,1278	0,5175486	0,0390168	101600,27	81780,853	1,2423479	67848,173	121002,44	0,5607174
3226,0914	0,4694744	0,0373905	56075,097	49758,361	1,1269482	46362,737	86281,03	0,5373457
18329,825	0,4520377	0,0805726	171261,11	157830,91	1,0850923	263421,19	227494,47	1,1579235
15961,348	0,4541188	0,0706399	159177,23	146022,36	1,0900881	229383,39	225953,6	1,0151792
13921,518	0,4212888	0,0492209	217273,82	214850	1,0112814	200068,62	282837,59	0,7073622
24898,086	0,4799483	0,0554278	365229,09	317014,31	1,1520902	357814,85	449198,51	0,7965628
1739,5333	0,1534267	0,0304595	41445,596	112534,4	0,3682927	24999,145	57109,685	0,4377391
2958,2541	0,1658524	0,0421587	50209,41	126116,3	0,3981199	42513,599	70169,509	0,60587

5803,1889	0,3082235	0,0535983	37592,958	50809,932	0,7398742	83398,667	108271,81	0,7702713
2172,9569	0,4445011	0,0467896	31479,444	29502,723	1,0670013	31227,952	46440,982	0,6724223
5160,82	0,4886465	0,0499045	72282,2	61623,242	1,1729698	74167,068	103413,85	0,717187
17108,914	0,4475126	0,0433109	255867,26	238186,61	1,0742302	245875,27	395025,32	0,6224291
67662,751	0,6087953	0,0709326	712615,87	487631,95	1,4613806	972393,51	953902,05	1,0193851
14530,686	0,3590074	0,0382768	188106,7	218277,44	0,861778	208823,09	379621,41	0,5500825
26831,179	0,4361459	0,033671	563859,18	538575,8	1,0469449	385595,68	796862,02	0,4838927
4583,5142	0,4578964	0,0384735	81560,892	74203,207	1,0991559	65870,503	119134,28	0,5529097
1055,0691	0,4681991	0,039896	18030,442	16042,932	1,1238869	15162,587	26445,48	0,5733527
26727,43	0,3965538	0,036647	416946,89	438012,54	0,9519063	384104,69	729320,18	0,5266613
9732,3073	0,3709242	0,038546	139225,17	156365,35	0,8903838	139864,73	252485,76	0,553951
6999,8033	0,4123034	0,0764523	64663,95	65336,106	0,9897123	100595,43	91557,81	1,0987094

3576,4269	0,4385223	0,045637	39844,669	37851,79	1,0526495	51397,471	78366,752	0,6558581
3808,0802	0,3181105	0,0492992	43232,639	56616,329	0,7636073	54726,603	77244,203	0,7084882
5626,0648	0,3296882	0,0478906	66243,931	83704,861	0,7913989	80853,184	117477,46	0,6882442
910,16449	0,5461399	0,1338623	47408,382	36162,56	1,3109797	13080,137	6799,2607	1,9237587
68,083862	0,5346433	0,0881331	7996,749	6230,9934	1,2833827	978,44537	772,51214	1,266576

157687,25	0,8825775	0,0749527	1490926,2	703738,35	2,1185803	2266151,7	2103823,4	1,0771587
4108,6185	0,6787172	0,0402511	52632,383	32305,175	1,6292245	59045,692	102074,59	0,5784563
118010,54	0,788287	0,0570623	1349142,7	712986,7	1,892241	1695950,6	2068099,9	0,8200525
95940,662	0,7994681	0,0988044	782954,94	407984,39	1,9190806	1378780,4	971016,19	1,4199356
7145,318	0,5852583	0,0628057	73466,366	52293,648	1,4048813	102686,64	113768,55	0,9025926
4502,0467	0,5858816	0,0638341	43771,568	31123,623	1,4063777	64699,72	70527,265	0,9173717
8403,3511	0,494507	0,0684993	64318,399	54183,961	1,1870376	120766,06	122677,83	0,9844164
8329,9366	0,4033952	0,0472451	94344,174	97429,897	0,9683288	119711,01	176313,15	0,6789681
41752,003	0,3707128	0,0826904	262343,62	294809,09	0,8898763	600025,51	504919,86	1,1883579
24715,084	0,3944021	0,0950199	147551,21	155851,68	0,9467412	355184,9	260104,16	1,3655487
13487,969	0,5309078	0,08182	93011,084	72983,312	1,2744158	193838,01	164849,37	1,1758493
16493,708	0,3228831	0,0876229	121111,9	156260,57	0,7750637	237034,03	188235,02	1,2592451
1135,0903	0,3107815	0,0264501	18512,079	24814,642	0,7460144	16312,586	42914,412	0,3801191
3502,8191	0,399552	0,0248999	54633,906	56963,53	0,9591032	50339,64	140675,93	0,3578412
236,15074	0,3939833	0,0215469	4000,4938	4230,0331	0,9457358	3393,7646	10959,847	0,3096544
2674,1462	0,4179794	0,0312323	35877,744	35758,407	1,0033373	38430,634	85621,055	0,4488456

12457,451	0,3830633	0,0583539	147160,47	160039,98	0,9195231	179028,26	213480,93	0,8386147
9390,0107	0,379633	0,0353055	168562,37	184971,42	0,9112887	134945,53	265964,21	0,5073823
4955,5507	0,3153007	0,0239199	117877,17	155744,5	0,7568625	71217,107	207173,03	0,3437566
7287,1173	0,4421334	0,0425434	121227,48	114223,55	1,0613177	104724,47	171286,63	0,611399
30990,804	0,3888201	0,0339352	595490,19	638019,28	0,933342	445374,39	913233,59	0,4876895
5963,3637	0,4072397	0,0365055	107122,65	109581,97	0,9775572	85700,567	163355,28	0,5246268
6050,9631	0,4427666	0,060417	69910,487	65777,199	1,0628377	86959,474	100153,27	0,8682639
6658,6051	0,4274688	0,0662289	59369,752	57858,71	1,0261161	95692,007	100539,29	0,9517871
10834,909	0,3999876	0,0935221	73444,419	76492,74	0,9601489	155710,42	115853,99	1,344023
5188,1473	0,2759309	0,0244713	98701,746	149015,85	0,6623574	74559,793	212009,56	0,3516813
27558,411	0,2189294	0,0780088	252955,38	481335,31	0,5255284	396046,85	353272,9	1,1210791

3730,2563

1987,9944

24876,272	0,4750392	0,1377114	159981,06	140296,58	1,1403062	357501,36	180640,61	1,9790753
3272,9208	0,2459719	0,0238457	74593,094	126334,24	0,5904424	47035,731	137253,88	0,3426914
4044,7881	0,2484481	0,0344378	63492,146	106461,41	0,5963865	58128,374	117451,99	0,4949118
3684,3598	0,2723826	0,0833584	29351,496	44890,96	0,6538398	52948,595	44199,01	1,1979588

35613,659

65778,532

4357,3834	0,3479611	0,0274882	102393,02	122587,88	0,8352622	62620,738	158518,08	0,3950385
7423,9516	0,3933953	0,0834055	64105,979	67885,552	0,9443243	106690,94	89010,369	1,1986349
14076,334	0,3134792	0,0330992	272388,92	361983,42	0,75249	202293,51	425277,43	0,4756742
1073,4223	0,317675	0,0115227	56435,696	74008,021	0,7625619	15426,344	93156,933	0,1655952
4442,8179	0,4156064	0,0643287	43796,777	43900,342	0,9976409	63848,531	69064,29	0,9244796
14612,992	0,3557648	0,0513909	198620,41	232578,08	0,8539945	210005,92	284349,72	0,738548
19316,505	0,37998	0,0742198	218684,04	239753,12	0,9121218	277600,96	260260,72	1,0666264
18084,489	0,2915735	0,1258978	126394,07	180587,05	0,6999066	259895,43	143644,19	1,8093

18302,646	0,832208	0,0504051	253303,63	126799,47	1,9976711	263030,6	363110,91	0,7243809
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41803,957	0,672009	0,0482218	417139,64	258591,54	1,6131218	600772,15	866910,73	0,6930035
18481,593	0,4694644	0,0536193	166132,23	147420,93	1,1269243	265602,28	344681,56	0,7705729
1052,4398	0,7621013	0,0183085	15039,424	8221,0332	1,8293836	15124,8	57483,648	0,2631148
922,50333	0,7625799	0,0177578	14521,825	7933,1159	1,8305323	13257,46	51949,077	0,2552011
581,55482	0,7218887	0,0215115	7448,4064	4298,343	1,7328553	8357,6285	27034,554	0,3091462
2230,0841	0,8295824	0,0283617	29664,814	14896,699	1,9913682	32048,938	78630,188	0,4075908
7804,9421	0,8669986	0,0299335	118875,72	57119,278	2,0811838	112166,22	260742,58	0,4301799
19766,748	0,9219934	0,0190957	404562,52	182795,62	2,213196	284071,47	1035139,1	0,2744283
10759,58	0,6618461	0,0251536	166115,06	104558,64	1,5887262	154627,86	427754,55	0,3614873
1319,1004	0,8939795	0,0178999	27852,166	12978,944	2,1459502	18957,029	73693,295	0,2572422
5218,9111	0,8481428	0,02695	86156,867	42318,365	2,0359215	75001,906	193651,93	0,3873026
12451,868	0,324244	0,0511565	94658,585	121617,47	0,7783305	178948,02	243407,4	0,735179
35558,088	0,8635287	0,0583348	352771,4	170186,27	2,0728546	511011,65	609552,09	0,8383396
4417,7151	0,5655523	0,0528674	28662,926	21113,278	1,3575782	63487,775	83562,202	0,7597667
21305,352	0,1688471	0,1078875	75948,642	187384,78	0,4053085	306183,03	197477,54	1,5504702
8318,3838	0,8607833	0,080294	62358,255	30179,222	2,0662645	119544,98	103599,04	1,1539198
9979,8185	0,5075672	0,0962428	79373,324	65146,179	1,218388	143421,76	103694,23	1,3831219
18154,961	1,0096831	0,0883513	130881,15	54000,769	2,4236906	260908,19	205486,16	1,2697118
12097,054	0,3071738	0,0618813	108438,91	147064,88	0,7373542	173848,93	195488,07	0,8893071
30905,402	0,5215435	0,0705467	272879,52	217965,78	1,2519374	444147,06	438084,39	1,0138391
18621,147	0,8085079	0,0971181	110038,98	56698,326	1,9407801	267607,84	191737,09	1,395702
46453,576	0,6339218	0,0974064	339331,4	222995,6	1,5216955	667592,66	476904,64	1,3998452
2385,9656	0,2070259	0,1606905	12375,281	24902,235	0,4969546	34289,139	14848,208	2,3093115
77096,858	0,1879598	0,1559848	428909,3	950623,18	0,4511875	1107972,8	494258,75	2,2416857
43130,326	0,2224522	0,1385773	235656,75	441317,4	0,5339847	619833,63	311236,48	1,9915198
22419,273	0,2210398	0,1480017	117378,25	221220,31	0,5305943	322191,39	151479,86	2,1269586
5553,8843	0,2358085	0,0732496	34378,67	60734,802	0,5660456	79815,865	75821,377	1,0526829
384,458	0,1763761	0,0581118	2107,6314	4978,0901	0,4233815	5525,1148	6615,8303	0,8351355
12111,076	0,3900398	0,0434172	197358,79	210792,67	0,9362697	174050,45	278946,19	0,6239571
22033,911	0,3707739	0,1468781	137630,33	154636,84	0,8900229	316653,28	150014,96	2,1108114
55888,619	0,2645756	0,1091366	281228,97	442810,86	0,6350995	803185,35	512097,96	1,5684213
6555,3812	0,1631121	0,0936518	57709,757	147391	0,3915419	94208,557	69997,372	1,3458871
4581,0763	0,135953	0,0952156	42092,923	128981,77	0,3263478	65835,468	48112,663	1,3683605
4115,2959	0,1055573	0,0899364	35954,085	141895,32	0,2533846	59141,654	45757,849	1,292492
8197,2832	0,2782813	0,0515868	103327,27	154681,65	0,6679995	117804,63	158902,72	0,7413632
46439,575	0,2064165	0,0921834	241367,71	487127,52	0,4954918	667391,44	503773,68	1,3247843
4502,3948	0,3159554	0,1709001	23000,183	30325,877	0,7584342	64704,722	26345,188	2,4560357
4186,7782	0,3824405	0,0821184	38205,538	41616,964	0,918028	60168,939	50984,674	1,1801378
2075,6575	0,2454135	0,1274636	11844,865	20106,641	0,5891021	29829,646	16284,312	1,8318027
3125,0836	0,3485102	0,0381054	59661,462	71315,898	0,8365801	44911,137	82011,661	0,5476189
3909,0866	0,3246243	0,0912393	28628,312	36738,604	0,7792433	56178,184	42844,351	1,3112157
2665,9692	0,3180354	0,168584	13801,676	18078,581	0,763427	38313,12	15813,889	2,4227514
1832,9255	0,2874632	0,1389076	9389,4308	13607,079	0,6900401	26341,301	13195,288	1,9962657
1502,4954	0,3997248	0,1220101	8115,7235	8458,1246	0,9595181	21592,63	12314,521	1,7534284
15340,313	0,3721402	0,0651892	200998	225005,45	0,8933028	220458,39	235319,77	0,936846
10984,588	0,3858299	0,0842828	111821,3	120735,93	0,9261642	157861,48	130330,16	1,2112429
16274,936	0,3377255	0,0497474	260778,85	321674,35	0,8106921	233890,02	327151,6	0,7149286
21217,676	0,6170218	0,1669215	129218,57	87243,354	1,481128	304923,02	127111,69	2,3988591
46548,861	0,5221978	0,2121153	183967,4	146762,05	1,253508	668962,02	219450,7	3,0483477
10369,635	0,442131	0,0553574	103831,62	97833,277	1,0613119	149023,88	187321,49	0,7955514

75200,645	0,7019376	0,6227738	190655,49	113151,09	1,6849637	1080721,9	120751,14	8,9499937
458,18087	0,4088408	0,0320545	7059,6703	7193,4642	0,9814006	6584,5993	14293,813	0,4606608
11179,769	0,5740808	0,0457958	147902,71	107327,51	1,3780503	160666,46	244122,21	0,6581395
10938,165	0,3598846	0,0512767	102285,16	118401,53	0,8638838	157194,33	213316,61	0,7369062
12955,169	0,3704376	0,084419	84362,015	94872,389	0,8892157	186181,05	153462,75	1,2132002
6744,0123	0,4399261	0,0360466	84054,443	79595,571	1,0560191	96919,408	187091,28	0,5180327
4988,0565	0,5569497	0,0387479	68530,734	51259,849	1,3369281	71684,253	128730,88	0,5568536
7817,2889	0,410724	0,0779861	73399,633	74447,773	0,9859211	112343,66	100239,49	1,1207525
3974,2396	0,4790339	0,0448503	41642,975	36214,575	1,1498955	57114,509	88611,242	0,6445515
9398,0661	0,2679845	0,0666372	81641,988	126914,67	0,6432825	135061,29	141033,36	0,9576549
3884,4141	0,5035838	0,0312268	58148,157	48102,993	1,2088262	55823,611	124393,41	0,4487666
2912,7239	0,4919764	0,0433857	34500,194	29213,605	1,1809632	41859,277	67135,594	0,6235035
10052,242	0,3171227	0,0509387	80359,709	105564,75	0,7612362	144462,57	197339,81	0,7320498
13405,776	0,4171862	0,0260097	242437,2	242090,24	1,0014332	192656,8	515415,28	0,3737895
1773,5307	0,3421766	0,0179188	40797,129	49669,21	0,8213766	25487,727	98976,144	0,2575138

1358,637	0,7944712	0,1330991	7797,4167	4088,6557	1,9070857	19525,216	10207,712	1,9127907
16270,761	0,4507098	0,0834317	95643,456	88402,838	1,0819048	233830,02	195019,04	1,1990112
424617,85	0,4175833	0,0885962	2264886,7	2259494,6	1,0023864	6102259,1	4792734,2	1,2732313
17596,31	0,5013144	0,1076293	95367,976	79250,198	1,2033784	252879,72	163489,95	1,54676
12714,524	0,2087109	0,0901981	108268,7	216105,41	0,5009995	182722,7	140962,22	1,296253
354,82986	0,3497919	0,0770037	2508,5915	2987,639	0,8396568	5099,3235	4607,9613	1,1066333
168,36596	0,3945737	0,0683056	1370,8293	1447,3155	0,9471531	2419,6173	2464,8943	0,9816313
41,709149	0,4754563	0,0802115	318,62227	279,173	1,1413076	599,40965	519,98981	1,1527335
63,351593	0,3850933	0,1174846	304,91066	329,8485	0,9243961	910,43709	539,23311	1,6883924
35773,718	0,6398587	0,083123	265781,62	173040,91	1,5359467	514110,5	430370,62	1,1945762
6117,2395	0,4982923	0,0879126	42508,889	35538,861	1,1961241	87911,943	69583,164	1,2634082
5053,8672	0,606798	0,0844292	34642,306	23783,216	1,4565863	72630,031	59859,234	1,2133472
1086,5684	0,5192903	0,0704005	7330,2948	5880,5664	1,2465287	15615,269	15434,11	1,0117376
2465,8508	0,6449373	0,0822449	19595,3	12657,337	1,5481376	35437,183	29981,825	1,1819555
4350,5184	0,6048864	0,0845211	26830,688	18478,466	1,4519976	62522,079	51472,596	1,2146673
13829,444	0,3751332	0,1139167	68201,996	75738,982	0,9004874	198745,41	121399,67	1,6371166
4452,1785	0,2987688	0,1108441	19784,929	27587,172	0,7171786	63983,055	40166,117	1,5929609
94566,035	0,4623678	0,1230962	484665,54	436679,17	1,1098893	1359025,4	768228,4	1,7690382
27781,214	0,2332913	0,082108	172874,14	308702	0,5600033	399248,79	338349,56	1,1799891
24820,109	0,2705821	0,0782189	175243,03	269804,79	0,6495179	356694,22	317316,05	1,1240977
1187087	0,3694387	0,1201827	5625670	6343658,1	0,886818	17059840	9877355,6	1,7271667
16910,615	0,356108	0,1156175	77892,835	91122,1	0,8548183	243025,48	146263,43	1,6615601
35341,725	0,3421276	0,1633745	129071,09	157162,44	0,8212591	507902,25	216323,33	2,3478848
79,992572	0,2491127	0,1299174	252,65493	422,51271	0,5979819	1149,5876	615,7189	1,8670656
119,14917	0,3486087	0,1321702	655,62489	783,47507	0,8368165	1712,314	901,48304	1,8994412
20654,601	0,2670417	0,0653972	188257	293683,82	0,6410193	296830,97	315833,22	0,9398346
829670,57	0,4149974	0,1211495	4238027,5	4254282,3	0,9961792	11923344	6848320,3	1,7410611
7681,8155	0,2329482	0,0547205	34290,649	61323,121	0,5591798	110396,75	140382,89	0,7863974
26126,919	0,6308981	0,106578	153934,32	101644,57	1,5144372	375474,63	245143,53	1,5316522
85818,968	0,4234436	0,0868955	471100,41	463474,47	1,0164538	1233319,8	987611,42	1,2487905
48743,533	0,4903372	0,1074137	256652,05	218050,87	1,1770283	700502,05	453792,48	1,5436616
16628,809	0,2045194	0,1009352	75685	154164,08	0,490938	238975,59	164747,31	1,4505583
9570,7598	0,5660482	0,0726774	57796,353	42535,835	1,3587685	137543,1	131688,28	1,0444597
63717,328	0,4480002	0,0353186	503434,56	468136,78	1,0754006	915693,12	1804075,2	0,5075693
13410,58	0,5127015	0,320047	24699,975	20069,652	1,2307127	192725,84	41901,911	4,5994523
36515,114	0,3873323	0,1294644	187733,94	201914,29	0,9297705	524765,24	282047,49	1,8605563

48144,122	0,7680239	0,2131602	166339,79	90225,505	1,8436005	691887,8	225858,84	3,0633638
5959,8639	0,5392946	0,2089978	18993,737	14672,101	1,2945479	85650,272	28516,4	3,0035443
30609,341	1,4351682	0,5035741	114917,76	33357,405	3,4450449	439892,32	60784,186	7,2369534
336,81775	0,5540968	0,119053	1757,2346	1321,1498	1,3300798	4840,4682	2829,1405	1,7109324

15075,821	0,6111977	0,0644556	166312,61	113357,79	1,4671476	216657,33	233894,52	0,9263035
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25102,718

23844,669

9598,9077	0,4375895	0,2691893	39716,047	37810,032	1,0504103	137947,62	35658,573	3,8685682
19001,906	0,6827465	0,1297332	131353,52	80147,527	1,6388967	273079,8	146469,11	1,8644191
16784,025	0,5369274	0,0847201	164411,74	127563,13	1,2888657	241206,23	198111,39	1,2175284
22702,141	0,3221578	0,054972	195284,82	252526,95	0,7733227	326256,53	412976,73	0,7900119

30695,863

11095,117

20376,174

15464,926	0,6072004	0,0769001	146318,12	100386,2	1,4575522	222249,22	201104,21	1,1051445
174,6469	0,5211002	0,1872373	547,9802	438,07808	1,2508734	2509,8818	932,75683	2,6908211
11986,016	0,3301125	0,1521094	68191,67	86055,224	0,7924176	172253,18	78798,676	2,1859908

15295,481	0,2497723	0,0526882	150940,07	251749,31	0,599565	219814,09	290301,85	0,7571915
18668,005	0,6499706	0,1109583	144243,13	92450,517	1,5602199	268281,25	168243,49	1,5946011
14226,315	0,6022349	0,0950414	120653,41	83460,623	1,4456328	204448,92	149685,52	1,3658564
4114,3118	0,3218944	0,0277113	79882,319	103382,05	0,7726904	59127,511	148470,34	0,3982446
3114,7927	0,3599591	0,0446169	41550,239	48087,067	0,8640627	44763,244	69811,903	0,6411979
4321,0137	0,356792	0,0280042	83343,334	97311,381	0,8564603	62098,062	154298,93	0,402453
3387,7085	0,3232022	0,0668793	33820,156	43592,247	0,7758296	48685,366	50654,063	0,9611345
3646,7808	0,3965952	0,1995789	21119,643	22184,366	0,9520057	52408,54	18272,38	2,8681836
42414,102	0,4378519	0,2095499	264412,37	251572,1	1,0510401	609540,65	202405,76	3,0114788
8743,3346	0,4247365	0,1914894	53914,351	52880,151	1,0195574	125652,03	45659,621	2,7519288
9017,7678	0,4093108	0,1942287	55496,105	56482,937	0,9825287	129595,95	46428,614	2,7912949
1895,5726	0,4196144	0,0601787	21790,229	21633,131	1,0072619	27241,613	31499,04	0,8648394
5962,4297	0,4014127	0,047175	79228,871	82224,319	0,9635698	85687,145	126389,58	0,6779605
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3914,3378	0,3093923	0,1040105	18055,106	24310,755	0,7426798	56253,649	37634,06	1,4947537
10584,485	0,3823052	0,0896843	85151,22	92787,315	0,9177032	152111,53	118019,38	1,2888691

9115,5624	0,6757158	0,1628625	49180,69	30320,646	1,6220199	131001,38	55970,895	2,3405268
5004,0884	0,3906032	0,0477187	54514,242	58140,951	0,9376221	71914,65	104866,42	0,6857738
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24931,949	0,4752587	0,0320873	371206,88	325382,28	1,1408331	358301,5	777003,58	0,4611324
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7706,8118	0,3841305	0,0531073	62881,558	68194,983	0,9220848	110755,97	145117,76	0,7632145
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4145,5935	0,0993682	0,0374444	80631,19	338036,59	0,238528	59577,066	110713,39	0,5381198
3884,1831	0,3932489	0,0351532	58185,873	61639,345	0,9439729	55820,291	110492,92	0,5051934
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175,99225	0,5850841	0,0263174	3271,2329	2329,1695	1,4044632	2529,2161	6687,2915	0,3782123
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1916,4352	0,5251149	0,0409128	25904,93	20551,145	1,2605103	27541,434	46841,899	0,5879658
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27846,631	0,4601607	0,0470636	368573,03	333673,68	1,1045913	400188,92	591680,76	0,6763595

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5821,5035	0,3405698	0,0515348	56462,736	69065,91	0,8175196	83661,868	112962,64	0,7406154
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14810,24 0,2673781 0,0624882 122761,47 191268,79 0,641827 212840,61 237008,73 0,8980286
5271,9153 0,4030332 0,0466163 71593,798 74001,842 0,9674597 75763,638 113091,72 0,6699309
3566,6929 0,3250654 0,0341663 59557,393 76326,07 0,7803021 51257,582 104392,21 0,4910097
4022,6611 0,3454067 0,0314273 77963,081 94029,933 0,8291304 57810,382 127998,81 0,4516478

4042,8885 0,4123187 0,0367349 53090,688 53640,552 0,9897491 58101,074 110055,76 0,527924
3227,2506 0,4438848 0,0370992 43269,035 40608,304 1,0655219 46379,396 86989,747 0,5331593
1391,2431 0,4093925 0,0227582 26929,804 27403,197 0,9827249 19993,804 61131,56 0,3270619
573,08839 0,4258753 0,0261213 10034,157 9815,3616 1,0222911 8235,9559 21939,474 0,3753944
1357,4419 0,4093493 0,0275104 21780,838 22166,06 0,9826211 19508,041 49342,924 0,3953564
2460,001 0,4529137 0,0356609 33991,024 31264,877 1,0871952 35353,114 68983,171 0,512489
12418,567 0,5431493 0,0675891 124291,98 95330,492 1,3038009 178469,46 183736,19 0,9713354
13495,941 0,4076618 0,0587106 119344,57 121958,07 0,9785705 193952,59 229872,49 0,8437399
4767,1554 0,4203034 0,0529222 55186,678 54698,989 1,0089159 68509,644 90078,553 0,7605544
18275,479 0,4545671 0,0468965 238453,14 218530,95 1,0911642 262640,18 389698,43 0,6739575
26459,776 0,5382778 0,047445 391469,02 302969,47 1,2921072 380258,17 557693,66 0,6818406
7320,2386 0,4250203 0,0535046 81815,773 80192,792 1,0202385 105200,46 136815,04 0,7689246
3430,1465 0,368795 0,0330835 51966,222 58700,804 0,8852728 49295,249 103681,5 0,4754489
18,574194 0,3140804 0,0039806 1602,2357 2125,1689 0,7539333 266,93306 4666,1643 0,0572061
966,49677 0,3107843 0,1341934 3944,4759 5287,3513 0,7460211 13889,698 7202,2679 1,9285173
597,69353 0,3860842 0,0479062 5918,1324 6385,7298 0,9267746 8589,5608 12476,337 0,6884682
13854,778 0,6412897 0,039375 195597,05 127062,09 1,5393816 199109,5 351867,42 0,5658651
69672,251 0,3287574 0,0426004 747561,87 947282,55 0,7891646 1001272,4 1635481,7 0,6122186
29888,832 0,3480382 0,0425813 339971,79 406933,96 0,8354471 429537,76 701923,14 0,6119442
24419,839 0,4168031 0,0785214 191912,29 191813,75 1,0005137 350941,88 310996,11 1,1284446

3748,8614	0,3235131	0,0495506	40255,11	51836,674	0,7765759	53875,558	75657,289	0,7121
17881,809	0,2257092	0,2819861	59046,604	108981,71	0,5418029	256982,68	63413,798	4,0524727
455,9001	0,3478291	0,0341597	6862,9535	8219,6444	0,8349453	6551,822	13346,124	0,4909157
2304,6618	0,3477482	0,0505569	23899,477	28630,664	0,8347511	33120,708	45585,476	0,7265627
30401,724	0,2769595	0,1800728	143479,72	215815,29	0,6648265	436908,62	168830,22	2,5878579
2010,6255	0,370665	0,0318208	30431,801	34202,196	0,8897616	28895,059	63185,81	0,457303
251,76824	0,3225196	0,0499986	2139,8724	2764,0101	0,7741912	3618,2065	5035,5035	0,7185392
2449,9688	0,3755002	0,0484928	27419,337	30419,687	0,9013682	35208,94	50522,362	0,6968981
8568,1605	0,3426225	0,0423674	111538,44	135617,76	0,8224471	123134,57	202234,58	0,60887
990,96932	0,3365906	0,0293225	14482,005	17923,985	0,8079679	14241,398	33795,469	0,4213996

1846,1249	0,340718	0,0488101	18142,208	22182,115	0,8178755	26530,992	37822,565	0,7014594
585,28254	0,3756345	0,030528	10316,935	11441,769	0,9016905	8411,2002	19172,019	0,4387227
12211,254	0,369321	0,1026682	78682,498	88752,793	0,8865355	175490,12	118938,96	1,4754638
1936,3619	0,4677784	0,1085536	15448,199	13757,693	1,1228771	27827,804	17837,84	1,5600434
1444,5927	0,3712534	0,0690454	13343,274	14972,694	0,8911739	20760,501	20922,363	0,9922637
18180,963	0,320426	0,1034465	113171,93	147135,99	0,7691655	261281,88	175752,38	1,4866478
20804,656	0,4471282	0,1636128	110924,3	103348,12	1,0733074	298987,44	127157,9	2,3513085
1672,6848	0,3696358	0,0341916	24093,031	27153,469	0,8872911	24038,452	48920,887	0,491374
14570,272	0,4089157	0,2228723	73787,261	75171,896	0,9815804	209391,99	65374,968	3,2029383
31525,915	0,4251091	0,2523545	158609,73	155430,9	1,0204517	453064,57	124927,08	3,6266322

13857,265	0,4616777	0,0374766	195302,5	176228,79	1,1082327	199145,23	369757,55	0,5385833
11088,951	0,4952988	0,0726632	91479,157	76941,888	1,1889383	159361,3	152607,52	1,0442559
2596,1126	0,4882811	0,0641546	25999,519	22182,133	1,1720928	37309,199	40466,538	0,9219766
670,18235	0,2356556	0,0604528	6765,9537	11960,769	0,5656788	9631,3105	11086,039	0,8687784
2115,5877	0,3106493	0,0288997	24496,726	32850,77	0,7456972	30403,49	73204,452	0,415323
11615,143	0,4123578	0,0282488	211735,3	213908	0,9898428	166923,3	411172,83	0,4059687
3375,2044	0,5851519	0,0279003	65342,43	46519,453	1,4046259	48505,667	120973,94	0,4009596
2126,9392	0,3972208	0,0220244	43885,978	46025,839	0,9535074	30566,624	96571,796	0,3165171
1202,8964	0,3815766	0,029808	19864,848	21687,597	0,9159543	17287,04	40354,776	0,4283765
22994,644	0,472291	0,0636016	180237,52	158980,36	1,1337094	330460,15	361541,66	0,9140306
7486,1396	0,4981576	0,0856766	54982,116	45979,33	1,1958007	107584,65	87376,742	1,2312733
4801,891	0,3963195	0,0749362	39489,375	41509,05	0,9513438	69008,835	64079,716	1,0769217
19281,907	0,4852655	0,0661814	181351,57	155686,09	1,164854	277103,74	291349,21	0,9511052

25437,775	0,5044792	0,0491657	309200,64	255331,87	1,2109755	365570,82	517388,79	0,7065689
33475,636	0,6139028	0,0431121	396896,59	269330,6	1,4736409	481084,36	776479,48	0,6195712
64437,965	0,6308938	0,0369687	882642,06	582822,51	1,5144269	926049,53	1743041,5	0,5312837
40754,365	0,3683609	0,0433162	438704,15	496142,16	0,8842308	585688,28	940857,17	0,622505
40685,351	0,566937	0,0327383	615928,1	452588,13	1,360902	584696,47	1242746	0,4704875
10837,322	0,6467528	0,0320261	193518,57	124650	1,5524956	155745,1	338389,99	0,4602533
4443,1204	0,4603923	0,1079612	25249,83	22847,482	1,1051472	63852,879	41154,779	1,5515301
816,88015	0,3138099	0,0231583	14211,018	18865,42	0,753284	11739,531	35273,681	0,3328128
5059,563	0,333229	0,030227	81210,827	101526,42	0,7998985	72711,886	167385,8	0,434397
6901,4882	0,3303304	0,044125	80554,952	101590,15	0,7929405	99182,522	156407,79	0,6341278
8878,6893	0,5421084	0,0774998	49594,947	38111,781	1,3013023	127597,23	114564,02	1,1137636
6829,4232	0,4614618	0,0286881	124841,55	112701,93	1,1077144	98146,863	238057,55	0,4122821
67003,586	0,4083901	0,0364956	884129,36	901879,62	0,9803186	962920,53	1835935,4	0,524485
21687,179	0,4439677	0,0448897	243673,83	228646,96	1,0657208	311670,34	483121,33	0,6451182
10565,593	0,3572438	0,0328879	146929,86	171337,83	0,8575448	151840,03	321261,04	0,4726375

8362,8275	0,3207286	0,0433493	79564,086	103344,5	0,7698918	120183,69	192917,31	0,6229803
82457,457	0,3653674	0,1301707	321788,56	366900,91	0,8770449	1185010,9	633456,51	1,870706
3378,268	0,361103	0,0499728	39853,278	45977,029	0,8668085	48549,695	67602,144	0,718168
421,93945	0,2807828	0,0256535	5204,9181	7722,383	0,6740041	6063,7673	16447,646	0,3686708
7425,5681	0,1675668	0,0605986	35372,492	87939,809	0,4022353	106714,17	122536,89	0,8708738
6656,5567	0,2853354	0,0452758	68972,397	100699,56	0,6849324	95662,568	147022,54	0,650666
3392,9598	0,3673378	0,0504944	38053,934	43156,07	0,8817748	48760,833	67194,807	0,7256637
707,86243	0,3693185	0,0598173	6719,5105	7579,5693	0,8865293	10172,818	11833,743	0,859645
2930,9031	0,3380057	0,064239	23319,089	28740,578	0,8113647	42120,533	45625,009	0,9231896
2444,3575	0,3208092	0,0745581	16831,137	21856,193	0,7700855	35128,299	32784,58	1,0714885
4641,1867	0,292038	0,0706417	31503,177	44938,954	0,7010216	66699,326	65700,402	1,0152042
4070,7288	0,3671957	0,0390977	57201,264	64895,71	0,8814337	58501,173	104116,75	0,5618805
6676,8056	0,5517149	0,0520759	102003,8	77021,077	1,3243622	95953,569	128212,95	0,7483922
14142,976	0,3215768	0,0375627	215693,22	279421,41	0,771928	203251,25	376516,79	0,5398199
781,4592	0,3300471	0,024663	14070,916	17760,469	0,7922604	11230,49	31685,526	0,354436
955,24856	0,433382	0,0355316	19443,622	18690,213	1,0403104	13728,048	26884,481	0,510631
1696,6149	0,4503297	0,0387723	31413,883	29060,222	1,0809925	24382,357	43758,38	0,5572043
467,49078	0,3047973	0,0497615	4046,5917	5530,7778	0,7316497	6718,3937	9394,6285	0,7151314
1544,3069	0,3273141	0,0325153	25077,856	31917,853	0,7857	22193,511	47494,781	0,4672831
4210,6211	0,3743235	0,0537796	41423,543	46100,76	0,8985436	60511,59	78294,071	0,7728758
5583,9067	0,3310459	0,0409815	66759,388	84010,211	0,794658	80247,322	136254,47	0,5889518
2193,569	0,1319925	0,0634144	7765,5356	24509,258	0,3168409	31524,174	34591	0,9113403
2565,6689	0,2572856	0,1354779	8369,0174	13550,863	0,6176003	36871,687	18937,912	1,9469774
3219,4606	0,1489307	0,0681588	17866,248	49975,49	0,3575002	46267,445	47234,704	0,9795223
18408,026	0,1378645	0,0649453	73350,646	221645,81	0,3309363	264545,04	283439,02	0,9333402
9651,4704	0,2141894	0,068937	54380,819	105768,35	0,5141502	138703,01	140004,28	0,9907055
5479,4986	0,1299205	0,0607453	26062,86	83570,365	0,3118673	78746,856	90204,434	0,8729821
3237,3394	0,2157102	0,0628288	18881,297	36464,406	0,5178007	46524,384	51526,345	0,9029242
396023,75	0,1487663	0,0615612	1825892,7	5113033,4	0,3571056	5691328,2	6433012,9	0,8847065
1176,0135	0,2571341	0,0938017	7101,6884	11505,615	0,6172368	16900,7	12537,226	1,3480415
232003,43	0,1250609	0,0694901	738761,83	2460882,7	0,300202	3334162,8	3338652,2	0,9986553
19173,055	0,1084626	0,0508115	68826,603	264353,09	0,2603586	275539,41	377336,99	0,730221
7717,8953	0,258005	0,0671333	49738,389	80310,356	0,6193272	110915,26	114963,78	0,9647844
18660,659	0,2882113	0,0748908	115815,16	167402,68	0,6918358	268175,66	249171,51	1,0762694
19303,29	0,1464256	0,0722075	69704,751	198314,02	0,3514867	277411,04	267330,65	1,0377076
6468,7713	0,1409778	0,0830777	21179,656	62585,838	0,3384097	92963,87	77864,136	1,1939241
11117,958	0,2414738	0,0890099	63892,485	110226,91	0,5796451	159778,17	124906,96	1,2791775
15856,574	0,190481	0,0745673	61863,288	135297,37	0,4572394	227877,66	212647,68	1,0716207
7027,555	0,16308	0,0688844	25292,532	64609,989	0,3914647	100994,25	102019,49	0,9899505
5280,2925	0,1531844	0,067181	18909,759	51425,591	0,3677111	75884,028	78598,013	0,9654701
3159,5751	0,2175346	0,0851269	13710,316	26255,911	0,5221802	45406,819	37116,066	1,2233737
5674,7195	0,1806982	0,0865314	22111,247	50976,18	0,4337564	81552,409	65579,88	1,2435584
3360,73	0,2031799	0,074583	15317,705	31406,602	0,4877225	48297,653	45060,279	1,0718454
10385,714	0,2028966	0,0766655	39903,236	81929,679	0,4870425	149254,96	135467,84	1,1017741
7686,8525	0,1657351	0,0402013	62935,114	158192,68	0,3978383	110469,13	191209,28	0,5777394
42253,173	0,3272625	0,1919343	186462	237356,96	0,7855763	607227,92	220143,9	2,7583227
59426,598	0,2391503	0,1931118	244001,32	425039,42	0,5740675	854030,27	307731,59	2,7752441
43013,158	0,2847275	0,2616267	171101,43	250341,06	0,6834733	618149,8	164406,62	3,7598839

205469,14	0,2586198	0,3365179	641848,05	1033899,5	0,6208031	2952833,7	610574,22	4,8361586
82388,278	0,2905597	0,2951907	299188,53	428960,69	0,6974731	1184016,7	279101,85	4,2422388
97924,558	0,2182213	0,3004514	315353,91	602017,45	0,5238285	1407291,4	325924,79	4,3178408
10553,894	0,3211158	0,2921315	41343,439	53635,568	0,7708213	151671,91	36127,209	4,1982736
50511,097	0,3542547	0,1303349	292861,28	344393	0,8503694	725904,02	387548,38	1,8730668
14899,662	0,1740381	0,2012597	53822,066	128832,06	0,4177692	214125,71	74032,027	2,8923389
22838,519	0,2112324	0,2381959	89596,511	176700,8	0,5070521	328216,44	95881,225	3,4231565
17392,819	0,2028872	0,2306787	58695,414	120519,55	0,4870198	249955,31	75398,448	3,3151254
75353,152	0,1614887	0,153448	337400,82	870385,87	0,3876451	1082913,6	491066,45	2,2052283
26132,079	0,2685651	0,2747459	93889,59	145638,34	0,6446763	375548,79	95113,629	3,9484225
37023,651	0,3105173	0,3281306	151798,34	203652,23	0,7453802	532073,51	112832,07	4,7156232
15563,55	0,2192752	0,2585285	55178,377	104830,44	0,5263583	223666,57	60200,509	3,71536

18912,598	0,5565283	0,073266	113008,29	84592,338	1,3359164	271796,33	258135,91	1,0529195
89987,875	0,6421574	0,1125289	529590,27	343563,05	1,5414646	1293231,9	799686,74	1,6171731
4617,0569	0,5533503	0,0307573	73828,189	55581,468	1,3282879	66352,551	150112,68	0,4420183
7289,9008	0,3677677	0,0506513	80911,141	91652,152	0,8828068	104764,47	143923,18	0,7279194
35276,497	0,6638393	0,0337265	593505,96	372451,78	1,5935109	506964,86	1045958,8	0,4846891
14800,015	0,4756261	0,0533898	107141,8	93842,851	1,1417151	212693,66	277206,98	0,7672738
12985,296	0,5501971	0,0454291	139477,42	105607,2	1,3207188	186614,01	285836,41	0,65287
3010,5539	0,6591343	0,079936	20207,011	12771,329	1,5822168	43265,209	37662,038	1,148775
24875,686	0,4975146	0,0993668	149156,97	124895,17	1,1942573	357492,93	250342,14	1,4280174
840,94439	0,5783441	0,0447914	10022,999	7219,7021	1,3882843	12085,362	18774,671	0,6437057
6058,5391	0,5342825	0,0382751	89546,135	69820,638	1,2825167	87068,35	158289,24	0,5500586

2187,3058	0,3991562	0,0421174	29502,698	30791,209	0,9581533	31434,163	51933,574	0,6052763
23669,087	0,4254916	0,0622398	221331,91	216701,03	1,0213699	340152,69	380288,35	0,8944599
16928,958	0,4193725	0,0831021	127528,52	126682,1	1,0066815	243289,08	203712,64	1,1942758
14000,098	0,4773452	0,0510196	156417,85	136509,13	1,1458417	201197,91	274406,02	0,7332125
1833,352	0,4513327	0,0331298	36407,62	33604,964	1,0834001	26347,43	55338,41	0,4761147
13537,242	0,3933878	0,086601	93152,371	98646,345	0,9443064	194546,13	156317,35	1,2445588
5078,5876	0,3723222	0,0861427	33296,016	37254,716	0,8937396	72985,292	58955,486	1,2379729
8911,3603	0,3675088	0,0892306	57972,245	65714,372	0,8821852	128066,75	99868,86	1,2823492
679,59439	0,33646	0,0374101	8940,6003	11069,835	0,8076544	9766,5727	18166,043	0,5376279
11065,991	0,2362222	0,0487857	92479,116	163091,31	0,5670389	159031,34	226828,45	0,7011084

4896,052	0,5200071	0,0377482	56270,519	45079,554	1,2482493	70362,039	129703,06	0,5424856
22814,438	0,5337391	0,032336	417023,69	325491,51	1,2812122	327870,38	705542,45	0,4647068
585,76434	0,4520502	0,0325774	7710,6596	7105,7973	1,0851224	8418,1242	17980,688	0,4681759
551,15175	0,3906381	0,0381177	5595,642	5967,3747	0,9377058	7920,7004	14459,224	0,5477957
146,26015	0,4230812	0,0263449	2316,4918	2280,9456	1,015584	2101,9308	5551,7412	0,3786075
306,09116	0,371432	0,0311596	3959,7551	4441,1647	0,8916028	4398,8908	9823,3497	0,4477995
2632,7326	0,410653	0,0429991	28998,807	29417,997	0,9857506	37835,471	61227,564	0,6179483
3821,1644	0,4170834	0,0663915	30078,084	30042,438	1,0011865	54914,637	57554,981	0,9541248
10178,783	0,3859398	0,0446148	100313,65	108280,03	0,926428	146281,11	228147,91	0,6411679
50173,246	0,4064419	0,0410222	587091,6	601748,88	0,9756422	721048,7	1223075,2	0,5895375
2311,0575	0,5066044	0,0756954	15876,274	13055,32	1,216077	33212,621	30531,014	1,0878322
2590,1038	0,6601331	0,1645774	21340,128	13467,08	1,5846143	37222,846	15737,908	2,3651712
18525,885	0,3861401	0,0290241	311322,54	335871,86	0,9269087	266238,82	638292,67	0,4171109

11589,841	0,4702668	0,0302092	186261,54	165001,08	1,1288504	166559,68	383652,61	0,4341419
17508,539	0,3346021	0,0780309	131929,58	164256,06	0,8031946	251618,35	224379,67	1,1213955

6896,8887	0,3826189	0,0494861	70511,318	76771,558	0,9184563	99116,422	139370,1	0,7111742
67,512358	0,18211	0,0095421	1067,9144	2442,9281	0,4371453	970,23218	7075,184	0,1371317
666,69347	0,5269915	0,0292267	11538,291	9121,0701	1,265015	9581,1713	22811,079	0,4200227
11708,591	0,4095732	0,0268441	205669,68	209192,79	0,9831586	168266,26	436170,26	0,3857811
11928,683	0,4838611	0,02449	236527,18	203642,45	1,1614827	171429,24	487083,44	0,3519505
70395,489	0,2656561	0,0429945	805692,7	1263448,7	0,6376933	1011666,2	1637313,2	0,6178819
40634,915	0,4540759	0,0777297	305838,33	280589,51	1,0899849	583971,64	522772,34	1,1170668
17736,046	0,5126867	0,0595522	156469,01	127140,59	1,230677	254887,9	297823,74	0,8558347
3517,8968	0,2744201	0,0385424	35790,116	54331,919	0,6587309	50556,325	91273,476	0,5538994
11394,874	0,4436951	0,0428942	141836,43	133171,43	1,0650665	163757,78	265650,67	0,6164403

5422,4584	0,3102729	0,0439315	81219,308	109049,43	0,7447935	77927,121	123429,74	0,631348
447,28117	0,3463887	0,0607955	2124,7602	2555,3722	0,8314876	6427,9577	7357,1451	0,8737027
8773,7775	0,4831274	0,0379512	94289,948	81303,944	1,1597217	126089,53	231185,96	0,545403
5256,7573	0,5357912	0,0477732	55042,928	42797,055	1,2861382	75545,801	110035,65	0,6865575
39390,531	0,5854594	0,054962	472391,4	336134,52	1,4053642	566088,37	716686,39	0,789869
28658,148	0,3556204	0,0560458	265657,48	311202,65	0,8536479	411851,38	511334,27	0,8054445
821,25378	0,496243	0,0783461	4679,0278	3927,9788	1,191205	11802,385	10482,385	1,1259256
10690,925	0,3885193	0,0620601	65019,166	69716,679	0,93262	153641,19	172267,34	0,8918765
61910,754	0,1225677	0,1423441	250072,54	849958,9	0,2942172	889730,54	434937,23	2,0456528

3824,0056	0,6066073	0,0371611	53604,289	36812,885	1,4561285	54955,469	102903,45	0,5340488
4675,2087	0,5638319	0,0374098	60264,045	44526,292	1,3534485	67188,262	124972,95	0,5376225
17653,46	0,6079982	0,0803782	140249,86	96096,61	1,4594673	253701,03	219630	1,1551292
39837,862	0,5576766	0,0407446	499443,45	373088,47	1,338673	572517,05	977745,61	0,5855481
12382,841	0,6656496	0,034972	190765,15	119388,16	1,5978565	177956,02	354079,06	0,5025884
8907,0582	0,4155453	0,0436085	68500,689	68672,754	0,9974944	128004,93	204250,5	0,6267056
8818,3989	0,4372949	0,0534348	64678,629	61616,124	1,049703	126730,79	165031,05	0,7679209
2650,1814	0,5989352	0,0392034	34174,123	23769,798	1,437712	38086,231	67600,797	0,5633991
1654,9018	0,534906	0,0406785	20916,704	16290,099	1,2840133	23782,89	40682,501	0,5845975
3869,8062	0,4623435	0,0480265	41013,716	36954,922	1,1098309	55613,678	80576,43	0,6901978
7498,6464	0,6288858	0,0388248	100000,34	66242,641	1,5096068	107764,39	193140,5	0,5579585
11245,34	0,7654012	0,0488668	130864,41	71226,289	1,8373049	161608,8	230122,35	0,7022734
2691,1374	0,4261202	0,0774485	22621,643	22115,662	1,0228789	38674,817	34747,427	1,1130268
1991,8198	0,5240766	0,0438867	23325,823	18541,724	1,258018	28624,799	45385,531	0,6307032

18131,25	0,3787703	0,0691291	142926,65	157197,34	0,909218	260567,44	262281,14	0,9934662
10822,299	0,4143406	0,0588652	119307,65	119955,1	0,9946025	155529,2	183848,88	0,8459622
11982,135	0,4340196	0,0461894	141248,26	135575,64	1,041841	172197,41	259413,21	0,6637958
12611,454	0,5877902	0,0329928	229474,67	162637,37	1,410959	181241,46	382248,24	0,474146
4726,3155	0,3418403	0,0366331	52377,697	63830,919	0,8205694	67922,726	129017,48	0,5264614
8137,5038	0,4187803	0,0207674	163106,75	162253,33	1,0052598	116945,52	391840,18	0,2984521
1384,581	0,4568049	0,120178	8227,0704	7502,7823	1,0965359	19898,062	11521,082	1,7271001
18738,647	0,4661699	0,0772027	240592,16	215003,34	1,1190159	269296,45	242720,13	1,1094937
29589,518	0,2756978	0,0498497	302176,29	456599,11	0,6617978	425236,25	593574,48	0,7163991
2844,7931	0,3606836	0,0618757	21676,936	25036,833	0,8658018	40883,032	45975,918	0,8892271
40783,947	0,3838812	0,0603914	340459,91	369468,16	0,9214865	586113,4	675327,13	0,8678955
62432,578	0,3677377	0,0636128	453211,51	513417,54	0,8827348	897229,76	981446,95	0,9141908
18082,541	0,3497	0,0375863	195924,26	233399,82	0,8394362	259867,43	481094,14	0,5401592
11108,408	0,4628461	0,1070306	78080,369	70276,992	1,1110374	159640,92	103787,26	1,5381553
21311,309	0,4321033	0,111054	141223,38	136152,91	1,037241	306268,64	191900,35	1,5959775
6971,1921	0,5079394	0,1131652	48349,025	39653,703	1,2192815	100184,25	61601,898	1,6263176

8186,5849	0,4083444	0,1158367	56150,315	57284,031	0,9802089	117650,88	70673,503	1,6647098
16160,311	0,4268648	0,1099367	102292,11	99829,694	1,0246662	232242,72	146996,52	1,5799199
10035,408	0,4877417	0,1144089	62644,465	53505,79	1,1707979	144220,64	87715,262	1,644191
45060,474	0,5256832	0,0999952	360617,42	285779,12	1,2618746	647572,14	450626,53	1,4370484
4690,4948	0,3528209	0,0335675	77056,295	90983,306	0,8469278	67407,941	139733,25	0,4824044
3739,6224	0,279563	0,0385535	60152,415	89635,745	0,6710762	53742,783	96998,355	0,5540587
12158,904	0,3791754	0,0717784	112844,78	123979,32	0,9101903	174737,78	169395,13	1,0315396

3204,6936	0,4325458	0,0348089	64132,681	61766,823	1,0383031	46055,225	92065,398	0,5002447
10466,844	0,4978087	0,0511273	176965,77	148093,08	1,1949632	150420,88	204721,41	0,7347589
8150,3939	0,4343788	0,0510546	130823,87	125466,08	1,0427031	117130,77	159640,68	0,733715
8399,3171	0,4235071	0,0444575	151527,94	149052,73	1,0166063	120708,09	188929,16	0,6389066
6148,6195	0,5200435	0,1327952	35883,48	28745,031	1,2483368	88362,911	46301,521	1,9084235
10487,271	0,3405797	0,0404211	181180,65	221615,95	0,8175434	150714,44	259450,58	0,5808985
7098,1758	0,3805963	0,0388973	138995,85	152140,64	0,9136011	102009,16	182484,93	0,5590004
16860,949	0,4344856	0,0333231	411790,16	394828,47	1,0429596	242311,72	505984,12	0,478892
6333,2064	0,3553833	0,0543878	79302,883	92960,796	0,8530788	91015,642	116445,39	0,7816165
7067,1577	0,3619599	0,0399638	124104,57	142835,18	0,8688656	101563,39	176839,03	0,5743268
18729,553	0,3378667	0,0304436	446064,65	549996,97	0,8110311	269165,76	615222,22	0,4375098
11341,378	0,3348379	0,0327899	239160,88	297552,42	0,8037605	162988,98	345880,45	0,4712292
9254,9694	0,4300184	0,0755535	99538,797	96430,237	1,0322364	133004,82	122495,5	1,0857936
6844,2865	0,3609193	0,0376454	129706,28	149712,75	0,8663677	98360,467	181809,24	0,5410092
17609,422	0,3431592	0,0296067	457732,04	555678,51	0,8237354	253068,15	594778,04	0,4254833
15853,127	0,3249885	0,0606631	203694,94	261107,97	0,7801176	227828,13	261330,75	0,8718
19694,199	0,4196855	0,070043	182160,71	180816,76	1,0074326	283028,86	281172,89	1,0066008
9935,9205	0,4098178	0,0764689	87393,906	88837,903	0,9837457	142790,89	129934,12	1,0989484

11292,69	0,5796324	0,1230269	66802,636	48011,9	1,3913766	162289,27	91790,385	1,7680421
81172,933	0,4072716	0,1228418	412545,6	421983,78	0,9776338	1166550,7	660792,57	1,7653812
60888,617	0,7434522	0,1248146	369349,7	206962,97	1,7846173	875041,21	487832,62	1,7937325

2240,8204

2582,1517

12785,824	0,6107816	0,103472	83421,873	56898,647	1,4661486	183747,37	123567,95	1,4870147
7439,1659	0,9079002	0,1967958	44407,789	20376,471	2,179366	106909,58	37801,443	2,828188
14839,423	0,6770972	0,1621884	78214,328	48121,95	1,6253358	213260,01	91494,981	2,3308383
16948,986	0,6405984	0,1593625	88275,468	57406,64	1,5377223	243576,91	106354,94	2,2902267
377,29747	48,308876	0,0423819	2139,4095	18,449089	115,96288	5422,2095	8902,3348	0,6090772
451,56144	0,6402519	0,068968	2525,4653	1643,2305	1,5368905	6489,4703	6547,4086	0,991151

4056,7165

2760,9604

381,94236

1460,6945

14036,627

102283,62

2447,477

23588,044

2618,0965

16182,648

5930,9485

2836,0497

2127,3303

2930,8975
1772,8528
5927,1349
3034,4619
7561,2625
124658,54
44191,051
18760,343
161317,28
16575,779
66678,7
17769,521
27086,077

2439,0567	0,5650932	0,0497716	21758,278	16040,295	1,3564762	35052,12	49004,981	0,7152767
2118,9029	0,497804	0,0485861	18525,791	15503,378	1,1949519	30451,133	43611,334	0,698239
13558,389	0,6276427	0,044471	170983,95	113488,22	1,5066229	194850,03	304881,7	0,6391005
13183,813	0,4530109	0,1051273	80838,03	74338,702	1,0874286	189466,94	125408,07	1,5108034
10045,522	0,462512	0,108064	62063,456	55901,164	1,1102355	144366	92959,023	1,5530068
10227,122	0,44439	0,0708641	87503,365	82029,196	1,0667344	146975,81	144320,15	1,0184012
5108,227	0,4403057	0,0642958	42359,598	40077,944	1,0569304	73411,245	79448,814	0,9240068
28507,069	0,4343776	0,041235	225631,8	216391,8	1,0427003	409680,19	691331,58	0,5925958
36480,988	0,5189064	0,049124	284043,59	228036,27	1,2456071	524274,81	742630,68	0,7059698
104030,98	0,5952834	0,3199059	436889,2	305742,25	1,4289461	1495047,9	325192,39	4,5974257
55766,908	0,811914	0,333488	336043,2	172422,14	1,9489563	801436,21	167223,11	4,7926164
1318,4539	0,1953946	0,0554697	12606,675	26877,941	0,4690343	18947,737	23768,924	0,7971643
26634,603	0,6902603	0,2041008	179760,97	108490,18	1,656933	382770,64	130497,27	2,9331697
15549,735	0,7196191	0,1920111	108326,79	62710,625	1,7274073	223468,03	80983,537	2,7594254
1451,2739	0,5021413	0,0440604	11011,583	9135,487	1,2053635	20856,517	32938,303	0,6331995
11242,104	0,4843299	0,0452275	87448,503	75217,529	1,162608	161562,29	248568,06	0,649972
11090,944	0,4334307	0,0459547	76676,704	73697,324	1,0404273	159389,95	241345,13	0,6604233
4622,5223	0,5847153	0,0513347	42666,056	30398,069	1,4035779	66431,096	90046,8	0,7377397
1865,7488	0,4705623	0,0541865	15245,137	13496,529	1,1295598	26813,01	34432,008	0,7787234
3751,2381	0,3759029	0,094022	25617,101	28389,793	0,9023349	53909,714	39897,439	1,3512074
41051,25	0,6905424	0,2704075	251736,27	151866,98	1,6576103	589954,86	151812,56	3,8860742
7942,7587	0,7274666	0,20774	58298,929	33385,311	1,7462449	114146,81	38234,142	2,985468
5622,5329	0,4719417	0,1482964	42621,408	37622,472	1,132871	80802,427	37914,158	2,131194

6259,0929	0,4752553	0,0528774	50615,309	44367,285	1,140825	89950,544	118369,83	0,759911
7954,4247	0,6314084	0,0441658	94638,849	62440,593	1,5156622	114314,46	180103,66	0,6347148
6141,8005	0,6771382	0,0423651	79963,882	49195,402	1,6254341	88264,914	144973,11	0,6088365
5259,258	0,5883849	0,0733517	43040,05	30473,278	1,4123866	75581,738	71699,179	1,0541507
1260,334	0,456462	0,0697997	8281,773	7558,3431	1,0957128	18112,486	18056,435	1,0031042
774,19034	0,4812437	0,0486852	6689,5394	5790,8066	1,1551999	11126,028	15901,98	0,6996631
8123,4167	0,4485772	0,0712685	59687,327	55431,019	1,0767857	116743,08	113983,3	1,0242121
13342,592	0,4997911	0,0981864	83633,34	69710,601	1,199722	191748,77	135890,4	1,4110546

5907,9124	0,4327009	0,0599846	58777,866	56589,256	1,0386754	84903,666	98490,491	0,8620494
21455,528	0,6285626	0,0429703	318711,39	211230,66	1,5088311	308341,24	499310,19	0,6175344
15107,982	0,4975951	0,053749	163172,49	136608,83	1,1944505	217119,51	281083,71	0,7724372
5542,9147	0,5970973	0,0491891	75316,895	52547,882	1,4333003	79658,219	112685,75	0,7069059
926,21716	0,4375533	0,0461862	9492,0457	9037,2603	1,0503234	13310,833	20053,968	0,6637506

8581,1511	0,4990079	0,0718036	79057,326	65999,801	1,1978419	123321,26	119508,64	1,0319025
4227,5338	0,3000624	0,0332974	59764,077	82972,97	0,7202837	60754,645	126962,97	0,4785226
33242,211	0,5052431	0,0439854	512053,87	422204,85	1,2128091	477729,77	755755,81	0,6321219
9299,6046	0,3339771	0,0304263	155784,72	194319,34	0,8016943	133646,28	305643,42	0,4372621
19882,686	0,3189909	0,0769259	151758,13	198189,92	0,7657208	285737,64	258465,3	1,1055164
8530,0072	0,2421018	0,0332237	110027,15	189325,82	0,5811524	122586,26	256744,67	0,4774637
17806,403	0,2498803	0,0296897	253800,11	423124,04	0,5998244	255899,01	599750,93	0,4266755
4250,7226	0,4161352	0,0432537	55197,154	55257,368	0,9989103	61087,895	98274,309	0,621606
4715,2504	0,4610072	0,0433089	65635,347	59311,382	1,1066231	67763,707	108874,82	0,6224002
15687,836	0,483891	0,0565217	180014,93	154977,58	1,1615546	225452,7	277554	0,8122841
1056,6258	0,2281398	0,0392237	13223,854	24147,097	0,5476374	15184,959	26938,461	0,5636906
11424,665	0,3062061	0,0417178	123071,74	167437,37	0,7350315	164185,9	273855,97	0,5995338
15935,792	0,3049497	0,0303361	216950,63	296374,35	0,7320155	229016,13	525307,38	0,4359659
3949,7907	0,289122	0,0409522	38072,059	54857,134	0,694022	56763,149	96448,727	0,5885319
4858,2203	0,5884985	0,2157381	20033,889	14181,685	1,4126593	69818,353	22519,062	3,1004113
880,20775	0,4773205	0,0675905	7083,7077	6182,4191	1,1457825	12649,623	13022,658	0,9713549
1862,89	0,3364821	0,0458703	16361,086	20256,208	0,8077073	26771,926	40612,161	0,6592096
956,12254	0,2771101	0,0333921	10304,198	15490,657	0,6651879	13740,608	28633,212	0,4798836
1738,34	0,3317491	0,0357211	21277,023	26718,318	0,7963459	24981,995	48664,188	0,5133548
724,61819	0,2355775	0,0273633	9070,4625	16039,967	0,5654913	10413,618	26481,431	0,3932423
139189,85	0,9849112	0,4042251	359892,86	152224,33	2,3642269	2000322,2	344337,47	5,8091912
2666,5443	0,5395724	0,0660488	17873,154	13799,375	1,2952147	38321,385	40372,322	0,9491994
4979,753	0,6203965	0,0726589	38917,611	26132,728	1,4892288	71564,922	68536,046	1,0441939
27539,879	0,667264	0,0381819	395832	247127,55	1,6017316	395780,53	721281,7	0,5487184
18102,805	0,7878749	0,0450385	287525,52	152029,22	1,8912517	260158,65	401940,48	0,6472567
6094,6365	0,5112993	0,0543885	63233,014	51520,093	1,2273467	87587,112	112057,36	0,7816275
7884,7913	0,5689935	0,0418453	100913,92	73884,22	1,3658386	113313,75	188426,98	0,6013669
14212,937	0,5244486	0,1512536	57256,758	45481,188	1,2589108	204256,67	93967,615	2,1736922
45285,186	0,7876339	0,2681131	182160,47	96346,882	1,8906733	650801,52	168903,28	3,8531017
8227,4858	0,6172294	0,0436728	103750,97	70025,062	1,4816263	118238,67	188389,45	0,6276289
9863,9194	0,4502786	0,05169	115473,39	106833,77	1,0808697	141756,15	190828,32	0,7428465
7618,4413	0,3888155	0,0525751	66768,876	71538,269	0,9333309	109485,98	144905,9	0,7555661
3622,0256	0,3790627	0,0300295	66681,778	73283,134	0,9099198	52052,778	120615,7	0,4315589
11343,742	0,4217465	0,040242	151165,84	149317,28	1,01238	163022,94	281888,11	0,578325
8122,4157	0,3637375	0,0254552	156066,77	178743,53	0,8731324	116728,69	319087,27	0,3658206
5288,4446	0,4087983	0,0280568	83413,108	85002,777	0,9812986	76001,184	188490,65	0,4032093
5270,7885	0,4513345	0,0319999	93059,409	85895,355	1,0834044	75747,445	164712,78	0,4598759
363,81832	0,3355457	0,0130297	8096,3328	10051,819	0,8054595	5228,4983	27922,152	0,1872527
1298,842	0,3450443	0,0216019	20591,819	24861,524	0,8282605	18665,89	60126,224	0,3104451
480,74919	0,2447191	0,0185911	3851,416	6556,3255	0,5874351	6908,9327	25859,085	0,2671762
25773,792	0,1969798	0,0550287	138966,67	293898,11	0,4728396	370399,78	468369,98	0,7908273
206422	0,3036279	0,1759404	658461,59	903434,54	0,7288426	2966527,5	1173249,4	2,5284714
6730,4996	0,4039748	0,0309022	91547,443	94406,07	0,9697199	96725,215	217799,87	0,4441014
5319,9478	0,488879	0,0460315	60069,701	51187,28	1,1735279	76453,922	115571,82	0,6615274
7992,267	0,4352851	0,0341003	104060,62	99591,091	1,0448788	114858,3	234375,12	0,4900618
6007,9024	0,4374735	0,0312186	79902,348	76087,913	1,0501319	86340,641	192446,35	0,4486479
463201,75	0,2797523	0,3470804	1000583,1	1490003,9	0,6715305	6656755,3	1334566,3	4,9879539
290816,33	0,3452924	0,3673492	753558,92	909155,31	0,8288561	4179373,6	791661,78	5,2792413

4540,4835	0,3007295	0,0512826	34933,164	48391,58	0,7218852	65252,101	88538,459	0,7369916
3570,2989	0,5031186	0,032535	56626,284	46887,346	1,2077093	51309,405	109737,21	0,4675662
9654,7711	0,2776624	0,0519403	99606,134	149443,45	0,6665139	138750,44	185882,02	0,7464436

6733,1481

8917,4073

5857,0784

6623,4376	0,3249361	0,101463	42860,079	54949,399	0,7799918	95186,607	65279,356	1,4581426
23871,365	0,1752167	0,0750825	116334,48	276592,84	0,4205983	343059,65	317935,15	1,079024

4880,2952

9151,4304

3767,2685	0,3005913	0,0435231	58392,223	80925,72	0,7215533	54140,09	86557,959	0,6254779
6149,3035	0,3361541	0,053173	83960,212	104050,24	0,8069199	88372,742	115647,1	0,7641587
20533,038	0,2143216	0,0915081	119100,62	231502,66	0,5144676	295083,96	224384,82	1,3150799
8507,0093	0,3194666	0,0725865	75087,476	97915,153	0,7668627	122255,75	117198,22	1,0431537
4176,0209	0,371803	0,067779	44143,893	49461,318	0,8924933	60014,344	61612,323	0,974064
3380,0592	0,3169588	0,0605224	34095,705	44813,08	0,7608427	48575,435	55848,032	0,8697788

2557,6431	0,4301778	0,0552871	25795,171	24980,341	1,0326188	36756,346	46261,082	0,7945414
16419,816	0,2850931	0,1095756	73246,469	107030,58	0,6843509	235972,12	149849,25	1,5747301
10148,773	0,3183911	0,1323568	56801,571	74320,294	0,7642808	145849,84	76677,398	1,9021229
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246,02534	0,3978046	0,0270714	5258,4655	5506,7731	0,9549087	3535,6742	9088,0277	0,3890475
380,67906	0,4549879	0,0310776	7513,1284	6879,0561	1,0921743	5470,8069	12249,31	0,4466216
623,64473	0,324207	0,0225279	10043,379	12905,221	0,7782415	8962,5101	27683,218	0,3237525
924,92853	0,4638586	0,0414185	14338,482	12877,322	1,1134677	13292,314	22331,274	0,5952331
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1975,0527	0,4149456	0,0748582	16870,513	16937,336	0,9960547	28383,836	26383,921	1,0758005
37278,455	0,3124882	0,1445979	171296,27	228361,14	0,7501113	535735,35	257807,73	2,0780422
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5933,0781	0,3467647	0,0387789	75971,376	91268,94	0,8323903	85265,328	152997,73	0,557298
7980,4594	0,3553451	0,0260009	147390,75	172793,65	0,8529871	114688,61	306930,1	0,3736636

680,72323	0,6526539	0,0611804	6486,3941	4140,2668	1,5666609	9782,7954	11126,488	0,8792348
22897,345	1,0487772	0,0648211	313784,99	124639,83	2,5175339	329061,85	353239,33	0,931555
28613,3	0,6954727	0,0884364	292376,46	175133,91	1,6694452	411206,86	323546,49	1,2709359
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43453,163	0,9536113	0,0555478	664561,35	290316,43	2,2890932	624473,18	782265,66	0,7982879
26479,432	0,7281699	0,3053903	104448,5	59755,436	1,747933	380540,66	86706,842	4,3888193
22642,23	0,785414	0,0679057	229466,81	121710,82	1,8853443	325395,55	333436,17	0,9758856
17183,873	0,6127534	0,0698035	154052,19	104734,57	1,4708819	246952,52	246175,07	1,0031581
3163,5597	1,3979828	0,0649222	44099,096	13141,223	3,3557832	45464,082	48728,435	0,9330093
13185,162	0,252764	0,0452978	105225,98	173426,62	0,6067464	189486,32	291077,52	0,6509823
35812,847	0,5916453	0,0639801	402200,2	283197,11	1,420213	514672,84	559749,89	0,9194693
15217,747	0,4351589	0,0541542	159840,4	153019,44	1,0445758	218696,97	281007,61	0,77826

11920,558	0,3597062	0,0300663	325808,48	377330,87	0,8634557	171312,47	396475,49	0,4320884
6018,1197	0,4274837	0,0585963	85334,032	83159,27	1,0261518	86487,476	102704,77	0,842098
5020,0627	0,3862269	0,0312411	125458,48	135321,08	0,927117	72144,22	160687,64	0,4489718
2037,9741	0,3157425	0,0441455	31146,086	41093,993	0,7579231	29288,091	46164,892	0,6344235
998,6217	0,3042495	0,043214	15379,444	21058,08	0,7303346	14351,371	23108,737	0,6210366
5602,7984	0,4137826	0,0938766	41950,728	42235,259	0,9932632	80518,819	59682,579	1,3491176

752,63163	0,261663	0,0443774	10836,853	17253,168	0,628108	10816,204	16959,795	0,6377556
1028,7825	0,2979445	0,0405979	17628,174	24647,899	0,7151999	14784,817	25340,81	0,583439

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29845,119	0,4061014	0,3867937	62223,75	63830,699	0,9748248	428909,55	77160,296	5,558682
118918,59	0,3643426	0,3782144	231195,18	264348,47	0,8745849	1709000,3	314421,12	5,4353864
1876,8051	0,3925775	0,0331843	20870,921	22147,473	0,9423613	26971,902	56557,088	0,4768969
164978,09	0,3062277	0,3544598	354572,89	482357,48	0,7350832	2370929,6	465435,27	5,0940051

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17625,145

9250,344	0,4264658	0,2351378	40684,366	39742,142	1,0237084	132938,35	39340,09	3,379208
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14878,757	0,3823433	0,1843517	67348,072	73380,323	0,9177947	213825,28	80708,528	2,6493518
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1009,8627
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2326,333
2684,2865
16522,79
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17516,645	0,5784893	0,0354903	320522,66	230818,87	1,3886328	251734,84	493561,74	0,5100372
2501,4981	0,4495364	0,0225878	46212,256	42825,287	1,0790881	35949,477	110745,58	0,3246132
880,66519	0,5251981	0,0307534	14500,327	11501,716	1,26071	12656,197	28636,324	0,441963
1669,7603	0,3224062	0,0346772	23153,87	29917,692	0,773919	23996,424	48151,489	0,4983527
8761,6655	0,4672046	0,0384362	134657,47	120069,11	1,1214997	125915,46	227953,33	0,5523739
2458,8842	0,3904495	0,034191	36008,708	38419,401	0,9372532	35337,065	71916,131	0,4913649
2257,1631	0,5339921	0,0722593	20842,984	16260,467	1,2818195	32438,094	31236,99	1,0384514
40325,712	0,431016	0,0348171	683247,85	660378,26	1,0346311	579528,03	1158215,5	0,5003629
43711,083	0,3662748	0,0388292	668182,91	759969,71	0,8792231	628179,81	1125726,5	0,5580217
2244,2751	0,5092437	0,0309891	38861,184	31790,57	1,2224123	32252,879	72421,471	0,4453497
19546,762	0,3880692	0,0806499	133162,95	142949,34	0,9315394	280910,01	242365,65	1,1590339

57259,753	0,3869914	0,0364118	677147,78	728937,13	0,9289522	822890,17	1572559,9	0,5232807
12956,32	0,4292352	0,0576012	103279,92	100237,1	1,0303562	186197,6	224931,43	0,8277972
9112,0138	0,3993919	0,0481969	100917,65	105263,03	0,9587189	130950,38	189057,93	0,6926469
27680,563	0,3460169	0,0364918	349498,99	420781,38	0,8305952	397802,33	758541,56	0,5244305
28434,109	0,3633684	0,0467427	311056,32	356615,12	0,8722466	408631,66	608311,26	0,6717477
47772,584	0,3577369	0,046657	522658,5	608642,38	0,8587284	686548,37	1023909,7	0,6705165
11920,928	0,5127441	0,0384401	168089,02	136567,26	1,2308149	171317,79	310116,66	0,5524301
15678,439	0,2274811	0,0297349	148264,66	271519,04	0,5460562	225317,66	527273,49	0,427326
5523,2323	0,3698775	0,0496204	49392,15	55629,857	0,8878712	79375,36	111309,73	0,7131035
248,39997	0,5173537	0,0279339	4539,4492	3655,304	1,2418801	3569,8004	8892,4338	0,4014425

2420,891	0,5363743	0,0286317	43985,622	34162,58	1,287538	34791,058	84552,72	0,4114718
3539,1446	0,48851	0,0579485	38282,326	32646,209	1,1726423	50861,68	61073,966	0,8327882
9603,2061	0,5011084	0,0571061	97027,994	80662,795	1,2028841	138009,39	168164,3	0,8206819
26230,898	0,3226427	0,0615714	173704,51	224283,41	0,7744867	376968,93	426023,81	0,8848541

44,488212	0,1051828	0,0658931	400,79999	1587,4167	0,2524857	639,34806	675,15691	0,9469622
377,77961	0,1773241	0,090089	2652,1782	6230,7858	0,4256571	5429,1384	4193,4056	1,2946848
256,93829	0,2468291	0,1008878	2307,3333	3894,2328	0,5925001	3692,5061	2546,7735	1,4498761
20916,463	0,1177458	0,0653328	266758,18	943800,93	0,2826424	300594,23	320152,58	0,9389093
18028,524	0,1961701	0,0958616	183510,91	389705,9	0,4708959	259091,15	188068,3	1,3776439
7662,1421	0,1880797	0,071131	100145,18	221817,6	0,4514754	110114,02	107718,74	1,0222364
27884,018	0,3285142	0,1072985	200736,15	254553,66	0,7885809	400726,22	259873,38	1,5420056
14640,349	0,1800473	0,0368827	285568,3	660741,24	0,4321938	210399,07	396943,12	0,5300484
4503,919	0,1950006	0,087074	50814,634	108557,71	0,4680887	64726,626	51725,172	1,2513564
14780,473	0,2063184	0,1353423	116567,34	235367,76	0,4952562	212412,83	109208,1	1,9450281

3302,1124	0,3971673	0,038116	37128,405	38944,012	0,953379	47455,249	86633,251	0,5477718
3179,8491	0,4701009	0,0566104	29652,858	26277,462	1,1284521	45698,181	56170,717	0,8135588
73,681852	0,4202273	0,0265187	971,85044	963,43654	1,0087332	1058,8951	2778,4881	0,3811048
2678,7926	0,4770814	0,0315	40317,464	35205,351	1,1452084	38497,407	85041,163	0,4526914
4627,1815	0,5290481	0,0279522	78516,516	61826,378	1,2699517	66498,053	165538,9	0,4017065
2575,8524	0,4592861	0,0358133	30410,315	27583,254	1,1024919	37018,036	71924,51	0,514679
8861,0058	0,402431	0,1198282	57103,262	59112,239	0,9660142	127343,1	73947,581	1,7220726
707,67583	0,5187238	0,0254915	10886,289	8742,8227	1,2451687	10170,136	27761,207	0,3663434
411,28905	0,5235086	0,0235733	6963,2815	5541,1269	1,2566544	5910,7086	17447,217	0,3387766
5030,5968	0,6190541	0,0640849	52453,101	35298,032	1,4860064	72295,608	78498,967	0,9209753
5088,0591	0,6686275	0,0690331	55129,586	34348,551	1,6050047	73121,408	73704,652	0,9920867
328,14358	0,4707991	0,020731	5712,2719	5054,5346	1,1301282	4715,8102	15828,668	0,2979284
3218,225	0,7769972	0,1090855	34655,593	18580,689	1,8651404	46249,688	29501,845	1,5676879
4691,804	0,4287734	0,0344673	61563,478	59814,058	1,0292476	67426,756	136123,17	0,4953364
1720,3875	0,3014749	0,0717611	14966,211	20680,86	0,7236745	24723,997	23973,831	1,031291

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11870,053	0,2729916	0,0240062	87499,782	133525,93	0,6553018	170586,66	494457,66	0,3449975
14676,718	0,3642705	0,025194	140575,75	160766,06	0,8744119	210921,74	582548,3	0,3620674
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7417,0873	0,2364647	0,0279013	58911,44	103786,59	0,5676209	106592,29	265832,76	0,400975
4934,2792	0,2255724	0,0362105	37738,856	69696,459	0,5414745	70911,41	136266,59	0,5203874

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12397,936 0,6538081 0,0508804 138324,58 88136,737 1,5694316 178172,96 243668,11 0,7312117
30397,972 0,7185814 0,0296578 534517,33 309880,15 1,7249163 436854,69 1024958,4 0,426217
4112,0186 0,818994 0,0263091 99322,046 50521,108 1,9659515 59094,555 156296,29 0,3780931
28269,325 0,4291547 0,0476132 331959,81 322240,11 1,0301629 406263,54 593728,58 0,684258
724,85576 0,6390707 0,0193226 8730,9553 5691,4223 1,5340551 10417,032 37513,313 0,2776889
57,1309 0,5299881 0,0126816 733,53039 576,58043 1,2722083 821,0384 4505,0252 0,1822495
244,73041 0,564923 0,0233971 2461,8577 1815,4389 1,3560675 3517,0646 10459,872 0,3362436
3624,435 0,4437313 0,038603 58009,497 54461,164 1,0651534 52087,404 93889,922 0,554771

1061,6465 0,1777156 0,0499082 11979,924 28082,536 0,4265969 15257,112 21272,001 0,7172392
1358,2876 0,2455048 0,0432289 20816,479 35322,806 0,5893212 19520,194 31420,818 0,6212503

3436,7174	0,2411081	0,0350656	48711,62	84164,463	0,5787671	49389,681	98008,321	0,5039335
3980,1213	0,1931416	0,0443101	53419,327	115220,72	0,4636261	57199,036	89824,168	0,6367889
1818,1869	0,2458322	0,0378075	38062,597	64501,17	0,5901071	26129,489	48090,653	0,5433382
850,26141	0,184953	0,0363116	14337,88	32294,715	0,4439699	12219,259	23415,696	0,5218405
631,88423	0,2044656	0,0285982	12556,994	25584,285	0,4908089	9080,9214	22095,281	0,4109892

6936,1598

9018,3872

12522,787

17410,1

4018,7211

1491,6322

9313,1908

2107,1595

5701,2671

7485,3991	0,4044875	0,0718176	57055,884	58762,906	0,9709507	107574,01	104227,91	1,0321037
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2865,7024

1353,5842

22573,889

9679,7713

3208,1314	0,446304	0,0570894	45147,909	42141,967	1,0713289	46104,631	56194,905	0,8204415
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7693,205	0,5179664	0,0535153	120040,98	96546,348	1,2433508	110560,43	143757,09	0,7690781
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2081,6572	0,4512087	0,0594543	27577,678	25461,743	1,0831025	29915,869	35012,725	0,8544285
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4594,0928

1759,9695	0,3644278	0,0593319	21646,673	24745,01	0,8747894	25292,837	29663,143	0,8526688
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11607,574

59525,802

1851,3939

8260,2948

132,89951

1834,9707

7340,2128	0,392324	0,0406788	97689,579	103731,66	0,9417528	105487,51	180443,38	0,5846017
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5549,7074	0,4320959	0,0487226	72574,797	69970,275	1,0372233	79755,838	113904,28	0,7002005
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3396,9172	0,4348931	0,0488213	45388,074	43477,766	1,0439376	48817,706	69578,627	0,7016193
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3265,7046	0,4692751	0,0546788	42496,56	37725,432	1,1264698	46932,026	59725,257	0,7857986
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1381,9796	0,5507776	0,0775428	12580,57	9515,5079	1,3221123	19860,677	17822,144	1,114382
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4854,9309	0,4822862	0,1622256	21208,432	18319,418	1,1577022	69771,082	29927,034	2,3313731
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5933,7798	0,4657104	0,1411893	30115,777	26939,285	1,117913	85275,412	42027,109	2,0290573
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7779,5153	0,3235489	0,0805725	52518,484	67620,774	0,776662	111800,81	96553,023	1,1579213
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2032,4148	0,3243474	0,0379499	28702,424	36865,152	0,7785788	29208,197	53555,175	0,5453852
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13891,16	0,4681897	0,0490808	122555,61	109048,39	1,1238644	199632,35	283026,59	0,7053484
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6445,5614	0,9691621	0,0570392	88775,032	38159,47	2,326422	92630,317	113002,4	0,8197199
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22202,759

2892,4843

59537,908

12500,935

6922,9934

17388,786

877,7854

1497,1017
19592,825
3611,9162
2771,5358
22296,575
5691,7949
3830,0111
9426,4834
4554,6294
232,61654

18799,884 0,8754302 0,0637578 265353,79 126273,35 2,1014236 270176,5 294863,84 0,9162755
7084,0925 0,8546278 0,0648859 99818,441 48656,595 2,0514884 101806,76 109177,64 0,9324873
20335,056 0,7469809 0,1210893 163180,36 91005,217 1,793088 292238,73 167934,4 1,7401958

58778,332

20757,401 0,8355109 0,0670465 298964,19 149064,77 2,0055993 298308,33 309597,04 0,9635374
23719,744 0,8535759 0,0784203 288122,25 140618,53 2,0489635 340880,69 302469,52 1,1269919

1245,3018 0,4274367 0,0283049 22407,604 21838,941 1,026039 17896,455 43996,003 0,4067746
1464,694 0,4290951 0,0379952 17633,649 17119,717 1,0300199 21049,38 38549,461 0,5460356
22355,491 0,3710811 0,0616542 232310,41 260800,15 0,8907603 321274,76 362594,99 0,886043
3288,5142 0,3372487 0,0210288 70588,713 87195,257 0,8095476 47259,826 156381,69 0,3022082
7535,9712 0,430451 0,0177934 216924,18 209938,55 1,0332747 108300,79 423526,96 0,2557117
32022,64 0,160059 0,084648 184445,55 480060,41 0,3842132 460203,09 378303,63 1,2164913

77,563856 0,4327256 0,0410488 4797,7862 4618,8749 1,0387348 1114,6841 1889,5514 0,58992

7266,7944 1,1623029 0,2348579 84100,396 30143,013 2,7900462 104432,4 30941,24 3,3751848
17165,092 0,860533 0,3018485 90422,849 43774,236 2,0656637 246682,6 56866,572 4,3379193
109813,35 0,9238045 0,2248341 658405,35 296907,54 2,2175434 1578147,3 488419,48 3,231131
44622,086 0,6924151 0,1386588 293816,62 176773,74 1,6621055 641271,99 321812,19 1,9926902
4484,3945 0,2964083 0,0432431 38888,36 54655,915 0,7115124 64446,036 103701,93 0,6214545
3374,3171 0,2402409 0,0497664 21096,124 36581,687 0,5766854 48492,916 67803,163 0,7152014
3251,0389 0,1932068 0,0492683 17592,681 37933,038 0,4637825 46721,262 65986,365 0,7080442
251769,59 0,8644024 0,3461862 1448727,2 698198,01 2,0749518 3618225,8 727266,29 4,9751045
14873,822 0,7463983 0,3327829 86433,657 48241,43 1,7916894 213754,35 44695,277 4,7824819
168043,4 0,7536159 0,330411 1002307,7 554062,72 1,8090149 2414981,8 508589,05 4,7483953
54645,239 0,8603487 0,3378654 313949,1 152017,19 2,0652211 785316,51 161736,71 4,8555241
366893,94 0,6101717 0,27229 2392421,9 1633404,2 1,4646846 5272698,5 1347438,1 3,9131286
108177,51 0,6990895 0,2939108 666286,72 397041,89 1,678127 1554638,3 368062,39 4,2238445

544,40006 0,2745041 0,0135884 18904,309 28689,3 0,6589324 7823,6707 40063,446 0,195282
723,4045 0,2685349 0,0283127 12695,802 19695,515 0,6446037 10396,176 25550,5 0,4068874
1225,5855 0,4286507 0,0321246 22887,873 22243,846 1,028953 17613,108 38151,016 0,4616681
31586,068 0,4755507 0,0290586 622095,29 544964,27 1,1415341 453929,03 1086979,8 0,4176058
3540,7568 0,1205663 0,0848388 44177,595 152645,54 0,289413 50884,849 41735,116 1,2192334
63293,445 0,3451347 0,086909 411406,72 496581,64 0,8284775 909601,43 728272,76 1,2489845
4481,8491 0,3286148 0,0300879 57581,411 72996,672 0,7888224 64409,456 148958,62 0,4323983
6073,1725 0,0947983 0,0624972 68484,144 300952,18 0,2275582 87278,65 97175,07 0,8981589
719,3983 0,5112661 0,0311338 10111,803 8239,2859 1,2272669 10338,602 23106,68 0,4474291
1131,9212 0,3614821 0,0338145 15432,964 17785,679 0,8677186 16267,043 33474,416 0,4859545
16128,465 0,5316071 0,1319476 143686,7 112598,8 1,2760945 231785,05 122233,86 1,8962427

2975,0031	0,6468488	0,0297833	62944,628	40538,142	1,552726	42754,302	99888,2	0,4280215
2833,7532	0,5829417	0,0354945	47896,505	34228,405	1,3993204	40724,374	79836,389	0,5100979
2433,4826	0,4181782	0,0432646	28944,614	28834,622	1,0038146	34972,014	56246,496	0,6217634
3631,9638	0,3439816	0,0355179	59514,793	72077,16	0,8257095	52195,602	102257,34	0,5104338
5523,8398	0,4557176	0,0425775	68717,422	62817,257	1,0939259	79384,091	129736,12	0,6118889
5306,6189	0,281145	0,0286493	80505,504	119289,76	0,6748736	76262,371	185227,13	0,4117236
195,00966	0,4068003	0,0235822	3924,9966	4019,444	0,9765024	2802,5187	8269,3503	0,3389043
10732,903	0,7910887	0,0897881	97513,014	51350,574	1,8989664	154244,47	119535,97	1,2903604
2188,6127	0,1485759	0,0507744	26594,205	74566,973	0,3566486	31452,945	43104,652	0,729688
19759,934	0,4350987	0,0710609	156409,26	149755,44	1,0444312	283973,55	278070,31	1,0212293
14955,256	0,3618872	0,06834	136759,61	157431,83	0,868691	214924,66	218836	0,9821266
1247,4957	0,3907609	0,0363765	16490,476	17580,453	0,9380006	17927,985	34294,046	0,5227725
1197,5278	0,4565916	0,0273061	24593,355	22438,704	1,0960238	17209,886	43855,736	0,3924204
913,97036	0,374303	0,0326522	9618,9538	10705,637	0,8984943	13134,832	27991,121	0,4692499
10923,884	0,4713761	0,0523076	104816,05	92633,522	1,1315131	156989,09	208839,31	0,751722
5501,3972	0,3677321	0,0321368	79121,148	89633,218	0,8827213	79061,565	171186,93	0,4618435
7367,7421	0,4264636	0,0574856	68744,192	67152,469	1,0237031	105883,14	128166,83	0,8261353
10469,976	0,4597214	0,0391726	141159,72	127915,74	1,1035368	150465,9	267277,87	0,5629568
11224,699	0,632004	0,0284529	137317,29	90513,497	1,5170918	161312,15	394501,6	0,4089011
8663,9064	0,4829178	0,0405052	66657,639	57502,219	1,1592186	124510,55	213896,06	0,5821077
8925,9974	0,5354139	0,086958	57095,187	44424,011	1,2852326	128277,11	102647,22	1,2496891
17001,405	0,563271	0,070506	91372,593	67578,176	1,3521021	244330,24	241134,07	1,0132548
27421,44	0,3405591	0,0969893	176432,09	215820,64	0,8174941	394078,42	282726,38	1,3938509
5303,0675	0,3097677	0,0638078	39070,731	52544,023	0,7435809	76211,333	83109,989	0,9169937
29724,574	0,562317	0,072064	202991,97	150385,37	1,349812	427177,18	412474,61	1,0356448
18072,564	0,4920354	0,1041429	143605,8	121585,99	1,1811049	259724,05	173536,18	1,4966564
54606,53	0,6746846	0,1332468	291459,41	179963,82	1,6195445	784760,21	409815,04	1,9149132
8628,5104	0,6479348	0,0524274	86987,885	55928,786	1,555333	124001,87	164580,03	0,7534442
7117,2776	0,5216137	0,0503889	69161,202	55235,902	1,252106	102283,67	141246,93	0,7241479
1959,4491	0,9317892	0,0776376	17022,271	7610,4047	2,2367104	28159,594	25238,401	1,115744
12419,116	0,9688304	0,0602978	128211,28	55129,798	2,3256258	178477,34	205963,1	0,8665501
14683,017	1,0663832	0,0741211	141476	55268,464	2,5597961	211012,27	198094,93	1,0652079
13224,744	0,7614757	0,0634222	107381,51	58746,415	1,8278819	190055,16	208519,22	0,9114515
23126,938	0,3589183	0,0691399	156406,78	181538,13	0,8615644	332361,36	334494,68	0,9936223
4170,3846	0,7880276	0,0917156	34851,121	18423,971	1,8916183	59933,343	45470,821	1,3180616
57429,875	0,760468	0,137079	267571,2	146577,18	1,8254628	825335,02	418954,53	1,9699871
4701,0395	0,3659849	0,1030476	28026,989	31902,241	0,8785273	67559,48	45620,064	1,4809159
1833,9257	0,7310465	0,062649	15234,61	8681,4896	1,7548383	26355,674	29273,035	0,9003396
13592,129	0,7977682	0,0773202	98142,095	51249,133	1,9150001	195334,92	175790,14	1,1111824
3183,8555	0,6056494	0,0617808	26362,855	18133,394	1,453829	45755,757	51534,742	0,8878624
7709,4734	0,7238895	0,0453294	157980,74	90915,886	1,7376583	110794,22	170076,79	0,6514365
18079,774	0,491753	0,0831591	174048,32	147445,24	1,1804268	259827,66	217411,84	1,1950943
8860,5973	0,6185	0,0350869	181467,47	122226,96	1,4846763	127337,23	252532,75	0,5042405
8659,3053	0,5827693	0,0840828	76926,213	54990,241	1,3989066	124444,43	102985,51	1,2083683
7330,8417	0,4710762	0,0348489	127018,68	112327,05	1,1307933	105352,84	210360,84	0,5008196
4676,5055	0,5152981	0,0554236	65453,645	52915,536	1,2369457	67206,897	84377,559	0,796502
10002,256	0,4979597	0,077444	96118,774	80412,196	1,1953258	143744,21	129154,63	1,1129622
3054,0914	0,6713528	0,0460958	64812,859	40217,797	1,6115467	43890,895	66255,345	0,6624506

1144,02	0,5091667	0,0434067	17605,107	14404,117	1,2222275	16440,917	26355,854	0,6238051
128,11936	0,3827819	0,0375657	1856,1346	2020,0679	0,9188477	1841,2263	3410,5452	0,5398627
1602,7095	0,4612712	0,0699786	14953,27	13504,787	1,107257	23032,825	22902,853	1,0056749
2946,4652	0,6165461	0,0398317	63848,656	43141,386	1,4799862	42344,179	73972,938	0,572428
2735,7442	0,5997852	0,0608483	35430,694	24608,882	1,4397523	39315,869	44960,103	0,8744613
4198,8013	0,6309143	0,0490254	68995,308	45557,209	1,5144762	60341,725	85645,369	0,7045533

28257,468	0,490311	0,2696774	206056,24	175074,17	1,1769654	406093,12	104782,48	3,8755823
607378,72	0,4447353	0,5750602	2835451,2	2656002,6	1,0675634	8728748,3	1056200,2	8,2642935
15497,656	0,4754021	0,5421957	70023,331	61360,603	1,1411774	222719,58	28583,139	7,7919918
58607,75	0,4475367	0,3660621	292362,24	272145,14	1,0742879	842262,47	160103,31	5,2607436
62138,843	0,2944645	0,1168307	368822,22	521785,66	0,7068462	893008,44	531870,96	1,6789946
1248,5123	0,3291037	0,0639007	12460,485	15772,85	0,7899958	17942,594	19538,307	0,918329
4144,1147	0,6180187	0,1964599	33605,803	22652,732	1,483521	59555,814	21093,943	2,8233609
3865,6267	0,1517394	0,1773439	23440,727	64354,777	0,3642422	55553,613	21797,353	2,5486403
1903,0093	0,4825505	0,0963683	14983,362	12935,239	1,1583367	27348,488	19747,251	1,3849263
2207,8153	0,4760251	0,0977401	17701,918	15491,676	1,1426729	31728,909	22588,638	1,4046402
2971,5176	0,3576672	0,0927805	19801,288	23063,344	0,858561	42704,212	32027,399	1,333365
13979,311	0,3263274	0,2199705	112961,44	144206,43	0,7833315	200899,18	63550,835	3,1612358

153722,66
5264,0623
170,96754
29,587804
13902,071

866,66684	0,5988569	0,0828606	4200,4641	2922,0131	1,437524	12455,024	10459,338	1,1908042
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81,425582

67,243819	0,0975868	0,0348789	280,51452	1197,4906	0,234252	966,37296	1927,9214	0,5012512
365332,43	0,1318267	0,0451667	1575028,7	4977291,6	0,3164429	5250257,8	8088533,2	0,6490989
394821,6	0,175874	0,0474585	1983054,1	4697220,5	0,4221761	5674052	8319294,1	0,6820353
145,6271	0,1320772	0,0378731	725,7269	2289,0397	0,3170443	2092,8331	3845,1328	0,5442811
779696,1	0,1682784	0,0479122	3743374,3	9267076,3	0,4039434	11205152	16273444	0,6885545
573,76497	0,1755634	0,0417919	3334,0443	7911,2536	0,4214306	8245,6792	13729,084	0,6005994
1466,1579	0,1653353	0,0410902	8438,9638	21263,338	0,3968786	21070,417	35681,491	0,5905139
86532,335	0,172122	0,0421545	477098,06	1154726,4	0,4131698	1243571,7	2052743,9	0,6058095
13338,546	0,1456196	0,0381799	80501,4	230298,68	0,3495522	191690,63	349360,62	0,5486899
181,36445	0,1888137	0,0675021	723,9323	1597,2477	0,4532373	2606,421	2686,7966	0,970085
995,292	0,2097728	0,0900118	2797,7813	5556,1308	0,5035485	14303,52	11057,353	1,2935754
842,22488	0,2015847	0,0538551	4644,0704	9597,3011	0,4838934	12103,765	15638,726	0,773961
1627,2035	0,2011358	0,0502451	9817,0345	20332,879	0,4828158	23384,833	32385,314	0,7220814
827,37795	0,2773474	0,047296	7208,6002	10827,662	0,6657577	11890,397	17493,601	0,6796998
444,66392	0,203271	0,0538871	2532,9354	5191,0656	0,4879413	6390,3447	8251,7709	0,774421
332,49311	0,1814844	0,0509956	1644,6756	3775,2785	0,4356435	4778,318	6520,0413	0,7328662
6434,7352	0,1854876	0,035611	46463,904	104353,92	0,4452531	92474,732	180695,14	0,5117721
272,87796	0,182161	0,0377808	1930,8986	4415,8256	0,4372678	3921,578	7222,6624	0,5429546
445,92279	0,2197724	0,0681654	2293,4929	4347,4256	0,527552	6408,4363	6541,7743	0,9796175
115,44304	0,1341645	0,0566863	430,1202	1335,5503	0,3220547	1659,0527	2036,5243	0,8146491
276,27462	0,1860246	0,0531267	1484,1317	3323,6096	0,4465421	3970,392	5200,2944	0,7634937
75355,952	0,1622655	0,0369574	449416,62	1153800,7	0,3895097	1082953,9	2038993	0,5311219
106594,89	0,1688497	0,0404248	625620,74	1543543,4	0,4053146	1531894,2	2636866,4	0,5809525
41,536973	0,2144392	0,0785618	220,0385	427,46683	0,5147499	596,93528	528,71726	1,1290255
2197,6907	0,1826162	0,0571515	10462,315	23866,921	0,4383605	31583,407	38453,799	0,8213339

16632,424	0,1593353	0,0276837	138264,33	361498,07	0,382476	239027,54	600802	0,3978474
5130,3946	2,3233569	0,0520069	105447,59	18907,263	5,5770943	73729,82	98648,288	0,7474009
3409,2974	2,5978135	0,0331143	91358,497	14650,381	6,2359128	48995,623	102955,55	0,4758911
5007,9396	2,711942	0,0376296	119157,3	18304,092	6,5098722	71969,997	133085,02	0,5407821
29775,545	0,4013944	0,0675759	258418,45	268200,82	0,963526	427909,69	440623,46	0,971146
20798,597	0,5646711	0,0814141	173386,4	127916,75	1,3554628	298900,37	255466,69	1,170017
15714,305	0,3559305	0,0570444	161480,63	189000,58	0,8543922	225833,09	275474,75	0,819796
6655,6131								
16768,221								
2090,9843	0,6352643	0,048491	26864,319	17616,893	1,5249181	30049,909	43121,095	0,6968726
24068,077	0,6031993	0,043693	327770,94	226369,31	1,4479477	345886,65	550844,95	0,6279202
16530,685	0,6225928	0,0468052	210787,44	141042,04	1,4945008	237565,44	353180,52	0,6726459
15355,104	0,5446519	0,0454419	191731,91	146650,41	1,3074079	220670,94	337906,2	0,6530538
15230,653								
7527,4084	0,6262221	0,0428425	110659,01	73615,008	1,5032127	108177,73	175699,73	0,6156967
46497,255	0,3727234	0,0684388	515037,93	575652,61	0,8947027	668220,38	679398,65	0,9835468
57933,712	0,5434732	0,0515112	738764,8	566286,2	1,3045785	832575,74	1124682,2	0,7402765
1418,189	1,6393207	0,3378621	7130,5362	1812,0333	3,9351021	20381,047	4197,5385	4,855476
7295,0923	0,1471685	0,4095429	66492,159	188218,98	0,3532702	104839,08	17812,769	5,8856138
12015,728	0,2684416	0,1419043	103272,81	160267	0,6443797	172680,18	84674,867	2,0393322
6431,3574	0,2189478	0,1198653	48278,161	91858,23	0,5255725	92426,189	53654,856	1,7226062
22062,404	0,3109403	0,0894121	111851,98	149856,16	0,7463956	317062,75	246749,75	1,2849567
12709,878	0,4000735	0,1915741	108385,55	112859,86	0,9603552	182655,94	66344,444	2,7531459
183,88091	0,1742284	0,2173539	997,26011	2384,5004	0,418226	2642,5855	845,99783	3,1236316
13089,692	0,3176957	0,2373907	73420,52	96275,11	0,7626116	188114,31	55139,867	3,4115843
10785,668	0,3802294	0,2367443	61814,519	67725,582	0,9127204	155002,77	45558,298	3,402295
18927,395	0,3592179	0,0436609	166401,35	192977,54	0,8622835	272008,98	433509,42	0,6274581
2404,6349	0,3867154	0,0442543	18719,752	20165,849	0,9282898	34557,438	54336,802	0,6359859
1045,5461	0,25263	0,0177042	18105,247	29855,72	0,6064247	15025,73	59056,544	0,2544295
5375,4848	0,3815391	0,0651295	32948,172	35974,953	0,9158642	77252,054	82535,319	0,9359878
11542,887	0,4935439	0,0460704	102393,3	86427,838	1,1847259	165884,9	250548,98	0,6620857
10178,497	0,3744862	0,0509075	92330,778	102711,38	0,8989342	146277	199940,85	0,7316014
1039,6517	0,517818	0,0344552	12917,058	10391,887	1,2429945	14941,02	30174,009	0,4951619
4394,142	0,5058713	0,0305081	58370,398	48068,498	1,2143171	63149,001	144031,77	0,438438
2421,4262	0,5090127	0,0281494	38124,673	31202,215	1,2218579	34798,749	86020,654	0,4045395
407,96198	0,3527769	0,2599063	1568,9648	1852,7677	0,8468222	5862,8947	1569,6503	3,7351597
10041,335	0,3625267	0,1754501	51398,834	59063,782	0,8702259	144305,82	57231,845	2,5214253
8613,6399	0,3514955	0,22014	32901,938	38995,059	0,8437463	123788,16	39128,008	3,1636714
233038,31	0,3554209	0,2139301	1043654,7	1223268,6	0,8531689	3349035,3	1089319,9	3,0744276
166916,11	0,3676697	0,2285242	675220,23	765060	0,8825716	2398781,2	730408,84	3,2841624
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21434,667	0,5013589	0,1281561	150644,38	125173,43	1,2034853	308041,44	167254,39	1,8417539
8662,0556	0,4192069	0,1115514	64871,083	64465,99	1,0062838	124483,95	77650,803	1,6031251
10664,826	0,4072408	0,1138563	84471,536	86410,599	0,9775599	153266,13	93669,214	1,6362487
23614,583	0,3739494	0,0916038	164800,08	183591,49	0,8976455	339369,4	257790,35	1,316455
18220,002	0,2812831	0,2013154	71429,249	105788,98	0,675205	261842,92	90504,744	2,8931402
12669,393	0,2397642	0,1910457	46734,852	81201,593	0,5755411	182074,12	66316,02	2,7455526
8869,3348	0,3041685	0,2033648	33752,424	46227,316	0,7301403	127462,8	43612,93	2,922592

52975,404	0,2687089	0,1995589	200870,72	311417,1	0,6450215	761319,01	265462,48	2,8678968
487083,96	0,6047454	0,2254263	2049942,1	1412137,4	1,4516591	6999970,8	2160724,2	3,239641
52508,71	0,6421025	0,2430667	213645,98	138611,18	1,5413329	754612,08	216025,95	3,4931548
45213,082	0,6007601	0,2227473	186669,06	129443,19	1,4420925	649765,3	202979,28	3,2011411
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52134,508	0,3555544	0,1529366	187967,73	220234,42	0,8534893	749234,35	340889,78	2,1978786
21394,92	0,5340988	0,2674879	70837,155	55251,929	1,2820757	307470,23	79984,641	3,8441159
224001,63	0,5754648	0,2861528	725200,69	524985,58	1,3813726	3219167,6	782804,34	4,1123527
243883,85	0,478696	0,2369078	908891,19	790969,98	1,1490843	3504898,5	1029446,3	3,4046443
74744,312	0,3249116	0,1993009	282747,33	362527,75	0,7799329	1074163,9	375032,48	2,864189
76224,122	0,456731	0,2541631	283244,55	258350,32	1,0963584	1095430,5	299902,41	3,6526231
185076,26	0,5173307	0,2497381	688325,37	554285,42	1,2418248	2659764,1	741081,34	3,5890312
82926,226	0,4609944	0,2803808	242474,92	219118,55	1,1065924	1191747,6	295762,91	4,029402
61409,56	0,5229522	0,3032568	192554,79	153391,15	1,2553188	882527,78	202500,2	4,3581575
540994,31	0,4138396	0,2573715	1655748,7	1666749,3	0,9934	7774726,1	2101998,1	3,6987313
31550,015	0,380388	0,226434	119469,45	130839,24	0,9131011	453410,92	139334,27	3,2541236
120101,97	0,5475213	0,2626996	437000,42	332497,79	1,3142957	1726007	457183,61	3,7753037
7019,3573	0,4467285	0,2512457	21844,494	20370,712	1,072348	100876,44	27938,215	3,6106975
37973,144	0,4341521	0,2904788	104485,45	100258,65	1,0421589	545718,85	130726,06	4,1745224
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6455,9363	0,5253104	0,0519666	77344,151	61336,561	1,2609796	92779,416	124232,4	0,7468214
15729,184	0,40278	0,0676962	122379,36	126575,07	0,966852	226046,91	232349,54	0,9728744
8228,3459	0,4292392	0,0285388	131358,64	127487,38	1,0303659	118251,03	288321,37	0,4101362
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10515,347	0,4362591	0,0270644	179137,53	171060,61	1,0472167	151117,93	388530,94	0,388947
33830,755	0,4980108	0,0556832	290892,91	243333,72	1,1954484	486187,83	607558,19	0,8002325
37071,814	0,6890683	0,1464858	192005,86	116080,73	1,6540717	532765,67	253074,39	2,1051742
11474,189	0,6825797	0,1376017	67033,892	40911,838	1,6384962	164897,62	83386,964	1,9774988
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34713,203	0,638198	0,1744111	152224,98	99366,136	1,5319603	498869,65	199030,88	2,5064938
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36158,443	0,4988487	0,1344867	201279,59	168088,82	1,1974598	519639,46	268862,6	1,9327324
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1173,2527	0,4579704	0,2329394	3376,9688	3071,8326	1,0993336	16861,024	5036,7285	3,3476143
41496,911	0,5825173	0,1755942	205001,57	146607,55	1,3983017	596359,54	236322,83	2,5234953
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30910,276	0,7031453	0,08977	315817,15	187110,69	1,6878627	444217,1	344327,45	1,2901008
8281,3815	0,4099422	0,0387766	76028,848	77261,606	0,9840444	119013,22	213566,52	0,5572653
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4983,1864

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13347,839 0,1570808 0,032898 111375,65 295375,9 0,3770641 191824,18 405733,55 0,4727836

6645,7179	0,3993428	0,0938824	44039,102	45941,011	0,9586011	95506,802	70787,696	1,3492006
11069,896	0,4731292	0,070843	103018,47	90707,52	1,1357214	159087,45	156259,5	1,0180978
15153,5	0,3581485	0,0399796	190610,18	221712,87	0,8597164	217773,66	379030,5	0,5745544
10101,864	0,3450824	0,0465279	114405,66	138112,37	0,828352	145175,69	217114,03	0,668661
5077,0628	0,4269917	0,0513896	60460,744	58987,77	1,0249708	72963,379	98795,459	0,7385297
3721,341	0,3513892	0,0651195	30937,772	36678,243	0,8434911	53480,057	57146,317	0,9358443
6762,4556	0,4312603	0,0549904	78493,129	75822,852	1,0352173	97184,46	122975,24	0,7902766
43188,25	0,2771143	0,033289	510156,61	766924,24	0,6651982	620666,08	1297373,8	0,4784019
10596,224	0,2214616	0,0297958	121901,24	229307,21	0,5316067	152280,23	355628,08	0,4282008
66766,92	0,3216837	0,0331624	934124,04	1209716,2	0,7721845	959519,37	2013332,9	0,4765826
13472,377	0,3425194	0,041783	155964,62	189691,91	0,8221996	193613,95	322436,9	0,6004708
802,62919	0,2326424	0,031381	11766,289	21069,711	0,5584457	11534,728	25576,893	0,4509824
3178,9716	0,249043	0,0363107	42905,915	71771,291	0,5978145	45685,57	87549,066	0,5218282
893,06805	0,2667043	0,0357965	11628,648	18163,819	0,6402094	12834,441	24948,464	0,5144381
72829,989	0,2759371	0,0380464	882180,91	1331850,4	0,6623723	1046652,8	1914243,6	0,546771
10361,661	0,3066615	0,036669	148454,06	201669,77	0,7361245	148909,28	282572,69	0,5269769
3681,7181	0,2383305	0,0199554	47969,42	83848,004	0,5720997	52910,63	184497,64	0,2867822
2404,931	0,2744276	0,0255132	26786,438	40662,593	0,6587489	34561,694	94262,272	0,3666546
2208,6313	0,3274006	0,0619394	18349,08	23347,627	0,7859077	31740,637	35657,958	0,8901417
663,80146	0,1793424	0,0361876	11115,636	25820,182	0,4305018	9539,6096	18343,32	0,5200591
18570,969	0,504713	0,0959103	162550,37	134168,76	1,2115366	266886,73	193628,48	1,3783444
15702,026	0,3835079	0,0452731	173530,73	188499,43	0,9205902	225656,63	346829,29	0,6506274
3687,9271	0,3038183	0,0763408	26977,266	36990,652	0,7292995	52999,86	48308,739	1,0971071
1661,01	0,4165156	0,0458257	25516,807	25521,311	0,9998235	23870,672	36246,218	0,65857
608,3444	0,3909383	0,0488639	8682,5255	9252,2154	0,9384266	8742,6262	12449,784	0,7022312
943,5628	0,4267983	0,0496402	11627,593	11349,458	1,0245065	13560,11	19008,044	0,713388
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6405,6727	0,3152326	0,0403638	53112,143	70189,253	0,7566991	92057,069	158698,55	0,5800751
14208,575	0,5424153	0,0960774	136111,4	104537,11	1,302039	204193,97	147886,76	1,3807454
6277,1012	0,4539147	0,0759378	60080,353	55139,929	1,0895979	90209,345	82661,085	1,0913158
35170,639	0,372942	0,114792	151932,38	169713,75	0,8952273	505443,55	306385,71	1,6496969
20758,559	0,4295813	0,1297723	105850,36	102649,03	1,0311871	298324,96	159961,37	1,8649813
9362,4199	0,4491385	0,1406214	46890,071	43491,913	1,0781331	134549,01	66578,915	2,0208952
883,77215	0,363784	0,1388639	4194,5473	4803,4079	0,873244	12700,848	6364,3036	1,9956383
16268,115	0,4168466	0,117797	94886,139	94827,532	1,000618	233792	138102,95	1,692882
22600,498	0,4043703	0,0921575	136006,7	140116,39	0,9706695	324795,81	245237,65	1,3244125
30703,998	0,3564728	0,127676	139215,93	162693,59	0,855694	441252,65	240483,69	1,8348548
60982,319	0,2639577	0,1795818	179332,39	283029,87	0,6336165	876387,82	339579,69	2,5808017
16568,008	0,266598	0,180558	52755,446	82436,272	0,6399543	238101,81	91760,042	2,5948311
13593,364	0,2934606	0,1945775	54382,671	77200,235	0,7044366	195352,67	69860,926	2,796308
4455,4702	0,3927894	0,1103427	22779,262	24159,495	0,94287	64030,36	40378,494	1,585754
20594,025	0,8587291	0,2774606	95895,466	46521,085	2,0613334	295960,41	74223,237	3,9874361
20458,706	0,5157367	0,2207859	68403,891	55253,618	1,2379984	294015,73	92663,093	3,172954
4143,5302	0,8828771	0,4328977	15936,089	7519,5078	2,1192995	59547,414	9571,6152	6,2212503
132914,16	0,8911713	0,2710343	681961,14	318791,24	2,1392092	1910133,2	490396,04	3,8950827
75503,039	0,9202499	0,262585	374684,34	169616,34	2,2090109	1085067,7	287537,51	3,7736562
231238,46	1,1539736	0,3881124	909838,34	328455,33	2,770052	3323169,3	595802,82	5,5776327
118628,38	1,6548366	0,5157613	485523,2	122225,78	3,972347	1704829,7	230006,35	7,4120986

201687,42	1,2279387	0,4219443	806695,44	273678,6	2,9476014	2898486	477995,36	6,0638371
144293,32	0,5312883	0,1415867	698477,17	547683,81	1,2753292	2073665,1	1019116,3	2,0347679
32431,248	1,0015345	0,1850229	471863,66	196272,09	2,4041302	466075,27	175282,37	2,6589969

8397,6419	0,602297	0,0631169	82977,499	57392,818	1,4457819	120684,02	133049,12	0,9070636
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35360,005	0,347581	0,0784848	355937,94	426605,3	0,8343496	508164,96	450532,89	1,1279198
4849,051	0,3643057	0,0494635	33403,655	38197,588	0,8744964	69686,58	98032,82	0,7108495
4161,3457	0,4638952	0,0624166	51009,628	45807,882	1,1135557	59803,444	66670,484	0,8970003
36164,609	0,6574041	0,0794708	416207,4	263745,66	1,5780635	519728,08	455067,95	1,1420889
9029,3291	0,502543	0,0842118	102988,79	85373,817	1,2063276	129762,1	107221,67	1,2102227
19714,845	0,549279	0,08361	217798,44	165184,66	1,318515	283325,57	235795,23	1,2015746
10417,957	0,374237	0,0663446	91019,958	101320,62	0,8983359	149718,33	157027,96	0,9534501
3351,2514	0,4724274	0,0582329	28227,525	24891,19	1,1340368	48161,434	57549,145	0,8368749
2353,679	0,4489333	0,0602657	17507,841	16246,459	1,0776404	33825,143	39055,004	0,8660899

12221,396	0,4939318	0,140859	65810,919	55505,863	1,1856571	175635,87	86763,306	2,0243105
10027,297	0,439847	0,0543928	85312,97	80801,861	1,0558293	144104,08	184349,84	0,7816881
40535,174	0,7734539	0,0799754	240073,61	129305,78	1,8566348	582538,25	506845,37	1,1493412
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23391,997	0,7074453	0,0981251	145557,04	85713,311	1,6981847	336170,57	238389,59	1,410173
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34218,807	0,878	0,1086877	178125,7	84516,208	2,1075922	491764,6	314836,03	1,5619705
3626,7433	0,738758	0,1037776	19734,716	11128,5	1,7733492	52120,578	34947,267	1,4914064
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9789,1715	0,3953578	0,0694721	80736,795	85072,495	0,9490352	140681,94	140907,9	0,9983964
22161,376	0,6221412	0,0382656	196257,39	131415,01	1,4934168	318485,1	579145,63	0,5499223
10291,206	0,4404488	0,035035	89411,75	84568,193	1,057274	147896,77	293740,77	0,5034942
142477,97	0,5855036	0,1085048	552154,07	392860,76	1,4054702	2047576,4	1313102,7	1,5593422
27973,149	0,4467808	0,0491188	189674,25	176856,83	1,0724734	402007,13	569500,14	0,7058947
25596,131	0,3974136	0,0602342	165181,3	173151,43	0,9539701	367846,59	424943,79	0,8656359
20166,912	0,4316562	0,0582307	142289,7	137323,04	1,0361677	289822,3	346327,54	0,8368445
6261,2562	0,4020866	0,041689	48640,122	50394,483	0,9651874	89981,634	150189,66	0,59912
11231,644	0,3840443	0,1726701	58001,002	62916,147	0,9218778	161411,96	65046,831	2,4814731

46117,751	0,444762	0,1683746	165765,02	155264,86	1,0676274	662766,45	273899,77	2,4197408
37237,367	0,5027822	0,2143967	125254,4	103781,76	1,2069019	535144,86	173684,38	3,081134
64993,952	0,6282583	0,2471368	233246,05	154662,14	1,5081005	934039,72	262987,79	3,5516468
3747,0567	0,5624188	0,1235523	19540,958	14474,18	1,3500563	53849,623	30327,698	1,7755922
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29868,172	0,4168234	0,147025	127237,31	127165,81	1,0005623	429240,84	203150,32	2,1129223
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17688,676

9245,9801	0,3187294	0,0348252	97756,411	127770,62	0,765093	132875,64	265496,65	0,5004795
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18286,32	0,4523586	0,0468355	212729,93	195908,68	1,0858627	262795,98	390436,98	0,6730817
8514,4709	0,3520567	0,050283	75927,072	89844,603	0,8450933	122362,99	169331,02	0,7226259

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27294,295

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394,6475 0,58603 0,0369875 6060,6895 4308,3415 1,4067338 5671,5499 10669,74 0,5315547
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630,86583 0,7060996 0,0439764 10513,723 6202,9532 1,6949544 9066,2857 14345,549 0,6319929
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2378,1087 0,400334 0,1029574 14542,542 15133,025 0,9609805 34176,226 23097,994 1,4796188
6949,4314 0,3603051 0,1191011 36678,447 42408,071 0,8648931 99871,524 58349,024 1,7116229
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3263,9767

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108994,95
10453,459

12579,609 0,3875011 0,1090861 74942,953 80568,602 0,9301757 180783,82 115318,21 1,5676954

688,1665 0,9005709 0,0459444 11555,897 5345,5661 2,1617723 9889,764 14978,244 0,6602752
1525,1315 0,4452909 0,1237715 8993,7302 8414,0283 1,0688971 21917,937 12322,153 1,7787426
1791,3685 0,8165273 0,0576618 30645,481 15635,207 1,9600304 25744,078 31066,841 0,8286674
2743,6354 0,9171912 0,0520042 41877,703 19020,893 2,2016687 39429,275 52757,975 0,7473614
23487,433 0,9995322 0,1315779 150947,2 62912,394 2,3993237 337542,1 178505,87 1,89093
18472,771 0,7726959 0,1765934 102491,28 55256,864 1,8548153 265475,5 104606,21 2,5378559
16657,809 0,7434627 0,0551107 192609,31 107925,99 1,7846425 239392,36 302260,94 0,7920056

19482,773	0,5854131	0,0849604	116430,62	82853,847	1,405253	279990,43	229315,95	1,220981
17847,885	0,5040436	0,0823862	97551,645	80625,876	1,2099297	256495,16	216636,85	1,1839867
261,20812	0,4765856	0,0244884	3123,2413	2730,0621	1,1440184	3753,8687	10666,598	0,3519274
689,74553	0,4511485	0,0210725	8987,083	8298,6452	1,0829579	9912,4565	32732,078	0,3028362
365,35178	0,4106453	0,0319661	3848,5427	3904,2482	0,9857321	5250,5359	11429,362	0,4593901
4840,6454	0,6374863	0,0718458	36418,281	23798,878	1,530252	69565,782	67375,461	1,0325092
12903,561	0,63479	0,0891234	77728,083	51010,057	1,5237796	185439,38	144783,02	1,2808089
4800,9834	0,5926439	0,0792388	36644,015	25758,296	1,4226102	68995,793	60588,801	1,1387549
3521,9229	0,4064759	0,0657122	26075,162	26723,919	0,9757237	50614,185	53596,218	0,9443611

7871,0947	0,4016377	0,0338417	127586,62	132336,19	0,9641098	113116,91	232585,51	0,4863455
2211,2419	0,4061587	0,0353104	30166,437	30941,134	0,9749622	31778,154	62622,985	0,5074519
7737,4055	0,4251273	0,0639597	79515,479	77918,507	1,0204954	111195,64	120973,22	0,9191757
9843,9108	0,4648916	0,1085654	59991,2	53758,086	1,1159475	141468,6	90672,606	1,5602133
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1864,8429	0,3146839	0,042403	20832,782	27579,138	0,7553819	26799,991	43979,024	0,6093812
19140,422	0,4222506	0,0621819	189384,92	186845,68	1,01359	275070,43	307813,48	0,893627
25772,877	0,5581607	0,0656211	330453,38	246637,39	1,3398349	370386,63	392752,69	0,9430531

57819,738	0,3026352	0,0597855	412920,59	568401,17	0,7264598	830937,81	967119,85	0,859188
1331,2083	0,4028659	0,0516845	12625,031	13055,091	0,9670581	19131,033	25756,436	0,7427671
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1609,4235	0,3727144	0,0654765	12877,733	14393,656	0,8946812	23129,313	24580,16	0,9409748
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6471,6155	0,7470386	0,4327343	47028,571	26225,676	1,7932263	93004,745	14955,172	6,2189016
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4575,3558	0,3612906	0,0799037	39885,137	45989,892	0,8672588	65753,258	57260,859	1,1483107
6786,2077	0,3210334	0,0706101	65499,737	84995,753	0,7706236	97525,806	96108,123	1,0147509
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4594,0928

1759,9695

59525,802

1851,3939

8260,2948

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2865,7024
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22573,889

73304,472 0,7106799 0,2383861 303127,45 177688,44 1,7059492 1053471,7 307503,13 3,4258893
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9698,8238

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4087,144 0,4876982 0,0278066 78247,019 66838,17 1,1706936 58737,079 146984,45 0,3996142
2012,6206 0,4693813 0,0293778 89246,484 79208,763 1,1267249 28923,73 68508,327 0,4221929
1475,5666 0,4454794 0,0325279 29958,129 28015,284 1,0693495 21205,632 45363,121 0,4674641
500,12307 0,4747807 0,0344772 7454,4962 6540,8343 1,1396858 7187,3582 14505,889 0,4954786
7488,9282 0,4682175 0,0906272 48292,845 42967,795 1,1239312 107624,73 82634,451 1,3024196
3181,133 0,2779957 0,0780324 26374,649 39523,609 0,6673138 45716,633 40766,831 1,1214174
24308,726 0,5958265 0,0465978 302515,5 211512,34 1,4302499 349345,06 521670,98 0,6696655
6151,5248 0,4813752 0,1275828 29503,641 25532,884 1,1555154 88404,665 48215,94 1,8335153
133606,58 0,4926968 0,1335521 586825,06 496177,22 1,1826925 1920084,1 1000408 1,9193011
65689,062 0,4018494 0,1022976 300595,57 311621,34 0,9646181 944029,28 642136,93 1,470137

38635,517 0,2946764 0,1851504 150103,93 212204,55 0,7073549 555237,93 208671,03 2,6608289
391136,27 0,3515377 0,4086812 1268502,3 1503236,3 0,8438476 5621089,4 957069,38 5,8732309
153293,35 0,1912324 0,3820843 551310,8 1200999,7 0,4590432 2203006,1 401202,9 5,4910025
123477,03 0,192621 0,3443641 450294,82 973870,37 0,4623765 1774510,5 358565,31 4,9489186
87813,546 0,1939915 0,3590194 293801,63 630927,39 0,4656663 1261984,2 244592,73 5,1595327
109780,44 0,2257877 0,3414475 394156,67 727237,92 0,5419914 1577674,4 321514,86 4,907003
18512,864 0,3021253 0,186529 85812,948 118324,24 0,7252356 266051,68 99249,261 2,6806414
19942,186 0,3115702 0,1435664 104559,34 139802,49 0,7479076 286592,72 138905,7 2,0632179
20402,519 0,4739108 0,0850993 151595,73 133259,55 1,1375975 293208,25 239749,62 1,2229769

2422,907	0,2975307	0,0313797	29432,414	41209,939	0,7142067	34820,031	77212,584	0,4509632
11321,638	0,4140545	0,0271406	166680,07	167700,4	0,9939157	162705,28	417146,99	0,390043
4195,1198	0,2973082	0,0310369	54285,168	76064,532	0,7136725	60288,818	135165,56	0,4460368
5968,277	0,4199653	0,0559966	58569,723	58098,873	1,0081043	85771,177	106582,9	0,8047367
7808,9552	0,438929	0,040284	99207,954	94158,627	1,0536258	112223,89	193847,72	0,5789281
13086,772	0,4225657	0,0423131	171461,9	169036,84	1,0143463	188072,35	309284,44	0,6080886
9782,1771	0,4201517	0,0364631	133480,65	132348,84	1,0085517	140581,42	268275,72	0,5240184
66029,539	0,485039	0,1177329	375585,63	322582,09	1,1643102	948922,33	560842,06	1,69196
75933,669	0,4866733	0,0453676	876942,27	750656,78	1,1682333	1091256,4	1673742,7	0,6519857

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4594,0928
1759,9695
11607,574
59525,802
1851,3939
8260,2948
132,89951
1834,9707

15485,012	0,4353358	0,0714751	182185,3	174339,92	1,0450005	222537,87	216649,15	1,0271809
3132,0546	0,4902347	0,0776246	33083,029	28113,127	1,1767822	45011,317	40348,717	1,1155576
3772,6518	0,4408006	0,0957046	31619,634	29882,89	1,0581184	54217,454	39419,74	1,3753884
17787,217	0,4944133	0,1007194	99376,433	83733,876	1,1868128	255623,28	176601,7	1,4474565
16706,599	0,4637019	0,0761614	178772,57	160609,01	1,1130918	240093,52	219357,69	1,0945298
9027,8259	0,5386221	0,0674038	126001,73	97454,131	1,2929337	129740,5	133936,39	0,9686726
797,89683	0,3637856	0,0370966	12496,398	14310,251	0,873248	11466,718	21508,626	0,5331218
3471,3235	0,473137	0,0389287	55936,487	49251,128	1,1357402	49887,012	89171,383	0,5594509
4427,6624	0,4117392	0,0462433	54901,267	55547,952	0,9883581	63630,729	95747,068	0,664571

3969,6425	0,2789761	0,0364178	51546,643	76973,509	0,6696673	57048,444	109002,87	0,5233664
7768,8973	0,3392608	0,0416392	91249,173	112047,77	0,8143774	111648,21	186576,41	0,5984048
17314,143	0,270942	0,0394122	156954,99	241327,43	0,6503819	248824,65	439309,46	0,5663995
5664,4313	0,3754655	0,0527111	55486,393	61563,658	0,9012849	81404,557	107461,78	0,757521
4317,7939	0,3666657	0,0407422	55856,517	63461,671	0,8801615	62051,789	105978,44	0,5855133
5223,4744	0,2779682	0,0470241	46726,357	70028,495	0,6672478	75067,485	111080,77	0,6757919
6552,9637	0,296827	0,0447096	57240,297	80335,295	0,7125174	94173,814	146567,29	0,6425296
5982,9654	0,3782893	0,0617845	57592,025	63422,912	0,9080634	85982,267	96835,954	0,8879168

2093,6617	0,4291997	0,1191534	11890,212	11540,86	1,030271	30088,387	17571,139	1,7123755
43513,261	0,4483476	0,1094342	274861,9	255392,2	1,0762345	625336,86	397620,25	1,5726987
2578,781	0,4310353	0,0875393	20768,838	20072,77	1,0346772	37060,124	29458,563	1,2580425
8512,0837	0,4413895	0,0424435	117335,86	110743,1	1,059532	122328,68	200551,12	0,6099626
9310,2361	0,382308	0,0318223	157632,2	171766,89	0,9177101	133799,07	292569,23	0,4573245
3010,0338	0,3676851	0,0394113	45056,835	51049,625	0,8826085	43257,734	76374,956	0,5663864

2940,5819	0,6845273	0,0474169	28948,228	17617,291	1,6431713	42259,629	62015,444	0,6814372
11643,819	0,5607621	0,0451329	118672,07	88161,26	1,3460795	167335,4	257989,67	0,6486128
9889,5078	0,6174441	0,0562351	90175,925	60841,635	1,4821417	142123,89	175860,19	0,8081641
8944,8637	0,3855138	0,086615	65615,416	70904,505	0,9254055	128548,24	103271,48	1,2447602
4409,7737	0,4610504	0,0498286	61278,734	55369,338	1,1067269	63373,648	88498,767	0,7160964
2349,5189	0,5696345	0,0756448	17144,534	12538,262	1,3673772	33765,357	31059,868	1,0871056

73511,135	0,9362892	0,0669682	632437,07	281394,26	2,2475123	1056441,7	1097701,4	0,9624126
32532,137	0,3450288	0,110754	191857,98	231650,08	0,8282232	467525,17	293733,35	1,5916652
3413,8525	0,5963508	0,0320433	42310,108	29556,312	1,4315084	49061,085	106538,82	0,4604996
6255,9974	0,6642658	0,0218298	110277,55	69159,708	1,5945347	89906,059	286580,71	0,3137199
6735,5818	0,4699954	0,0338407	71461,991	63341,653	1,128199	96798,252	199037,76	0,4863311
4995,2108	0,6763694	0,0265792	79134,781	48740,654	1,6235888	71787,068	187936,75	0,3819746
1679,2798	0,6173974	0,0379867	22685,692	15307,181	1,4820294	24133,231	44207,08	0,5459133
8364,7615	0,6685982	0,058254	86832,956	54103,741	1,6049344	120211,48	143591,12	0,8371791

2823,869
109579,91
79,539306
39,029183

28,050415
105,47347
91,809958
627187,39
252091,25
409686,06
513289,87
7822,2717
8621,3122
43132,058
25460,473
6283,7259

5212,0084	0,6852898	0,0832548	43992,28	26743,001	1,6450016	74902,706	62603,076	1,19647
31814,423								
78,120456								

9536,0322	0,3940227	0,0614748	89197,63	94306,151	0,9458305	137044,03	155121	0,8834654
3421,9859	0,3951999	0,0836582	24370,727	25689,731	0,9486564	49177,972	40904,356	1,2022674
28395,682	0,3378938	0,0773599	180521,62	222565,06	0,8110959	408079,43	367059,58	1,1117526
4533,0173	0,5389143	0,067911	44733,938	34580,031	1,293635	65144,803	66749,387	0,9759611
12707,826	0,4463334	0,0959059	89263,652	83314,996	1,0713996	182626,44	132503,03	1,3782813
12464,67	0,3291188	0,0707795	119178,31	150852,49	0,7900321	179132	176105,56	1,0171854
8605,394	0,2505862	0,1299234	56160,568	93364,598	0,6015189	123669,66	66234,367	1,8671524
1005,6027	0,2949063	0,0479336	9067,9493	12809,521	0,707907	14451,696	20979,06	0,6888629
1454,0364	0,3993897	0,0780356	9896,7524	10322,95	0,9587136	20896,218	18632,996	1,1214631
1635,5689	0,2925363	0,0568172	12283,341	17492,212	0,7022177	23505,054	28786,507	0,8165303

5457,1266	0,4475441	0,0414086	71121,31	66202,111	1,0743058	78425,343	131787,27	0,5950904
2359,2293	0,485595	0,0501214	26582,294	22804,794	1,165645	33904,907	47070,287	0,7203038
14032,54	0,4111284	0,0802605	111240,9	112718,44	0,9868917	201664,14	174837,43	1,153438
33616,579	0,3814795	0,1299857	201704,52	220268,48	0,9157212	483109,87	258617,6	1,8680472
14225,224	0,4690423	0,1346196	92055,514	81760,92	1,1259109	204433,24	105669,75	1,9346431
145,24568	0,3122041	0,0148059	4008,1393	5348,2549	0,7494294	2087,3516	9809,9763	0,2127785
1223,8895	0,3233268	0,0304072	17645,216	22734,91	0,7761287	17588,735	40250,055	0,4369866
4083,9579	0,2911101	0,0431583	61584,525	88129,693	0,6987943	58691,289	94627,437	0,6202354
962,11715	0,3241526	0,0379085	9136,2283	11741,549	0,778111	13826,758	25379,99	0,5447897
997,42762	0,2589072	0,0168964	15481,568	24910,285	0,621493	14334,211	59031,852	0,2428216
2877,7078	0,3629887	0,0346064	37952,858	43557,133	0,8713351	41356,054	83155,255	0,4973354

9838,9071	0,7414433	0,053745	114530,24	64350,239	1,7797951	141396,7	183066,36	0,7723794
14059,649	0,5428584	0,0537209	146999,99	112807,68	1,3031026	202053,74	261716,48	0,7720329
3170,338	0,5943149	0,0491444	35126,338	24622,047	1,4266213	45561,494	64510,623	0,7062634
552,38873	0,5755906	0,0579496	4953,739	3585,3155	1,3816745	7938,4773	9532,2271	0,832804
1470,9153	0,5154337	0,0497254	17004,324	13743,41	1,2372711	21138,787	29580,752	0,7146129
1652,6825	0,56958	0,0507377	17354,422	12692,973	1,3672464	23750,997	32573,038	0,7291612
10312,692	0,3088952	0,1066608	56211,722	75809,515	0,7414864	148205,54	96686,775	1,5328419
29667,615	0,705438	0,0866944	220898,74	130449,47	1,6933663	426358,6	342209,28	1,2459002
3585,958	0,4855274	0,1110292	22470,389	19279,899	1,1654827	51534,444	32297,429	1,5956206
25599,852	0,7147871	0,0724613	248433,77	144791,11	1,7158082	367900,05	353289,81	1,0413548
6591,5659	0,4590826	0,0518312	61732,875	56018,77	1,1020034	94728,573	127173,82	0,7448748
2036,3476	0,4616145	0,0351021	28025,928	25292,311	1,1080809	29264,716	58012,108	0,5044588

950,7425	0,5409274	0,0238224	22602,247	17406,866	1,2984674	13663,291	39909,632	0,3423557
21554,765	0,6577156	0,0500274	267786,85	169612,97	1,5788111	309767,39	430858,89	0,7189532
3962,5359	0,6993739	0,0260178	108631,18	64707,255	1,6788099	56946,313	152301,03	0,3739063
6364,8661	0,6260854	0,027525	158105,37	105201,27	1,5028846	91470,63	231239,58	0,3955665
4017,1602	0,5479614	0,039614	67689,658	51461,242	1,3153522	57731,328	101407,65	0,5692996
15070,572	0,4639931	0,0400155	211524,65	189914,18	1,1137907	216581,89	376618,19	0,5750702
61720,544	0,4583125	0,0741494	526890,92	478924,41	1,1001547	886997	832381,33	1,0656138
77684,007	0,5112022	0,0848254	626967,77	510928,9	1,2271135	1116410,8	915810,34	1,2190415

16776,142
6596,1671
644,35077
924,36965
3869,4226
2953,1876

2965,9831	0,7110925	0,0264978	62733,475	36752,015	1,7069398	42624,674	111933,28	0,3808043
26120,034	0,5622528	0,0450309	335970,31	248929,98	1,3496579	375375,69	580047,15	0,6471469
24658,65	0,5267918	0,0545798	277801,61	219686,64	1,2645357	354373,88	451790,61	0,7843764
17570,25	0,3877141	0,0407167	203821,64	219001,25	0,9306871	252505,2	431524,72	0,5851466
6833,8414	0,4064204	0,0748635	51614,289	52905,693	0,9755904	98210,358	91284	1,075877

12938,16	0,4554174	0,1092193	72784,692	66579,168	1,0932052	185936,62	118460,33	1,5696108
2670,647	0,3457493	0,1676394	13068,811	15746,452	0,8299528	38380,346	15930,902	2,409176
3218,8798	0,303467	0,1076957	16679,244	22896,698	0,7284563	46259,098	29888,656	1,5477142
4213,3019	0,4220441	0,0563141	31945,407	31532,511	1,0130943	60550,116	74817,842	0,8093005
7048,7417	0,6177324	0,0377819	88770,545	59865,474	1,4828337	101298,73	186564,08	0,5429702

4436,952	0,6101808	0,0399218	78247,88	53422,222	1,4647066	63764,231	111141,05	0,5737235
47416,679	0,3068689	0,0550415	385936,28	523926,86	0,7366224	681433,59	861471,99	0,7910107
29605,681	0,500363	0,082641	236133,73	196598,74	1,2010948	425468,55	358244,32	1,1876491
27232,868	0,4983083	0,0491594	356295,1	297865,15	1,1961624	391368,43	553971,09	0,7064781
34282,142	0,3808624	0,0526493	376923,73	412281,01	0,9142398	492674,79	651141,15	0,7566329
3859,8272	0,5644248	0,0353374	72411,063	53444,96	1,3548717	55470,268	109227,75	0,5078404
8946,5718	0,3967704	0,0374211	107881,79	113270,49	0,9524263	128572,79	239078,19	0,5377855
3950,4629	0,3642116	0,0287532	57465,062	65729,157	0,8742705	56772,809	137392,12	0,4132173
9443,3608	0,3876138	0,0330537	122707,7	131880,49	0,9304462	135712,23	285697,12	0,4750213
1638,2138	0,388691	0,0432042	21385,049	22919,954	0,9330319	23543,065	37917,941	0,6208951
2953,3628	0,4091371	0,0368188	37924,502	38615,257	0,9821119	42443,306	80213,398	0,5291299

11010,848	0,4349886	0,0415727	148571,49	142287,12	1,0441668	158238,87	264857,35	0,5974494
20119,207	0,478525	0,0869353	147024,06	127994,63	1,1486737	289136,72	231427,37	1,2493627
6480,8684	0,5630997	0,09932	58255,349	43098,131	1,3516908	93137,721	65252,39	1,4273457
4316,8261	0,3245663	0,0301012	42761,681	54885,703	0,7791042	62037,881	143410,33	0,4325901

493977,59	0,4569752	0,0485906	5884802,4	5364722,1	1,0969445	7099040,4	10166114	0,6983042
6724,9212	0,3979172	0,0517244	81798,048	85636,342	0,9551791	96645,047	130014,61	0,7433399
9341,6417	0,3811161	0,0472472	109794,81	120014,16	0,9148488	134250,4	197718,57	0,6789974
6536,2781	0,5340459	0,0503198	81185,408	63329,686	1,2819487	93934,023	129894,65	0,7231554
20552,407	0,4192199	0,0323005	355028,15	352800,22	1,006315	295362,33	636287	0,4641967
6125,9323	0,486721	0,0615454	64351,144	55078,751	1,1683479	88036,869	99535,133	0,8844803
5098,4475	0,3823133	0,038945	66387,863	72339,777	0,9177228	73270,702	130914,1	0,5596853

2216,5428	1,5542196	0,0240016	47916,856	12843,514	3,7308212	31854,333	92349,602	0,344932
21119,711	0,4582465	0,0900311	156631,19	142392,46	1,0999964	303515,15	234582,42	1,2938529
3041,064	0,5628702	0,0481741	37777,944	27960,051	1,35114	43703,675	63126,541	0,6923185
2966,9699	1,3225759	0,0348866	48578,606	15301,442	3,174773	42638,856	85046,223	0,501361
1935,1801	0,9320586	0,0402175	21402,055	9565,7755	2,237357	27810,82	48117,808	0,5779735
643,64561	1,7033967	0,0260922	10706,77	2618,488	4,0889131	9249,9463	24668,119	0,3749757
12965,87	0,8092042	0,0441689	135368,1	69689,303	1,9424516	186334,83	293552,12	0,634759
18538,51	0,4996023	0,081898	139363,15	116206,79	1,1992686	266420,24	226360,9	1,1769711
21060,482	1,1364199	0,0352706	315091,55	115506,35	2,7279153	302663,96	597112,04	0,5068797

11908,682	0,5397297	0,1023031	87161,674	67275,536	1,2955924	171141,8	116405,85	1,4702164
8739,8376	0,345539	0,1414087	45250,983	54555,544	0,8294479	125601,77	61805,523	2,0322095
24439,465	0,4736504	0,1387925	140142,79	123259,6	1,1369726	351223,92	176086,29	1,9946125
7750,885	0,7983258	0,1101342	62135,784	32424,221	1,9163385	111389,36	70376,734	1,5827582
7399,4391	0,431022	0,1048894	58297,031	56344,944	1,0346453	106338,66	70545,145	1,5073846
19057,423	0,5899047	0,154617	102263,12	72217,945	1,4160348	273877,64	123255,67	2,2220287

6385,4345	0,4775547	0,0496981	75371,375	65749,322	1,1463445	91766,222	128484,37	0,7142209
15913,382	0,4660478	0,0630858	162144,83	144937,43	1,1187229	228694,06	252249,83	0,9066173
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15415,76 0,5364105 0,1015729 105764,89 82139,529 1,2876247 221542,65 151770,36 1,4597227

39543,515	0,9937319	0,254699	176337,44	73923,616	2,3854006	568286,94	155255,89	3,6603245
19099,332	0,6969334	0,1233243	104478,81	62451,784	1,6729516	274479,91	154870,84	1,772315
333899,53	0,9425584	0,360334	1241330,1	548639,34	2,2625612	4798530	926638,87	5,1784251
95904,674	0,7744752	0,3397453	329306,37	177133,44	1,8590864	1378263,2	282284,05	4,8825402
258019,6	0,830436	0,3119488	946869,75	474998,24	1,9934174	3708045,9	827121,52	4,4830726
31771,432	0,6325251	0,1992619	134662,75	88690,62	1,5183427	456592,93	159445,61	2,8636281
8509,2274	0,5171119	0,2810985	28397,227	22877,014	1,2412995	122287,63	30271,341	4,0397164
15206,499	0,5689864	0,3034557	51714,155	37863,038	1,3658216	218535,32	50111,107	4,3610156
218433,99	1,2627261	0,3584728	795645,78	262493,49	3,0311067	3139154	609346,14	5,1516762
363918,3	1,1661709	0,3283898	1361508,1	486369,09	2,799331	5229935	1108190,1	4,7193481
1205,6086	0,4876435	0,0355791	15820,111	13514,969	1,1705622	17326,017	33885,35	0,5113129
1821,2485	0,6076546	0,0288622	26447,389	18131,51	1,4586424	26173,488	63101,507	0,4147839
2599,2847	0,5938054	0,0375786	25784,175	18089,102	1,4253983	37354,786	69169,33	0,5400484
7422,3099	0,5763896	0,046351	93604,072	67652,914	1,3835926	106667,34	160132,84	0,6661178
1313,0596	0,379536	0,0324493	14996,965	16461,082	0,9110558	18870,215	40464,95	0,4663348
56284,594	0,6226058	0,0465442	625826,11	418743,86	1,494532	808875,98	1209271,4	0,6688953
10839,712	0,4315179	0,0329791	128545,73	124098,57	1,0358357	155779,45	328684,43	0,4739484
7704,0721	0,5230842	0,0527689	71197,355	56702,237	1,2556357	110716,6	145996,36	0,7583518
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7582,8622	0,4173038	0,0553365	91638,586	91481,641	1,0017156	108974,67	137031,9	0,7952504
1968,1429	0,4861141	0,0392404	30103,553	25798,083	1,1668911	28284,534	50156,023	0,563931
2670,2275	0,3335759	0,0710769	16131,215	20145,605	0,8007312	38374,318	37568,17	1,0214583
7495,1596	0,4974912	0,0405089	145419,46	121771,33	1,1942011	107714,28	185024,96	0,5821608
2381,0642	0,4082713	0,0391053	33020,061	33692,784	0,9800336	34218,7	60888,455	0,5619899
880,62163	0,4273807	0,0438151	11715,569	11419,745	1,0259046	12655,571	20098,581	0,6296749
276,77444	0,4400572	0,0304855	4442,9013	4205,963	1,0563339	3977,575	9078,8833	0,4381128
4623,7682	0,4959807	0,0407362	68385,07	57438,683	1,1905752	66449,001	113505,15	0,5854272
60,672046	0,3432148	0,0122177	2120,2265	2573,4998	0,8238689	871,92884	4965,9131	0,1755828
937,79163	0,5099919	0,0616125	8569,3191	6999,8864	1,2242083	13477,171	15220,791	0,8854449
5215,0862	0,4129457	0,0552275	61713,315	62257,818	0,9912541	74946,937	94429,209	0,7936838
621,54275	0,3704902	0,028864	9076,9605	10206,377	0,8893421	8932,3022	21533,481	0,4148099
1953,099	0,3318509	0,1444026	8814,4108	11065,173	0,7965904	28068,336	13525,368	2,0752363
13546,8	0,3812882	0,2172197	62358,003	68131,307	0,9152621	194683,49	62364,512	3,121703
7497,1556	0,4666912	0,082011	54601,262	48739,497	1,1202672	107742,97	91416,451	1,1785949
3034,4647	0,4422436	0,0463409	30928,683	29134,518	1,0615821	43608,836	65481,327	0,6659736
1473,5335	0,5008486	0,070758	13921,404	11579,359	1,2022603	21176,414	20824,965	1,0168763
6456,7871	0,4688419	0,0601315	58027,064	51559,909	1,1254299	92791,644	107377,73	0,864161
8604,6575	0,3856006	0,0708977	94197,354	101767,46	0,9256137	123659,07	121367,2	1,0188838
8577,0421	0,452362	0,0531355	78156,241	71975,635	1,0858708	123262,21	161418,41	0,7636192
58476,392	0,3681419	0,0583595	443801,93	502206,02	0,8837049	840374,7	1002003,5	0,8386944
11203,392	0,3218868	0,0527848	94727,37	122597,13	0,772672	161005,95	212246,53	0,7585799
1745,3	0,404111	0,0597136	15027,667	15491,691	0,9700469	25082,018	29227,833	0,8581552
1400,7635	0,3735235	0,0468746	14143,757	15774,473	0,8966231	20130,623	29883,213	0,6736432
11042,699	0,3410866	0,0654563	100768,06	123073,95	0,8187603	158696,61	168703,29	0,9406847
34186,494	0,3877567	0,0418	452469,35	486113,6	0,9307893	491300,22	817857,9	0,6007159
2576,7551	0,3807266	0,0458237	31995,437	35009,246	0,9139139	37031,009	56231,959	0,6585403

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1898,097	0,3146073	0,0413458	22905,609	30330,601	0,755198	27277,891	45907,895	0,5941874
20918,285	0,415796	0,0520532	238072,44	238526,58	0,9980961	300620,41	401863,71	0,7480656

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262814,07
87353,555

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3120,8561	0,5589385	0,1191845	28754,892	21431,65	1,3417022	44850,382	26185,092	1,7128213
28694,406	0,6765803	0,198756	182870,03	112598,12	1,6240948	412372,44	144370,04	2,8563574
56410,771	0,635839	0,2477594	366495,19	240120,41	1,5262975	810689,28	227683,68	3,5605946
93401,218	0,3817273	0,1969168	313377	341996,62	0,9163161	1342285,6	474318,16	2,8299267
58480,693	0,4049662	0,2259628	204748,83	210625,31	0,9720998	840436,52	258806,71	3,2473521
57191,489	0,2811156	0,2224491	132487,69	196335,39	0,6748029	821909,13	257099,16	3,1968565
31297,262	0,5802222	0,3314504	117228	84167,61	1,3927924	449778,56	94425,188	4,7633324

3112,1348	0,7104374	0,0698972	37815,35	22174,317	1,7053671	44725,046	44524,447	1,0045054
1583,8192	0,6185731	0,0430214	28864,691	19439,445	1,4848516	22761,349	36814,711	0,6182678
4678,1079	0,6643	0,0442875	111502,08	69924,062	1,5946167	67229,926	105630,41	0,6364637
6179,8551	0,5254468	0,0781911	57646,506	45703,782	1,2613071	88811,804	79035,294	1,123698
2090,8777	0,6468362	0,079051	21831,886	14060,632	1,5526959	30048,377	26449,736	1,1360558
3781,7189	0,5269715	0,0559789	44951,787	35535,933	1,2649671	54347,759	67556,123	0,8044831

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23844,669

6858,5081	0,5301577	0,0386098	84900,017	66713,022	1,2726154	98564,848	177636,66	0,5548677
16784,025	0,5369274	0,0847201	164411,74	127563,13	1,2888657	241206,23	198111,39	1,2175284

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11095,117
20376,174

6039,8156	0,4994252	0,0339401	89210,036	74413,407	1,1988436	86799,271	177955,31	0,4877588
1865,6435	0,4909326	0,0393929	23945,347	20319,228	1,1784576	26811,497	47359,925	0,566122
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19819,448	0,4768544	0,0338165	316427,27	276436,91	1,1446636	284828,83	586088,34	0,4859828

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9367,9465
27294,295

161902,14	0,6052733	0,2143914	1141313,7	785527,62	1,4529263	2326724,7	755170,86	3,0810573
120169,87	0,606299	0,2242571	799647,16	549438,96	1,4553885	1726982,7	535857,52	3,2228393
62471,416	0,6347087	0,1821541	303621,19	199280,84	1,5235845	897787,91	342959,13	2,6177694
49379,831	0,6352387	0,1716832	265044,32	173815,88	1,5248568	709646,4	287621,75	2,4672905
189574,51	0,6272903	0,2353365	989191,9	656931,24	1,5057769	2724409,2	805546,69	3,3820624
81030,461	0,6042972	0,1490323	490382,79	338059,05	1,4505833	1164503,3	543710,81	2,1417696
73471,073	0,4495574	0,1744098	411108,34	380959,74	1,0791385	1055865,9	421255,34	2,5064749
25372,824	0,4023783	0,0904877	206035,66	213312,25	0,9658876	364637,39	280400,76	1,3004151
9548,6823	0,5251653	0,2631165	57898,819	45928,429	1,2606314	137225,82	36290,704	3,781294

16337,203 0,4362329 0,2129066 99123,24 94659,674 1,0471538 234784,87 76734,123 3,0597192

7302,3509 0,4317551 0,0951532 43649,705 42116,453 1,036405 104943,39 76743,079 1,3674639
4310,5531 0,5719084 0,0853197 22118,813 16111,77 1,3728357 61947,73 50522,382 1,2261443
8742,2213 0,6648384 0,0789648 49645,474 31107,959 1,5959091 125636,03 110710,38 1,1348171
6767,6036 0,6720867 0,0897134 36523,935 22639,154 1,6133083 97258,443 75435,81 1,2892875
4393,7654 0,7972976 0,2074874 17483,683 9135,2489 1,9138704 63143,589 21176,062 2,9818381
2163,8269 0,8056298 0,1630939 8502,6257 4396,6864 1,9338713 31096,744 13267,366 2,3438522
4151,8333 0,3063675 0,0560387 27612,822 37547,069 0,7354188 59666,74 74088,661 0,8053424

2412,6774 0,2611037 0,0308581 34736,292 55421,507 0,6267656 34673,019 78186,285 0,4434668
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8167,8399 0,2925808 0,0513695 64559,453 91922,526 0,7023246 117381,49 159001,75 0,7382402
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12835,987 0,5564646 0,0583958 118774,51 88918,803 1,3357637 184468,27 219810,16 0,8392163
9225,905 0,3872894 0,0697656 83891,265 90237,927 0,9296675 132587,13 132241,41 1,0026143
6823,4835 0,817747 0,0483006 92136,13 46937,39 1,9629581 98061,503 141271,07 0,6941372

7431,268 0,3471503 0,0530622 37160,037 44592,985 0,8333157 106796,08 140048,25 0,7625664
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4958,9745 0,5325013 0,0676592 43803,585 34268,642 1,2782411 71266,31 73293,375 0,9723431

2363,2383
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1885,1785
4217,9794

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519,26157 0,4516539 0,0304111 8009,3469 7387,5305 1,0841711 7462,401 17074,76 0,4370428
148,19587 0,3973252 0,0266189 2251,4318 2360,5902 0,953758 2129,7493 5567,3121 0,3825453
7319,2703 0,4624833 0,077607 50503,914 45492,194 1,1101666 105186,54 94312,013 1,1153038
10256,996 0,4747284 0,0579438 103553,6 90871,543 1,1395603 147405,12 177016,3 0,8327206

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1887,8238 0,4166437 0,0379402 20484,433 20481,751 1,000131 27130,254 49757,843 0,5452458
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2545,1933 0,3791744 0,0266048 35842,271 39378,976 0,910188 36577,429 95666,715 0,3823423
3945,2456 0,357682 0,0242263 61628,564 71778,259 0,8585965 56697,831 162849,76 0,3481604
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2718,0906 0,3192762 0,0419142 26986,941 35212,351 0,7664055 39062,166 64848,925 0,6023564
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11044,555 0,3711705 0,0663184 82784,292 92914,281 0,8909749 158723,28 166538,36 0,9530734
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35538,475 0,4657141 0,0877563 232199,74 207706,61 1,1179218 510729,79 404967,93 1,2611611
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244871,23 0,443695 0,1523195 1476929,3 1386702 1,0650661 3519088,3 1607615,6 2,189011
274125,59 0,4836658 0,1580725 1862887 1604534,6 1,1610139 3939507,9 1734176,4 2,2716881
98815,003 0,4222709 0,1764722 459322,49 453142,16 1,0136388 1420088,1 559946,69 2,536113
11730,132 0,4275457 0,1373467 61966,096 60378,114 1,0263006 168575,82 85405,29 1,9738335
16569,607 0,3520106 0,1523864 84224,267 99675,723 0,8449828 238124,78 108734,18 2,1899718
7308,4587 0,5097881 0,1220649 51884,737 42399,219 1,2237192 105031,17 59873,557 1,7542163
8367,7583 0,3798995 0,093484 53015,159 58135,206 0,9119286 120254,55 89510,086 1,3434749
65469,279 0,4561032 0,2347708 303963,37 277629,78 1,0948515 940870,73 278864,71 3,3739326
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5717,4225 0,3584313 0,0463492 70606,067 82062,375 0,8603951 82166,102 123355,49 0,666092
1399,9188 0,2809316 0,0296779 27085,965 40165,353 0,6743614 20118,484 47170,433 0,4265062
2074,0718 0,2928258 0,0682676 20419,959 29050,492 0,7029127 29806,857 30381,487 0,9810862
915,61332 0,3139667 0,028974 14292,434 18964,025 0,7536604 13158,443 31601,228 0,4163902
2546,0073 0,4017863 0,0712949 23849,505 24728,182 0,9644666 36589,127 35710,925 1,024592
2280,9269 0,4122374 0,0628809 24717,439 24978,363 0,989554 32779,609 36273,751 0,903673

3290,2692 0,3762033 0,0313751 64218,232 71112,136 0,9030559 47285,048 104868,64 0,4508979
6748,5673 0,326764 0,0411135 98147,498 125127,56 0,7843795 96984,87 164144,73 0,5908497
5752,0887 0,3709444 0,051321 68844,666 77316,014 0,8904322 82664,297 112080,61 0,7375432
3744,894 0,5321254 0,0434054 72525,764 56778,803 1,2773387 53818,542 86277,162 0,6237867
6586,9883 0,4005427 0,077117 67360,565 70059,137 0,9614815 94662,788 85415,47 1,1082628
2546,9656 0,4555208 0,0484688 40503,633 37041,938 1,0934534 36602,898 52548,561 0,6965538
4888,6604 0,5136292 0,0384815 105765,93 85783,544 1,2329396 70255,814 127039,22 0,5530246
2476,9955 0,2618053 0,0500186 25564,693 40678,982 0,6284497 35597,345 49521,481 0,7188263

3955,8245	0,6331415	0,0294202	68438,402	45030,526	1,5198224	56849,863	134459,38	0,4228032
1251,3366	0,651757	0,0461163	18000,14	11505,304	1,564508	17983,182	27134,37	0,6627455
31089,221	0,7229675	0,0479389	399306,95	230089,09	1,735445	446788,76	648517,59	0,6889385
4023,7475	0,2421804	0,062273	34275,046	58958,563	0,5813413	57825,996	64614,657	0,8949362
2683,7876	0,5668954	0,0262402	47622,229	34995,702	1,3608022	38569,192	102277,7	0,3771027
701,1893	0,683459	0,0292881	11874,018	7237,576	1,640607	10076,917	23941,127	0,420904
81666,5	0,2841708	0,2553857	151434,78	222000,6	0,6821368	1173643,9	319777,06	3,6701941
23068,329	0,3176542	0,3114901	38206,223	50105,74	0,7625119	331519,09	74057,973	4,4764807
22052,05	0,3017169	0,2483797	47860,268	66082,039	0,7242553	316913,95	88783,631	3,5695088
27769,891	0,3394382	0,2333835	67749,868	83148,747	0,8148032	399086,07	118988,24	3,3539959
10817,919	0,4094557	0,2294502	32741,357	33311,765	0,9828767	155466,24	47147,129	3,29747
4774,9606	0,25781	0,2288643	9386,2809	15167,071	0,6188592	68621,814	20863,719	3,2890499
11878,71	0,8897568	0,1683505	92352,394	43239,908	2,1358139	170711,07	70559,385	2,4193957
1797,1595	0,3959008	0,0373399	25819,686	27168,927	0,9503388	25827,3	48129,735	0,5366184
6758,3511	0,5233798	0,0810646	77824,921	61945,488	1,2563453	97125,474	83369,93	1,1649941
6655,6131								
16768,221								
1721,0491	0,5581553	0,0482619	21258,581	15866,721	1,339822	24733,504	35660,595	0,6935808
1645,6784	0,4923014	0,0475308	20907,02	17691,676	1,1817433	23650,339	34623,383	0,6830742
15230,653								
5457,194	0,4877256	0,0321466	88788,806	75838,657	1,1707592	78426,311	169759,47	0,4619849
8427,1282	0,5220952	0,0511474	75636,293	60351,551	1,2532618	121107,77	164761,64	0,7350483
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368,57546	0,6251786	0,0531226	3501,0251	2332,9158	1,5007078	5296,864	6938,2041	0,7634344
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1534,8668	0,3628899	0,0330514	23859,214	27389,817	0,871098	22057,845	46438,843	0,474987
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262814,07								
87353,555								
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153722,66								
5264,0623								
170,96754								
29,587804								
13902,071								
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13954,102	0,3656366	0,1445053	80037,995	91191,526	0,8776911	200536,9	96564,665	2,076711
20733,375	0,4827708	0,1027391	193257,26	166764,17	1,1588657	297963,04	201806,16	1,4764814
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6963,0161 0,2773596 0,0636858 41671,542 62589,916 0,6657868 100066,75 109333,94 0,9152396

27294,295

2587,2784 0,3464688 0,0627506 17863,543 21478,868 0,8316799 37182,242 41231,161 0,9017995
30994,768 0,3410041 0,0498151 247445,93 302293,39 0,8185621 445431,36 622196,65 0,7159013
3255,1605 0,2894136 0,0435173 26637,718 38342,987 0,694722 46780,495 74801,508 0,6253951

2052,6445 0,4031824 0,0414109 28945,946 29908,462 0,967818 29498,922 49567,786 0,5951228
448,406 0,388266 0,0465235 5805,1631 6228,6364 0,9320119 6444,1228 9638,2752 0,6685971
5993,7931 0,3995292 0,0359425 101362,19 105690,35 0,9590486 86137,874 166760,82 0,5165354
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4558,2557 0,5305991 0,0396984 74748,63 58687,375 1,2736748 65507,509 114822,27 0,5705122

9202,5345 0,4375441 0,0472757 164917,88 157019,6 1,0503013 132251,27 194656,61 0,6794081
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2019,4441 0,8031961 0,0853375 21072,764 10929,691 1,9280294 29021,793 23664,208 1,2264004
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4895,0483

4008,5147

2397,3739

10268,199

1805,0497 0,3801519 0,0537131 18513,226 20287,702 0,9125344 25940,693 33605,375 0,7719209
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1795,5156 0,2009672 0,0393198 24906,646 51629,505 0,4824111 25803,676 45664,375 0,5650724
280,44332 0,2863664 0,020599 5230,4077 7608,8925 0,6874072 4030,3012 13614,396 0,2960323
440,34688 0,3708653 0,0479023 5841,6365 6561,8485 0,8902425 6328,3039 9192,5982 0,688413
1664,3929 0,3166774 0,0466431 18229,315 23980,662 0,7601673 23919,288 35683,558 0,6703168

1505,1647 0,5074926 0,0430028 17314,034 14212,696 1,218209 21630,992 35001,569 0,6180006
2325,6979 0,6989017 0,0499455 22362,583 13329,497 1,6776764 33423,022 46564,67 0,7177764
29446,103 0,8434246 0,0557181 277829,82 137227,29 2,0245959 423175,22 528483,94 0,8007343
50567,286 0,8882979 0,0762647 385328,91 180709,45 2,1323118 726711,52 663049,32 1,0960143
7332,1617 0,6088551 0,0626203 51359,029 35140,731 1,4615242 105371,81 117089,28 0,899927
10845,035 0,6591916 0,0668751 79197,623 50050,497 1,5823544 155855,94 162168,41 0,9610746
6164,1881 0,7296095 0,0562514 65084,311 37161,544 1,7513888 88586,651 109582,77 0,8083994

39525,059	0,9378347	0,0554915	422585,94	187714	2,2512223	568021,7	712271,8	0,7974789
36755,785	0,7045975	0,0616799	344157,26	203480,97	1,6913487	528223,97	595911,5	0,8864134
511,60812	0,376517	0,045996	5815,2159	6434,1205	0,903809	7352,4119	11122,872	0,6610174
2025,0815	0,3160071	0,0612228	25735,785	33927,239	0,7585582	29102,809	33077,25	0,8798437
480,55623	0,2393864	0,0392405	7929,4212	13799,077	0,5746342	6906,1596	12246,424	0,5639328
820,23378	0,2971855	0,1037822	8155,3375	11432,003	0,7133778	11787,726	7903,4156	1,4914724
4284,6752	0,3235941	0,050337	46387,396	59718,287	0,7767704	61575,835	85119,848	0,7234016
17661,085	0,3126545	0,0979811	101803,25	135645,34	0,7505105	253810,62	180249,9	1,4081041
33360,884	0,4096786	0,0515128	361478,4	367575,91	0,9834116	479435,23	647623,8	0,740299
30459,963	0,4518769	0,0673535	300107,02	276671,18	1,0847065	437745,59	452240,35	0,967949
9206,2916	0,4970127	0,042844	127861,55	107171,77	1,1930525	132305,26	214879,34	0,6157189
3476,7233	0,3997282	0,0512865	42265,882	44048,697	0,9595263	49964,613	67790,189	0,7370478
507,43089	0,4224805	0,0749599	2410,631	2377,0156	1,0141418	7292,3802	6769,3639	1,0772622
2841,4865	0,5139178	0,0320199	21698,378	17589,015	1,2336324	40835,511	88741,322	0,4601634
1055,0129	0,6373649	0,0212056	14482,49	9465,9246	1,5299604	15161,78	49751,685	0,3047491
7218,9402	0,3432081	0,0353016	126628,14	153702,39	0,8238528	103744,68	204493,17	0,5073259
8067,8786	0,3233019	0,0793121	58725,629	75670,62	0,7760691	115944,93	101723,16	1,1398085
650,39354	0,1365388	0,0313406	10816,969	33003,296	0,3277542	9346,922	20752,435	0,4504012
2292,5464	0,3363406	0,0339764	34072,399	42201,838	0,8073677	32946,595	67474,682	0,4882808
23160,63	0,3249601	0,074552	179865,48	230582,19	0,7800493	332845,56	310664,1	1,0714001
21478,083	0,3165887	0,0383613	308520,86	405972,96	0,7599542	308665,37	559888,77	0,5512977
25629,901	0,321882	0,037342	364295,52	471481,92	0,7726606	368331,9	686355,52	0,5366488
22639,569	0,3899558	0,0486546	275187,17	293981,98	0,9360682	325357,29	465311,64	0,6992245
1401,3121	0,4581283	0,0754075	11232,67	10214,187	1,0997125	20138,507	18583,192	1,0836947
1585,5385	0,469146	0,0185305	49488,85	43944,782	1,1261599	22786,057	85563,827	0,2663048
845,16831	0,6489668	0,0358847	15539,14	9974,9889	1,5578102	12146,065	23552,344	0,5157051
2826,1422	0,5887626	0,0362881	52963,184	37475,017	1,4132931	40614,996	77880,584	0,5215035
2198,5134	0,4982124	0,0369439	40508,201	33871,651	1,1959323	31595,23	59509,586	0,5309267
10434,508	0,4746223	0,1023202	79409,232	69699,677	1,1393056	149956,19	101978,93	1,4704624
1876,7577	0,4714736	0,0314392	33755,142	29825,687	1,1317473	26971,221	59694,818	0,4518185
3324,5463	0,4622976	0,0421512	44386,558	39997,954	1,1097207	47777,65	78871,959	0,6057622
2561,0253	0,4170801	0,0406459	37137,249	37093,53	1,0011786	36804,953	63008,157	0,58413
1878,1924	0,3265593	0,0529446	18145,393	23147,933	0,7838883	26991,839	35474,668	0,7608764
5166,4263	0,2952496	0,0817936	33272,158	46946,103	0,708731	74247,637	63164,151	1,1754712
4498,7926	0,2734535	0,2494951	13102,498	19960,829	0,6564105	64652,954	18031,588	3,5855386
69434,344	0,1837995	0,1625936	209599,22	475065,31	0,4412008	997853,39	427042,2	2,3366623
5339,9564	0,2756293	0,1460161	29742,211	44952,696	0,6616335	76741,469	36571,005	2,0984238
10379,573	0,5148211	0,1168601	64908,935	52523,791	1,2358006	149166,7	88820,515	1,6794172
42420,967	0,2597814	0,2031522	133220,78	213634,71	0,6235914	609639,32	208813,69	2,9195371
5120,1501	0,2863978	0,0548892	42287,3	61510,356	0,6874826	73582,594	93281,521	0,7888228
230,12991	0,4830456	0,0233423	3932,5056	3391,4789	1,1595253	3307,2382	9858,9222	0,3354564
835,55269	0,5406867	0,0618416	9369,3101	7218,8802	1,2978897	12007,877	13511,169	0,8887371
2610,451	0,4780159	0,0333621	28892,311	25179,545	1,1474517	37515,259	78246,005	0,4794527
15180,179	0,3594694	0,0465043	117419,8	136077,82	0,8628872	218157,07	326425,59	0,668321

8368,4455	0,5584545	0,0294019	146861,86	109554,23	1,3405403	120264,43	284622,34	0,4225404
16639,857	0,7408164	0,0346031	283360,84	159344,54	1,7782902	239134,36	480878,11	0,4972869
147464,29	0,7416076	0,0518893	1904328	1069733,3	1,7801895	2119235,7	2841900,9	0,7457106
48187,106	0,4961445	0,0675366	514262	431801,54	1,1909684	692505,53	713495,67	0,9705813
17329,263	0,3981005	0,0761117	170634,71	178559,32	0,9556191	249041,95	227682,06	1,0938145
6488,5127	0,632844	0,0444184	92182,003	60681,653	1,5191083	93247,578	146077,1	0,6383449
3744,8897	0,6252354	0,0483271	49773,115	33163,413	1,5008442	53818,481	77490,433	0,6945177
8213,4734	0,5926943	0,0413286	115338,85	81068,632	1,422731	118037,3	198735,92	0,5939404
4697,3404	0,6033657	0,0425643	68701,693	47434,544	1,4483473	67506,321	110358,64	0,6116995
1570,2736	0,5529649	0,0530231	18487,425	13927,936	1,3273629	22566,683	29614,888	0,7620047
6393,63	0,394759	0,0699045	59171,441	62443,622	0,9475978	91884,001	91462,358	1,00461
3770,8299	0,4731783	0,1208258	24229,204	21331,541	1,1358393	54191,272	31208,824	1,7364086
12142,631	0,4761022	0,0375198	146726,77	128385,82	1,142858	174503,92	323632,26	0,5392043
5345,0467	0,6737748	0,0528918	61177,695	37825,64	1,6173605	76814,623	101056,19	0,7601179

6689,4535	0,3651554	0,0430528	81642,578	93142,286	0,8765361	96135,334	155377,82	0,6187198
7753,4184	0,308038	0,0592055	68959,17	93260,051	0,7394288	111425,76	130957,77	0,8508527
29003,202	0,3372501	0,0720418	190078,66	234795,21	0,8095508	416810,22	402588,33	1,0353261
2184,8843	0,3840818	0,0371491	29407,737	31896,708	0,9219678	31399,364	58813,948	0,5338761
35181,899	0,4572848	0,0664355	387028,04	352584,8	1,0976878	505605,37	529564,86	0,9547563
6355,0201	0,3442993	0,0653253	50219,988	60764,281	0,8264722	91329,131	97282,68	0,9388016

5946,0041	0,4680331	0,0487966	51350,958	45706,707	1,1234884	85451,09	121852,71	0,7012654
4737,8105	0,3991889	0,1190179	19113,773	19946,923	0,9582316	68087,923	39807,539	1,7104278
57577,111	0,347541	0,1063348	252592,01	302775,99	0,8342538	827450,97	541470,14	1,5281562
85346,712	0,4050488	0,1444367	337864,35	347490,47	0,9722982	1226532,9	590893,49	2,0757258
31157,29	0,4574954	0,0823725	248627,43	226396,79	1,0981933	447766,99	378248,83	1,1837895
20413,165	0,3781224	0,0692463	109611,87	120762,79	0,9076626	293361,25	294790,71	0,9951509
21231,031	0,3519554	0,0809177	98557,939	116657,29	0,8448503	305114,95	262378,18	1,1628823

18631,504	0,5244187	0,1048301	116887,77	92853,629	1,258839	267756,68	177730,44	1,5065325
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2801,1969
22233,063
6788,5831

16265,95	0,5244938	0,0705658	145975,92	115944,14	1,2590194	233760,88	230507,46	1,0141142
18648,989	0,3747676	0,0700183	132380,19	147152,92	0,8996097	268007,95	266344,46	1,0062456

10360,932
3263,9767

7673,1192	0,2975065	0,0540375	61155,194	85633,709	0,7141486	110271,77	141996,14	0,7765829
37021,983	0,3136354	0,082622	236948,63	314729,19	0,7528651	532049,55	448088,9	1,187375
47029,044	0,5862656	0,1301361	277010,33	196838,23	1,4072994	675862,81	361383,65	1,8702086
19521,017	0,6040629	0,1459765	115850,83	79895,977	1,4500208	280540,04	133727,15	2,0978541

108994,95
10453,459

19285,205	0,2437358	0,0597096	171175,25	292569,87	0,5850748	277151,14	322983,06	0,8580981
6208,2915	0,298199	0,0256759	67607,595	94448,97	0,7158108	89220,469	241794,75	0,3689926
6919,2154	0,3738311	0,0407531	87808,773	97852,161	0,8973616	99437,284	169783,81	0,58567
5676,6995	0,4551681	0,096398	37104,145	33959,283	1,0926068	81580,864	58888,153	1,3853527
2986,0683	0,3787788	0,0320515	42431,011	46666,545	0,9092383	42913,323	93164,741	0,4606176

39818,821	0,3982199	0,0450009	415998,53	435187,89	0,9559056	572243,41	884845,41	0,6467157
2246,7006	0,2951092	0,0287126	23751,029	33527,992	0,708394	32287,737	78247,982	0,4126335
18640,642								
37463,409								
10369,466	0,416303	0,0641628	83312,047	83369,308	0,9993132	149021,45	161611,79	0,9220951
3786,183	0,4241505	0,0784564	33346,079	32751,618	1,0181506	54411,914	48258,424	1,1275112
9065,8008	0,2367759	0,0542908	82057,622	144374,15	0,5683678	130286,25	166985,92	0,780223
3206,6282	0,3310751	0,0954307	22204,207	27939,374	0,7947281	46083,028	33601,636	1,3714519
4486,5022	0,2960879	0,0883846	32735,486	46058,103	0,7107433	64476,326	50761,139	1,2701907
4207,0765	0,344893	0,0970083	28356,206	34250,875	0,8278973	60460,649	43368,232	1,394123
13170,546	0,4303823	0,113306	79940,088	77378,112	1,0331098	189276,27	116238,78	1,6283402
4983,3001	0,2657347	0,046564	47524,215	74503,139	0,637882	71615,898	107020,56	0,6691789
14646,662	0,7828001	0,0473078	145976,21	77685,351	1,87907	210489,81	309603,74	0,6798684
26349,063	0,5977619	0,0553928	205472,07	143196,52	1,4348957	378667,1	475676,58	0,79606
12844,341								
31077,884								
23015,105								
7026,7434	0,4964007	0,0326251	67648,084	56771,591	1,1915834	100982,59	215378,54	0,468861
13906,159	0,5350464	0,0308076	146929,02	114399,48	1,2843504	199847,9	451387,22	0,4427416
5354,4286	0,4817497	0,0423433	65539,762	56674,971	1,1564146	76949,452	126452,88	0,6085227
1065,7109	0,402887	0,0287573	19856,357	20531,666	0,9671089	15315,523	37058,734	0,413277
9382,5927	0,385364	0,074533	85506,954	92435,38	0,9250457	134838,92	125885,13	1,0711267
12535,195	0,4638139	0,0576366	121662,41	109274,94	1,1133605	180145,53	217486,83	0,8283055
54279,072	0,5181603	0,0975831	456610,17	367104,21	1,2438162	780054,26	556234,62	1,4023835
1363,3567	0,3852225	0,0997015	6968,5514	7535,9645	0,924706	19593,044	13674,383	1,4328283
5979,4925	0,3220143	0,0521394	53528,92	69250,246	0,772978	85932,357	114682,84	0,7493044
56029,142	0,432305	0,0500229	576894,22	555922	1,0377251	805204,84	1120070,4	0,7188877
79988,89	0,4717453	0,0472749	858513,66	758136,79	1,1323994	1149534,7	1691994,5	0,6793962
21405,092	0,622199	0,0700648	205675,01	137708,31	1,4935555	307616,41	305504,2	1,0069139
24491,579	0,4233548	0,060377	213673,79	210259,06	1,0162406	351972,87	405644,23	0,8676886
39579,956	0,5325769	0,1009089	242180,14	189436,71	1,2784224	568810,64	392234,44	1,4501803
18562,099	0,5361679	0,0454591	251024,91	195040,1	1,2870426	266759,24	408325,06	0,6533012
11414,442	0,2261487	0,0478277	83613,732	154025,05	0,542858	164039	238657,75	0,6873399
11071,28	0,6100811	0,0656326	136760,05	93385,536	1,4644672	159107,34	168685,69	0,9432178
513,93973	0,4272124	0,0284828	16933,753	16512,669	1,0255007	7385,9198	18043,888	0,4093308
1320,5191	0,3638492	0,0777616	14202,259	16260,876	0,8734006	18977,416	16981,631	1,1175261
203,32653	0,5513425	0,0089596	19172,722	14486,727	1,3234682	2922,042	22693,656	0,1287603
1042,5779	0,5072849	0,0312767	24974,42	20509,327	1,2177103	14983,073	33334,046	0,4494826
530,0506	0,556752	0,0443024	11155,121	8346,8076	1,3364536	7617,4521	11964,376	0,6366777
9825,332	0,5092265	0,0403804	120914,95	98918,372	1,222371	141201,61	243319,39	0,5803138
16694,08	0,6291831	0,0770094	145426,56	96288,546	1,5103204	239913,61	216779,7	1,1067162
5717,074	0,4087407	0,0832899	47715,415	48631,627	0,9811602	82161,094	68640,682	1,1969737
21159,833	0,798423	0,1049026	188215,6	98204,302	1,9165718	304091,76	201709,36	1,5075739
7024,6576	0,6341724	0,0992606	52567,607	34531,764	1,5222972	100952,61	70769,876	1,4264913

13653,706	0,7267993	0,0896578	83277,48	47733,247	1,7446431	196219,86	152286,92	1,2884879
42911,939	0,4453051	0,0674352	247711,51	231737,59	1,0689311	616695,15	636343,5	0,969123
10988,053	0,6399891	0,0802836	58382,254	38002,853	1,5362598	157911,28	136865,55	1,1537694
11775,258	0,4749695	0,1381771	67147,964	58894,545	1,1401389	169224,34	85218,589	1,9857679
4729,7256	0,9924009	0,037068	39552,588	16603,348	2,3822056	67971,734	127595,96	0,5327107
3352,1606	0,4165114	0,0498869	38576,458	38583,66	0,9998134	48174,5	67195,157	0,7169341
8260,7036	0,4743904	0,0900643	61293,265	53825,089	1,138749	118716,05	91720,105	1,2943296
7496,816	0,5363278	0,138161	39604,466	30762,513	1,2874262	107738,09	54261,445	1,9855366
4445,7724	0,3927612	0,0396044	58980,053	62558,245	0,9428022	63890,99	112254,58	0,5691615
1841,9172	0,4242666	0,0425803	29528,789	28994,44	1,0184294	26470,522	43257,476	0,6119294
12746,861	0,4648721	0,0528009	97984,713	87807,729	1,1159008	183187,42	241413,78	0,758811
1997,2788	0,5575019	0,0192831	16466,12	12304,186	1,3382536	28703,252	103576,42	0,2771215
2477,5004	0,4707083	0,0460658	15380,407	13612,062	1,1299101	35604,602	53781,761	0,66202
4922,4315	0,6005418	0,0312053	40193,819	27882,004	1,4415685	70741,145	157743,2	0,4484577
13470,526	0,6596041	0,0316514	108004,16	68212,679	1,5833444	193587,34	425589,78	0,4548684
1109,8358	0,5914433	0,0322618	9918,1354	6985,9403	1,419728	15949,649	34400,893	0,4636405
33630,654	0,4218157	0,0348362	337522,29	333340,17	1,0125461	483312,16	965394,2	0,5006371
5201,4426	0,4534092	0,0392988	62479,508	57405,72	1,0883847	74750,863	132356,12	0,5647707
19579,693	0,4388081	0,0627099	136442,98	129534,2	1,0533356	281383,27	312226,66	0,9012148
7257,0625	0,4746237	0,0817289	64401,645	56526,942	1,1393088	104292,55	88794,328	1,1745406
12655,506	0,3595872	0,0733699	102264,69	118475,74	0,8631699	181874,54	172489,1	1,0544118
7664,4134	0,3880268	0,0588566	74098,135	79552,433	0,9314377	110146,66	130221,74	0,8458393
479,35587	0,289461	0,0252133	7120,3142	10247,479	0,6948357	6888,909	19011,989	0,3623455
13088,75	0,5236499	0,1003677	91397,755	72711,383	1,2569938	188100,78	130408,02	1,4424019
6518,1287	0,3079074	0,1046029	39172,66	52999,383	0,7391154	93673,194	62313,074	1,5032671
395,71812	0,3928504	0,0593593	3395,6383	3600,8265	0,9430164	5686,936	6666,4927	0,8530627
529,75433	0,3990596	0,0316603	6490,948	6776,0757	0,9579214	7613,1943	16732,428	0,4549964
3262,428	0,4524143	0,0398435	42810,563	39420,54	1,0859964	46884,937	81881,122	0,5725976
14496,665	0,4645694	0,0337125	226427,15	203041,98	1,1151741	208334,17	430008,81	0,4844881
1590,2025	0,4316045	0,0332344	20951,159	20222,277	1,0360435	22853,085	47848,154	0,4776169
1779,2969	0,3810866	0,0357332	24836,518	27150,322	0,914778	25570,595	49793,902	0,5135286
1225,7738	0,5494945	0,0401138	17420,524	13207,049	1,3190323	17615,814	30557,441	0,576482
511,48085	0,3272918	0,2015286	2348,5305	2989,2962	0,7856466	7350,5828	2538,0069	2,8962029
913,33714	0,8949438	0,0263424	21904,818	10196,516	2,148265	13125,732	34671,794	0,3785709
1642,6933	0,5881352	0,0404475	22301,339	15796,53	1,4117872	23607,44	40613,019	0,5812776
2918,1415	0,593927	0,0430338	41260,414	28940,662	1,4256901	41937,134	67810,452	0,6184465
5365,2951	0,4979968	0,0512271	55131,185	46118,872	1,1954149	77105,617	104735,57	0,7361932
114257,49	0,2758625	0,3936294	398604,69	601946,21	0,6621932	1642014,8	290266,69	5,6569179
27166,676	0,353616	0,1620354	130583,95	153838,79	0,8488363	390417,17	167658,87	2,3286401
133998,85	0,2672458	0,1895406	761397,35	1186884,1	0,6415094	1925721,5	706966,35	2,7239224
591,23327	0,2290037	0,2127727	1535,1609	2792,6683	0,5497111	8496,7192	2778,708	3,0577949
6711,405	0,2865463	0,260498	17514,417	25462,957	0,6878391	96450,803	25763,749	3,7436633
5123,6001	0,4092585	0,0454025	63834,383	64977,777	0,9824033	73632,174	112848,43	0,6524874
8646,6275	0,4121626	0,039169	128478,21	129858,03	0,9893744	124262,23	220751,83	0,5629047

19809,161	0,4948247	0,0716289	188537,34	158728,14	1,1878003	284681	276552,74	1,0293914
23129,232	0,3853918	0,0306223	418750,95	452648,72	0,9251124	332394,34	755306,75	0,4400786
5320,0661	0,4356859	0,0394192	73205,081	69996,397	1,0458407	76455,622	134961,24	0,5665006
5996,9573	0,4361499	0,0408874	75565,848	72176,822	1,0469545	86183,347	146670,09	0,5876

13707,489	0,3638507	0,1831232	81403,37	93202,397	0,8734043	196992,78	74853,916	2,6316963
33217,395	0,4021018	0,1761168	202844,27	210152,53	0,965224	477373,13	188610,04	2,5310059
10944,928	0,7206508	0,2094848	76567,035	44261,375	1,7298838	157291,52	52246,889	3,0105432
7749,7114	0,4758431	0,0989734	62216,119	54468,712	1,1422359	111372,49	78300,915	1,4223651
1603,3937	0,3804924	0,0979566	8941,455	9789,7181	0,9133516	23042,658	16368,407	1,407752
57578,09	0,4526499	0,0744728	471495,7	433933,52	1,086562	827465,03	773142,89	1,0702615

53549,169

13335,389	0,2972957	0,1888188	62253,545	87233,532	0,7136424	191645,26	70625,312	2,7135492
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11038,59

15956,955

7101,2452	0,4488009	0,1057966	41654,766	38665,079	1,0773227	102053,27	67121,654	1,5204224
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1786,3547	0,3595415	0,0238542	29709,756	34423,738	0,8630601	25672,023	74886,476	0,3428125
2113,2663	0,4684561	0,0288945	37149,452	33036,305	1,1245039	30370,128	73137,342	0,4152479
2035,4094	0,3980244	0,0839169	12327,384	12902,36	0,9554364	29251,233	24255,047	1,2059854
10757,494	0,3829086	0,0338367	142132,22	154634,13	0,9191517	154597,87	317923,73	0,4862734
8007,2736	0,4705569	0,0394969	121310	107397,07	1,1295466	115073,96	202731,64	0,5676172
6524,1154	0,5841853	0,0528033	73180,271	52185,675	1,4023057	93759,23	123554,96	0,7588463
4410,1103	0,5728763	0,0860789	37355,763	27164,685	1,3751591	63378,485	51233,368	1,2370548
10010,318	0,509027	0,0581244	121157,12	99155,329	1,2218921	143860,07	172222,36	0,8353159

983,9956	0,4086345	0,0612457	6378,3868	6502,5515	0,9809052	14141,177	16066,362	0,8801729
4847,7616	0,5762472	0,0513868	54920,67	39704,062	1,3832507	69668,05	94338,706	0,7384885
9459,9949	0,4561863	0,0411118	117659,87	107446,93	1,095051	135951,28	230103,92	0,5908256
1225,685	0,4105058	0,0365237	16482,977	16727,24	0,9853973	17614,538	33558,665	0,5248879
2337,0542	0,5898664	0,1368917	11117,859	7851,9121	1,4159429	33586,224	17072,287	1,9672949

2467,8143	0,5450182	0,0313576	43189,327	33012,119	1,3082871	35465,401	78699,154	0,4506453
9092,9037	0,5300695	0,0556978	100731,15	79166,034	1,2724037	130675,75	163254,4	0,8004424
10670,795	0,3866116	0,0429655	122667,62	132179,17	0,9280405	153351,91	248357,25	0,617465
4462,8992	0,4493858	0,0469986	49088,689	45506,141	1,0787267	64137,123	94958,063	0,6754258
1254,7837	0,4103484	0,0374897	13892,618	14103,903	0,9850194	18032,722	33470,08	0,5387714
13047,28	0,512598	0,0791687	91242,393	74152,828	1,2304641	187504,8	164803,5	1,1377477
10617,866	0,4320024	0,0765787	83589,44	80607,073	1,0369988	152591,25	138652,98	1,1005263
5959,3216	0,437843	0,0966668	44363,067	42209,589	1,0510187	85642,478	61648,055	1,3892162

10680,143	0,1341174	0,044105	60037,566	186485,91	0,3219416	153486,25	242152,8	0,6338405
5523,0641	0,1047757	0,0417274	25916,625	103044,76	0,2515084	79372,943	132360,63	0,5996718
6338,6425	0,066212	0,0479185	23454,805	147571,66	0,1589384	91093,767	132279,57	0,6886458
1536,176	0,0988924	0,0515789	7026,1383	29597,949	0,237386	22076,661	29783,006	0,7412502
12020,264	0,1341366	0,0585983	60627,651	188291,82	0,3219877	172745,36	205129,86	0,8421269

4622,035	0,2331972	0,0689845	20888,993	37316,602	0,5597775	66424,093	67001,051	0,9913888
7902,8486	0,2456574	0,0703162	35743,709	60614,67	0,5896874	113573,25	112390,11	1,0105271
20623,367	0,3856482	0,0703749	182239,17	196860,42	0,9257278	296382,1	293050,08	1,0113701
8376,8395	0,3851094	0,0760595	62394,745	67495,034	0,9244346	120385,06	110135,28	1,0930653

8592,7762 0,4699667 0,0565142 80324,431 71201,394 1,12813 123488,33 152046,24 0,8121761

13778,617 0,585294 0,0720622 152785,98 108747,01 1,4049671 198014,97 191204,5 1,0356188
4744,1967 0,4147009 0,0659591 43124,685 43321,038 0,9954675 68179,701 71926,344 0,94791
10463,103 0,3538969 0,0754779 86129,929 101387,69 0,8495108 150367,12 138624,67 1,0847068
4807,7349 0,3947738 0,0644198 47712,929 50349,563 0,9476334 69092,82 74631,343 0,9257882
4090,96 0,60467 0,0423674 63284,66 43600,147 1,4514781 58791,918 96559,248 0,6088688
12233,333 0,5532337 0,0545974 139408,14 104975,38 1,3280079 175807,42 224064,35 0,7846291
22356,85 0,5980403 0,0578477 257861,63 179623,93 1,4355639 321294,29 386477,59 0,83134

10759,905 0,5866477 0,1110068 104379,36 74121,676 1,4082165 154632,52 96930,126 1,5952988
51330,185 0,6730404 0,0931436 642718,51 397820,94 1,6155975 737675,28 551086,75 1,3385829
8519,371 0,4090639 0,0231982 148778,81 151515,76 0,9819362 122433,41 367243,44 0,3333849
7263,7232 0,3238338 0,0359934 79467,438 102229,19 0,7773459 104388,27 201807,11 0,5172675
33509,755 0,6035241 0,0652767 328242,33 226572,86 1,4487275 481574,69 513349,44 0,9381031
101015,05 0,6093534 0,1476118 471639,4 322439,9 1,4627203 1451705,4 684329 2,1213559
4296,2903 0,4087321 0,055862 37905,512 38634,165 0,9811397 61742,757 76909,005 0,8028027
4579,2677 0,2530799 0,0378676 66942,619 110192,75 0,6075047 65809,476 120928,51 0,5442015
6796,3538 0,4277871 0,0340906 103231,7 100529,46 1,0268801 97671,617 199361,53 0,4899221
2671,9431 0,4543221 0,0477181 31763,941 29125,841 1,0905759 38398,973 55994,332 0,6857654
46439,899 0,3960242 0,0760917 625191,87 657657,2 0,9506349 667396,1 610315,08 1,0935271
5276,4115 0,5807977 0,0587559 55353,405 39703,375 1,3941738 75828,254 89802,286 0,8443911

30738,228

1161,1999

2783,5186 0,360282 0,0620793 34918,783 40376,115 0,8648376 40002,444 44838,103 0,8921529
12065,63 0,3683506 0,0964551 80942,799 91542,911 0,8842061 173397,33 125090,68 1,3861731

2112,1722 0,9919106 0,0390561 36445,148 15306,472 2,3810286 30354,404 54080,475 0,5612821
2835,285 0,6072478 0,0491773 30002,911 20582,842 1,4576661 40746,389 57654,3 0,7067363
4228,1038 0,5953172 0,0480866 45793,291 32045,082 1,4290271 60762,836 87926,842 0,6910613
2242,0394 0,8166047 0,0377058 39516,223 20159,117 1,960216 32220,749 59461,466 0,5418761

2801,1969

22233,063

6788,5831

947,87732 0,2779333 0,0522028 12056,701 18071,569 0,667164 13622,115 18157,578 0,7502165

11442,048 0,4630047 0,0499247 119224,77 107272,65 1,1114181 164435,72 229186,15 0,7174767
24249,976 0,4065546 0,0989054 133817,31 137120,16 0,9759127 348500,74 245183,52 1,4213873
19862,454 0,5617185 0,0670517 216964,1 160907,79 1,3483754 285446,88 296226,11 0,9636115
15601,571 0,5338093 0,0488468 227246,83 177345,27 1,2813808 224212,97 319398,21 0,7019857
8607,665 0,4182172 0,060271 75307,889 75014,719 1,0039082 123702,3 142815,99 0,8661656

18640,642

37463,409

2647,7269 0,540581 0,0447251 38064,763 29333,931 1,2976359 38050,957 59199,968 0,642753
5921,1684 0,5107804 0,1025363 37608,009 30672,847 1,226101 85094,171 57747,067 1,473567
249,60536 0,3554431 0,0555627 2966,605 3476,9426 0,8532223 3587,1234 4492,3154 0,7985021
260,8518 0,4806494 0,1122066 1834,2992 1589,8263 1,1537734 3748,748 2324,7465 1,6125405
295,46507 0,3419711 0,0402184 4717,3176 5746,6347 0,8208835 4246,1814 7346,5065 0,5779865
4899,8808 0,3368601 0,0383851 85541,668 105787,9 0,8086148 70417,064 127650,68 0,5516388

5149,7199	0,4406494	0,0344006	92640,509	87582,16	1,0577555	74007,547	149698,34	0,4943779
1106,9165	0,3731604	0,0329187	16915,579	18884,23	0,8957516	15907,695	33625,805	0,47308
3178,7132	0,3338457	0,0325401	56893,65	70994,706	0,8013788	45681,856	97685,961	0,4676399
3808,9372	0,314103	0,0311151	70674,778	93734,67	0,7539876	54738,918	122414,55	0,4471602

3557,9173	0,336365	0,0387347	37273,595	46163,461	0,8074264	51131,467	91853,553	0,5566629
18647,057	0,5636045	0,056105	230180,47	170138,24	1,3529026	267980,19	332360	0,806295
7266,3092	0,5270393	0,0473502	98507,062	77863,208	1,2651298	104425,43	153459,05	0,6804775
4711,3245	0,4361367	0,0511538	48085,725	45930,529	1,046923	67707,289	92101,153	0,7351405
101694,37	0,5293384	0,0557349	1093610,8	860671,24	1,2706487	1461468	1824607,5	0,8009767
16682,333	0,342145	0,0494624	207799,37	253012,45	0,8213009	239744,79	337272,91	0,7108332
18476,724	0,4504692	0,050572	197597,39	182735,98	1,0813273	265532,3	365354,56	0,7267798
2870,1043	0,3252964	0,0439609	29475,3	37747,392	0,7808566	41246,783	65287,651	0,6317701
6809,7054	0,2912585	0,0422485	64153,013	91758,523	0,6991505	97863,495	161182,25	0,6071605

27180,009	0,3876411	0,1290063	173494	186450,09	0,9305118	390608,78	210687,47	1,8539725
16806,741	0,4048436	0,113291	114716,3	118044,51	0,9718054	241532,68	148350,23	1,6281248
5260,779	0,4605763	0,1568209	26747,879	24193,334	1,1055888	75603,597	33546,422	2,2537007
56539,522	0,5347922	0,1278452	378305,29	294689,92	1,2837402	812539,59	442249,91	1,837286
111812,98	0,5711012	0,1622756	680993,22	496749,73	1,370898	1606884,4	689031,35	2,3320918
6729,1633	0,3935744	0,2142431	26649,011	28207,343	0,9447544	96706,011	31409,009	3,0789259
5743,882	0,3973816	0,1995281	22172,618	23244,333	0,9538935	82546,356	28787,339	2,8674535
6006,6255	0,2651164	0,078316	27309,325	42912,352	0,6363978	86322,29	76697,266	1,1254937
1730,1444	0,4202953	0,0707236	13469,449	13350,675	1,0088965	24864,215	24463,463	1,0163817
7883,4091	0,3149371	0,0517687	61923,042	81909,907	0,7559897	113293,88	152281,37	0,7439773

3647,6258	0,4081551	0,0579682	32866,839	33545,996	0,9797544	52420,683	62924,645	0,8330708
7484,3843	0,2743992	0,295588	23845,164	36201,4	0,6586807	107559,43	25320,328	4,2479477
1847,1823	0,314413	0,3250705	5711,4665	7567,5454	0,7547317	26546,187	5682,405	4,6716464
1610,9602	0,3599877	0,0794491	11702,164	13542,114	0,8641313	23151,398	20276,625	1,1417777

6007,3981	0,4462984	0,0331339	61579,424	57480,194	1,0713155	86333,393	181306,91	0,4761727
7228,2916	0,3532439	0,0263481	91232,674	107592,9	0,8479432	103879,07	274338,66	0,3786527
86,986235	0,743529	0,0148233	1711,5386	958,95174	1,7848016	1250,0948	5868,2075	0,2130284
266,18334	0,8273495	0,0167704	5912,9554	2977,3062	1,9860085	3825,3685	15872,197	0,2410107
12667,537	0,2869701	0,082603	122649,33	178047,75	0,6888564	182047,44	153354,4	1,1871028
3347,7583	0,2207048	0,056697	16098,512	30386,58	0,5297902	48111,233	59046,464	0,814803

9235,7959	0,3859523	0,045303	87589,254	94542,064	0,926458	132729,28	203867,23	0,6510574
4528,7636	0,5314585	0,0625369	45028,363	35295,94	1,2757377	65083,672	72417,458	0,898729
1701,7546	0,4942679	0,0293934	26177,571	22063,521	1,1864639	24456,221	57895,772	0,4224181
9288,5206	0,5404854	0,0442234	95220,078	73392,644	1,2974063	133486,99	210036,55	0,6355417

426,79257	0,3275102	0,0235071	5965,0834	7587,5153	0,7861709	6133,5124	18155,897	0,3378248
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431,51322
4053,3277
3540,6644

6402,6149	0,2700002	0,0524364	55035,08	84914,796	0,6481212	92013,125	122102,49	0,7535729
1177,7161	0,4259675	0,0362246	15404,048	15064,904	1,0225122	16925,17	32511,457	0,5205909

723,23365	0,4686397	0,0580381	6584,472	5853,1518	1,1249447	10393,72	12461,357	0,8340761
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8525,2125	0,4827602	0,0280675	126050,64	108773,11	1,1588401	122517,36	303739,75	0,4033629
4411,215	0,5338235	0,0288802	80688,191	62968,045	1,2814149	63394,36	152742,09	0,4150419
4562,4433	0,5533831	0,0305831	80711,076	60759,635	1,3283667	65567,689	149181,65	0,4395158
3238,2031	0,6245826	0,0336314	57742,584	38513,615	1,4992772	46536,796	96285,225	0,4833223

31662,846	1,3055885	0,2423347	146248,98	46665,34	3,1339957	455032,43	130657,5	3,4826354
19632,71	1,2117477	0,2268043	91851,464	31577,794	2,9087359	282145,19	86562,35	3,2594446
98230,938	0,7157835	0,2390051	449750,16	261756,56	1,7182001	1411694,4	410999,37	3,4347848
43359,951	0,6743951	0,2590428	173628,69	107254,37	1,6188496	623133,62	167385,27	3,7227505
79491,004	0,7156649	0,2810699	306397,54	178354,26	1,7179154	1142379,4	282815,8	4,0393057
34504,739	0,6894658	0,2534643	141190,43	85310,107	1,6550258	495873,78	136132,51	3,6425815
10586,521	0,4471312	0,130626	56015,844	52189,587	1,0733146	152140,8	81044,52	1,8772496

47806,556	0,390609	0,2472757	163769,75	174662,37	0,9376361	687036,58	193333,02	3,5536432
4242,5782	0,3769071	0,0426022	60516,845	66888,261	0,9047454	60970,851	99585,78	0,6122445
4873,4872	0,4001182	0,0366429	81790,655	85157,589	0,9604623	70037,757	132999,41	0,526602
14139,382	0,3041844	0,0576883	114785,18	157201,52	0,7301786	203199,59	245099,67	0,8290488

5140,4062	0,5408957	0,0423229	49744,99	38312,79	1,2983912	73873,698	121456,75	0,6082305
4834,3138	0,4372947	0,0510591	42773,067	40747,795	1,0497026	69474,79	94680,661	0,7337801
1441,1142	0,4658384	0,0505564	15569,525	13923,488	1,1182201	20710,51	28505,069	0,7265553
1040,392	0,2960773	0,0279706	10385,865	14613,207	0,7107177	14951,66	37195,85	0,4019712
2259,9526	0,2974778	0,0182941	34070,232	47712,09	0,7140797	32478,183	123534,55	0,2629077
2687,844	0,4739066	0,0366466	33392,398	29353,696	1,1375875	38627,487	73344,948	0,526655
841,27906	0,2849558	0,0317219	7754,6647	11336,878	0,6840212	12090,172	26520,426	0,4558815

11375,622	0,4712327	0,1601996	63443,966	56087,084	1,1311689	163481,1	71009,052	2,3022572
8503,325	0,5132277	0,0744707	80938,501	65698,135	1,2319756	122202,81	114183,47	1,070232
3862,1265	0,2943806	0,1312099	31229,354	44193,84	0,706645	55503,311	29434,728	1,8856403
22960,35	0,3338587	0,1379572	164006,28	204647,18	0,8014099	329967,3	166430,93	1,9826081
4949,6205	0,2755902	0,0923272	24707,133	37347,922	0,6615397	71131,882	53609,584	1,3268501

51753,107	0,5737546	0,1905686	272224,59	197655,6	1,3772673	743753,17	271572	2,7386961
86412,73	0,6031406	0,2592667	459210,02	317176,3	1,4478069	1241852,8	333296,69	3,7259681
4665,0154	0,3441755	0,0449619	35075,156	42454,879	0,8261749	67041,771	103754,93	0,6461551
7450,0486	0,4028399	0,1573315	41586,162	43005,532	0,9669956	107065,98	47352,566	2,2610387
2986,4578	0,5448084	0,0695617	17248,56	13189,156	1,3077835	42918,919	42932,531	0,999683
5565,8001	0,5392553	0,0658813	39261,589	30330,628	1,2944536	79987,11	84482,184	0,9467926

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13785,592
5874,2885
6896,4299

3034,67	0,2690836	0,0334062	60883,997	94259,215	0,6459209	43611,785	90841,629	0,4800859
9604,4853	0,5987251	0,0665898	103530,55	72035,899	1,4372077	138027,78	144233,59	0,9569739
17910,293	0,3783149	0,0518932	253343,52	278974,35	0,9081248	257392,03	345137,57	0,7457665

35613,659
65778,532

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5641,529

1705,337

6507,4392 0,2530866 0,0384514 80504,586 132513,29 0,6075208 93519,574 169237,87 0,5525925

1808,5341

2293,5387

31799,141 0,4190347 0,1981546 185125,79 184045,36 1,0058705 456991,15 160476,42 2,8477153
8940,8957 0,2214148 0,1127138 66399,145 124929,13 0,5314945 128491,21 79323,874 1,6198303
205,31091 0,5956656 0,1625097 1085,6421 759,26267 1,4298636 2950,5598 1263,3766 2,3354555
450,05252 0,2999559 0,2050201 2017,6521 2802,1849 0,7200282 6467,7854 2195,163 2,9463805

5242,1232 0,7225194 0,0651978 59512,048 34313,367 1,7343692 75335,491 80403,435 0,9369686
659,11226 0,6215541 0,0520257 9329,2822 6252,8386 1,4920075 9472,2202 12668,966 0,7476711
1821,2866 0,5767922 0,0947972 13513,203 9759,9339 1,3845588 26174,036 19212,456 1,3623472
1095,3943 0,4515092 0,0645645 10277,389 9482,528 1,0838238 15742,107 16965,898 0,9278676
372,48333 0,6391743 0,0702146 3943,6661 2570,3292 1,5343039 5353,0247 5304,9262 1,0090668
44895,193 0,3828512 0,0961056 200839,43 218537,99 0,9190138 645196,86 467144,49 1,3811505

229,68468 0,3200355 0,0246679 2803,1668 3648,8724 0,7682282 3300,8397 9311,077 0,3545068
4582,0121 0,5536503 0,0368597 51140,685 38480,343 1,329008 65848,916 124309,41 0,5297179
13688,07 0,7674435 0,060653 133133,12 72268,268 1,8422071 196713,71 225678,46 0,8716548
2501,2453 0,726856 0,030761 42036,656 24092,824 1,7447791 35945,844 81312,232 0,4420718
2792,5844 0,8531332 0,0355125 50237,029 24530,988 2,0479008 40132,731 78636,746 0,5103559

10581,999 0,6267852 0,1087681 122294,68 81282,444 1,5045646 152075,8 97289,584 1,5631252
2576,5432 0,4346471 0,0407997 39628,408 37981,995 1,0433472 37027,963 63150,957 0,5863405
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13271,872 0,4618347 0,2061426 60749,893 54798,277 1,1086095 190732,44 64381,996 2,9625121
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5641,529

4735,4737 0,335829 0,0479105 54979,634 68201,131 0,8061396 68054,34 98839,925 0,6885309

1705,337

1808,5341

2293,5387

22696,151 0,4284434 0,0487143 276094,07 268455,03 1,0284555 326170,46 465903,22 0,700082
1418,3711 0,5618002 0,0622866 16159,61 11982,761 1,3485715 20383,665 22771,689 0,8951319
3402,5306 0,3132383 0,0629058 24623,251 32747,527 0,7519118 48898,377 54089,338 0,9040299
155,46452 0,4870534 0,0447366 2261,3426 1934,1838 1,1691457 2234,2085 3475,1117 0,642917
55,252079 0,4245227 0,0339946 939,39736 921,84171 1,0190441 794,03751 1625,3192 0,4885425

2823,869

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43132,058
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4758,1466 0,5820564 0,0522704 46764,738 33470,437 1,3971953 68380,177 91029,461 0,7511873
3524,7884 0,989312 0,0480553 51157,417 21541,863 2,3747908 50655,365 73348,584 0,6906114
8525,9307 0,3790165 0,0653913 71832,241 78953,115 0,9098088 122527,68 130383,18 0,9397506

701,78805 0,2639153 0,0285031 8939,3727 14110,758 0,6335147 10085,522 24621,426 0,4096238
8725,7137 0,3726689 0,1924162 38268,926 42779,038 0,8945719 125398,79 45348,119 2,7652479
3422,5635 0,342292 0,0647366 31129,089 37885,898 0,8216537 49186,272 52869,066 0,9303412
2252,1391 0,3514832 0,0573854 22506,097 26674,943 0,8437168 32365,895 39245,853 0,8246959

2506,5969 0,3334136 0,0562696 20344,701 25420,024 0,8003415 36022,753 44546,237 0,8086598
2044,7543 0,3778916 0,0540612 18358,33 20238,294 0,9071086 29385,53 37822,928 0,7769237
4594,6411 0,4339537 0,0723307 41511,364 39850,298 1,0416826 66030,411 63522,7 1,0394774
45685,293 0,2222547 0,0733854 506033,91 948498,36 0,5335106 656551,52 622539,42 1,0546345
33028,066 0,2401465 0,0688896 411004,61 712981,54 0,576459 474652,25 479434,63 0,990025
13721,151 0,2700916 0,0796393 146078,69 225311,7 0,6483405 197189,12 172291,11 1,1445113

8505,6242 0,4017397 0,0924028 58718,384 60888,787 0,9643546 122235,85 92049,443 1,3279368
1442,6049 0,3193457 0,035696 19387,669 25291,373 0,7665724 20731,934 40413,59 0,5129941
2312,5904 0,4144045 0,0444282 24937,159 25068,619 0,994756 33234,651 52052,311 0,6384856
1379,9662 0,2750315 0,0321503 17057,524 25836,969 0,6601984 19831,741 42922,286 0,4620383

14967,675 0,3437083 0,0945499 66328,729 80393,241 0,8250535 215103,14 158304,46 1,3587939
14042,521 0,8273083 0,0988266 104680,69 52711,712 1,9859095 201807,59 142092,48 1,4202552
3139,4504 0,9567749 0,0775595 29268,218 12743,667 2,2966873 45117,604 40477,937 1,1146221
16992,182 0,8358306 0,0663484 173891,59 86669,884 2,0063669 244197,69 256105,5 0,9535043

8481,3926 0,2861863 0,0614047 77911,419 113412,33 0,6869749 121887,61 138122,87 0,8824578
1395,8831 0,728168 0,0843142 12331,332 7054,8265 1,7479285 20060,486 16555,72 1,2116952
718,38607 0,367781 0,1176986 3951,0312 4475,3719 0,8828386 10324,055 6103,608 1,6914675
224,2891 0,2931787 0,0365977 2687,7578 3819,1408 0,7037598 3223,2988 6128,5039 0,525952

7273,4414 0,4692356 0,0660868 56954,033 50564,008 1,126375 104527,93 110058,95 0,9497449
499,98776 0,2883071 0,0218485 10538,832 15228,08 0,6920657 7185,4136 22884,34 0,3139882
7048,7417 0,6177324 0,0377819 88770,545 59865,474 1,4828337 101298,73 186564,08 0,5429702

28608,988 0,5609311 0,1280083 141866,46 105360,57 1,3464853 411144,89 223493,22 1,8396303
64,113542 0,4093328 0,035567 889,31913 905,08433 0,9825815 921,38719 1802,6112 0,5111403

35024,968	0,4669159	0,0761783	240574,09	214643,69	1,1208067	503350,09	459776,15	1,0947721
15981,667	0,5102415	0,0740381	121335,83	99065,229	1,2248074	229675,4	215857,4	1,0640145
1356,8391	0,403504	0,0388931	21218,008	21906,081	0,9685899	19499,377	34886,4	0,5589392
2363,2163	0,4124157	0,0360601	42001,071	42426,096	0,989982	33962,205	65535,505	0,518226
626,28833	0,6199586	0,0686599	6084,1781	4088,3417	1,4881775	9000,5017	9121,6025	0,9867237
1208,3829	0,5521166	0,0633258	16102,248	12149,647	1,3253264	17365,887	19081,99	0,9100669
3400,0361	0,5187312	0,0858352	32756,195	26306,256	1,2451865	48862,528	39611,212	1,233553
1445,3782	0,3721967	0,087411	14177,723	15868,72	0,8934383	20771,789	16535,428	1,2561991
2772,3181	0,3855355	0,0411775	39607,808	42798,088	0,9254574	39841,479	67326,01	0,5917695
15706,87								
19223,379								
50627,511								
12653,278	0,2411671	0,0708948	220470,48	380838,12	0,5789087	181842,52	178479,73	1,0188413
1677,4906	0,6487593	0,0734944	13121,432	8425,6917	1,5573121	24107,518	22824,727	1,0562018
2468,8252	0,594025	0,0782591	18750,95	13150,022	1,4259254	35479,928	31546,831	1,1246749
2151,6895	0,4787483	0,0321155	38363,84	33382,803	1,1492097	30922,315	66998,57	0,4615369
2404,898	0,4521099	0,1963732	12134,999	11181,592	1,0852657	34561,219	12246,567	2,822115
490,60754	0,3355409	0,0604379	4529,6763	5623,7976	0,805448	7050,6088	8117,5429	0,8685644
31313,735	0,2593645	0,0383888	389746,81	626008,2	0,6225906	450015,29	815700,75	0,5516916
11390,411	0,4356308	0,0528473	122939,18	117565,44	1,0457085	163693,63	215534,59	0,7594773
27525,454	0,2315771	0,0963145	145844,66	262363,17	0,5558885	395573,23	285787,34	1,3841524
274,88029	0,6618735	0,0564459	2675,0271	1683,686	1,5887922	3950,3539	4869,7981	0,8111946
85,051529	0,3204533	0,0657485	1705,8375	2217,588	0,769231	1222,2908	1293,5892	0,9448833
423,51972	0,3531361	0,0584618	6652,3843	7847,7142	0,8476843	6086,4778	7244,3822	0,8401652
5500,4652	0,369978	0,0700503	83483,077	94000,575	0,8881124	79048,17	78521,658	1,0067053
6487,3048	0,2469756	0,0890603	102909,91	173584,54	0,5928518	93230,218	72841,708	1,2799016
21286,035	0,4709612	0,0647647	202036,69	178711,74	1,1305172	305905,42	328667,45	0,9307445
10211,233	0,5297534	0,0620904	105961,6	83326,414	1,2716448	146747,46	164457,65	0,8923115
20674,511	0,5261591	0,0716714	196155,6	155307,18	1,2630169	297117,1	288462,52	1,0300024
6891,1022	0,583318	0,0816605	57147,164	40812,881	1,4002237	99033,264	84387,212	1,1735577
18039,34	0,4942785	0,0322132	292223,87	246292,9	1,1864892	259246,59	559998,81	0,4629413
8417,2077	0,323323	0,0446589	71067,509	91567,731	0,7761196	120965,2	188477,68	0,6418012
8771,4865	0,1853494	0,033808	89176,97	200433,1	0,4449214	126056,6	259450,04	0,4858608
13847,35	0,3288301	0,0430758	172674,61	218758,46	0,7893391	199002,74	321464,82	0,6190498
1590,4276	0,4819781	0,0543563	21387,508	18485,908	1,1569629	22856,319	29259,288	0,7811646
1333,42	0,4674976	0,0320325	27031,506	24087,892	1,1222031	19162,818	41627,125	0,4603445
1046,9675	0,4670369	0,0476007	14255,192	12715,393	1,1210972	15046,158	21994,797	0,6840781
3147,7254	0,4066559	0,0848299	27178,37	27842,247	0,9761558	45236,526	37106,335	1,2191052
582,99057	0,2769441	0,0329169	6166,5842	9275,994	0,6647896	8378,2618	17710,998	0,4730542
10780,745	0,4458324	0,0549937	134213,22	125409,83	1,070197	154932,02	196035,95	0,7903245
1034,2956	0,3802004	0,0341816	17727,616	19424,314	0,9126508	14864,048	30258,818	0,4912303
2878,5922	0,3982109	0,0331109	33827,261	35388,453	0,9558841	41368,763	86937,846	0,475843
915,31405	0,4026295	0,0462899	9064,6272	9378,9089	0,9664906	13154,142	19773,495	0,6652411

6378,23	0,3068735	0,0583074	54333,192	73758,785	0,7366335	91662,685	109389,7	0,8379462
46134,11	0,3494805	0,120329	232590,02	277252,89	0,8389093	663001,56	383399,63	1,7292702
464,41838	0,491021	0,0402265	6096,2336	5172,1301	1,1786698	6674,2397	11545,087	0,5781021
3742,6205	0,4091929	0,0399692	46917,639	47765,682	0,9822458	53785,869	93637,623	0,5744045
3828,4125	0,5076014	0,0611996	35108,046	28813,221	1,21847	55018,801	62556,154	0,8795106
42615,831								
126658,42	0,5717524	0,3848424	581643,81	423796,21	1,3724611	1820230,8	329117,64	5,5306389
191052,95	0,6474194	0,3825882	940085,09	604908,06	1,5540958	2745656,1	499369,63	5,4982442
77372,489	0,6102569	0,3392191	356321,1	243240,99	1,4648892	1111933,9	228090,01	4,8749784
153515,45	0,5428265	0,366676	581596,98	446343,28	1,3030262	2206198	418667,78	5,2695671
371645,15	0,4665662	0,3521012	1489317,6	1329786,7	1,1199673	5340979	1055506,5	5,0601099
878142,2	0,4624644	0,3086638	3757190,6	3384487,4	1,110121	12619939	2844979,6	4,4358627
4108,542	0,4850776	0,0545689	47087,046	40438,792	1,1644029	59044,592	75290,955	0,7842189
3630,5954	0,3158018	0,0597614	32974,15	43497,764	0,7580654	52175,936	60751,482	0,8588422
7859,6742	0,2743191	0,1040322	46550,874	70693,549	0,6584883	112952,79	75550,38	1,4950658
2633,316	0,5469698	0,0572272	32796,749	24979,02	1,3129718	37843,856	46015,135	0,8224219
6419,4513	0,4886349	0,0728048	53207,96	45362,819	1,1729421	92255,084	88173,417	1,0462914
11049,374	0,3970266	0,0465062	120478,86	126415,15	0,9530413	158792,53	237589,31	0,6683488
10064,92	0,3431504	0,0935082	61309,936	74431,066	0,8237143	144644,77	107636,75	1,3438233
16431,49	0,2930448	0,0709125	110322,3	156832,91	0,7034385	236139,88	231715,03	1,0190961
22162,004	0,3614368	0,0482024	234249,68	269994,28	0,8676098	318494,12	459770,11	0,6927247
7241,196	0,3475949	0,050087	70313,917	84270,553	0,834383	104064,52	144572,35	0,7198093
3986,6592	0,43835	0,0829961	34206,082	32508,003	1,0522357	57292,993	48034,285	1,1927521
4793,9194	0,5652753	0,0827831	28322,067	20872,423	1,3569132	68894,274	57909,404	1,1896906
6132,9797	0,606108	0,1070664	44596,182	30651,772	1,45493	88138,149	57282,011	1,5386706
2311,5497	0,6955088	0,0968681	10853,697	6501,0425	1,6695318	33219,695	23862,852	1,3921092
1832,0666	0,6985352	0,0853932	10112,506	6030,8484	1,6767966	26328,957	21454,486	1,2272006
760,2446	0,7347873	0,0887941	4121,9531	2336,9496	1,7638177	10925,611	8561,8867	1,2760752
3261,0807	0,5159716	0,1279276	15525,616	12535,191	1,2385624	46865,575	25491,608	1,8384708
273,36154	0,7017492	0,0790933	1853,9204	1100,5685	1,6845116	3928,5277	3456,1906	1,1366641
18790,99	0,893122	0,1166914	153700,37	71692,227	2,1438918	270048,68	161031,52	1,6769927
10155,074	1,0648789	0,1345124	81784,882	31994,9	2,556185	145940,39	75495,446	1,9331019
21417,273	1,4160881	0,1494225	178366,16	52472,302	3,3992439	307791,47	143333,61	2,1473782
37154,491	0,8788826	0,1300453	321433,56	152359,05	2,109711	533953,84	285704,13	1,8689049
1960,8742	0,3871979	0,0451583	27417,299	29498,479	0,9294479	28180,074	43422,184	0,6489787
3381,8941	0,2899452	0,0275222	68382,206	98250,587	0,6959979	48601,806	122878,6	0,395527
4282,1039	0,2524359	0,0389659	55455,627	91517,151	0,6059588	61538,881	109893,57	0,5599862
7363,9115	0,2141443	0,0548584	55805,561	108562,24	0,5140421	105828,09	134234,86	0,7883801
2408,6936	0,2520317	0,0394801	29069,838	48050,222	0,6049886	34615,768	61010,263	0,5673761
16669,149	0,446767	0,0660325	146413,77	136523,94	1,0724403	239555,33	252438,54	0,9489649
14152,302	0,4181426	0,1470327	67986,791	67734,209	1,003729	203385,26	96252,73	2,1130337
9899,4085	0,3292881	0,0490796	88326,75	111744	0,7904384	142266,17	201700,92	0,7053323
122478,57	0,5996805	0,21087	889308,36	617789,3	1,4395011	1760161,5	580825	3,0304506

84519,047	0,5890578	0,1914616	637620,68	450933,39	1,4140019	1214638,4	441441,31	2,7515285
19415,479	0,5532139	0,2496798	137025,04	103184,58	1,3279604	279023,32	77761,502	3,5881935
335183,11	0,5527156	0,219715	2287382,6	1724030,8	1,3267644	4816976,5	1525535,5	3,1575643
45894,6	0,4537323	0,0982348	364291,4	334469,96	1,0891603	659559,51	467192,76	1,4117503
15213,204	0,683819	0,1831077	118156,1	71981,832	1,6414711	218631,68	83083,368	2,6314735
141460,04	0,4755117	0,1530779	1012735,2	887243,16	1,1414404	2032947,6	924104,88	2,19991

3989,8804	0,2822257	0,0303069	52868,743	78038,757	0,6774678	57339,286	131649,18	0,4355461
4657,3515	0,3093319	0,0399158	75446,543	101606,74	0,7425349	66931,632	116679,25	0,5736378
1832,3677	0,2941341	0,0432194	28324,368	40116,471	0,7060533	26333,284	42396,922	0,6211131
4129,4796	0,251922	0,0278533	65065,705	107595,48	0,6047253	59345,491	148258,25	0,4002846

6408,1069	0,4884406	0,1137853	50239,868	42849,389	1,1724757	92092,051	56317,541	1,6352285
9473,8348	0,4691933	0,0896338	95696,471	84967,344	1,1262735	136150,18	105694,86	1,2881437
10738,631	0,5154521	0,1092748	92010,617	74363,111	1,2373153	154326,79	98271,806	1,5704075
3671,9093	0,5045671	0,0633052	37172,067	30690,625	1,2111864	52769,666	58003,274	0,9097705
4275,7551	0,3871852	0,0300866	86302,566	92856,62	0,9294175	61447,642	142115,08	0,4323795
3158,0361	0,460499	0,0329113	61087,276	55262,436	1,1054033	45384,702	95955,933	0,4729744

7651,9325	0,6310558	0,0577549	129781,59	85674,833	1,5148157	109967,29	132489,78	0,8300058
888,99305	0,6697185	0,0549451	17200,97	10699,626	1,6076235	12775,878	16179,658	0,789626
10467,169	0,5118702	0,085895	113145,48	92084,24	1,2287171	150425,56	121859,98	1,2344131
10010,011	0,5335519	0,0795567	114215,04	89177,343	1,280763	143855,66	125822,4	1,1433231

2372,9433	0,6496149	0,0542902	31103,072	19945,974	1,5593659	34101,992	43708,472	0,7802147
3027,4869	0,591959	0,0462684	42911,604	30198,893	1,4209661	43508,556	65433,193	0,664931
13828,157	0,5964925	0,0477285	175605,86	122642,76	1,4318485	198726,92	289725,48	0,6859145
3629,1159	0,4351282	0,0629435	38344,664	36710,956	1,0445019	52154,674	57656,705	0,9045726
4409,7066	0,5193077	0,0908783	44447,439	35655,777	1,2465705	63372,683	48523,216	1,3060281
10689,676	0,4710009	0,0515928	123704,72	109413,9	1,1306125	153623,24	207193	0,74145

6698,3837
13356,955
9367,9465
27294,295

3074,7359	0,402628	0,0452485	28313,99	29295,779	0,966487	44187,58	67952,162	0,6502748
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2395,3318	0,640316	0,0359161	34912,335	22713,94	1,5370444	34423,742	66692,49	0,5161562
677,00452	0,3201513	0,0258454	9401,6382	12233,655	0,7685061	9729,3531	26194,396	0,3714288
11331,853	0,4660165	0,056951	100294,39	89656,797	1,1186479	162852,09	198975,35	0,8184536

46476,465	0,449287	0,0679461	358490,38	332400,42	1,0784895	667921,61	684019,99	0,976465
6418,7767	0,4012974	0,085704	42144,725	43750,684	0,9632929	92245,389	74894,71	1,2316676
42901,429	0,3218033	0,0407618	526966,52	682182,34	0,7724717	616544,12	1052491,1	0,5857951
43360,764	0,3967883	0,0477921	665901,53	699131,85	0,9524692	623145,3	907278,54	0,6868291
22985,645	0,4663446	0,0684465	224561,84	200602,79	1,1194353	330330,82	335819,1	0,983657
3353,1945	0,3556898	0,0296248	49434,824	57898,793	0,8538144	48189,358	113188,92	0,4257427
153306,42	0,4512192	0,1290912	1060473	979084,1	1,0831276	2203194,1	1187582,7	1,8551921

22132,894	0,6676849	0,1771289	96560,495	60247,061	1,602742	318075,78	124953,59	2,5455514
13888,107	0,8626567	0,2317807	56809,111	27433,924	2,0707614	199588,48	59919,163	3,3309624
11254,476	0,7928341	0,1865705	52201,105	27428,706	1,903156	161740,09	60322,929	2,6812373

19422,784	0,7680435	0,2820486	74014,827	40145,865	1,8436476	279128,3	68863,255	4,0533707
5386,0106	0,9374147	0,1032638	58382,07	25945,118	2,2502141	77403,323	52157,8	1,484022
10640,045	0,7038124	0,0807452	112959,28	66861,015	1,6894641	152909,99	131773,11	1,1604036
7643,6567	0,5435763	0,0848105	74172,111	56844,453	1,3048259	109848,36	90126,255	1,2188275
8856,7562	0,5019511	0,0871506	73178,859	60734,036	1,2049069	127282,03	101625,82	1,2524576
852,51293	0,3937183	0,057332	5977,4003	6324,6232	0,9450998	12251,616	14869,765	0,823928
2523,3398	0,4368553	0,0631822	16705,131	15930,163	1,0486478	36263,367	39937,501	0,9080029
3936,4519	0,5258251	0,0772851	30788,11	24392,127	1,262215	56571,455	50934,187	1,1106775
1499,3237	0,6246124	0,0803269	13306,4	8874,7859	1,4993488	21547,05	18665,27	1,1543926
1760,5873	0,5139292	0,0816963	14617,769	11849,11	1,2336597	25301,715	21550,4	1,1740717
1916,7306	0,3726838	0,1052768	9668,2155	10807,214	0,8946076	27545,679	18206,574	1,5129523
3808,9693	0,4231566	0,058305	24042,702	23669,555	1,0157649	54739,38	65328,386	0,8379111
8432,1483	0,3102323	0,0311835	118815,97	159549,61	0,7446961	121179,91	270403,8	0,4481443
2363,2383								
1970,0712								
10215,177								
1885,1785								
4217,9794								
20174,986	0,7474064	0,0596909	150932,88	84126,917	1,7941092	289938,34	337990,9	0,8578288
6425,3086	0,6746083	0,0692965	54920,229	33914,748	1,6193613	92339,26	92721,933	0,9958729
25025,104	0,7500981	0,0895376	167980,92	93293,169	1,8005704	359640,25	279492,7	1,2867608
11384,823	0,5977543	0,0665163	78600,877	54778,809	1,4348774	163613,33	171158,52	0,955917
6301,6255	0,4781543	0,068505	39834,255	34705,364	1,1477838	90561,788	91987,825	0,9844975
3455,9874	0,5325459	0,0553473	24928,311	19500,41	1,2783481	49666,613	62441,816	0,7954063
8768,0587								
3730,2563								
1987,9944								
35613,659								
65778,532								
9476,2992	0,5102988	0,0519932	111658,74	91154,071	1,2249452	136185,59	182260,32	0,7472037
6738,0098	0,2685218	0,0584821	60375,585	93667,69	0,6445722	96833,145	115214,88	0,840457
6983,2886	0,3476918	0,0675947	54240,908	64989,091	0,8346156	100358,09	103311,19	0,9714154
3944,5866								
1402,9235	0,7130654	0,1039705	6705,1166	3917,2826	1,7116755	20161,665	13493,477	1,4941787
1196,9468	0,6884937	0,1012	5988,481	3623,4699	1,6526923	17201,536	11827,54	1,4543629
2725,1369	0,7145005	0,0941156	16313,218	9511,4124	1,7151205	39163,431	28955,214	1,3525519
3024,5628	0,6557406	0,0932698	17558,457	11154,811	1,5740703	43466,534	32428,103	1,3403971
1858,1377	0,7316018	0,1040401	9445,3311	5378,3664	1,756171	26703,629	17859,815	1,4951796
1598,9072	0,5774117	0,1072832	8346,4878	6021,7969	1,386046	22978,181	14903,613	1,541786
236,49344	0,7910556	0,0942484	1953,5038	1028,7627	1,8988867	3398,6896	2509,2555	1,3544613
1002,634	0,6492678	0,1167189	4728,2666	3033,7937	1,5585327	14409,033	8590,1576	1,6773887
15386,375	0,8199077	0,1010286	120642,64	61297,646	1,9681448	221120,35	152297,18	1,4519005
10976,856	0,5682529	0,0938964	81173,958	59509,05	1,3640607	157750,36	116903,9	1,349402
4559,8937	0,3792169	0,0662165	43124,25	47374,185	0,9102901	65531,049	68863,363	0,9516098

1040,5955	0,3606239	0,0349803	11988,271	13848,729	0,8656586	14954,584	29748,077	0,5027076
5322,8647	0,4154795	0,0418339	60692,21	60854,301	0,9973364	76495,841	127238,06	0,6012025
23385,038	0,3427431	0,3331491	75347,422	91581,461	0,8227366	336070,56	70193,905	4,7877456
68314,927	0,3233099	0,2624459	241072,23	310624,8	0,7760881	981766,05	260300,94	3,7716577
267678,46	0,3534962	0,2851574	1021548,9	1203877,7	0,8485488	3846855,1	938704,35	4,0980476
77016,504	0,2413276	0,2453613	285603,69	493020,15	0,5792941	1106818	313890,13	3,5261318
518169,93	0,3127524	0,2671294	1849108,7	2463029,8	0,7507455	7446712,9	1939771,6	3,8389637
168277,79	0,3320007	0,2929049	589069,05	739154,44	0,7969499	2418350,3	574513,32	4,2093894
17694,367	0,4546021	0,0821586	158272,73	145038,26	1,0912481	254288,91	215368,51	1,1807154
15374,226	0,6177721	0,0808561	157727,17	106361,93	1,4829289	220945,75	190142,99	1,1619979
3019,6291	0,4268478	0,0662202	36708,876	35826,63	1,0246254	43395,63	45599,834	0,951662
1186,7968	0,498171	0,0466978	15792,484	13206,263	1,1958329	17055,669	25414,415	0,6711021
3226,2246	0,3334286	0,035419	49345,518	61652,8	0,8003776	46364,651	91087,296	0,5090134
1421,9204	0,2652723	0,0617667	19861,064	31190,233	0,6367719	20434,673	23020,828	0,8876602
29142,503	0,5429197	0,0969828	224853,15	172532,65	1,3032499	418812,13	300491,41	1,3937574
1590,8915	0,4739541	0,1037827	5138,8133	4516,838	1,1377015	22862,987	15329,062	1,4914798
3725,3187	0,5926703	0,0442784	51540,889	36228,192	1,4226735	53537,222	84134,037	0,6363325
8534,2587	0,7614477	0,2164872	94575,404	51742,341	1,8278146	122647,36	39421,543	3,111176
3868,2643	0,3401228	0,0596277	53089,951	65025,617	0,8164467	55591,519	64873,588	0,8569207
7046,0142	0,562187	0,0730779	64662,307	47915,758	1,3494998	101259,53	96417,881	1,0502153
16963,161	0,5583856	0,1701109	78133,754	58292,462	1,3403749	243780,62	99718,233	2,4446946
9688,1701	0,2504799	0,0424568	88711,406	147541,58	0,6012638	139230,43	228188,65	0,6101549
5122,2229	0,3721218	0,0404684	69201,992	77471,398	0,8932586	73612,382	126573,25	0,5815793
11887,385	0,4236479	0,1544972	57506,796	56548,62	1,0169443	170835,74	76942,401	2,2203068
13252,433	0,4978491	0,1728534	59053,377	49414,559	1,1950603	190453,09	76668,627	2,4841072
5755,3187	0,4480542	0,1886682	23849,484	22174,627	1,0755303	82710,716	30504,976	2,7113844
11710,485	0,4689361	0,1789344	49955,518	44379,023	1,1256561	168293,47	65445,685	2,5714984
2528,289	0,5268141	0,1808972	11856,376	9375,6745	1,2645892	36334,494	13976,383	2,5997065
5254,6143	0,4925343	0,156573	25970,157	21965,747	1,1823024	75515,002	33560,162	2,2501382
4812,9813	0,4663348	0,17281	21654,062	19344,142	1,1194119	69168,216	27851,283	2,483484
38721,821	0,4014779	0,0485437	448366,62	465242,69	0,9637263	556478,22	797669,54	0,69763
30627,876	0,388691	0,0480441	330032,5	353720,45	0,933032	440158,69	637495,42	0,69045
24556,589	0,5655093	0,0499208	339580,78	250156,22	1,3574748	352907,13	491910,58	0,7174213
10678,262	0,5561337	0,0618069	130378,23	97663,836	1,3349694	153459,22	172768,25	0,8882374
4833,1379	0,4188412	0,0495236	41821,117	41596,244	1,0054061	69457,891	97592,572	0,7117129
6558,3603	0,3394337	0,1100606	41947,112	51481,956	0,8147925	94251,37	59588,608	1,5817012
22335,601	0,3352944	0,1306344	106315,1	132092,02	0,8048563	320988,92	170977,97	1,87737
50650,405	0,4656983	0,2227861	304867,9	272718,72	1,117884	727906,04	227349,9	3,2016994
42074,319	0,3814081	0,1159283	331009,02	361541,28	0,9155497	604657,57	362933,86	1,6660269
16862,498	0,3844707	0,1992081	101018,3	109457,31	0,9229014	242333,98	84647,666	2,8628549
15747,527	0,4040181	0,2409854	87610,451	90336,452	0,9698239	226310,53	65346,396	3,4632442
25217,844	0,469226	0,2632671	139632,53	123968,81	1,1263521	362410,15	95788,071	3,7834581
6426,0663	0,2089363	0,0221633	72292,796	144141,53	0,5015404	92350,15	289941,16	0,3185134

4454,9009	0,3568535	0,0410782	59260,804	69180,787	0,8566078	64022,179	108449,18	0,5903427
1595,6413	0,2360233	0,036141	12845,68	22673,064	0,5665613	22931,247	44150,41	0,5193892
2767,3476	0,3984113	0,0618109	20022,505	20936,045	0,9563652	39770,047	44771,188	0,8882955
6125,8809	0,3852079	0,0413923	64996,091	70291,051	0,9246709	88036,131	147995,79	0,5948556
762,25161	0,304341	0,0316387	6599,8376	9034,012	0,7305544	10954,454	24092,352	0,454686
37125,106	0,4446562	0,1591742	161036,92	150872,14	1,0673735	533531,54	233235,77	2,2875202
5432,6006	0,4454934	0,085019	48028,95	44912,763	1,0693831	78072,875	63898,627	1,221824
4600,5563	0,447127	0,0665193	44863,153	41799,094	1,0733044	66115,418	69161,183	0,9559614
3052,1706	0,3570082	0,0503916	33354,131	38920,585	0,8569792	43863,29	60569,02	0,7241869
15706,87								
19223,379								
50627,511								
9754,1738	0,4713217	0,1228329	54754,167	48395,796	1,1313827	140178,98	79410,09	1,765254
327905,9	0,8468306	0,3141617	2108598,2	1037302	2,0327716	4712394,4	1043748,9	4,5148737
9629,0265	0,8916325	0,2463577	79967,247	37362,352	2,1403162	138380,46	39085,547	3,540451
28002,062	0,6648901	0,1494782	202325,99	126768,03	1,5960332	402422,64	187332,03	2,1481785
20318,382	0,7366516	0,2411384	99987,502	56544,653	1,7682928	291999,11	84260,249	3,4654432
21293,577	0,9006949	0,2019911	130110,58	60178,703	2,1620702	306013,81	105418,38	2,9028508
80125,088	0,6951834	0,1834025	687298,93	411864,38	1,6687506	1151492	436881,15	2,63571
28098,349	0,4564569	0,0717837	215106,28	196318,51	1,0957005	403806,4	391430,91	1,031616
1540,93	0,3940902	0,0461746	16737,567	17693,128	0,9459925	22144,981	33371,824	0,6635832
12535,891	0,4126418	0,0288437	208126,54	210117,46	0,9905247	180155,53	434614,44	0,414518
3331,3029	0,3849029	0,0383939	40880,84	44246,258	0,9239389	47874,751	86766,452	0,5517657
1108,2521	0,4113019	0,0482935	13005,012	13172,188	0,9873084	15926,89	22948,254	0,6940349
13338,989	0,183112	0,0655626	82320,652	187283,71	0,4395505	191697	203454,27	0,9422118
8065,1692	0,3636283	0,0535137	71371,273	81766,177	0,8728704	115905,99	150712,26	0,7690548
1890,4786	0,2404071	0,0368021	22217,697	38499,91	0,5770844	27168,407	51368,837	0,5288889
1554,0114	0,4878544	0,0583419	19349,768	16523,174	1,1710685	22332,976	26636,28	0,838442
691,27154	0,3174789	0,0391779	9339,6628	12255,31	0,7620911	9934,387	17644,434	0,5630324
6957,1078	0,3029101	0,3701035	10909,688	15003,983	0,7271195	99981,842	18797,735	5,318824
7381,9301	0,2750677	0,4369091	8382,3065	12694,976	0,6602854	106087,04	16895,802	6,2788993
5413,194	0,3861246	0,0617392	37716,789	40692,57	0,9268716	77793,98	87678,443	0,8872646
7583,1479	0,3320797	0,0554662	77621,698	97375,298	0,7971395	108978,78	136716,63	0,7971142
8257,3752	0,2872267	0,0502845	84804,852	122999,63	0,6894724	118668,22	164213,04	0,722648
24744,939	0,4115707	0,0944235	179416,43	181604,14	0,9879534	355613,95	262063,48	1,3569764
633,24765	0,9853434	0,0369212	10700,228	4523,9038	2,3652642	9100,5154	17151,31	0,5306018
2998,6718	0,523121	0,0277138	41245,269	32845,805	1,2557241	43094,45	108201,57	0,3982793
1275,3693	0,4142989	0,0386608	16114,465	16203,543	0,9945025	18328,561	32988,663	0,5556018
2809,4674	0,5707183	0,0457558	39172,639	28593,608	1,3699788	40375,358	61401,369	0,6575645
9598,0731	0,268149	0,0948786	62874,371	97679,942	0,6436774	137935,63	101161,65	1,363517
1806,0865	0,4766846	0,0602956	19082,873	16677,1	1,1442561	25955,593	29953,846	0,8665195

30102,806	0,6750375	0,2267556	106411,04	65669,955	1,6203915	432612,82	132754,39	3,2587458
2240,8204	0,8313647	0,1558508	16015,127	8025,0308	1,9956468	32203,231	14377,981	2,2397603
2582,1517	0,6323717	0,1652878	16726,15	11018,73	1,5179745	37108,565	15622,159	2,37538
3914,1565	0,5006659	0,054101	31402,031	26128,69	1,2018219	56251,043	72348,993	0,7774959
4196,1172	0,4043963	0,088179	33401,454	34408,527	0,9707319	60303,151	47586,364	1,267236
5385,6604	0,2443305	0,0343617	67889,854	115753,76	0,5865024	77398,29	156734,31	0,4938184
7756,7558	0,23896	0,0793229	60879,786	106134,33	0,5736107	111473,73	97787,11	1,1399634
9311,6467	0,2877691	0,0430277	120238,79	174063,79	0,6907743	133819,34	216410,31	0,6183594
15791,653	0,3450318	0,0417426	233946,02	282464,87	0,8282305	226944,67	378310,43	0,5998901
15356,585	0,3328722	0,0395912	229963,34	287798,78	0,7990421	220692,23	387878,51	0,5689726
1879,4178	0,2901108	0,0414302	26603,557	38201,789	0,6963956	27009,449	45363,48	0,5954007
19084,675	0,2816608	0,0515328	219383,47	324478,12	0,6761118	274269,29	370340,13	0,7405875
36476,802	0,9104945	0,267957	161849,55	74052,906	2,1855936	524214,65	136129,33	3,8508574
12059,209	0,5425115	0,1216298	70538,19	54165,57	1,3022699	173305,05	99146,846	1,7479633
54907,033	0,8082362	0,270532	259349,62	133676,55	1,940128	789078,81	202959,5	3,8878633
1946,7314	0,8853975	0,2392694	9093,8873	4278,7725	2,1253495	27976,825	8136,1493	3,438583
2235,2144	0,7972615	0,0518506	17879,671	9342,5768	1,9137836	32122,666	43108,718	0,7451548
7722,1334	0,435706	0,1434164	67793,886	64819,388	1,045889	110976,16	53844,135	2,0610631
4458,0728	0,4448014	0,0552694	31677,178	29668,002	1,067722	64067,763	80660,76	0,7942866
3700,3746	0,5028318	0,1050261	24294,548	20127,692	1,207021	53178,746	35232,892	1,5093495
644,46517	0,3040767	0,0280786	11751,632	16099,892	0,72992	9261,7244	22952,211	0,4035221
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858,80187	0,5824364	0,0536128	9805,46	7013,3806	1,3981075	12341,995	16018,59	0,7704795
2671,8778	0,5232415	0,0466747	36071,363	28718,933	1,2560133	38398,034	57244,72	0,6707699
1269,3427	0,5343407	0,0390898	20681,275	16123,785	1,2826564	18241,951	32472,503	0,5617661
3073,6467	0,5340057	0,0361399	52925,801	41288,533	1,2818523	44171,928	85048,63	0,5193726
1207,8449	0,4921378	0,039606	21154,404	17906,966	1,1813506	17358,155	30496,549	0,5691842
3664,6316	0,3827117	0,0492636	48034,865	52286,887	0,918679	52665,076	74388,197	0,7079762
1111,6332	0,3663169	0,0507773	15257,704	17351,628	0,8793241	15975,48	21892,31	0,7297302
285,59725	0,2879921	0,0413183	4249,7041	6147,323	0,6913097	4104,3693	6912,1299	0,5937923
2391,3236	0,3798478	0,0587055	26865,007	29463,565	0,9118043	34366,139	40734,22	0,8436675
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1208,9592	0,4144894	0,0397918	11662,422	11721,501	0,9949597	17374,17	30382,098	0,5718555
1072,9853	0,536659	0,042126	11729,481	9105,1756	1,2882213	15420,064	25470,838	0,6054007
1061,6255	0,501731	0,0758535	7332,9953	6088,6133	1,2043786	15256,811	13995,731	1,0901046
10213,993	0,4755716	0,0291981	125855,03	110245,95	1,1415842	146787,12	349816,64	0,4196116
1451,3297	0,3289961	0,0535216	11441,617	14487,871	0,7897376	20857,319	27116,719	0,7691682
1114,4571	0,3332793	0,0544766	8138,5848	10172,988	0,8000191	16016,062	20457,526	0,7828934
893,88012	0,3044583	0,0753797	5573,8814	7626,7194	0,730836	12846,111	11858,374	1,0832945
1761,6495	0,2423834	0,0453244	12778,559	21962,76	0,5818285	25316,98	38867,554	0,6513654
1672,9008	0,3771262	0,0764064	11177,426	12347,044	0,9052714	24041,558	21894,778	1,0980498

8018,7817	0,2890416	0,0599662	73134,628	105407,29	0,6938289	115239,35	133721,67	0,8617851
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1108,3358	0,2385688	0,0421458	6587,9214	11503,834	0,5726718	15928,092	26297,65	0,605685

6698,3837	0,4426152	0,0457934	90787,639	85449,268	1,0624742	96263,672	146274,1	0,6581047
13356,955	0,5979008	0,0381406	236770,97	164970,86	1,4352291	191955,19	350203,5	0,5481247
9367,9465	0,3602977	0,0475324	115166,08	133159,18	0,8648753	134628,44	197085,63	0,6830962

27294,295

1484,1852	0,3284592	0,0445798	12725,135	16139,458	0,7884487	21329,491	33292,792	0,6406639
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1449,9684	0,2138594	0,0485454	30419,564	59256,032	0,5133581	20837,756	29868,275	0,6976552
754,85365	0,2038311	0,0471637	14328,872	29285,283	0,4892858	10848,137	16004,968	0,6777981

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31576,923	0,3289528	0,0574784	314807,69	398675,58	0,7896338	453797,61	549370,16	0,8260325
21638,952	0,3589329	0,0637742	200832,04	233092,18	0,8615992	310977,25	339305,8	0,9165103
2244,3985	0,3582978	0,0514459	28734,827	33409,685	0,8600748	32254,652	43626,416	0,7393377
7730,7489	0,4563349	0,0757168	84781,141	77396,892	1,0954076	111099,98	102100,8	1,0881401
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1172,082	0,3722756	0,0256365	22277,035	24928,766	0,8936277	16844,2	45719,354	0,368426
149,32835	0,2429649	0,0423358	1036,366	1776,9597	0,5832242	2146,0244	3527,2318	0,608416

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2771,9147	0,4132846	0,0827359	24037,769	24229,971	0,9920676	39835,682	33503,183	1,1890119
16037,198	0,4548508	0,1014215	116887,36	107054,89	1,0918452	230473,44	158124,18	1,4575471
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10441,591	0,4431744	0,1056331	52737,57	49573,931	1,0638166	150057,97	98847,726	1,5180721
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31009,46	0,4872434	0,0570036	278094,99	237768,93	1,1696019	445642,5	543991,31	0,8192089
4344,3063	0,4321901	0,0693984	31293,749	30164,124	1,0374493	62432,804	62599,497	0,9973372

26285,086	0,335052	0,109674	159851,99	198753,01	0,8042746	377747,67	239665,55	1,576145
21885,393	0,5662952	0,6569692	63933,782	47032,218	1,3593614	314518,9	33312,663	9,4414218
20450,544	0,5535967	0,6985326	56621,725	42608,624	1,3288795	293898,44	29276,437	10,038737
633119,94	0,3222824	0,1984659	3743138,6	4838460,5	0,7736218	9098680,1	3190069,4	2,8521888

28202,111	0,4633572	0,2464689	56381,622	50690,856	1,1122642	405297,58	114424,61	3,5420491
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52870,394	0,4014685	0,3267543	67561,339	70105,931	0,9637036	759809,9	161804,73	4,6958448

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526,35523 0,3016284 0,0280515 7338,8083 10135,876 0,7240428 7564,3453 18763,861 0,4031337

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11305,721 0,3923827 0,0495639 83437,916 88585,282 0,9418937 162476,54 228103,87 0,7122919

12304,66 0,4883826 0,0586398 90583,365 77267,39 1,1723363 176832,48 209834,47 0,8427237

5658,6736 0,483584 0,0827667 24591,678 21184,792 1,1608175 81321,812 68368,968 1,189455

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10393,921 0,552424 0,1038098 81494,554 61455,958 1,3260643 149372,9 100124,64 1,4918694

5728,8654 0,4570303 0,075212 46192,486 42105,059 1,0970768 82330,55 76169,542 1,0808854

281,77823	0,3787388	0,0654729	2811,2449	3092,1945	0,9091423	4049,4854	4303,7359	0,9409233
26809,573	0,5201178	0,1589458	139489,75	111724,53	1,248515	385285,18	168671,2	2,284238
53012,794	1,1042755	0,1481017	537641,26	202825,75	2,6507544	761856,35	357948,7	2,1283953
53549,169								
7579,1722								
14439,705								
4983,1864								
3645,9868								
10814,251								
3573,6876								
972,42614								
2383,5149								
17625,145								
7087,3579	0,4474268	0,0350799	93805,645	87340,356	1,0740241	101853,69	202034,53	0,50414
8984,8107	0,3564975	0,0427215	86324,541	100875,5	0,8557533	129122,32	210311,14	0,6139586
18229,937	0,7304959	0,0505978	306909,04	175024,89	1,7535165	261985,69	360290,81	0,7271506
6594,9691	0,4173126	0,0330796	120712,74	120503,48	1,0017366	94777,482	199366,64	0,4753929
59374,581	0,4159496	0,2622242	235536,08	235898,25	0,9984647	853282,74	226426,77	3,768471
35394,95	0,4487881	0,1810802	202975,14	188412,39	1,0772919	508667,17	195465,63	2,6023356
22183,697	0,4324056	0,1400296	138722,09	133647,94	1,0379665	318805,88	158421,49	2,0123904
31152,72	0,3102626	0,2485581	126503,71	169856,36	0,7447688	447701,31	125333,76	3,5720729
2934,8977	0,3016761	0,0557205	30773,207	42495,189	0,7241574	42177,94	52671,768	0,8007694
5006,8689	0,5177713	0,0830724	45165,766	36339,534	1,2428824	71954,61	60271,154	1,1938482
2110,105	0,4077045	0,0314155	31220,177	31900,518	0,978673	30324,697	67167,673	0,4514776
679,28223	0,3813169	0,0237375	12883,213	14074,923	0,915331	9762,0866	28616,425	0,3411358
1749,9493	0,3987245	0,0373335	22807,151	23829,013	0,9571169	25148,835	46873,38	0,536527
9077,2154	0,3727903	0,0984658	54806,039	61245,15	0,8948633	130450,29	92186,489	1,4150695
14791,16	0,3057027	0,1168368	74093,892	100969,7	0,733823	212566,41	126596,73	1,679083
1899,6441	0,4840327	0,0403982	15036,887	12941,694	1,1618948	27300,126	47023,042	0,5805691
27540,093	0,4145642	0,0508117	225081,82	226181,21	0,9951393	395783,61	542002,73	0,7302244
9243,4841	0,5805694	0,0358277	114951,88	82484,025	1,3936259	132839,77	257998,52	0,5148858
3420,8334	0,5701888	0,0325332	51927,091	37938,768	1,3687079	49161,41	105148,93	0,4675407
3944,6645	0,7340144	0,039109	64863,316	36813,111	1,7619624	56689,479	100863,37	0,5620423
1518,4044	0,7323135	0,0396555	21215,282	12068,678	1,7578794	21821,261	38289,87	0,5698964
2169,2009	0,4701381	0,0518173	15669,638	13884,859	1,1285414	31173,974	41862,522	0,744675
328,201	0,2203063	0,1190711	1693,6535	3202,621	0,5288336	4716,6353	2756,3449	1,711192
28178,663	0,3114923	0,1652647	192007,35	256790,22	0,7477207	404960,61	170506,27	2,3750481
10174,234	0,5160939	0,0861692	74924,271	60478,6	1,2388559	146215,73	118072,76	1,2383529
37800,009	0,748221	0,1368155	146197,06	81398,552	1,7960646	543230,7	276284,63	1,9661995
9908,4651	0,4419859	0,0453905	95571,047	90079,474	1,0609636	142396,33	218294,01	0,6523144
10468,849								

9316,2377	0,376163	0,0492061	75408,179	83512,269	0,9029593	133885,32	189330,79	0,7071503
12844,341								
31077,884								
23015,105								

1657,2929	0,5620102	0,0363644	25776,827	19107,029	1,3490756	23817,252	45574,554	0,5225998
1440,9685	0,526046	0,0390031	20812,921	16482,279	1,2627453	20708,417	36944,929	0,5605212

34985,194	1,0540154	0,2288319	231885,16	91650,304	2,5301079	502778,48	152886	3,2885843
39422,771	0,5645165	0,1253582	303355,07	223863,1	1,3550919	566551,69	314481	1,8015451
17274,633	0,7950883	0,263548	89742,068	47020,653	1,908567	248256,85	65546,429	3,7874961

1841,7477	0,5492623	0,0890316	12484,584	9468,9581	1,318475	26468,085	20686,439	1,2794897
695,17056	0,5670826	0,1271435	4022,2613	2954,8257	1,3612516	9990,4206	5467,6043	1,8272025
1958,8302	0,6176741	0,1259989	10515,052	7091,857	1,4826937	28150,7	15546,41	1,8107525
7466,9259	0,6331929	0,1781688	29841,62	19633,345	1,5199458	107308,53	41909,28	2,5604957
8409,347	0,4706386	0,1319546	41825,224	37021,898	1,1297428	120852,23	63729,073	1,8963438

19256,045	0,3618876	0,0637366	129489,46	149062,57	0,868692	276732,07	302119,28	0,9159696
9289,1164	0,3973106	0,0639239	67486,556	70761,173	0,953723	133495,55	145315,33	0,9186612
3355,3742	0,4423427	0,0771108	22495,564	21185,851	1,0618202	48220,684	43513,664	1,1081734

5653,8852	0,3999591	0,0506277	68783,914	71643,904	0,9600805	81252,996	111675,75	0,7275796
6585,5062	0,4331655	0,1032214	38185,711	36724,419	1,0397907	94641,488	63799,8	1,4834136
2132,1472	0,3979354	0,0582519	25389,524	26579,69	0,9552227	30641,469	36602,223	0,8371478
1723,5294	0,3750358	0,0714658	17122,788	19019,966	0,9002534	24769,15	24116,857	1,0270472

5631,719	0,575336	0,1088356	30905,244	22377,86	1,3810634	80934,442	51745,178	1,5640963
7386,3307	0,5317544	0,0567974	68167,807	53404,296	1,276448	106150,28	130046,99	0,8162456
253712,6	0,5813602	0,1931272	1563110,3	1120088,2	1,3955243	3646149,2	1313707,4	2,7754652
141724,29	0,5190216	0,1852891	850947,14	683006,91	1,2458836	2036745,2	764881,83	2,6628233

5408,1928

1359,711	0,5435877	0,0231739	30987,331	23747,75	1,3048534	19540,65	58674,189	0,3330366
3167,1081	0,6677059	0,0443413	58052,317	36219,485	1,6027925	45515,078	71425,698	0,6372367

381,94236

1460,6945

2618,0965	0,3016619	0,031804	45052,792	62217,009	0,7241234	37625,134	82319,773	0,4570607
16182,648	0,3017555	0,0273872	335127,57	462660,98	0,724348	232563,74	590882,69	0,393587
5930,9485	0,3505326	0,0399879	89136,613	105934,06	0,8414349	85234,723	148318,58	0,5746732

5054,4849	0,4283228	0,0350753	64032,973	62278,828	1,028166	72638,907	144103,99	0,5040729
3570,2442	0,5045352	0,0418274	48163,271	39767,88	1,2111098	51308,619	85356,544	0,6011094
3531,1806	0,4675615	0,0374049	46141,693	41111,445	1,1223564	50747,229	94404,196	0,5375527
7097,0692	0,5006071	0,0406299	110794,17	92199,341	1,2016807	101993,25	174676,08	0,5838994
3833,8588	0,4539539	0,0357859	62332,438	57201,875	1,0896922	55097,072	107133,19	0,5142857

13327,489	0,3593777	0,1645175	61556,834	71356,417	0,8626671	191531,73	81009,537	2,3643109
6450,823	0,4707183	0,2060813	27491,837	24330,477	1,1299342	92705,932	31302,328	2,9616306
4448,8547	0,423842	0,179775	21931,119	21555,827	1,0174102	63935,287	24746,797	2,5835783
2750,417	0,5549426	0,0806333	34713,995	26059,401	1,3321102	39526,736	34110,187	1,1587956

67297,213	0,3205237	0,2024825	296128,73	384882,59	0,7694002	967140,3	332360,65	2,9099121
93558,134	0,4584235	0,3244244	363108,55	329972,32	1,1004212	1344540,7	288381,92	4,6623612
552944,33	0,3727267	0,3478006	1693259	1892521,4	0,8947106	7946461,9	1589831,6	4,9983041
9884,0338	0,6496464	0,5082559	4559,7605	2923,9702	1,5594415	142045,22	19446,962	7,3042369
5525,8574	0,4607304	0,100881	31146,174	28162,148	1,1059587	79413,086	54776,002	1,4497788
92040,326	0,5711165	0,4283665	85854,24	62624,596	1,3709348	1322728	214863,49	6,156132
15437,519	0,4173048	0,0451043	113890,63	113695,31	1,0017179	221855,35	342262,36	0,6482026
13801,374	0,3030418	0,029284	113132,91	155522,9	0,7274357	198342,02	471293,96	0,4208457
4183,7225	0,3086874	0,0473194	26428,303	35666,318	0,7409877	60125,026	88414,445	0,6800362
982,15327	0,4150469	0,043076	10351,144	10389,606	0,9962981	14114,701	22800,478	0,6190528
26,579832	0,2185844	0,0051526	1107,3195	2110,3852	0,5247002	381,98352	5158,5113	0,0740492
1042,5657	0,2736903	0,0362005	11792,886	17950,172	0,656979	14982,898	28799,758	0,5202439
2957,8527	0,3449292	0,041282	33930,837	40980,061	0,8279841	42507,831	71649,858	0,5932717
6111,2621	0,4037354	0,081187	54676,41	56417,151	0,9691452	87826,042	75273,863	1,1667535
1548,3848	0,4800282	0,0360668	19784,402	17169,757	1,152282	22252,115	42930,972	0,5183231
1736,8488	0,6157576	0,0378361	26420,016	17874,39	1,4780933	24960,565	45904,525	0,5437496
2917,404	0,5049086	0,028387	52521,372	43334,24	1,2120063	41926,535	102772,55	0,4079546
26682,927	0,444867	0,0562454	314649,01	294648,4	1,0678796	383465,12	474402,26	0,8083122
43668,787	0,4738875	0,0489272	562511,12	494497,14	1,1375417	627571,96	892525,08	0,7031421
8762,0935	0,4576405	0,0843826	60237,475	54834,044	1,0985415	125921,61	103837,67	1,2126776
19235,99	0,4339642	0,0786967	143184,72	137451,87	1,041708	276443,86	244432,13	1,1309637
8528,5132	0,3521399	0,0614167	84888,198	100424,57	0,8452931	122564,79	138863	0,882631
4345,4599	0,3224178	0,0564983	56009,785	72369,034	0,7739468	62449,383	76913,067	0,8119476
3836,3793	0,2688611	0,0549852	44456,902	68884,117	0,6453868	55133,294	69771,09	0,7902026
737,48576	0,4586916	0,0636665	6826,2427	6199,6737	1,1010648	10598,54	11583,579	0,9149625
8320,936	0,400437	0,0718639	64236,606	66827,663	0,9612278	119581,66	115787,38	1,0327694
1394,446	0,6388838	0,5243139	6686,8877	4360,2369	1,5336065	20039,834	2659,5635	7,5350085
6609,9718	0,6673185	0,3257427	33249,945	20757,054	1,6018625	94993,088	20292,001	4,6813071
5943,6903	0,8425869	0,428443	31188,227	15419,984	2,0225849	85417,837	13872,769	6,1572304
40213,723	0,3500136	0,1354586	124393,07	148053,66	0,8401891	577918,62	296871,02	1,9466993
89971,192	0,4709938	0,1747833	275475,83	243655,49	1,1305956	1292992,1	514758,58	2,5118417
9007,9917	0,6212417	0,060077	100062,69	67099,53	1,4912577	129455,46	149940,65	0,863378
5023,064	0,3441051	0,2233422	13173,064	15947,907	0,8260058	72187,352	22490,441	3,2096904
30758,815	0,3242405	0,176735	94323,216	121187,9	0,7783221	442040,44	174039,21	2,53989
89864,656	0,6888473	0,2349886	520846,97	314988,8	1,6535412	1291461,1	382421,3	3,3770636
45941,31	0,6182456	0,224358	249281,64	167972,13	1,4840655	660230,8	204767,88	3,2242889
10467,283	0,7952802	0,3371244	42373,622	22196,44	1,9090278	150427,2	31048,723	4,8448758
33057,232	0,8524449	0,3777012	138113,28	67495,851	2,0462485	475071,39	87522,173	5,4280119
32430,858	0,8176164	0,3852605	130269,24	66374,339	1,9626446	466069,66	84179,042	5,5366473
326,37643	0,6629826	0,1598652	2769,5597	1740,2696	1,5914544	4690,4141	2041,5724	2,2974517
611,55254	0,7702756	0,1994295	4331,1369	2342,4143	1,8490055	8788,731	3066,5093	2,8660376

7940,6402	0,3350944	0,0306771	135991,46	169064,47	0,8043764	114116,36	258845,46	0,4408668
14982,527	0,535376	0,0470285	223910,26	174230,04	1,2851415	215316,58	318584,1	0,6758548
1017,0098	0,43792	0,0371966	14512,201	13805,319	1,0512036	14615,63	27341,494	0,5345586
182004,76	0,8943535	0,3026689	895574,86	417158,03	2,146848	2615623	601332,87	4,349709
68054,527	0,5540487	0,2926482	358060,12	269225,35	1,3299644	978023,79	232547,23	4,2056996
5475,8984	0,260832	0,4176093	9915,7421	15836,974	0,6261134	78695,116	13112,492	6,0015378
6181,8622	0,2781514	0,048376	75594,008	113217,62	0,6676877	88840,649	127787,74	0,6952204
15620,658	0,3472119	0,221367	41050,094	49252,406	0,8334637	224487,27	70564,541	3,1813043
7299,7321	0,3191025	0,1458623	25732,449	33593,777	0,7659886	104905,76	50045,359	2,0962135
1437,4822	0,3333298	0,032767	22639,355	28294,227	0,8001404	20658,314	43869,818	0,4709004
1456,993	0,3447723	0,0391806	18331,19	22149,615	0,8276076	20938,707	37186,592	0,5630714
1611,9555	0,3391143	0,0296905	23196,271	28495,748	0,8140257	23165,702	54291,912	0,4266879
1841,8175	0,3959862	0,0386022	25676,377	27012,301	0,9505439	26469,089	47712,782	0,5547589
2073,9378	0,3975987	0,0294145	40083,795	41998,311	0,9544144	29804,931	70507,282	0,4227213
386,59531	0,3723168	0,0416385	4879,9037	5460,1748	0,8937266	5555,8305	9284,5712	0,5983939
4865,0343	0,4838582	0,1229103	31089,86	26767,549	1,1614758	69916,278	39581,99	1,7663659
8864,2325	0,5096407	0,0517666	125602,94	102670,02	1,2233654	127389,47	171234,74	0,7439464
5509,5007	0,3324285	0,0995697	29935,401	37514,122	0,7979769	79178,022	55333,118	1,4309337
8869,6114	0,4421893	0,0490405	151320,37	142559,81	1,0614518	127466,77	180862,92	0,7047701
1619,2496	0,4504331	0,055468	23261,491	21513,705	1,0812406	23270,525	29192,482	0,797141
15428,375	0,3095901	0,077249	141168,99	189959,16	0,7431545	221723,94	199722,75	1,1101587
14337,24	0,2933654	0,058562	157657,09	223878,56	0,7042081	206043,05	244821,69	0,8416046
984,55022	0,3854849	0,0554497	9728,9437	10513,958	0,925336	14149,147	17755,729	0,7968779
590,36552	0,3480648	0,0164418	13179,982	15774,754	0,8355111	8484,2486	35906,403	0,2362879
2616,1842	0,3367592	0,0520619	24218,929	29960,107	0,8083726	37597,652	50251,37	0,7481916
8058,3736	0,5338975	0,109214	39223,72	30605,456	1,2815924	115808,33	73785,177	1,5695338
3855,0577	0,3195575	0,0957484	18639,178	24298,849	0,7670807	55401,725	40262,366	1,3760176
16051,229	0,2474137	0,1670309	127802,81	215191,24	0,5939034	230675,08	96097,341	2,4004314
17145,938	0,3017534	0,1601844	164527,94	227140,96	0,7243429	246407,35	107038,76	2,3020386
25664,858	0,3756771	0,2267145	213421,68	236663,74	0,9017929	368834,27	113203,43	3,2581546
8847,3129	0,4356858	0,1249615	61568,176	58869,568	1,0458405	127146,32	70800,324	1,7958437
27373,049	0,6381829	0,0698164	383543,21	250366,97	1,5319242	393382,99	392071,67	1,0033446
12654,069	0,5846415	0,0653376	184875,51	131733,93	1,4034009	181853,89	193672,07	0,9389784
47280,136	0,4624336	0,1671117	200673,94	180779,65	1,1100472	679471,31	282925,27	2,4015929
11855,083	0,333755	0,0423449	138368,74	172710,27	0,8011611	170371,52	279965	0,6085458
2709,3197	0,3560892	0,0315614	28452,923	33287,1	0,8547733	38936,118	85842,786	0,4535747
1764,1671	0,4568535	0,0353607	22069,184	20124,137	1,0966525	25353,161	49890,678	0,5081743
830,17598	0,4523521	0,0382772	10057,768	9262,6006	1,085847	11930,608	21688,51	0,5500889
1316,9672	0,3631826	0,059428	11875,134	13621,389	0,8718005	18926,371	22160,725	0,8540502
800,25186	0,4049926	0,0487694	10717,323	11024,203	0,972163	11500,563	16408,897	0,7008736
1678,3024	0,5796057	0,0673249	17444,678	12538,287	1,3913127	24119,184	24928,405	0,9675382
983,99247	0,4003583	0,1554498	6132,0299	6380,6277	0,9610387	14141,132	6329,9706	2,2339964

5258,3074	0,7331331	0,036372	37571,77	21349,453	1,7598469	75568,077	144570,15	0,5227087
15677,322	0,9445121	0,0958441	100441,7	44301,094	2,2672509	225301,6	163571,09	1,3773925
9000,9598	0,6656876	0,099892	57171,624	35778,161	1,5979475	129354,4	90106,928	1,4355656
58338,786	0,3877487	0,260728	239382,73	257187,81	0,9307701	838397,14	223753,48	3,7469681
62686,366	0,3851488	0,2973985	239522	259074,55	0,9245292	900876,99	210782,4	4,2739669
102627,86	0,3605151	0,3495058	378669,41	437567,13	0,8653973	1474883,4	293637,11	5,02281
11637,413	0,4089284	0,0589297	114534,3	116679,94	0,9816109	167243,34	197479,68	0,8468889
6111,636	0,336144	0,0409894	75492,703	93559,413	0,8068959	87831,415	149103,02	0,5890653
193254,82	0,7465741	0,3625058	855627,94	477441,29	1,7921113	2777299,6	533108,27	5,2096353
107958,68	0,4421393	0,2463656	374428,34	352790,99	1,0613319	1551493,5	438205,18	3,540564
5933,0781	0,3467647	0,0387789	75971,376	91268,94	0,8323903	85265,328	152997,73	0,557298
7980,4594	0,3553451	0,0260009	147390,75	172793,65	0,8529871	114688,61	306930,1	0,3736636
10082,534	0,3202627	0,0642752	117679,21	153073,96	0,7687735	144897,9	156865,17	0,9237099
10003,418	0,2934444	0,0297674	174365,34	247538,24	0,7043976	143760,9	336052,98	0,4277924
8549,8088	0,4402331	0,0465503	111363,45	105382,36	1,0567561	122870,83	183668,24	0,6689825
10876,968	0,5527023	0,0641045	81279,812	61263,148	1,3267325	156314,85	169675,49	0,9212577
7802,6578	0,6025568	0,0677107	51453,639	35573,455	1,4464054	112133,39	115235,24	0,9730825
9741,7204	0,6143442	0,3752525	32197,258	21833,081	1,4747006	140000,01	25960,438	5,3928215
6402,6599	0,6047165	0,2545794	29011,722	19986,173	1,4515897	92013,772	25149,952	3,6586063
121451,45	0,7429923	0,2908514	506661,03	284080,32	1,7835133	1745400,5	417572,18	4,1798774
668,46746	0,4200049	0,0553658	7019,1114	6962,0269	1,0081994	9606,6655	12073,657	0,7956715
20980,444	0,4963115	0,0678574	156430,22	131302,87	1,1913694	301513,72	309184,12	0,9751915
7012,827	0,5551351	0,048606	84244,282	63219,3	1,3325722	100782,59	144279,03	0,6985256
8817,7743	0,3362358	0,0530152	79970,859	99082,22	0,8071161	126721,81	166325,25	0,7618916
41454,038	0,3091704	0,047415	306879,81	413502,75	0,742147	595743,41	874281,25	0,6814093
8749,0993	0,4500825	0,07228	69163,58	64016,7	1,080399	125734,87	121044,58	1,0387485
1463,9841	0,2147629	0,0460817	14025,13	27205,422	0,515527	21039,178	31769,284	0,6622491
3059,6606	0,2955768	0,0430487	36567,506	51538,634	0,7095164	43970,93	71074,426	0,6186604
31619,639	0,2989433	0,1081821	197072,29	274627,92	0,7175974	454411,49	292281,52	1,5547048
10985,582	0,3134026	0,0751922	76347,648	101484,79	0,7523063	157875,77	146099,98	1,0806009
1636,4228	0,4854929	0,049798	14381,591	12340,477	1,1653999	23517,325	32861,204	0,7156562
1209,735	0,4239095	0,0650239	9520,3163	9355,913	1,0175721	17385,319	18604,478	0,9344696
911,1408	0,4013458	0,0328596	11692,512	12136,6	0,9634093	13094,168	27728,302	0,4722311
2702,4173	0,4951389	0,054984	23986,297	20181,067	1,1885544	38836,923	49149,15	0,7901851
9377,4163	0,5200928	0,1611008	28291,822	22661,466	1,2484551	134764,53	58208,385	2,3152082
700,04748	0,159109	0,1032423	3107,072	8135,131	0,3819326	10060,508	6780,6248	1,483714
969,58254	0,2976349	0,1047278	5601,2722	7839,9054	0,7144566	13934,044	9258,1241	1,5050613
52332,374	0,2261192	0,2212667	152634,99	281206,04	0,542787	752077,91	236512,64	3,1798635
2271,8848	0,5970394	0,0262698	44273,633	30892,289	1,4331613	32649,664	86482,733	0,3775281

5591,8834	0,4721592	0,0535149	47319,002	41749,861	1,133393	80361,958	104492,13	0,7690719
7672,2981	0,7519822	0,0580344	86919,228	48152,21	1,8050932	110259,97	132202,48	0,8340234
6190,5481	0,2908913	0,0303002	80988,378	115984,47	0,6982691	88965,475	204307,38	0,4354492
25605,775	0,374685	0,0623578	270560,15	300819,1	0,8994115	367985,17	410626,73	0,8961549
7381,8361	0,3312553	0,0500698	93970,756	118178,31	0,7951608	106085,69	147430,94	0,7195619
89445,23	0,9399946	0,2919493	535537,15	237340,67	2,256407	1285433,4	306372,46	4,1956558
75466,69	0,9160403	0,2822258	432701,83	196780,51	2,1989059	1084545,3	267398,29	4,0559171
16456,695	0,3088608	0,1396046	82431,766	111183,36	0,7414038	236502,11	117880,73	2,0062829
13386,587	0,45104	0,1292751	61869,952	57144,26	1,0826976	192381,04	103551,16	1,8578357
36003,084	0,9655739	0,3666871	197625,6	85263,984	2,3178087	517406,76	98184,749	5,2697264
20169,123	0,2808638	0,1643456	94488,458	140149,29	0,6741986	289854,07	122723,81	2,3618406
3018,08	0,6384734	0,0384517	41245,996	26912,057	1,5326214	43373,368	78490,194	0,552596
2487,0401	0,3244132	0,0304863	48880,423	62768,869	0,7787367	35741,699	81578,844	0,4381246
3517,3511	0,487193	0,0434697	46355,1	39637,331	1,1694809	50548,482	80914,972	0,6247111
9582,6898	0,2977204	0,0272426	146085,44	204411,92	0,714662	137714,55	351753,87	0,3915083
3005,4502	0,5679869	0,0371882	49512,044	36314,536	1,3634222	43191,863	80817,281	0,5344385
23600,982	0,4102949	0,2243754	145799,78	148036,46	0,984891	339173,94	105185,26	3,2245389
1838,0313	0,3822337	0,10872	11384,286	12407,514	0,9175316	26414,677	16906,1	1,5624347
20645,688	0,2468003	0,1386273	87818,192	148233,65	0,5924309	296702,88	148929,41	1,9922383
12962,527	0,2268779	0,1831326	42272,119	77619,3	0,5446084	186286,8	70782,188	2,6318316
50884,388	0,474081	0,09217	407139,17	357765,37	1,1380061	731268,66	552071,31	1,3245909
6182,859	0,4607012	0,0454299	84757,274	76641,785	1,1058886	88854,973	136096,66	0,6528814
5885,8599	0,3930497	0,0596363	63166,083	66949,057	0,9434947	84586,746	98695,853	0,8570446
13327,932								
32714,614	0,6521814	0,1065651	224733,88	143551,61	1,5655267	470147,57	306991,92	1,5314656
4563,1801	0,5234729	0,0530399	83964,049	66820,102	1,2565687	65578,278	86032,94	0,7622462
14139,431	0,6442327	0,0949836	110846,96	71678,512	1,5464462	203200,3	148861,86	1,3650259
3216,1814								
1779,3628	0,8250416	0,0364992	26130,144	13193,921	1,9804685	25571,541	48750,704	0,5245369
459,26716	0,5531839	0,0276829	8077,9326	6083,2916	1,3278884	6600,2106	16590,307	0,3978353
2393,5574	0,5526926	0,0630991	12981,28	9784,5706	1,3267092	34398,242	37933,317	0,9068082
16314,051	0,5856949	0,0825324	89992,851	64009,506	1,4059295	234452,15	197668,56	1,1860872
4144,9499	0,6946492	0,0456139	24956,828	14966,898	1,6674683	59567,818	90870,418	0,6555249
38583,817	0,6706304	0,0487131	233784,08	145224,42	1,6098125	554494,95	792063,16	0,7000641
6965,7594	0,5500362	0,050805	47346,267	35859,349	1,3203326	100106,18	137107,85	0,7301273
5278,282	0,4912793	0,0539951	36261,493	30748,589	1,1792897	75855,135	97754,747	0,7759739
5681,1975	0,3002924	0,0320267	65741,603	91201,904	0,7208359	81645,507	177389,43	0,4602614
13963,929	0,435591	0,0832402	80696,353	77176,125	1,0456129	200678,13	167754,6	1,1962601
16818,745	0,4645406	0,1519828	64493,179	57835,97	1,115105	241705,2	110662,15	2,1841723
3962,1994	0,3177021	0,0716144	22828,139	29933,556	0,762627	56941,477	55326,884	1,0291828
3357,5076	0,2507882	0,1240478	11284,092	18744,223	0,6020037	48251,343	27066,25	1,7827125

83377,934	0,4448835	0,331118	379003,49	354899,08	1,067919	1198239,2	251807,29	4,7585565
33479,056	0,4628833	0,2947056	164606,75	148143,98	1,1111268	481133,51	113601,68	4,2352675
13092,348	0,5584634	0,234342	75643,125	56426,445	1,3405616	188152,47	55868,56	3,3677702
59893,677	0,5322696	0,2404598	348545	272794,21	1,2776847	860742,75	249079,81	3,4556905
37633,853	0,3098736	0,0782962	310254,91	417101,81	0,743835	540842,85	480659,77	1,1252093
6054,2376	0,2471734	0,0471205	62186,109	104809,26	0,5933265	87006,532	128484,18	0,677177
41939,748	0,2135302	0,0880062	225445,56	439835,49	0,5125679	602723,63	476554,36	1,2647532
26339,182	0,2366851	0,0707582	267796,7	471348,56	0,56815	378525,1	372241,94	1,0168792
11170,158	0,3495463	0,1430142	73144,688	87173,818	0,8390672	160528,34	78105,253	2,0552822
2469,4998	0,4653771	0,2015876	15912,243	14244,076	1,117113	35489,623	12250,255	2,8970517
23085,268	0,6809939	0,0838144	250969,54	153527,33	1,6346896	331762,53	275433,17	1,2045119
2451,0331	0,7834526	0,1159482	21914,481	11652,695	1,8806362	35224,236	21139,027	1,666313
2100,4039	0,6964104	0,1665226	11131,739	6658,9495	1,6716959	30185,28	12613,325	2,3931263
23071,033	0,2373237	0,0759728	115472,04	202695,25	0,569683	331557,94	303675,03	1,0918183
314,05487	0,2060262	0,0189718	2147,2568	4341,7957	0,494555	4513,3388	16553,79	0,2726469
19257,762	0,3923374	0,0477276	222492,07	236245,07	0,941785	276756,75	403493,39	0,6859016
31272,107	0,3816589	0,3344395	84521,076	92256,621	0,9161519	449417,05	93506,022	4,8062899
49189,332	0,3013364	0,1029543	319244,02	441345,89	0,723342	706908,7	477778,23	1,4795749
24808,056	0,310121	0,1149142	154536,67	207590,89	0,744429	356521,02	215883,36	1,651452
3144,2499	0,3401252	0,0451143	34157,265	41836,201	0,8164523	45186,578	69695,248	0,6483452
5284,4482	0,5756876	0,0545287	77741,74	56256,837	1,3819074	75943,752	96911,367	0,7836413
1985,8086	0,6620878	0,046016	31816,971	20019,404	1,5893066	28538,411	43154,767	0,6613038
62318,464	0,4983473	0,1114126	448991,05	375330,21	1,1962561	895589,8	559348,22	1,601131
13306,107	0,7500365	0,3324153	57292,016	31821,428	1,8004225	191224,45	40028,563	4,7772
6053,5382	0,822862	0,1168804	41664,303	21093,325	1,9752364	86996,481	51792,604	1,6797086
1670,6282	1,3813328	0,0390228	30002,565	9048,3208	3,3158158	24008,897	42811,599	0,5608036
2968,6669	0,5257078	0,0500346	30995,427	24561,855	1,2619335	42663,244	59332,271	0,7190563
5783,5681	0,599576	0,039014	98864,8	68691,882	1,4392501	83116,692	148243,37	0,5606773
17337,558	0,5532937	0,0374187	304586,46	229331,01	1,3281521	249161,15	463339,04	0,5377513
4815,4567	0,4622106	0,043372	63237,755	56996,008	1,109512	69203,791	111026,89	0,6233066
3324,7322	0,8096517	0,0428479	61547,046	31667,727	1,9435259	47780,322	77593,847	0,6157746
1064,8779	0,8549077	0,0378819	23649,891	11524,387	2,0521604	15303,551	28110,492	0,5444071
639,56369	0,8836338	0,024983	20536,16	9681,772	2,1211158	9191,2842	25599,985	0,3590347
13959,918	0,3380207	0,2217602	55702,783	68650,153	0,8114007	200620,49	62950,501	3,1869561
5408,1928								
286,9787	0,590597	0,0355199	8140,9408	5742,3719	1,4176966	4124,2223	8079,3893	0,5104621
7010,6842	0,6328379	0,086709	56058,862	36902,833	1,5190937	100751,8	80852,985	1,246111
13254,448	0,5180827	0,1234873	69559,534	55932,666	1,2436299	190482,05	107334,48	1,7746585
3297,1831	0,4600102	0,0513404	37110,974	33608,015	1,1042299	47384,409	64222,007	0,737822

75423,235	0,3550704	0,2116384	475523,65	557911,84	0,8523276	1083920,8	356377,78	3,0414939
32984,572	0,5030331	0,1677275	455586,71	377296,22	1,207504	474027,19	196655,78	2,4104412
15369,344	0,4072624	0,2327518	105298,24	107709,67	0,9776117	220875,59	66033,191	3,3449177
23789,368	0,3456136	0,076952	169210,14	203959,3	0,829627	341881,27	309145,59	1,1058908
90072,996	0,4300857	0,2685287	524645,39	508181,47	1,0323977	1294455,2	335431,5	3,8590745

2630,245	0,5244386	0,0320905	50460,159	40083,153	1,258887	37799,722	81963,345	0,4611784
3362,0194	0,5169631	0,0368025	51294,543	41335,151	1,2409424	48316,182	91352,969	0,5288956
16036,28	0,3690116	0,0452559	206132,57	232709,7	0,8857928	230460,24	354346,83	0,6503804
17378,394	0,5075954	0,0472215	239339,39	196428,48	1,2184557	249748,01	368018,4	0,6786292
4217,1984	0,4049633	0,0901391	34201,118	35182,979	0,9720927	60606,113	46785,444	1,2954053
8410,1159	0,4008559	0,0548113	129122,35	134190,28	0,9622332	120863,28	153437,62	0,787703
6776,1002	0,3955749	0,0695666	58458,642	61564,156	0,9495565	97380,549	97404,51	0,999754
11982,135	0,4340196	0,0461894	141248,26	135575,64	1,041841	172197,41	259413,21	0,6637958

7863,7579	0,3995705	0,0557472	76302,603	79552,5	0,9591478	113011,47	141061,02	0,8011531
528,59823	0,4109067	0,035538	6471,6271	6561,1227	0,9863597	7596,5798	14874,182	0,5107225

22233,063
6788,5831

6245,2999	0,2802475	0,0469726	74698,139	111039,09	0,6727193	89752,324	132956,31	0,6750512
5980,2884	0,2923743	0,0475889	71302,428	101595,15	0,701829	85943,796	125665,67	0,6839083
4920,4744	0,3288794	0,0451923	65265,019	82670,733	0,7894574	70713,018	108878,58	0,6494667

204,88306	0,3589484	0,0347063	2008,2345	2330,7213	0,8616365	2944,4111	5903,3472	0,4987698
2299,8648	0,5344072	0,041344	33642,466	26225,478	1,2828161	33051,769	55627,505	0,5941624
933,23023	0,5481245	0,040096	14832,435	11273,043	1,3157437	13411,619	23274,907	0,5762265

238,86318	0,6111503	0,0225667	4998,8058	3407,4237	1,4670338	3432,7455	10584,78	0,3243096
137005,61	0,2125252	0,1087653	467712,1	916802,97	0,5101555	1968932,1	1259645	1,5630849

3356,5216	0,4796048	0,0816983	25049,89	21758,566	1,1512657	48237,173	41084,338	1,1741013
2723,4215	0,5694811	0,0788428	20334,026	14874,83	1,367009	39138,778	34542,434	1,1330637
14215,388	0,4350016	0,0808133	93559,853	89599,701	1,0441983	204291,88	175904,14	1,1613819

671,38421	0,6688003	0,0259272	12749,431	7941,4955	1,6054194	9648,5826	25895,011	0,3726039
423,84512	0,5138522	0,0219358	6171,2312	5003,127	1,2334748	6091,1541	19322,053	0,3152436

475,98525	0,4194803	0,0441705	3694,4087	3668,946	1,0069401	6840,4692	10776,077	0,6347829
3646,3649	0,3849662	0,0423996	34485,247	37318,028	0,9240908	52402,562	86000,043	0,6093318

6763,3031	0,2831839	0,2022135	25516,956	37537,75	0,6797679	97196,639	33446,355	2,9060458
9296,7658	0,4238704	0,1313853	68545,674	67368,2	1,0174782	133605,49	70759,551	1,8881619
5647,7784	0,3535821	0,1265921	32121,354	37845,264	0,8487549	81165,234	44613,974	1,8192783

75263,003
15079,69

47238,216	0,5167566	0,1308347	325982,91	262794,76	1,2404468	678868,87	361052,67	1,8802488
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8025,6486

57,321263	0,0603566	0,0555752	6015,7538	41521,485	0,1448829	823,77414	1031,4177	0,7986814
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10390,954	0,3625057	0,0874459	66511,078	76434,084	0,8701756	149330,26	118827,18	1,2567012
4559,6301	0,483205	0,1083688	32079,059	27656,557	1,1599079	65527,261	42075,099	1,5573881

13327,932
3216,1814

53534,866	0,3288362	0,251617	185391,6	234865,04	0,7893537	769359,15	212763,35	3,6160323
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24955,938	0,5326838	0,1345737	164341,37	128524,32	1,2786791	358646,25	185444,43	1,9339823
97675,133	0,5020042	0,2079576	487225,19	404324,7	1,2050344	1403706,8	469687,67	2,9885963
16976,045	0,2854106	0,1864369	76770,979	112055,96	0,6851128	243965,79	91055,166	2,6793185

7492,4368	0,4629224	0,0493232	92804,844	83516,138	1,1112205	107675,15	151905,07	0,7088318
254,98627	0,273815	0,0267273	2504,2513	3810,0313	0,6572784	3664,4533	9540,2896	0,3841029

19276,29	0,9310331	0,2692271	146291,15	65457,713	2,2348955	277023,02	71598,622	3,869111
4789,8763	0,9787074	0,2809906	36033,404	15337,704	2,349335	68836,17	17046,396	4,0381656
18490,216	0,6080949	0,2190144	132436,88	90728,868	1,4596995	265726,2	84424,667	3,1474948

1148,7491	0,488671	0,018816	22535,813	19211,648	1,1730286	16508,88	61051,614	0,2704086
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222,67982	0,3482722	0,0193687	3655,2228	4372,2303	0,8360087	3200,1715	11496,895	0,2783509
688,31778	0,3183463	0,0341583	7394,4637	9676,422	0,7641733	9891,938	20150,845	0,4908945

6120,2569	0,319432	0,0508471	77194,643	100673,84	0,7667796	87955,308	120365,92	0,7307326
877,02246	0,3741111	0,0264684	20999,175	23383,503	0,8980337	12603,847	33134,748	0,3803816
2695,4236	0,4759227	0,0894746	22336,917	19552,161	1,142427	38736,414	30125,023	1,2858551

436,56732	0,3708937	0,024421	7472,3855	8393,0099	0,8903106	6273,9871	17876,715	0,3509586
2256,2986	0,4385014	0,0609373	20281,351	19267,875	1,0525993	32425,672	37026,589	0,8757402

10875,084	0,4375603	0,2693562	32592,117	31030,056	1,0503402	156287,78	40374,362	3,8709659
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75263,003
15079,69

2916,2605	0,3389144	0,0886139	22542,427	27708,853	0,813546	41910,102	32909,749	1,2734859
2762,2773	0,3975776	0,0484428	42200,957	44218,941	0,9543638	39697,182	57021,392	0,6961805
3535,4932	0,3625589	0,0526543	47829,686	54957,486	0,8703034	50809,206	67145,356	0,7567047

617,19968	0,4474903	0,0283269	10287,606	9577,2023	1,0741765	8869,8872	21788,456	0,4070911
2048,3183	0,5207791	0,0576552	20781,878	16624,138	1,2501026	29436,749	35527,039	0,8285731
1017,5643	0,4178331	0,0428267	9555,4095	9526,9602	1,0029862	14623,599	23760,054	0,6154699

6579,0823	0,3202732	0,198622	25005,589	32525,532	0,7687988	94549,17	33123,627	2,8544329
7446,5508	0,2654213	0,1129925	29811,057	46789,619	0,6371297	107015,71	65903,072	1,623835

20978,674	0,4797101	0,1403492	125453,9	108946,49	1,1515185	301488,27	149474,85	2,0169833
175,73923	0,4645965	0,0414291	4069,0895	3648,6251	1,1152392	2525,58	4241,9316	0,5953844

17591,92	0,5777413	0,0482459	243635,28	175676,93	1,3868371	252816,64	364630,38	0,6933504
6852,4167	0,4198007	0,0499297	79071,888	78466,975	1,0077091	98477,307	137241,18	0,7175492
7272,0767	0,534542	0,04721	85978,601	67006,434	1,2831395	104508,32	154036,9	0,6784629

1959,2619	0,2129294	0,0601691	18434,106	36065,708	0,5111256	28156,904	32562,598	0,8647008
546,66237	0,1370934	0,0590687	3967,857	12057,228	0,3290853	7856,1827	9254,6952	0,8488862
683,53758	0,1908944	0,0599558	5649,1564	12328,162	0,4582319	9823,2409	11400,686	0,8616359
2405,2453	0,4819674	0,0698474	15071,996	13027,5	1,156937	34566,21	34435,736	1,0037889
877,75572	0,4408687	0,0349422	9135,8633	8632,7313	1,0582819	12614,385	25120,21	0,5021608
730,39978	0,462645	0,0453209	6301,4535	5674,1502	1,1105546	10496,706	16116,176	0,6513149
7978,6314	0,4796759	0,0424031	100487,95	87271,818	1,1514364	114662,34	188161,72	0,6093819
14590,308	0,4325637	0,0463263	160124,77	154211,37	1,038346	209679,92	314946,5	0,6657636
9396,2428	0,4582763	0,0525544	97229,762	88385,237	1,1000679	135035,09	178790,71	0,755269
7713,7288	0,2985038	0,1043222	51613,472	72031,286	0,7165424	110855,38	73941,383	1,4992332
40676,501	0,4864067	0,1511819	307733,55	263562,27	1,1675933	584569,27	269056,71	2,172662
9878,4753	0,3487632	0,1883997	67955,847	81171,59	0,8371876	141965,34	52433,611	2,7075255
46234,464	0,3566067	0,1505606	334736,39	391040,15	0,8560154	664443,75	307082,03	2,1637338
39838,265	0,3711205	0,1110589	237187,42	266246,94	0,890855	572522,85	358712,91	1,5960475
7150,3967	0,3180266	0,1960099	43811,202	57389,134	0,7634059	102759,63	36479,77	2,8168936
35091,781	0,3471544	0,2309004	212932,9	255521,84	0,8333256	504310,26	151978	3,3183109
46681,715	0,2755696	0,1020772	449911,7	680148,86	0,6614901	670871,28	457317,88	1,4669693
2122,6178	0,4747149	0,0423114	32749,257	28739,321	1,1395279	30504,52	50166,604	0,6080643
460,31763	0,5404188	0,0401514	7546,554	5817,3634	1,2972465	6615,3071	11464,54	0,5770233
1066,1176	0,5059226	0,0461239	7729,3164	6364,5088	1,2144404	15321,367	23114,23	0,6628543
3053,4013	0,5595229	0,0466447	27053,561	20142,554	1,3431048	43880,976	65460,775	0,67034
2462,7234	0,7340885	0,0710687	19284,612	10943,857	1,7621404	35392,239	34652,701	1,0213414
2987,2154	0,2328151	0,0305903	38053,498	68091,263	0,5588602	42929,808	97652,522	0,439618
3356,2457	0,3419202	0,0514341	33873,225	41270,499	0,8207612	48233,207	65253,331	0,7391685
24239,727	0,2139263	0,0510864	177229,21	345127,15	0,5135186	348353,46	474484,87	0,7341719
5967,6211	0,4199353	0,039877	80319,451	79679,443	1,0080323	85761,751	149650,59	0,5730799
9123,5595	0,6397249	0,207189	50840,189	33107,153	1,5356255	131116,31	44034,956	2,9775506
1955,0552	0,5758936	0,1307227	21025,904	15209,69	1,3824019	28096,449	14955,739	1,87864
5388,6185	0,2557907	0,0314773	68041,14	110814,04	0,6140119	77440,801	171190,72	0,4523656
103,87079	0,2037022	0,0230162	1776,4989	3633,0982	0,4889763	1492,7457	4512,9461	0,3307697
834,24982	0,3383085	0,0619144	8309,0563	10231,673	0,8120916	11989,154	13474,244	0,889783
7205,4863	0,3472399	0,0717142	64936,922	77905,839	0,8335309	103551,33	100474,97	1,0306182
15846,682	0,4015437	0,1641787	78185,817	81115,354	0,9638843	227735,51	96520,915	2,3594421
6322,3438	0,387697	0,2822199	42088,629	45225,172	0,9306461	90859,535	22402,19	4,0558327
1621,9563	0,2581079	0,3237218	13210,582	21322,033	0,6195742	23309,424	5010,3407	4,6522634
6151,8388	0,3573789	0,0355812	76830,812	89560,083	0,8578689	88409,177	172895,71	0,511344
5321,0966	0,4181267	0,0571889	55381,087	55177,431	1,0036909	76470,432	93044,27	0,8218715

14518,922	0,4632755	0,0672941	119435,37	107399,34	1,1120681	208654,02	215753,13	0,9670961
2414,4834	0,3822761	0,0568064	21855,032	23816,733	0,9176335	34698,973	42503,727	0,8163749
4652,9015	0,7612794	0,0454128	65265,308	35714,635	1,8274107	66867,68	102457,84	0,6526361
4952,3981	0,7837201	0,048548	66917,149	35570,044	1,8812782	71171,8	102010,44	0,6976914
3909,3097	0,9391049	0,0526772	56961,758	25268,368	2,2542714	56181,389	74212,582	0,7570332
5240,2638	0,920093	0,0542453	68928,41	31208,614	2,2086341	75308,769	96603,009	0,7795696
2691,5102								
2612,7594								
2769,0086								
16377,269								
1825,121	0,4691274	0,0776012	15047,045	13361,903	1,1261154	26229,14	23519,223	1,1152214
527,06055	0,3336283	0,0498739	5300,1044	6618,0416	0,8008569	7574,4815	10567,857	0,7167471
524,2856	0,2956239	0,0298408	8195,8132	11549,425	0,7096295	7534,6022	17569,446	0,4288469
1800,3635	0,3032296	0,0539888	16607,269	22815,739	0,7278865	25873,346	33346,987	0,7758826
8340,4149	0,2996734	0,1449513	38933,081	54122,585	0,71935	119861,6	57539,411	2,0831217
1205,7225	0,4650211	0,0364552	20111,279	18016,688	1,1162584	17327,655	33074,091	0,5239042
1027,462	0,3963051	0,0329728	13253,405	13931,752	0,9513093	14765,84	31160,908	0,4738578
1744,852	0,3584742	0,0613153	11981,574	13923,995	0,8604983	25075,58	28457,053	0,8811728
4284,245	0,2860363	0,0537726	38909,252	56668,235	0,6866149	61569,652	79673,34	0,7727761
15453,764	0,3262639	0,0428222	167437,1	213791,56	0,7831792	222088,81	360882,31	0,6154051
13699,794	0,3671951	0,1043459	91889,916	104250,69	0,8814322	196882,19	131292,13	1,4995735
15697,532	0,3471249	0,1251855	98406,463	118098,87	0,8332549	225592,04	125394,18	1,7990631
742,32041	0,283244	0,0412406	7909,1944	11632,671	0,6799122	10668,02	17999,75	0,592676
363,31949	1,512354	0,0327602	3920,0396	1079,804	3,6303252	5221,3294	11090,269	0,4708028
14477,996	0,4784614	0,0636904	93288,078	81224,524	1,1485211	208065,87	227318,17	0,9153068
9809,751	0,2965459	0,0636494	52569,849	73850,39	0,7118425	140977,69	154121,56	0,9147175
186,05431	0,1261946	0,0760884	366,96147	1211,4004	0,3029234	2673,8198	2445,2375	1,0934806
1027,1602	0,3226371	0,0392582	9390,8482	12125,465	0,7744733	14761,503	26164,213	0,5641868
2498,4611	0,2273712	0,0274544	21960,008	40235,09	0,5457925	35905,832	91004,186	0,3945514
2834,3134	0,2329944	0,0356318	21880,509	39121,892	0,5592907	40732,426	79544,476	0,5120711
1773,0515	0,247136	0,0458951	13191,46	22236,412	0,5932369	25480,841	38632,718	0,6595663
4342,0658	0,4421721	0,1450874	33172,265	31253	1,0614106	62400,605	29927,235	2,0850775
17790,671	0,3963647	0,3016504	88304,08	92809,768	0,9514524	255672,91	58977,774	4,3350723
2554,2398	0,5767694	0,1756255	15512,618	11204,456	1,3845043	36707,438	14543,671	2,5239459
20914,015	0,3837991	0,1124697	58378,919	63366,551	0,9212892	300559,05	185952,43	1,6163223
31337,815	0,5689957	0,1045403	231325,46	169364,49	1,3658439	450361,35	299767,87	1,502367
5282,5536	0,3586563	0,0810427	39221,413	45556,748	0,8609353	75916,523	65182,387	1,1646785
7104,1413	0,2966022	0,048487	71307,284	100153,8	0,7119778	102094,89	146516,51	0,6968149

1477,3976	0,3998003	0,041244	13284,95	13842,825	0,9596994	21231,946	35820,935	0,5927245
534,90626	0,5347682	0,0382993	5706,6759	4445,551	1,2836825	7687,2336	13966,488	0,5504056
29618,472	0,5944718	0,1474873	170284,04	119330,28	1,4269978	425652,37	200820,52	2,1195661
8523,0551	0,683195	0,0886702	81904,998	49942,887	1,6399733	122486,35	96120,895	1,2742947
1747,4308	0,5758896	0,0498878	27205,379	19679,926	1,3823923	25112,641	35027,184	0,7169472
13108,57	0,7060422	0,0413573	136648,16	80627,098	1,6948167	188385,61	316959,24	0,5943528
311,37906	0,4287354	0,0234244	4313,6654	4191,4575	1,0291564	4474,8843	13292,916	0,3366368
2455,6771	0,2982495	0,0326628	29945,328	41827,059	0,715932	35290,975	75182,658	0,4694031
62,395251	0,4013933	0,0163536	1314,307	1364,0637	0,9635232	896,69332	3815,3737	0,2350211
367,41516	0,4029789	0,0438563	3602,4699	3724,1402	0,9673293	5280,189	8377,7013	0,630267
1007,56	0,4124483	0,0532998	11966,16	12086,297	0,9900601	14479,825	18903,624	0,7659814
432,63008	0,2420175	0,0882951	2715,7248	4674,626	0,5809502	6217,4044	4899,819	1,2689049
3151,1699	0,3960934	0,0599937	30638,454	32223,829	0,9508012	45286,027	52525,006	0,8621803
8247,7378	0,3725181	0,0622004	79866,504	89315,176	0,8942098	118529,72	132599,5	0,8938926
2014,9685	0,2942559	0,0627669	18582,67	26308,185	0,7063456	28957,473	32102,422	0,9020339
1183,8365	0,6610681	0,072434	10062,538	6341,1687	1,5868586	17013,126	16343,663	1,0409616
2505,5196	0,5151159	0,0756956	22720,209	18374,489	1,2365083	36007,271	33099,921	1,0878355
1557,3027	0,2992277	0,045046	20353,912	28337,013	0,7182801	22380,276	34571,379	0,6473643
3993,9701	0,4083833	0,0455839	68332,397	69705,434	0,9803023	57398,06	87618,065	0,6550939
27294,295	0,2719084	0,031284	290883,66	445661,07	0,6527015	392251,2	872467,25	0,4495884
6698,3837								
13356,955								
9367,9465								
11727,585	0,2922601	0,1600592	124324,37	177212,62	0,7015549	168539,23	73270,294	2,3002395
6996,31	0,2960778	0,1493976	68230,295	96001,788	0,710719	100545,22	46830,128	2,1470201
13966,454	0,4055451	0,2384575	102295,17	105080,94	0,9734893	200714,41	58569,995	3,4269152
73605,808								
36683,675								
6624,8629	0,286139	0,1888038	31783,977	46274,219	0,6868615	95207,09	35088,607	2,7133334
63148,844	0,2825827	0,2239853	334452,43	493056,58	0,6783247	907523,34	281932,97	3,218933
2801,1969								
29902,264	0,5010257	0,1066926	242057,83	201264,43	1,2026856	429730,79	280265,5	1,5332989
25982,374	0,5676944	0,073392	166362,69	122081,33	1,3627202	373397,35	354021,91	1,0547295
82317,676	0,5917092	0,0661408	538582,36	379185,48	1,4203665	1183002,1	1244583,2	0,9505207
6105,6012	0,4036703	0,0702928	39051,183	40300,955	0,968989	87744,689	86859,505	1,010191
5941,3371	0,272532	0,3508094	19636,948	30016,797	0,6541987	85384,02	16936,084	5,0415444
20084,028	0,258989	0,3134915	67754,674	108984,8	0,6216892	288631,17	64065,624	4,5052425
19563,608	0,6807083	0,2191817	71901,524	44003,273	1,634004	281152,11	89257,48	3,1498997

32217,109	0,4396577	0,145731	114380,74	108379,26	1,0553748	462997,84	221072,45	2,0943262
11535,915	0,6354483	0,0384432	226173,54	148275,53	1,5253599	165784,7	300076,93	0,552474
32198,393	0,3511256	0,0344437	469801,67	557390,99	0,8428584	462728,87	934811,43	0,494997
20319,11	0,3504366	0,0391114	289283,47	343892,03	0,8412043	292009,57	519518,75	0,5620771
31949,712	0,3525442	0,1119371	172281,77	203579,33	0,8462636	459155,03	285425,46	1,6086688
1081,8287	0,484621	0,0702509	10779,91	9266,6095	1,1633068	15547,154	15399,491	1,0095888
6812,3687	0,4832663	0,1107716	53220,652	45877,693	1,1600551	97901,771	61499,251	1,5919181
1281,5321	0,3435537	0,0538202	17934,735	21747,444	0,8246824	18417,127	23811,342	0,7734603
1968,5132	0,3693754	0,0558396	28831,603	32516,869	0,886666	28289,855	35252,968	0,8024815
1644,3128	0,3534688	0,1101559	13645,399	16082,114	0,8484829	23630,714	14927,138	1,5830706
37002,633	0,3361778	0,1030173	326963,18	405170,4	0,806977	531771,47	359188,48	1,4804803
294,42602	0,3068767	0,0822719	1860,5939	2525,7803	0,7366412	4231,249	3578,6947	1,1823442
13781,394	0,5201275	0,0836629	86007,106	68886,241	1,2485382	198054,88	164725,27	1,2023345
27465,298	0,3318897	0,0473154	242688,98	304624,08	0,7966835	394708,71	580473	0,6799777
10399,981	0,3451188	0,0490234	91630,474	110606,16	0,8284392	149459,99	212143,26	0,7045239
9007,4177	0,3250133	0,0546644	81649,612	104655,24	0,780177	129447,21	164776,58	0,7855923
19032,002	0,5008457	0,151231	120872,72	100538,46	1,2022535	273512,3	125847,22	2,1733678
11079,072	0,5639002	0,1511478	69560,138	51388,52	1,3536124	159219,32	73299,591	2,172172
20251,444	1,0670744	0,2460201	104244,5	40697,375	2,5614552	291037,12	82316,212	3,5355991
5954,5725	0,7252786	0,1829734	33082,36	19002,009	1,7409927	85574,227	32543,372	2,6295439
36518,367	0,4796484	0,0860752	294147,91	255476,35	1,1513704	524812	424261,1	1,2370024
32394,048	0,3858337	0,1087832	213080,88	230065,89	0,9261733	465540,67	297785,42	1,5633427
14405,013	0,3066294	0,1065768	81710,612	111012,69	0,7360475	207017,03	135160,87	1,5316343
257808,74	0,9368687	0,422154	938424,84	417281,06	2,2489035	3705015,5	610698,27	6,0668511
118793,3	1,3603078	0,3391465	590235,11	180757,27	3,2653465	1707199,8	350271,37	4,8739348
21498,333	1,2546433	0,041897	331784,64	110165,07	3,0117044	308956,39	513123,32	0,6021094
3872,5412	0,4694651	0,053034	44243,678	39260,499	1,126926	55652,983	73019,914	0,7621617
2453,0762	0,6137521	0,0468739	30362,754	20608,961	1,4732792	35253,597	52333,548	0,6736329
5179,6401	0,692421	0,0648594	61712,056	37128,526	1,6621198	74437,535	79859,457	0,9321067
2447,7404	0,7349061	0,0632537	32550,255	18451,448	1,764103	35176,915	38697,161	0,9090309
7396,4671	0,3239266	0,1666425	48424,62	62276,972	0,7775686	106295,95	44385,241	2,3948491
3576,6645	0,2921969	0,255984	16214,803	23117,666	0,7014031	51400,885	13972,22	3,6787915
15676,103	0,304051	0,2291447	67934,011	93078,368	0,7298582	225284,08	68411,372	3,2930794
12844,341	0,4564984	0,0499014	96830,089	88364,738	1,0958001	184588,33	257394,54	0,7171416
31077,884	0,8994459	0,0720429	280042,93	129705,22	2,1590721	446625,83	431380,11	1,0353417
23015,105	0,4565079	0,1194045	145391,44	132677,88	1,0958228	330754,2	192749,13	1,7159828
2426,5895	0,4343828	0,0539218	25418,539	24377,317	1,0427127	34872,952	45002,037	0,7749194
1383,6455	0,4721157	0,095336	10372,335	9152,4216	1,1332886	19884,617	14513,352	1,3700914

17175,626	0,2940379	0,1017731	143384,65	203145,51	0,7058224	246833,99	168763,94	1,4625991
1175,2041	0,3165068	0,0438603	21407,378	28176,582	0,7597578	16889,068	26794,259	0,6303241
11139,407	0,4831352	0,064793	150734,93	129972,99	1,1597404	160086,42	171922,98	0,9311519
958,34308	0,2728373	0,0531212	11181,163	17072,268	0,6549314	13772,52	18040,697	0,763414
2031,4423	0,4089133	0,1727232	10750,142	10951,937	0,9815745	29194,221	11761,261	2,4822355
6465,4199	0,486898	0,0666624	54646,509	46755,46	1,1687728	92915,707	96987,565	0,9580167
5647,9483	0,6640733	0,1509666	18648,393	11698,586	1,5940725	81167,676	37411,901	2,1695683
585,8418	0,3412833	0,0189632	10416,028	12714,376	0,8192323	8419,2374	30893,679	0,272523
431,51322								
4053,3277								
3540,6644								
11236,231	0,2734378	0,1282349	81621,016	124351,62	0,6563728	161477,88	87622,223	1,8428873
6666,1284	0,3030253	0,0963936	55323,874	76057,422	0,7273961	95800,125	69155,321	1,3852893
27268,533	0,363956	0,111275	218063,94	249599,05	0,8736569	391880,97	245055,24	1,5991536
9520,6937	0,3643234	0,093737	71963,098	82286,903	0,8745389	136823,59	101568,17	1,347111
7725,3906	0,4699127	0,1594861	48481,611	42980,138	1,1280004	111022,97	48439,286	2,2920026
26577,187	0,3848214	0,0319738	371118,32	401754,87	0,9237432	381945,52	831216,51	0,4595018
29242,102	0,352452	0,0500448	250760,51	296392,42	0,8460422	420243,48	584318,71	0,7192025
3911,017	0,4119611	0,0323455	59902,6	60575,551	0,9888907	56205,926	120913,92	0,4648425
3420,8187	0,4649637	0,039051	48122,309	43115,688	1,1161206	49161,199	87598,775	0,5612087
10954,591	0,5519542	0,032111	177548,5	134005,29	1,3249365	157430,4	341147,56	0,461473
759,33722	0,5419786	0,0583045	5521,1401	4243,7967	1,3009907	10912,571	13023,648	0,8379043
1802,7613	0,4401017	0,0862206	10285,14	9735,654	1,0564406	25907,805	20908,698	1,2390922
1211,3478	0,3866081	0,0231821	21447,182	23110,387	0,9280321	17408,496	52253,509	0,3331546
3520,5471	0,4047896	0,0660755	29283,653	30137,268	0,9716758	50594,413	53280,651	0,9495832
6857,0104	0,4274561	0,0619155	65510,613	63845,171	1,0260856	98543,324	110747,87	0,8897989
6782,906	0,2682311	0,0769069	50896,088	79046,588	0,6438746	97478,356	88196,351	1,1052425
679,46982	0,4379223	0,1476868	16586,238	15778,248	1,0512091	9764,7825	4600,7487	2,1224334
1057,3495	0,5726389	0,0580802	10863,85	7903,3431	1,3745892	15195,358	18204,999	0,8346805
4119,6044	0,4950055	0,1138545	23986,287	20186,497	1,1882343	59203,573	36183,061	1,6362235
46516,068	0,5725741	0,3805288	213194,54	155114,46	1,3744336	668490,74	122240,61	5,4686469
20181,339	0,724876	0,1058585	194399,64	111722,25	1,7400262	290029,64	190644,43	1,5213119
17055,556	0,5343704	0,0463714	261201,62	203629,85	1,2827276	245108,44	367803,54	0,6664113
12713,584	0,3266759	0,0303755	146346,33	186626,2	0,7841682	182709,19	418547,5	0,4365316
2000,7404	0,5209716	0,04661	17849,52	14273,17	1,2505645	28752,999	42925,107	0,6698411
682,58604	0,5276612	0,0544872	5405,0677	4267,3069	1,2666227	9809,5662	12527,461	0,783045
8551,407	0,4282883	0,0433325	125178,25	121758,87	1,0280833	122893,8	197344,02	0,6227389

2463,4689	0,4309009	0,0950163	15100,518	14598,977	1,0343546	35402,953	25926,798	1,3654965
12287,159	0,4154323	0,0609098	115716,58	116038,81	0,9972231	176580,95	201726,99	0,8753462
9509,3739	0,3555879	0,06934	69976,106	81980,534	0,8535698	136660,92	137141,31	0,9964971
5821,7933	0,2627147	0,0313185	71187,357	112882,44	0,6306327	83666,033	185889,72	0,4500842
5705,8944	0,4241306	0,0424537	72352,403	71065,902	1,0181029	82000,43	134402,77	0,6101097
2137,945	0,2951126	0,032541	26963,031	38061,767	0,708402	30724,79	65700,115	0,467652
1931,8138	0,334949	0,0453849	18204,545	22641,703	0,8040272	27762,442	42565,121	0,6522345
12201,127	0,4765314	0,0922704	85418,461	74673,784	1,1438882	175344,59	132232,27	1,3260348
2914,5254	0,3712085	0,0420477	30255,498	33954,261	0,8910663	41885,167	69314,693	0,6042754
9372,7877	0,2617545	0,0542856	90069,455	143347,92	0,6283276	134698,01	172657,12	0,7801475
10901,667	0,3370976	0,071387	88351,432	109185,71	0,8091849	156669,81	152712,24	1,0259152
13720,974	0,3656265	0,1103125	99259,74	113094,99	0,877667	197186,58	124382,72	1,5853213
41962,959	0,2968206	0,1078129	246263,75	345632,33	0,7125021	603057,2	389220,14	1,5493987
9310,9195	0,2892576	0,0364229	114311,83	164632,01	0,6943475	133808,89	255633,84	0,5234397
1347,3569	0,4257089	0,0607749	10531,721	10306,105	1,0218916	19363,107	22169,628	0,8734069
15717,276	0,2853838	0,053589	145090,7	211796,22	0,6850486	225875,79	293292,83	0,7701375
4924,793	0,5457198	0,0532551	57811,02	44131,52	1,3099712	70775,081	92475,523	0,7653385
11116,15	0,4224229	0,0357206	187958,39	185362,64	1,0140036	159752,18	311197,18	0,5133471
3949,8904	0,2907022	0,0541803	45200,915	64774,914	0,6978151	56764,583	72902,71	0,7786347
511,91514	0,8602384	0,0355953	6490,2777	3143,058	2,0649564	7356,8241	14381,557	0,5115457
3738,0194	0,8444216	0,0370051	53921,799	26601,92	2,026989	53719,746	101013,53	0,5318074
2832,3726	0,2377656	0,0270344	30350,402	53176,943	0,5707436	40704,534	104769,35	0,3885157
17063,667	0,2958727	0,0726823	92157,112	129757,32	0,7102267	245225,02	234770,69	1,04453
12111,653	0,6454291	0,0769033	140084,78	90417,056	1,5493181	174058,73	157492,07	1,1051905
44712,03	0,4308792	0,1075796	347211,31	335696,1	1,0343025	642564,59	415618,19	1,5460454
54019,505	0,5272116	0,1228637	351035,79	277379,53	1,2655432	776323,98	439670,18	1,7656962
3950,5963	0,4579991	0,1512281	8683,6134	7898,4842	1,0994025	56774,727	26123,421	2,1733266
44320,62	0,7726237	0,2640065	84194,987	45396,892	1,8546421	636939,56	167876,98	3,7940851
821,9486	2,1513073	0,0304931	14136,93	2737,5407	5,1640986	11812,37	26955,21	0,4382222
1808,7602	2,6951083	0,0304668	33210,574	5133,4354	6,4694638	25994,017	59368,248	0,4378438
10281,342	1,0191392	0,0421145	142288,02	58162,455	2,4463894	147755	244128,27	0,6052351
4638,8832	0,3631896	0,1128326	15282,602	17529,592	0,8718174	66666,221	41112,96	1,6215378
2173,1752	0,42935	0,1123617	6343,0479	6154,5243	1,0306317	31231,09	19340,89	1,6147701
5342,3449	0,5061647	0,1414141	16749,6	13785,435	1,2150215	76775,795	37778,015	2,0322877
463,23621	0,3793122	0,0537059	6140,4351	6743,8875	0,9105186	6657,2505	8625,4235	0,7718172
2035,5055	0,3287067	0,0431127	25869,109	32785,427	0,7890429	29252,614	47213,636	0,6195798
7113,126	0,4517462	0,0985882	42695,696	39372,909	1,0843927	102224,01	72149,897	1,4168282
4867,3909	0,4775732	0,0437006	66363,02	57888,746	1,146389	69950,146	111380,43	0,6280291

426,81145	0,2623942	0,0444808	6529,9447	10367,241	0,6298633	6133,7837	9595,411	0,6392414
1414,0349	0,4598627	0,0656051	19638,565	17790,554	1,103876	20321,349	21553,732	0,9428227
6362,1404	0,3034407	0,050177	59993,221	82363,791	0,7283931	91431,459	126794	0,7211024
3214,831	0,3473618	0,0437822	39890,09	47839,966	0,8338235	46200,911	73427,81	0,6292018
3467,6709	0,3648206	0,0435386	43208,962	49340,375	0,8757323	49834,519	79645,884	0,6257011
101333,03	0,5962097	0,119898	827464,45	578173,55	1,4311697	1456275,1	845160,34	1,7230756
32317,947	0,4513026	0,0852927	266959,66	246425,55	1,0833279	464447,01	378906,21	1,2257572
85114,656	0,4271204	0,0930641	669207,78	652707,42	1,0252799	1223198	914580,51	1,3374415
4009,375	0,4216013	0,0815663	26161,239	25850,226	1,0120314	57619,446	49154,79	1,1722041
413,09228	0,4697869	0,0262649	7852,6482	6963,4297	1,1276984	5936,6231	15727,913	0,3774578
963,54936	0,4729152	0,0343027	14590,733	12852,918	1,1352078	13847,34	28089,578	0,4929708
14760,641	0,7235188	0,376886	38416,778	22119,69	1,7367684	212127,82	39164,737	5,4162963
5547,1286	0,4845226	0,0317777	90230,559	77579,609	1,1630706	79718,779	174560,42	0,456683
54535,628	0,2331172	0,108226	293563,05	524608,21	0,5595853	783741,28	503904,98	1,5553354
17197,052	0,2311087	0,0978405	106098,21	191249,21	0,5547642	247141,91	175766,25	1,4060829
38728,2	0,2370647	0,1155849	212932,15	374181,53	0,5690611	556569,9	335062,89	1,6610909
5873,9279	0,187471	0,2098654	20946,498	46546,303	0,4500142	84415,27	27989,029	3,0160128
4250,9633	0,4728344	0,1496447	20337,595	17918,37	1,1350137	61091,354	28407,035	2,1505713
39462,948	0,4998848	0,1882173	179454,3	149551,88	1,1999468	567129,09	209666,94	2,7049047
111885,2	0,3292769	0,1200901	563341,71	712719,3	0,7904118	1607922,3	931676,79	1,725837
49861,264	0,2743052	0,1093313	213327,37	323981,72	0,658455	716565,15	456056,46	1,5712203
22077,255	0,6115546	0,0832247	232410,36	158317,23	1,4680042	317276,19	265272,94	1,1960368
1257,139	0,5723461	0,0439349	17590,738	12803,633	1,3738864	18066,57	28613,646	0,631397
14894,922	0,4227775	0,0404847	190838,56	188045,2	1,0148548	214057,59	367914,77	0,581813
2893,2039	0,4049483	0,1086421	19162,439	19713,292	0,9720568	41578,751	26630,598	1,5613149
2546,1251	0,5913909	0,0464726	34257,223	24131,563	1,4196023	36590,82	54787,702	0,6678656
4650,62	0,358087	0,0482558	48400,626	56308,038	0,8595687	66834,892	96374,231	0,6934934
15641,625	0,4408451	0,0515072	160652,52	151813,16	1,0582253	224788,6	303678,3	0,7402195
24679,398	0,4140408	0,0502744	250495,18	252036,91	0,9938829	354672,05	490893,67	0,7225028
8941,8775	0,4077866	0,0516321	90418,808	92370,601	0,97887	128505,32	173184,6	0,7420136
35285,242	0,2903692	0,103923	193960,02	278272,09	0,6970157	507090,53	339532,4	1,4934967
6522,0753	0,4229411	0,1380659	37404,642	36842,876	1,0152476	93729,912	47238,85	1,9841701
99184,104	0,4141015	0,1352832	532976,37	536178,15	0,9940285	1425392,5	733159,13	1,9441789
8804,3006	0,4016102	0,1193749	54221,108	56243,403	0,9640439	126528,18	73753,375	1,7155578
5499,1376	0,504636	0,0410357	78217,606	64570,509	1,2113519	79029,091	134008,6	0,5897315
2180,6673	0,4893782	0,0351601	33417,005	28446,63	1,1747263	31338,76	62021,145	0,5052915
24984,888	0,5173816	0,0695188	191759,57	154402,39	1,2419469	359062,3	359397,74	0,9990667
2602,9525	0,6580462	0,0618848	25082,15	15878,749	1,5796049	37407,497	42061,259	0,8893575
2934,6067	0,595012	0,0469529	41064,472	28750,7	1,4282947	42173,759	62501,072	0,6747686
218824,29	0,8624214	0,3057071	1462739,9	706570,51	2,0701967	3144763,1	715797,3	4,393371

51757,526	0,4950602	0,206957	267268,06	224903,9	1,1883656	743816,67	250088,26	2,9742167
87941,985	0,3194191	0,3385577	216687,93	282606,26	0,7667485	1263830	259754,78	4,8654735
62891,366	0,6437692	0,2187945	466128,41	301636,08	1,5453337	903823,08	287444,87	3,1443354
78,718054	0,6169576	0,0190503	2755,4218	1860,5473	1,4809738	1131,2713	4132,1269	0,2737746
3054,6275	0,7347203	0,0328118	58951,687	33425,826	1,7636569	43898,599	93095,446	0,471544
26096,243	0,472834	0,0978711	230004,99	202645,29	1,1350127	375033,78	266638,94	1,4065229
26395,219	0,3865752	0,0840715	209717,69	226000,32	0,9279531	379330,42	313961,6	1,2082064
29752,186	0,3720799	0,0545094	316623,97	354499,41	0,893158	427573,98	545817,16	0,7833649
2009,7385	0,4117652	0,0453436	26657,18	26969,477	0,9884204	28882,311	44322,469	0,6516404
1416,443	0,6467897	0,0587063	12694,217	8176,1857	1,5525843	20355,957	24127,6	0,8436793
22189,062	0,3701985	0,1102512	125289,6	140989,99	0,8886418	318882,99	201259,15	1,5844397
49908,378	0,3351614	0,1144989	250822,44	311759,97	0,804537	717242,23	435885,24	1,6454841
9103,199	0,5153924	0,0564798	94823,283	76645,194	1,2371719	130823,7	161176,22	0,8116812
3692,6582	0,6367019	0,0495951	57020,795	37308,268	1,5283689	53067,852	74456,08	0,7127403
1184,982	0,3686774	0,040022	13107,443	14810,828	0,8849905	17029,589	29608,295	0,5751628
432,11036	0,4428801	0,0474658	3970,8415	3735,1182	1,06311	6209,9354	9103,6181	0,6821393
7152,0446	0,259054	0,0745329	51918,573	83491,141	0,6218453	102783,31	95958,209	1,0711258
10451,864	0,2517478	0,0580403	100013,31	165500,79	0,6043072	150205,61	180079,35	0,8341079
7203,7344	0,2638992	0,0836716	49185,647	77644,053	0,633476	103526,16	86095,382	1,2024589
5068,6833	0,3330626	0,087335	38733,286	48446,942	0,7994991	72842,955	58037,261	1,2551067
1222,5489	0,232733	0,0229811	13815,759	24730,036	0,5586631	17569,47	53198,069	0,3302652
15323,838	0,2629942	0,0496757	176430,55	279470,26	0,6313035	220221,62	308477,85	0,7138977
2127,9644	0,7340444	0,1532498	23835,836	13527,452	1,7620344	30581,357	13885,594	2,2023803
2379,3968	0,2854074	0,1503854	14318,101	20899,124	0,6851053	34194,737	15821,989	2,161216
14978,443	0,4745389	0,0675469	159248,57	139801,43	1,1391054	215257,89	221748,93	0,970728
119894,19	0,3246097	0,1615427	863219,13	1107815,5	0,7792084	1723020,9	742182,8	2,3215586
49529,52	0,3717893	0,1455164	376483,54	421848,96	0,8924605	711797,61	340370,72	2,0912422
3617,2125	0,384406	0,0414127	44439,106	48159,621	0,9227462	51983,608	87345,469	0,5951495
2230,1672	0,4331913	0,0474227	30006,719	28856,7	1,0398527	32050,133	47027,388	0,6815206
1058,6128	0,3739015	0,0377432	14093,928	15703,003	0,8975307	15213,514	28047,797	0,5424139
3571,886	0,284658	0,0651952	28700,82	42002,859	0,6833063	51332,214	54787,542	0,9369322
628,79599	0,3568298	0,041555	4633,1473	5409,0738	0,8565509	9036,5398	15131,64	0,597195
3441,4085	0,2635753	0,0658956	19061,424	30127,183	0,6326985	49457,098	52225,15	0,9469977
7369,9266	0,2348743	0,0564799	56094,253	99492,594	0,5638033	105914,53	130487,59	0,8116828
774,35096	0,3287025	0,0512631	9072,7972	11498,632	0,7890327	11128,336	15105,427	0,7367111
1238,4655	0,6727609	0,0428232	18848,536	11671,451	1,6149266	17798,209	28920,43	0,6154199
1453,6743	0,4537333	0,028545	23026,825	21141,77	1,0891626	20891,013	50925,708	0,4102253

7584,249	0,3650525	0,1049255	42502,436	48502,757	0,8762891	108994,6	72282,196	1,5079038
12911,779								
14277,646								
14188,239	0,5186944	0,0325365	337780,28	271288,07	1,2450982	203901,72	436071,64	0,4675877
476,00045	0,3064917	0,0478602	5481,2594	7450,2282	0,735717	6840,6877	9945,6358	0,687808
1813,8684	0,3464371	0,0580837	18181,578	21863,267	0,8316039	26067,427	31228,545	0,8347308
12459,983	0,4557696	0,0674018	131871,53	120535,11	1,0940507	179064,64	184861,18	0,9686438
54278,322	0,5448269	0,0737162	382933,76	292801,32	1,307828	780043,48	736314,8	1,0593886
88682,947	0,6160484	0,0741804	614769,9	415724,59	1,4787913	1274478,5	1195503,4	1,0660601
62724,011	0,3371553	0,0394079	504251,78	623053,61	0,8093233	901417,99	1591660,5	0,5663381
101807,59	0,4666561	0,0623152	769227,33	686697,8	1,1201832	1463095,2	1633752,1	0,895543
10294,546	1,3126299	0,1235737	95994,079	30465,624	3,1508982	147944,77	83306,952	1,7758995
25932,741	0,5921713	0,1179807	156426,36	110045,04	1,4214757	372684,07	219804,92	1,695522
2214,8931	0,556524	0,0299497	23936,467	17917,774	1,3359063	31830,625	73953,817	0,4304122
2569,5991	0,4521644	0,0286138	27512,819	25348,174	1,0853965	36928,168	89802,683	0,4112145
4394,2162	0,3205823	0,0881429	30044,737	39042,425	0,7695408	63150,068	49853,307	1,2667177
2137,5584	0,2459417	0,0509586	21902,652	37099,88	0,5903699	30719,235	41946,968	0,7323351
3083,3349	0,4810736	0,0357708	48079,541	41634,823	1,1547915	44311,158	86196,881	0,5140692
2472,9521	0,3922955	0,0294334	41134,486	43681,817	0,9416844	35539,238	84018,47	0,4229932
3008,0673	0,3946939	0,0403204	43966,127	46405,105	0,9474416	43229,474	74604,099	0,5794517
34931,188	1,0366146	0,1849915	265174,29	106566,82	2,4883382	502002,35	188825,95	2,6585454
7551,5699	0,6429942	0,2328816	37862,162	24530,492	1,5434734	108524,96	32426,652	3,3467829
2249,9654	0,5240108	0,0240562	34862,373	27715,621	1,2578601	32334,655	93529,571	0,3457158
6769,3504	0,4506002	0,0559814	72850,686	67351,95	1,0816418	97283,546	120921,5	0,8045182
42615,831								
42903,419	0,4373962	0,2365538	150910,33	143731,47	1,0499464	616572,71	181368,51	3,3995577
1860,5776	0,554173	0,0408227	16054,818	12068,909	1,3302626	26738,693	45577,065	0,5866699
1686,8268	0,5374705	0,0457993	14465,234	11211,888	1,2901693	24241,689	36830,812	0,6581905
4893,3861	0,6804773	0,065372	31595,929	19343,07	1,6334496	70323,727	74854,416	0,9394733
1886,4299	0,426016	0,0532135	21866,599	21382,734	1,0226288	27110,222	35450,185	0,7647413
1862,0854	0,5233968	0,0302336	39127,197	31142,653	1,2563861	26760,363	61589,957	0,4344923
27235,624	0,3196493	0,1485244	135692,24	176843,52	0,7673012	391408,03	183374,7	2,1344713
3833,312	0,4289514	0,0590161	43043,103	41802,612	1,029675	55089,213	64953,678	0,8481308
3931,3805	0,4267097	0,059332	37545,319	36654,829	1,0242939	56498,573	66260,746	0,8526703
14984,662	0,3966117	0,4563341	38750,72	40702,608	0,9520451	215347,26	32837,044	6,5580586
3457,2472	0,3977792	0,19369	12777,739	13381,966	0,9548477	49684,719	17849,38	2,7835543
37800,009	0,748221	0,1368155	146197,06	81398,552	1,7960646	543230,7	276284,63	1,9661995
10468,849								

8591,6232	0,3045633	0,0802952	39393,932	53883,983	0,731088	123471,75	107000,4	1,1539373
4324,9338	0,2709997	0,0636502	24674,325	37930,139	0,6505203	62154,397	67948,448	0,9147287
6134,2759	0,3144314	0,0711243	32913,8	43607,386	0,7547758	88156,777	86247,275	1,0221399
6991,7197	0,3733644	0,0913726	35582,522	39701,944	0,8962413	100479,26	76518,819	1,3131313
310,22011	0,2458138	0,0269783	6038,5157	10233,682	0,5900629	4458,2287	11498,871	0,3877101
1900,1864	0,3883747	0,0749789	17556,428	18831,859	0,9322727	27307,919	25342,952	1,0775351
4541,263	0,4324502	0,0841189	31248,01	30101,923	1,0380736	65263,303	53986,221	1,2088882
4204,2579	0,698123	0,0712462	43763,794	26115,055	1,6758071	60420,143	59010,308	1,0238913
7373,2675	0,2659615	0,0720592	64876,827	101619,92	0,6384263	105962,55	102322,3	1,0355763
4475,1344	0,2849457	0,0460624	57526,227	84103,036	0,683997	64312,957	97153,704	0,6619712
8255,8608	0,2117672	0,0452196	94446,576	185795,62	0,5083359	118646,45	182572,75	0,6498585
3119,9105	0,3650191	0,038198	37973,871	43338,834	0,8762089	44836,792	81677,278	0,5489506
1661,4502	0,6373969	0,0318524	29939,715	19567,964	1,5300373	23876,998	52160,946	0,4577562
11691,398	0,3531014	0,0920287	77476,792	91407,15	0,847601	168019,18	127040,74	1,3225614
9099,4293	0,3981704	0,0639915	64583,346	67570,876	0,9557867	130769,53	142197,42	0,9196336
12160,519	0,4099228	0,0464185	123374,42	125380,8	0,9839977	174760,99	261975,52	0,667089
1994,4618	0,5726606	0,1168268	10407,012	7570,7122	1,3746411	28662,767	17071,954	1,6789389
5415,5214	0,2853977	0,1088391	32893,493	48013,946	0,6850821	77827,428	49757,142	1,5641459
14645,393	0,3456596	0,0715453	125359,36	151083,17	0,8297374	210471,57	204701,1	1,0281897
2633,7657	0,3425092	0,0464717	31851,484	38740,508	0,8221752	37850,319	56674,626	0,667853
2099,3522	0,4414299	0,0517523	27845,889	26278,905	1,0596289	30170,167	40565,401	0,7437414
64497,332	0,4914765	0,3174599	257707,5	218440,05	1,179763	926902,71	203166,85	4,5622733
97441,324	0,3013507	0,1536231	482089,56	666443,76	0,7233762	1400346,7	634288,04	2,2077457
62673,239	0,5170237	0,3856319	245131,06	197513,05	1,2410879	900688,34	162520,88	5,5419855
3720,813	0,3153093	0,0242716	81161,907	107231,75	0,7568832	53472,47	153298,89	0,3488119
16903,664	0,363023	0,1117793	102941,61	118131,24	0,8714173	242925,59	151223,55	1,6064005
4295,6281	0,6004244	0,1001836	27894,473	19353,868	1,4412867	61733,24	42877,549	1,4397568
2197,8023	0,1727515	0,063404	19535,911	47110,72	0,4146808	31585,01	34663,484	0,9111897
723,01837	0,6222288	0,0658872	6664,9239	4462,2409	1,4936271	10390,627	10973,577	0,9468769
3358,8885	0,4963384	0,0874833	29231,943	24535,093	1,1914339	48271,188	38394,614	1,2572385
24610,032	0,5010401	0,0891676	169647,41	141053,11	1,2027201	353675,17	275997,33	1,2814442
29387,893	0,8538056	0,1067963	173873,31	84836,325	2,0495148	422338,67	275176,97	1,5347893
15924,69	0,7246306	0,0933401	103328,12	59403,194	1,739437	228856,57	170609,23	1,3414079
4296,5775	0,8088053	0,0370301	94850,925	48854,607	1,941494	61746,885	116029,26	0,5321665
2331,5864	0,6776105	0,0411912	39549,502	24314,694	1,6265679	33507,646	56603,983	0,5919662
7559,3387	0,4311435	0,0554119	84900,675	82034,625	1,0349371	108636,61	136420,81	0,7963346
1072,5732	1,0881884	0,0378014	24482,304	9372,5144	2,6121384	15414,141	28373,889	0,5432509
2627,9017	1,0096343	0,0528641	44028,897	18166,933	2,4235734	37766,046	49710,487	0,7597199

2509,2299 0,5192312 0,0655611 25069,422 20113,676 1,2463869 36060,592 38273,153 0,9421903
2573,7817 0,5200108 0,0462006 30132,889 24139,95 1,2482581 36988,277 55708,821 0,6639573

6003,9621 0,7094449 0,047598 78071,102 45843,69 1,7029847 86284,015 126139,08 0,6840387
13972,589 0,4729392 0,0765717 98469,621 86737,091 1,1352654 200802,57 182477,3 1,1004249

10963,597 0,2701576 0,1126868 59963,057 92464,388 0,6484989 157559,81 97292,605 1,6194429
15571,666 0,2902517 0,1247432 89451,88 128387,46 0,6967338 223783,2 124829,76 1,7927071

4208,536 0,2785962 0,0507941 47741,129 71388,04 0,6687553 60481,624 82854,798 0,7299713
11418,078 0,3214256 0,2294811 70142,379 90909,217 0,7715651 164091,24 49756,078 3,2979134
5337,1301 0,3599215 0,1962718 37076,222 42913,665 0,8639724 76700,852 27192,54 2,8206579

700,32475 0,4232374 0,0555896 4951,594 4873,8141 1,0159587 10064,492 12598,116 0,7988887
857,21305 0,2935107 0,0398001 8264,3891 11729,912 0,7045568 12319,162 21537,985 0,5719738

1470,6887 0,4336516 0,0608702 11718,485 11257,408 1,0409576 21135,53 24161,054 0,8747768
2361,0921 0,4123917 0,0545523 19574,127 19773,357 0,9899243 33931,677 43281,276 0,7839805
3287,6592 0,3611224 0,0418016 34156,431 39402,702 0,8668551 47247,539 78649,104 0,6007384

1862,4936 0,2939331 0,0600188 17023,157 24126,789 0,7055708 26766,229 31031,846 0,8625407
3607,4957 0,3339726 0,0706346 30468,969 38006,234 0,8016835 51843,966 51072,646 1,0151024

1656,8054 1,1873702 0,0335644 6531,0115 2291,4071 2,8502188 23810,248 49362,026 0,4823596
3162,2206 0,5810449 0,0347121 21953,52 15739,917 1,3947672 45444,839 91098,473 0,498854

2184,538 0,2726821 0,0461997 31427,193 48012,776 0,654559 31394,387 47284,676 0,6639442
25122,556 0,3785705 0,0861627 189152,85 208148,89 0,9087382 361040,74 291571,22 1,2382592

3350,8286 0,3477779 0,035388 52312,851 62663,454 0,8348223 48155,358 94688,279 0,5085673
10369,448 0,4924027 0,0490414 137248,62 116116,92 1,1819864 149021,2 211442,81 0,7047825
5031,1393 0,5001614 0,0442514 58748,078 48931,83 1,2006107 72303,404 113694,46 0,6359448

9292,8291
75263,003
15079,69

4408,3866 0,4060567 0,0530217 41068,083 42133,319 0,9747175 63353,713 83143,093 0,7619841
7004,1413 0,7863326 0,127614 54195,866 28712,29 1,8875494 100657,77 54885,35 1,8339642

8663,2783 0,1550493 0,1317226 58558,285 157335,44 0,3721875 124501,52 65769,121 1,8930088
6686,8653 0,1458012 0,0976181 54590,345 155977,77 0,349988 96098,139 68500,294 1,4028865

4429,2691 0,4055284 0,0538963 47642,685 48942,133 0,9734493 63653,819 82181,309 0,7745535
836,90285 0,5174003 0,0709843 6888,4617 5546,3022 1,2419918 12027,281 11789,966 1,0201285
160,47164 0,4353136 0,0663243 1240,1357 1186,7927 1,0449472 2306,1667 2419,4983 0,9531591
1155,5771 0,4950882 0,0773859 8568,6534 7210,0445 1,1884328 16607,006 14932,663 1,1121262

16603,298 0,5272436 0,0650418 1403394,5 1108859,1 1,2656203 238608,97 255271,05 0,9347279
2382,0106 0,8891623 0,1964123 79084,807 37052,709 2,1343866 34232,3 12127,605 2,8226761

2530,7557	0,1535649	0,1008261	18151,622	49241,513	0,3686244	36369,943	25100,198	1,4489903
18904,895	0,3147993	0,1329045	128957,74	170655,98	0,7556591	271685,62	142244,21	1,9099942
21368,659	0,2896172	0,1736649	102381,54	147266,92	0,6952107	307092,83	123045,34	2,4957698
178,33392	0,2627539	0,035486	1943,4983	3081,3634	0,6307267	2562,8686	5025,4795	0,5099749
42890,288	0,4998147	0,1896432	210170,45	175174,38	1,1997785	616384	226163,03	2,7253969
38058,537	0,4693644	0,1263749	207626,6	184281,08	1,1266843	546946,05	301155,73	1,8161569
3020,7146	0,4105076	0,058129	26264,467	26653,569	0,9854015	43411,231	51965,667	0,8353829
3191,9606	0,437615	0,0386389	44347,389	42216,648	1,0504716	45872,237	82610,11	0,555286
2508,7886	0,421286	0,0311731	36823,762	36413,218	1,0112746	36054,25	80479,389	0,4479936
2874,0483	0,4670477	0,0517674	33005,375	29439,564	1,1211231	41303,463	55518,497	0,7439586
47292,639	0,2842132	0,0426713	399686,4	585845,47	0,6822386	679650,98	1108300	0,6132374
3314,7741	0,7927252	0,0443913	35617,09	18717,321	1,9028947	47637,212	74671,71	0,6379553
2394,9589	0,7962874	0,0379242	37233,031	19478,991	1,9114456	34418,384	63151,193	0,5450156
6621,4223	0,3293183	0,0456975	87763,819	111021,62	0,7905111	95157,646	144896,91	0,6567265
928,33936	0,3455775	0,045494	13729,03	16550,163	0,8295405	13341,331	20405,744	0,6538027
4215,1381	0,1349758	0,0533779	32238,539	99500,974	0,3240022	60576,504	78967,902	0,7671029
13496,115	0,178625	0,1777718	63411,401	147888	0,4287799	193955,08	75918,199	2,5547903
5812,3946	0,6688277	0,0226044	79313,354	49401,481	1,6054853	83530,963	257135,48	0,324852
3563,5123	0,7088099	0,0198686	62352,567	36646,5	1,7014603	51211,873	179353,93	0,2855353
7773,9869	0,6725928	0,0283931	112395,8	69615,471	1,6145233	111721,36	273798,83	0,4080418
823,05779	0,5583456	0,034042	14699,69	10967,635	1,3402789	11828,311	24177,731	0,4892234
19843,386	0,4370432	0,1310596	115549,29	110141,47	1,0490989	285172,85	151407,29	1,8834816
18837,368	0,9626729	0,2190272	132234,55	57223,461	2,310845	270715,19	86004,707	3,1476788
6018,9435	1,3742199	0,1749341	44426,393	13467,679	3,2987417	86499,314	34406,915	2,5140096
1063,9818	0,3893345	0,0412437	18126,765	19395,695	0,9345767	15290,673	25797,416	0,5927211
7742,5264	0,3766616	0,0479297	90964,619	100607,2	0,9041562	111269,23	161539,22	0,6888063
5405,3294	0,3518034	0,0399052	77075,645	91269,382	0,8444852	77680,956	135454,35	0,5734844
10987,968	0,4745228	0,081794	129053,4	113297,48	1,1390668	157910,06	134337,17	1,1754755
254,15227	0,5318729	0,0724584	1376,7705	1078,3547	1,2767326	3652,4677	3507,5601	1,041313
3637,8165	0,3975637	0,0349717	52781,154	55306,998	0,9543305	52279,712	104021,61	0,5025851
744,30057	0,3220756	0,0434354	9161,5674	11850,043	0,7731253	10696,477	17135,805	0,6242179
13189,52	1,4617606	0,1215155	72673,73	20711,385	3,5088784	189548,96	108541,9	1,7463207
10345,664	0,4905499	0,0753852	96079,728	81593,673	1,1775389	148679,39	137237,43	1,0833735
12349,243	0,4518113	0,0794713	96059,755	88571,155	1,084549	177473,19	155392,43	1,1420968
16972,373	0,4637259	0,0996627	64311,082	57773,991	1,1131494	243913,02	170298,08	1,4322711
13379,081	0,3407227	0,0397793	139707,62	170815,39	0,8178866	192273,16	336332,74	0,5716754

18351,598	0,3134123	0,0456196	158169,25	210239,31	0,7523296	263734,1	402274	0,6556081
16893,903	0,2572188	0,040177	143347,59	232164,43	0,6174399	242785,3	420486,87	0,5773909
16003,134	0,2998228	0,0464378	134141,76	186383,42	0,7197086	229983,9	344614,56	0,6673656
43240,47	0,4338255	0,0838445	256532,07	246339,76	1,041375	621416,54	515722,15	1,2049445
60641,699	0,3946571	0,2051267	322465,34	340385,51	0,9473533	871492,71	295630,46	2,9479124
49540,887	0,4269536	0,2007331	291090,66	284024,34	1,0248793	711960,95	246799,84	2,8847708
4871,6545	0,3157456	0,0467793	54982,036	72542,324	0,7579304	70011,419	104141,26	0,6722736
1907,555	0,5369801	0,0441679	45425,97	35241,467	1,288992	27413,814	43188,751	0,6347443
5140,1032	0,4650154	0,0689037	70695,393	63333,244	1,1162446	73869,344	74598,416	0,9902267
9094,2285	0,5096748	0,0605833	102142,26	83487,269	1,2234471	130694,79	150111,14	0,8706535
25300,826	0,2342024	0,0857778	165558,54	294488,37	0,5621904	363602,69	294957,83	1,2327277
9292,8291								
6294,9075	0,5492492	0,0852659	63989,657	48534,246	1,3184434	90465,243	73826,806	1,2253712
84293,583	0,3253021	0,0667997	520293,9	666300,05	0,7808703	1211398,2	1261886,1	0,9599901
7521,6543	0,4952249	0,0902991	40006,886	33654,274	1,1887609	108095,04	83297,074	1,2977051
7320,933	0,4356864	0,0948443	32599,865	31170,928	1,045842	105210,44	77188,927	1,363025
4195,5882	0,3508368	0,1203248	44435,837	52763,808	0,8421651	60295,549	34868,871	1,7292085
6449,5267	0,5150757	0,1126605	38675,067	31280,086	1,2364118	92687,303	57247,437	1,6190647
6949,4044	0,4777471	0,0726028	100499,01	87633,803	1,1468064	99871,135	95718,173	1,0433874
3641,109	0,3246799	0,0502205	48668,468	62445,366	0,7793768	52327,029	72502,394	0,7217283
12685,255	0,2759497	0,0486743	138169,09	208587,84	0,6624024	182302,07	260615,2	0,6995067
1658,1523	0,303217	0,0561858	17291,591	23756,876	0,7278563	23829,603	29511,947	0,8074561
1469,2702	0,455897	0,0297822	25381,08	23192,701	1,0943564	21115,146	49333,896	0,4280048
5525,885	0,9632608	0,0891401	47084,257	20362,907	2,3122562	79413,483	61991,009	1,2810484
19207,686	0,4424117	0,0844373	158265,83	149028,2	1,0619858	276037,09	227478,58	1,2134641
7666,6536	0,4110932	0,0570657	95134,849	96406,706	0,9868074	110178,85	134347,88	0,8201011
6955,4695	0,5456887	0,0824967	68380,714	52203,134	1,3098967	99958,297	84312,138	1,1855742
9631,8806	0,6513149	0,0831602	102152,66	65338,117	1,5634467	138421,48	115823,14	1,1951107
3791,6035	0,4258586	0,0685213	32968,683	32251,067	1,0222509	54489,813	55334,634	0,9847325
20162,404	0,3698723	0,1080199	116898,2	131663,06	0,8878587	289757,52	186654,56	1,5523731
11107,014	0,3102027	0,13107	66901,287	89845,61	0,744625	159620,89	84741,104	1,88363
1694,9214	0,7742132	0,0490204	27479,302	14786,08	1,8584576	24358,019	34575,834	0,704481
19384,888	0,6556325	0,0999816	121096,17	76944,549	1,5738109	278583,7	193884,62	1,436853
6134,8168	0,6796514	0,0935254	42810,13	26240,267	1,6314671	88164,551	65595,204	1,3440701
9224,1238	0,5192447	0,1310054	64216,021	51520,405	1,2464192	132561,54	70410,233	1,8827027
5465,821	0,3768151	0,0710139	53845,565	59529,141	0,9045245	78550,292	76968,365	1,020553
20866,509	0,4824238	0,0515641	238873,77	206275,49	1,1580327	299876,34	404671,49	0,7410365

1905,2387	0,6532633	0,124832	11577,523	7383,0415	1,5681238	27380,526	15262,419	1,7939834
5084,2315	0,7527878	0,0977589	36347,509	20114,535	1,8070271	73066,401	52007,853	1,4049109
7629,1575	0,646929	0,0816693	57411,576	36970,115	1,5529185	109639,99	93415,273	1,1736837
10313,6	0,6614453	0,0705557	85937,655	54124,949	1,5877642	148218,59	146176,76	1,0139682
16303,959	0,3539322	0,0320771	173997,5	204800,4	0,8495955	234307,11	508274,52	0,4609854
7393,4188	0,444789	0,0747147	58532,459	54821,468	1,0676923	106252,15	98955,388	1,0737379
15686,551	0,5569079	0,0613301	153093,32	114519,86	1,3368276	225434,24	255772,42	0,881386
7979,7573	0,4227544	0,0413144	108093,29	106516,9	1,0147994	114678,52	193146,97	0,5937371
4590,894	0,5857695	0,0923852	33059,074	23511,039	1,4061086	65976,559	49692,952	1,3276845
911,30093	0,5545673	0,0727644	7956,8851	5977,1856	1,3312093	13096,469	12524,002	1,0457096
12024,871	0,4563962	0,2464985	53956,254	49250,164	1,0955548	172811,58	48782,733	3,5424743
13768,312	0,2785573	0,2161261	75456,311	112846,71	0,668662	197866,88	63705,004	3,1059865
3564,8196	0,4681279	0,0332231	35825,334	31881,126	1,1237161	51230,661	107299,53	0,4774547
7535,9288	0,4465734	0,0503628	71744,161	66927,049	1,0719756	108300,18	149632,89	0,7237726
11336,535	0,3881799	0,0595237	134884,45	144756,07	0,9318052	162919,38	190454,12	0,8554258
967,48007	0,3876572	0,0685449	11628,835	12496,728	0,9305504	13903,829	14114,554	0,9850704
244,87725	0,29443	0,0373588	1331,6968	1884,218	0,7067636	3519,1748	6554,7351	0,5368905
26204,647	0,8064994	0,1296507	156692,23	80937,793	1,9359588	376591,68	202117,29	1,8632333
1026,1113	0,4723618	0,054001	9231,1151	8141,1801	1,1338792	14746,429	19001,7	0,7760584
4895,0426	0,6004982	0,0567488	71476,71	49586,196	1,4414639	70347,534	86258,075	0,8155472
374,53386	0,6329004	0,0262194	8464,1039	5571,2614	1,5192437	5382,4931	14284,599	0,3768039
6852,629	0,6458125	0,1028931	77059,492	49708,155	1,5502384	98480,359	66599,484	1,4786955
12799,341	0,6744393	0,1297343	100675,52	62185,475	1,6189556	183941,62	98658,101	1,864435
17941,457	0,5941238	0,0878032	139497,56	97813,234	1,4261624	257839,89	204337,22	1,2618352
16191,037	0,3300953	0,1100094	105859,76	133597,88	0,7923761	232684,3	147178,7	1,5809644
6918,8324	0,2918949	0,1326713	24182,067	34512,372	0,7006782	99431,779	52150,166	1,9066436
1152,1836	0,6128477	0,03433	14056,743	9555,207	1,4711082	16558,236	33561,986	0,4933628
13995,885	0,3441985	0,0624036	144062,82	174361,59	0,8262303	201137,38	224280,04	0,8968135
1567,777	0,5379949	0,1277931	10057,891	7788,1925	1,2914281	22530,803	12268,089	1,8365374
5247,465	0,3422603	0,0713844	52982,589	64488,847	0,8215775	75412,259	73509,935	1,0258785
8628,1447	0,2226114	0,2063936	37835,15	70803,703	0,5343668	123996,61	41804,323	2,9661194

<i>IR.N116</i>	<i>IR.N114</i>	<i>IR.N(116/11</i>	<i>IR.N117</i>	<i>IR.N115</i>	<i>IR.N(117/115)</i>
0,4332989	0,5667011	0,7645987	0,5877663	0,4122337	1,4258087
0,4768773	0,5231227	0,9115974	0,5622091	0,4377909	1,2841953
0,503054	0,496946	1,012291	0,5305444	0,4694556	1,1301269
0,3812961	0,6187039	0,6162821	0,6233233	0,3766767	1,6547965
0,4022663	0,5977337	0,6729857	0,6126955	0,3873045	1,5819478
0,5159782	0,4840218	1,0660226	0,3525755	0,6474245	0,5445816
0,1488601	0,8511399	0,174895	0,6696118	0,3303882	2,0267426
0,4481305	0,5518695	0,8120225	0,6743998	0,3256002	2,0712515
0,5099445	0,4900555	1,0405851	0,6602037	0,3397963	1,9429398
0,4869655	0,5130345	0,9491867	0,6613345	0,3386655	1,9527659
0,4708596	0,5291404	0,8898576	0,6324198	0,3675802	1,7204946
0,48486	0,51514	0,9412197	0,447994	0,552006	0,8115745
0,5107578	0,4892422	1,0439776	0,6628833	0,3371167	1,9663316
0,4708811	0,5291189	0,8899346	0,5258884	0,4741116	1,1092079
0,4955317	0,5044683	0,9822851	0,6120243	0,3879757	1,577481
0,4790277	0,5209723	0,9194878	0,7525007	0,2474993	3,040416
0,4704269	0,5295731	0,8883134	0,7570503	0,2429497	3,1160788
0,4659034	0,5340966	0,8723204	0,7453277	0,2546723	2,9266142
0,3653842	0,6346158	0,5757565	0,7208847	0,2791153	2,5827483
0,5337352	0,4662648	1,1447042	0,7576744	0,2423256	3,1266791
0,5488468	0,4511532	1,2165421	0,4777817	0,5222183	0,914908
0,5398626	0,4601374	1,1732637	0,5214911	0,4785089	1,0898253
0,5206208	0,4793792	1,0860311	0,5966615	0,4033385	1,4793071
0,493653	0,506347	0,9749304	0,4672263	0,5327737	0,8769697
0,533672	0,466328	1,1444131	0,6124471	0,3875529	1,5802929
0,5657938	0,4342062	1,3030531	0,5480592	0,4519408	1,2126792
0,4895788	0,5104212	0,9591663	0,7426092	0,2573908	2,8851433
0,5050484	0,4949516	1,0203994	0,7385459	0,2614541	2,8247634
0,3931649	0,6068351	0,647894	0,5760704	0,4239296	1,3588824
0,4059698	0,5940302	0,6834161	0,5610499	0,4389501	1,2781632
0,345047	0,654953	0,5268272	0,5369124	0,4630876	1,1594186
0,5130321	0,4869679	1,0535235	0,7282053	0,2717947	2,6792473
0,435344	0,564656	0,7709899	0,5882947	0,4117053	1,4289221
0,4890077	0,5109923	0,9569766	0,6380767	0,3619233	1,7630161
0,5912695	0,4087305	1,4465997	0,4095843	0,5904157	0,6937218
0,4187185	0,5812815	0,7203368	0,6376259	0,3623741	1,7595789
0,444591	0,555409	0,8004749	0,6003976	0,3996024	1,5024877
0,5425537	0,4574463	1,1860487	0,6469641	0,3530359	1,832573
0,4853813	0,5146187	0,9431862	0,6968421	0,3031579	2,2986107
0,6017382	0,3982618	1,5109112	0,7333499	0,2666501	2,7502333
0,4575094	0,5424906	0,8433499	0,8384837	0,1615163	5,1913245
0,4324232	0,5675768	0,7618763	0,8505115	0,1494885	5,6894786
0,4820569	0,5179431	0,9307139	0,67647	0,32353	2,0909033
0,4167572	0,5832428	0,7145519	0,6894114	0,3105886	2,2196927
0,4354923	0,5645077	0,7714551	0,5962992	0,4037008	1,4770819
0,4428256	0,5571744	0,7947703	0,6190004	0,3809996	1,6246745
0,4730312	0,5269688	0,8976454	0,5598852	0,4401148	1,2721343
0,5000427	0,4999573	1,0001706	0,8152085	0,1847915	4,4115054
0,3901513	0,6098487	0,6397509	0,6303457	0,3696543	1,7052304
0,4936887	0,5063113	0,9750695	0,5944809	0,4055191	1,4659751

0,4013327 0,5986673 0,6703768 0,4902014 0,5097986 0,9615589
0,3848416 0,6151584 0,6255976 0,4483221 0,5516779 0,8126518
0,4078091 0,5921909 0,6886447 0,4937708 0,5062292 0,9753899
0,4115364 0,5884636 0,6993406 0,4986131 0,5013869 0,9944679

0,4422957 0,5577043 0,793065 0,511136 0,488864 1,0455587
0,468274 0,531726 0,8806678 0,2921818 0,7078182 0,4127922
0,4088148 0,5911852 0,6915172 0,7119972 0,2880028 2,4721879
0,4164419 0,5835581 0,7136253 0,4994458 0,5005542 0,9977857
0,479987 0,520013 0,9230289 0,516442 0,483558 1,0680043
0,3808862 0,6191138 0,6152121 0,7266078 0,2733922 2,6577488
0,4036498 0,5963502 0,6768671 0,5324109 0,4675891 1,1386299
0,4496325 0,5503675 0,8169678 0,5341228 0,4658772 1,1464884
0,3752065 0,6247935 0,6005289 0,4945813 0,5054187 0,9785578
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0,5554358 0,4445642 1,2493939 0,3872591 0,6127409 0,6320111
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0,4167477 0,5832523 0,7145239 0,6349424 0,3650576 1,7392938
0,594945 0,405055 1,4688005 0,5487909 0,4512091 1,2162672
0,3598129 0,6401871 0,5620434 0,5705923 0,4294077 1,3287893
0,4118216 0,5881784 0,7001645 0,6342334 0,3657666 1,733984
0,3277197 0,6722803 0,4874749 0,4963006 0,5036994 0,9853112
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0,4960173 0,5039827 0,9841951 0,6872988 0,3127012 2,197941

0,5853902	0,4146098	1,4119062	0,845307	0,154693	5,4644167
0,5749974	0,4250026	1,3529267	0,8492513	0,1507487	5,6335547
0,4788187	0,5211813	0,9187182	0,7729321	0,2270679	3,40397
0,586627	0,413373	1,4191227	0,8346397	0,1653603	5,0474017
0,5101667	0,4898333	1,0415109	0,6375647	0,3624353	1,7591134
0,5001274	0,4998726	1,0005097	0,6469266	0,3530734	1,8322724
0,4749764	0,5250236	0,9046763	0,6216551	0,3783449	1,643091
0,3302591	0,6697409	0,4931148	0,6759287	0,3240713	2,0857412
0,3407034	0,6592966	0,516768	0,6116466	0,3883534	1,5749741
0,4917279	0,5082721	0,9674502	0,6416166	0,3583834	1,7903079
0,4245358	0,5754642	0,7377274	0,607669	0,392331	1,5488683
0,3665892	0,6334108	0,5787542	0,5951706	0,4048294	1,4701765
0,3856782	0,6143218	0,6278114	0,5846724	0,4153276	1,4077377
0,5491853	0,4508147	1,2182062	0,5604406	0,4395594	1,2750054
0,5797076	0,4202924	1,3792961	0,5872671	0,4127329	1,4228747
0,5934332	0,4065668	1,4596203	0,5009199	0,4990801	1,0036862
0,5630719	0,4369281	1,288706	0,4551341	0,5448659	0,8353138
0,5312244	0,4687756	1,1332168	0,4106423	0,5893577	0,6967624
0,570809	0,429191	1,3299649	0,4047548	0,5952452	0,6799798
0,569378	0,430622	1,3222225	0,542305	0,457695	1,1848611
0,5641668	0,4358332	1,2944559	0,4459888	0,5540112	0,8050177
0,4225923	0,5774077	0,7318784	0,3981672	0,6018328	0,6615912
0,5129356	0,4870644	1,0531167	0,3897448	0,6102552	0,6386586
0,4327857	0,5672143	0,763002	0,5298068	0,4701932	1,1267853
0,3980452	0,6019548	0,6612544	0,5318516	0,4681484	1,1360746
0,5693076	0,4306924	1,3218427	0,7455172	0,2544828	2,9295386
0,4747002	0,5252998	0,9036748	0,6514085	0,3485915	1,8686873
0,3727042	0,6272958	0,5941441	0,611724	0,388276	1,5754878
0,3386422	0,6613578	0,5120408	0,5883875	0,4116125	1,4294694
0,4327728	0,5672272	0,762962	0,6507029	0,3492971	1,8628925
0,4058873	0,5941127	0,6831824	0,5545899	0,4454101	1,2451219
0,3936236	0,6063764	0,6491407	0,5198533	0,4801467	1,0826969
0,3761794	0,6238206	0,603025	0,5659834	0,4340166	1,3040596
0,39951	0,60049	0,6653067	0,5836601	0,4163399	1,4018836
0,3657016	0,6342984	0,5765449	0,5352258	0,4647742	1,1515824
0,3969631	0,6030369	0,6582733	0,5510193	0,4489807	1,2272672

0,4503701	0,5496299	0,819406	0,8657518	0,1342482	6,4488883
0,3659526	0,6340474	0,5771691	0,8927189	0,1072811	8,3213025
0,4028297	0,5971703	0,6745642	0,8779544	0,1220456	7,1936573
0,3808303	0,6191697	0,6150662	0,8047536	0,1952464	4,1217344
0,3976558	0,6023442	0,6601803	0,6125653	0,3874347	1,5810801
0,3915437	0,6084563	0,6435034	0,6437728	0,3562272	1,8071972
0,4330684	0,5669316	0,7638812	0,8052764	0,1947236	4,1354842
0,3512953	0,6487047	0,5415336	0,4581062	0,5418938	0,84538
0,4850555	0,5149445	0,9419567	0,4514209	0,5485791	0,8228913
0,4305403	0,5694597	0,7560504	0,8446528	0,1553472	5,437192
0,3903906	0,6096094	0,6403946	0,8445591	0,1554409	5,4333142
0,3730381	0,6269619	0,5949933	0,450061	0,549939	0,8183834
0,4145871	0,5854129	0,708196	0,5464718	0,4535282	1,2049345
0,4355312	0,5644688	0,7715772	0,7796631	0,2203369	3,5385038
0,4904331	0,5095669	0,9624509	0,6359134	0,3640866	1,7465992

0,4447387	0,5552613	0,8009538	0,4401198	0,5598802	0,7860965
0,4910271	0,5089729	0,9647411	0,5068539	0,4931461	1,0277967
0,4468395	0,5531605	0,8077935	0,5792144	0,4207856	1,376507
0,3927147	0,6072853	0,6466725	0,8738633	0,1261367	6,9279095
0,4047225	0,5952775	0,6798889	0,8738142	0,1261858	6,9248204
0,4165869	0,5834131	0,7140514	0,847	0,153	5,5359475
0,454233	0,545767	0,8322836	0,8612919	0,1387081	6,2093818
0,4124002	0,5875998	0,7018386	0,5748248	0,4251752	1,3519715
0,6065977	0,3934023	1,5419272	0,4605015	0,5394985	0,8535733
0,4519209	0,5480791	0,8245542	0,8055917	0,1944083	4,1438141
0,4140155	0,5859845	0,7065297	0,8404792	0,1595208	5,2687741
0,4355019	0,5644981	0,7714852	0,6256396	0,3743604	1,671223
0,387044	0,612956	0,6314384	0,44471	0,55529	0,8008607
0,3462641	0,6537359	0,5296697	0,4303003	0,5696997	0,7553108
0,4367568	0,5632432	0,7754321	0,5720865	0,4279135	1,3369208
0,3773623	0,6226377	0,6060705	0,5182922	0,4817078	1,0759474
0,3973908	0,6026092	0,6594502	0,3752406	0,6247594	0,6006161
0,4428793	0,5571207	0,7949433	0,3956643	0,6043357	0,6547096
0,4399675	0,5600325	0,7856108	0,545961	0,454039	1,202454
0,4067574	0,5932426	0,6856511	0,8444726	0,1555274	5,4297341
0,4070371	0,5929629	0,6864461	0,5132295	0,4867705	1,0543562
0,3696737	0,6303263	0,58648	0,5017086	0,4982914	1,0068577
0,3312256	0,6687744	0,4952726	0,5251522	0,4748478	1,1059377
0,2857008	0,7142992	0,3999737	0,4608278	0,5391722	0,8546952
0,2862015	0,7137985	0,4009556	0,4448162	0,5551838	0,8012054
0,4371278	0,5628722	0,7766023	0,8475965	0,1524035	5,5615296
0,280291	0,719709	0,3894504	0,733443	0,266557	2,7515427
0,4716428	0,5283572	0,8926589	0,5125306	0,4874694	1,0514106
0,4918266	0,5081734	0,9678324	0,5546358	0,4453642	1,2453534
0,4594215	0,5405785	0,84987	0,3334061	0,6665939	0,5001637
0,4462242	0,5537758	0,805785	0,3010405	0,6989595	0,4306981
0,4481762	0,5518238	0,8121727	0,3680261	0,6319739	0,5823439
0,4362017	0,5637983	0,7736841	0,5144386	0,4855614	1,0594716
0,4505591	0,5494409	0,8200319	0,7141029	0,2858971	2,4977623
0,4509531	0,5490469	0,8213379	0,8089492	0,1910508	4,234211
0,4344114	0,5655886	0,7680696	0,7782129	0,2217871	3,5088293
0,3879058	0,6120942	0,6337354	0,5214595	0,4785405	1,0896872
0,3623464	0,6376536	0,5682496	0,5052047	0,4947953	1,0210376
0,3881992	0,6118008	0,634519	0,4187352	0,5812648	0,7203863
0,4572654	0,5427346	0,8425211	0,5133126	0,4866874	1,0547071
0,3445861	0,6554139	0,5257534	0,7803167	0,2196833	3,552007
0,351526	0,648474	0,5420819	0,6329848	0,3670152	1,7246829
0,5123209	0,4876791	1,0505286	0,7374489	0,2625511	2,8087821
0,3603956	0,6396044	0,5634663	0,789339	0,210661	3,7469641
0,4478398	0,5521602	0,8110687	0,8157319	0,1842681	4,426876
0,4496866	0,5503134	0,8171465	0,819758	0,180242	4,5480978
0,4269586	0,5730414	0,7450746	0,8038647	0,1961353	4,0985223
0,4025321	0,5974679	0,67373	0,8820159	0,1179841	7,4757148
0,424323	0,575677	0,7370852	0,859402	0,140598	6,1124792
0,3957682	0,6042318	0,654994	0,5648044	0,4351956	1,2978174
0,4601171	0,5398829	0,8522536	0,7047317	0,2952683	2,3867506
0,3493736	0,6506264	0,5369803	0,8582993	0,1417007	6,0571268

0,4074513	0,5925487	0,687625	0,8021704	0,1978296	4,0548564
0,3772303	0,6227697	0,6057301	0,7617931	0,2382069	3,1980318
0,3512334	0,6487666	0,5413863	0,3934545	0,6065455	0,6486808
0,3948711	0,6051289	0,6525404	0,5038073	0,4961927	1,0153461
0,4128533	0,5871467	0,7031518	0,7214948	0,2785052	2,590597
0,3898722	0,6101278	0,639001	0,8190856	0,1809144	4,5274752
0,432728	0,567272	0,7628227	0,4119815	0,5880185	0,7006269
0,4894615	0,5105385	0,9587162	0,6875456	0,3124544	2,200467
0,4933627	0,5066373	0,9737987	0,4309286	0,5690714	0,7572486
0,4739148	0,5260852	0,9008327	0,334312	0,665688	0,5022052
0,4239346	0,5760654	0,735914	0,5417537	0,4582463	1,1822325
0,631816	0,368184	1,7160336	0,6758307	0,3241693	2,0848076
0,3810649	0,6189351	0,6156782	0,4844241	0,5155759	0,9395787
0,5372222	0,4627778	1,1608644	0,5827173	0,4172827	1,396457
0,3931833	0,6068167	0,6479442	0,4626934	0,5373066	0,8611346
0,4598741	0,5401259	0,8514201	0,5330119	0,4669881	1,1413822
0,4347955	0,5652045	0,769271	0,8755	0,1245	7,0321294
0,4754728	0,5245272	0,906479	0,7859937	0,2140063	3,6727587
0,4677218	0,5322782	0,878717	0,588641	0,411359	1,4309665

0,3660959	0,6339041	0,5775257	0,7707991	0,2292009	3,3629843
0,4506778	0,5493222	0,8204253	0,3410913	0,6589087	0,5176609
0,3588849	0,6411151	0,5597822	0,7471001	0,2528999	2,9541331
0,4034152	0,5965848	0,6762077	0,7187175	0,2812825	2,5551444
0,4789557	0,5210443	0,9192226	0,648207	0,351793	1,8425809
0,5001284	0,4998716	1,0005138	0,6994947	0,3005053	2,3277288
0,5003573	0,4996427	1,0014303	0,7136091	0,2863909	2,4917308
0,4266837	0,5733163	0,7442378	0,7469537	0,2530463	2,9518462
0,4337839	0,5662161	0,7661102	0,698928	0,301072	2,3214641
0,3914651	0,6085349	0,6432911	0,716505	0,283495	2,5273989
0,3831068	0,6168932	0,6210262	0,7725489	0,2274511	3,3965501
0,4758358	0,5241642	0,9077992	0,7652288	0,2347712	3,2594658
0,3780102	0,6219898	0,6077434	0,7529549	0,2470451	3,0478447
0,4489251	0,5510749	0,8146354	0,7307164	0,2692836	2,7135569
0,4499795	0,5500205	0,818114	0,7388705	0,2611295	2,8295169

0,4086216	0,5913784	0,6909647	0,7733879	0,2266121	3,4128279
0,3992143	0,6007857	0,664487	0,3322318	0,6677682	0,4975256
0,5065392	0,4934608	1,0265032	0,2887568	0,7112432	0,4059888
0,5498468	0,4501532	1,2214658	0,4426761	0,5573239	0,7942888
0,5238207	0,4761793	1,1000491	0,3395231	0,6604769	0,5140576
0,6257662	0,3742338	1,6721266	0,6143164	0,3856836	1,5927989
0,3608216	0,6391784	0,5645085	0,7664445	0,2335555	3,2816374
0,4485045	0,5514955	0,8132515	0,8049313	0,1950687	4,126399
0,3781734	0,6218266	0,6081655	0,7787329	0,2212671	3,5194241

0,4056117	0,5943883	0,682402	0,7608827	0,2391173	3,1820475
0,4497678	0,5502322	0,8174145	0,770612	0,229388	3,3594266

0,3458801	0,6541199	0,5287718	0,6807576	0,3192424	2,1324156
0,5128295	0,4871705	1,0526693	0,5670298	0,4329702	1,3096279
0,5055659	0,4944341	1,0225144	0,6437388	0,3562612	1,8069291
0,4083255	0,5916745	0,6901186	0,763076	0,236924	3,2207633
0,4158817	0,5841183	0,7119818	0,7759453	0,2240547	3,4631958
0,3669285	0,6330715	0,5796004	0,7589874	0,2410126	3,1491609
0,3237368	0,6762632	0,4787142	0,695977	0,304023	2,2892244
0,3026198	0,6973802	0,433938	0,6609109	0,3390891	1,949077
0,3987393	0,6012607	0,6631721	0,7445321	0,2554679	2,9143866
0,5808523	0,4191477	1,3857938	0,4150104	0,5849896	0,709432
0,5363878	0,4636122	1,1569752	0,5232108	0,4767892	1,0973628
0,5201459	0,4798541	1,0839668	0,6120007	0,3879993	1,5773239
0,5106065	0,4893935	1,0433453	0,6632683	0,3367317	1,969723
0,4049413	0,5950587	0,6805064	0,6845242	0,3154758	2,1698155
0,5276881	0,4723119	1,117245	0,2652387	0,7347613	0,3609863
0,4880306	0,5119694	0,9532416	0,2170289	0,7829711	0,2771863
0,511147	0,488853	1,0456049	0,342474	0,657526	0,5208523
0,5449489	0,4550511	1,1975552	0,3185326	0,6814674	0,4674216
0,3890437	0,6109563	0,6367784	0,724389	0,275611	2,6283026
0,4332845	0,5667155	0,764554	0,684408	0,315592	2,1686477

0,3759809	0,6240191	0,6025151	0,6887015	0,3112985	2,2123507
0,3536291	0,6463709	0,5470992	0,661475	0,338525	1,9539917
0,5587513	0,4412487	1,2662959	0,6274904	0,3725096	1,6844946
0,3202407	0,6797593	0,4711089	0,6607268	0,3392732	1,9474769
0,2453962	0,7546038	0,3251987	0,5657453	0,4342547	1,3027962
0,2799063	0,7200937	0,3887081	0,6529421	0,3470579	1,8813633
0,4287246	0,5712754	0,7504692	0,7521864	0,2478136	3,0352906
0,3834096	0,6165904	0,6218223	0,6657961	0,3342039	1,9921849
0,4337718	0,5662282	0,7660724	0,3212524	0,6787476	0,4733016
0,4189413	0,5810587	0,7209965	0,3096554	0,6903446	0,448552

0,4138823	0,5861177	0,7061419	0,7922688	0,2077312	3,8139134
0,3359833	0,6640167	0,5059863	0,6436457	0,3563543	1,8061963
0,3550624	0,6449376	0,5505375	0,7001241	0,2998759	2,3347122
0,4757195	0,5242805	0,9073758	0,7780736	0,2219264	3,5059975
0,2995441	0,7004559	0,4276416	0,7113705	0,2886295	2,4646489
0,2539415	0,7460585	0,3403774	0,6758914	0,3241086	2,0853853
0,3917989	0,6082011	0,644193	0,6858216	0,3141784	2,1829051
0,3738514	0,6261486	0,5970649	0,764159	0,235841	3,2401443
0,3952525	0,6047475	0,6535828	0,7511353	0,2488647	3,0182476
0,4475738	0,5524262	0,8101967	0,6877329	0,3122671	2,2023872
0,422914	0,577086	0,732844	0,8111532	0,1888468	4,2952977
0,4194602	0,5805398	0,7225347	0,8227472	0,1772528	4,6416607
0,4762163	0,5237837	0,9091851	0,4717753	0,5282247	0,8931337
0,5869494	0,4130506	1,4210108	0,497179	0,502821	0,9887792
0,6092954	0,3907046	1,5594787	0,4855697	0,5144303	0,9438978
0,516489	0,483511	1,0682054	0,455493	0,544507	0,8365237
0,5416643	0,4583357	1,1818069	0,4405522	0,5594478	0,7874767
0,5298002	0,4701998	1,1267555	0,5174286	0,4825714	1,0722321

0,5162292	0,4837708	1,0670947	0,4233097	0,5766903	0,7340329
0,5014716	0,4985284	1,0059036	0,4723248	0,5276752	0,8951053
0,4779764	0,5220236	0,9156222	0,4895175	0,5104825	0,9589309
0,5717592	0,4282408	1,3351349	0,7744974	0,2255026	3,4345388
0,5123139	0,4876861	1,0504991	0,4615353	0,5384647	0,8571319
0,4314909	0,5685091	0,7589869	0,7062775	0,2937225	2,4045738
0,377954	0,622046	0,6075983	0,6958323	0,3041677	2,2876601
0,378996	0,621004	0,6102955	0,7276792	0,2723208	2,6721394
0,3438087	0,6561913	0,5239458	0,7529589	0,2470411	3,0479102
0,3688043	0,6311957	0,5842947	0,7119103	0,2880897	2,4711414
0,4149923	0,5850077	0,7093792	0,607191	0,392809	1,5457666
0,365174	0,634826	0,5752347	0,7488391	0,2511609	2,981511
0,3076431	0,6923569	0,4443418	0,7758788	0,2241212	3,461871
0,4441161	0,5558839	0,7989369	0,7067156	0,2932844	2,4096591

0,4577113	0,5422887	0,8440364	0,4282365	0,5717635	0,748975
0,4095667	0,5904333	0,6936713	0,7261031	0,2738969	2,6510085
0,3730488	0,6269512	0,5950204	0,7325315	0,2674685	2,7387583
0,454307	0,545693	0,8325322	0,6114475	0,3885525	1,5736545
0,4066255	0,5933745	0,6852765	0,6696344	0,3303656	2,0269495
0,4672045	0,5327955	0,8768926	0,6198818	0,3801182	1,6307609
0,5076514	0,4923486	1,0310812	0,3475785	0,6524215	0,5327515
0,4587683	0,5412317	0,8476377	0,4219285	0,5780715	0,7298899
0,4336292	0,5663708	0,7656279	0,6883108	0,3116892	2,2083238
0,5212926	0,4787074	1,0889587	0,6354597	0,3645403	1,7431808
0,439376	0,560624	0,7837266	0,2148175	0,7851825	0,2735893
0,6062225	0,3937775	1,5395054	0,1974248	0,8025752	0,2459891
0,6159282	0,3840718	1,60368	0,3050519	0,6949481	0,4389564
0,6349863	0,3650137	1,7396233	0,3981542	0,6018458	0,6615552
0,5604729	0,4395271	1,2751726	0,3453921	0,6546079	0,5276321
0,5193562	0,4806438	1,080543	0,2346958	0,7653042	0,3066699
0,5518724	0,4481276	1,2315071	0,3520074	0,6479926	0,5432276
0,5279747	0,4720253	1,1185304	0,2461532	0,7538468	0,3265294
0,4424636	0,5575364	0,7936049	0,3092997	0,6907003	0,4478058
0,5057764	0,4942236	1,0233755	0,2822295	0,7177705	0,3932029
0,5301293	0,4698707	1,1282453	0,2819077	0,7180923	0,3925786
0,5314688	0,4685312	1,1343294	0,3042696	0,6957304	0,4373384
0,5720756	0,4279244	1,3368615	0,2446604	0,7553396	0,3239078
0,5034551	0,4965449	1,0139164	0,6429516	0,3570484	1,8007408

0,4340148	0,5659852	0,7668306	0,6927503	0,3072497	2,2546813
0,359364	0,640636	0,5609488	0,7801824	0,2198176	3,5492271
0,4009551	0,5990449	0,6693241	0,8380146	0,1619854	5,1733942
0,4645101	0,5354899	0,8674488	0,7800374	0,2199626	3,546228
0,4455797	0,5544203	0,8036856	0,7867404	0,2132596	3,6891196
0,4404236	0,5595764	0,7870661	0,7788568	0,2211432	3,5219577
0,3952504	0,6047496	0,6535771	0,7155897	0,2844103	2,5160474
0,3955991	0,6044009	0,654531	0,6948683	0,3051317	2,2772732

0,4283711	0,5716289	0,7493868	0,7731732	0,2268268	3,4086492
0,4424297	0,5575703	0,7934957	0,7566071	0,2433929	3,108584
0,4932099	0,5067901	0,9732035	0,8119116	0,1880884	4,3166477
0,4029527	0,5970473	0,6749092	0,8655057	0,1344943	6,4352614
0,4317308	0,5682692	0,7597295	0,8632201	0,1367799	6,3110139
0,385348	0,614652	0,6269368	0,8224813	0,1775187	4,6332089
0,4073418	0,5926582	0,6873132	0,8170032	0,1829968	4,4645751
0,4054607	0,5945393	0,6819746	0,8196321	0,1803679	4,5442248
0,4013654	0,5986346	0,6704681	0,7931323	0,2068677	3,8340071
0,4417359	0,5582641	0,7912668	0,750455	0,249545	3,0072937
0,4458011	0,5541989	0,8044063	0,7909373	0,2090627	3,783254
0,2826058	0,7173942	0,3939337	0,8426991	0,1573009	5,3572409
0,2798381	0,7201619	0,3885767	0,8367228	0,1632772	5,1245547
0,296268	0,703732	0,4209956	0,818409	0,181591	4,5068796
0,2853938	0,7146062	0,3993721	0,8279297	0,1720703	4,8115785
0,3001041	0,6998959	0,4287839	0,8204448	0,1795552	4,569319
0,2996551	0,7003449	0,427868	0,8172414	0,1827586	4,4716992
0,3067808	0,6932192	0,4425452	0,8488132	0,1511868	5,6143337
0,3439947	0,6560053	0,5243779	0,7534989	0,2465011	3,056777
0,2983181	0,7016819	0,4251472	0,8187839	0,1812161	4,518273
0,27376	0,72624	0,3769553	0,8358563	0,1641437	5,0922226
0,4161529	0,5838471	0,7127771	0,6621474	0,3378526	1,9598707
0,3728994	0,6271006	0,5946405	0,7776512	0,2223488	3,4974382
0,4455314	0,5544686	0,8035288	0,7579167	0,2420833	3,1308092
0,3795315	0,6204685	0,6116853	0,8227895	0,1772105	4,6430068
0,3076513	0,6923487	0,444359	0,7564287	0,2435713	3,1055739
0,4865462	0,5134538	0,9475948	0,7574809	0,2425191	3,123386
0,4607922	0,5392078	0,8545726	0,786612	0,213388	3,6862983
0,3910218	0,6089782	0,6420948	0,8387723	0,1612277	5,2024099
0,3314491	0,6685509	0,4957724	0,7547029	0,2452971	3,0766885
0,4517744	0,5482256	0,8240665	0,8124089	0,1875911	4,3307432
0,4740204	0,5259796	0,9012143	0,8167209	0,1832791	4,4561581
0,4338279	0,5661721	0,7662474	0,7791267	0,2208733	3,5274824
0,5776639	0,4223361	1,3677825	0,9094766	0,0905234	10,046861
0,4902445	0,5097555	0,9617248	0,8175197	0,1824803	4,4800428
0,3003557	0,6996443	0,4292976	0,8096195	0,1903805	4,2526387
0,354487	0,645513	0,5491556	0,8733533	0,1266467	6,8959785
0,311808	0,688192	0,4530829	0,8749106	0,1250894	6,9942809
0,4111823	0,5888177	0,6983186	0,8776125	0,1223875	7,1707718
0,4056346	0,5943654	0,6824666	0,868378	0,131622	6,5975114
0,3880845	0,6119155	0,6342125	0,8592992	0,1407008	6,1072787
0,423668	0,576332	0,7351109	0,8728527	0,1271473	6,8648953
0,3714074	0,6285926	0,5908556	0,8700923	0,1299077	6,6977736
0,3848984	0,6151016	0,6257476	0,8753073	0,1246927	7,0197152
0,3866417	0,6133583	0,6303685	0,8636682	0,1363318	6,3350443
0,3636165	0,6363835	0,5713796	0,8714687	0,1285313	6,7802084
0,3708479	0,6291521	0,5894409	0,8700203	0,1299797	6,6935081
0,4043116	0,5956884	0,67873	0,8706157	0,1293843	6,7289146
0,3697742	0,6302258	0,5867329	0,8724321	0,1275679	6,8389626
0,4238315	0,5761685	0,7356034	0,8748927	0,1251073	6,9931376
0,4078001	0,5921999	0,6886189	0,8703115	0,1296885	6,7107834
0,3984213	0,6015787	0,6622928	0,8760226	0,1239774	7,0659888

0,3722508	0,6277492	0,5929929	0,8648774	0,1351226	6,4006869
0,3636318	0,6363682	0,5714174	0,8440969	0,1559031	5,4142392
0,3516592	0,6483408	0,5423987	0,872772	0,127228	6,8599055
0,4113646	0,5886354	0,6988446	0,7825638	0,2174362	3,5990499
0,4273328	0,5726672	0,7462149	0,8536573	0,1463427	5,8332738
0,3929928	0,6070072	0,6474268	0,8302201	0,1697799	4,8899798
0,3613621	0,6386379	0,5658325	0,8255599	0,1744401	4,7326265
0,4270302	0,5729698	0,7452928	0,8538366	0,1461634	5,8416572
0,4347376	0,5652624	0,76909	0,7099476	0,2900524	2,4476525
0,3789614	0,6210386	0,610206	0,8268785	0,1731215	4,77629
0,3680593	0,6319407	0,582427	0,8211494	0,1788506	4,5912604
0,3945081	0,6054919	0,6515497	0,8708467	0,1291533	6,7427375
0,461879	0,538121	0,8583179	0,7313606	0,2686394	2,7224619
0,397315	0,602685	0,6592417	0,872803	0,127197	6,861822
0,36202	0,63798	0,5674473	0,869214	0,130786	6,6460799
0,4018466	0,5981534	0,671812	0,7481232	0,2518768	2,9701947
0,2550266	0,7449734	0,3423297	0,674709	0,325291	2,0741701
0,3567948	0,6432052	0,5547139	0,8543318	0,1456682	5,8649161
0,401796	0,598204	0,6716706	0,8582236	0,1417764	6,0533595
0,3877402	0,6122598	0,6332936	0,8311343	0,1688657	4,9218649
0,3873709	0,6126291	0,6323091	0,8393736	0,1606264	5,2256249
0,3544452	0,6455548	0,5490552	0,8173201	0,1826799	4,4740553
0,3928457	0,6071543	0,6470277	0,8301718	0,1698282	4,8883047
0,3568578	0,6431422	0,5548661	0,8324067	0,1675933	4,9668255
0,3856503	0,6143497	0,6277373	0,8326192	0,1673808	4,9744
0,3788511	0,6211489	0,6099198	0,8332357	0,1667643	4,9964878
0,3578271	0,6421729	0,557213	0,7936336	0,2063664	3,8457503
0,3686969	0,6313031	0,5840251	0,8044681	0,1955319	4,1142559
0,3369906	0,6630094	0,5082743	0,8074792	0,1925208	4,1942446
0,2952805	0,7047195	0,4190044	0,8193322	0,1806678	4,5350206
0,4475498	0,5524502	0,810118	0,7649694	0,2350306	3,2547644

0,3992736	0,6007264	0,6646512	0,8579385	0,1420615	6,0392042
0,3830691	0,6169309	0,6209271	0,8473758	0,1526242	5,5520409
0,387539	0,612461	0,6327571	0,8480508	0,1519492	5,5811474
0,4223753	0,5776247	0,731228	0,886163	0,113837	7,7844918
0,405687	0,594313	0,6826149	0,8863014	0,1136986	7,7951818
0,2702747	0,7297253	0,3703786	0,792494	0,207506	3,8191377
0,457657	0,542343	0,8438516	0,8475707	0,1524293	5,560417
0,3607966	0,6392034	0,5644472	0,7366301	0,2633699	2,7969405
0,381708	0,618292	0,6173588	0,8610243	0,1389757	6,195504
0,3634026	0,6365974	0,5708516	0,8721327	0,1278673	6,8206066
0,3808047	0,6191953	0,6149993	0,8583276	0,1416724	6,0585401
0,4103411	0,5896589	0,6958958	0,8600137	0,1399863	6,143558
0,2884941	0,7115059	0,4054696	0,7741207	0,2258793	3,4271423
0,2526588	0,7473412	0,3380769	0,7175718	0,2824282	2,5407224
0,3356254	0,6643746	0,505175	0,7946601	0,2053399	3,8699742
0,4295268	0,5704732	0,7529307	0,8361769	0,1638231	5,1041446
0,4013975	0,5986025	0,6705576	0,8353567	0,1646433	5,0737379
0,4096463	0,5903537	0,6938997	0,8616513	0,1383487	6,2281118
0,4238431	0,5761569	0,7356382	0,8618945	0,1381055	6,2408391

0,4787458	0,5212542	0,9184498	0,8649672	0,1350328	6,4056087
0,477519	0,522481	0,9139452	0,8497436	0,1502564	5,6552892
0,4661797	0,5338203	0,8732897	0,8695488	0,1304512	6,6657023
0,5022173	0,4977827	1,0089086	0,7134921	0,2865079	2,4903048
0,4886774	0,5113226	0,9557123	0,8557513	0,1442487	5,9324719
0,4128774	0,5871226	0,7032218	0,8693449	0,1306551	6,6537383
0,4710371	0,5289629	0,8904917	0,8203824	0,1796176	4,5673846
0,4069324	0,5930676	0,6861485	0,8397147	0,1602853	5,2388759
0,6255019	0,3744981	1,6702406	0,9477373	0,0522627	18,134088
0,3677783	0,6322217	0,5817236	0,7333399	0,2666601	2,7500926
0,3817297	0,6182703	0,6174154	0,8305019	0,1694981	4,8997727
0,4145656	0,5854344	0,7081334	0,8147322	0,1852678	4,3975922
0,4065349	0,5934651	0,685019	0,787632	0,212368	3,7088076
0,4105147	0,5894853	0,6963952	0,8012652	0,1987348	4,0318318
0,4253567	0,5746433	0,7402098	0,8087262	0,1912738	4,2281083
0,4090954	0,5909046	0,6923204	0,7160941	0,2839059	2,5222944
0,4093871	0,5906129	0,6931564	0,6479542	0,3520458	1,8405392
0,3878143	0,6121857	0,6334914	0,7807386	0,2192614	3,5607653
0,3612596	0,6387404	0,5655813	0,8086563	0,1913437	4,2261979
0,3965107	0,6034893	0,6570303	0,8098816	0,1901184	4,2598813
0,375898	0,624102	0,6023022	0,7892742	0,2107258	3,7455043
0,4465155	0,5534845	0,8067354	0,8047285	0,1952715	4,1210746
0,4055842	0,5944158	0,6823242	0,8459342	0,1540658	5,4907351
0,4010664	0,5989336	0,6696341	0,8468446	0,1531554	5,5293152
0,3683366	0,6316634	0,5831217	0,7977782	0,2022218	3,9450657
0,3705771	0,6294229	0,5887569	0,7652954	0,2347046	3,2606741
0,3786154	0,6213846	0,6093092	0,818549	0,181451	4,5111287
0,3552449	0,6447551	0,5509764	0,6587125	0,3412875	1,9300806
0,4141502	0,5858498	0,706922	0,8989344	0,1010656	8,8945676
0,3821081	0,6178919	0,618406	0,897111	0,102889	8,7192081
0,3981375	0,6018625	0,6615091	0,900904	0,099096	9,0912266
0,4228254	0,5771746	0,7325778	0,8918072	0,1081928	8,2427569
0,4965255	0,5034745	0,9861979	0,8573098	0,1426902	6,0081886
0,4070566	0,5929434	0,6865015	0,8366547	0,1633453	5,1219993
0,340119	0,659881	0,5154247	0,7856977	0,2143023	3,666305
0,415443	0,584557	0,7106971	0,8561237	0,1438763	5,950414
0,462248	0,537752	0,8595934	0,869719	0,130281	6,6757135
0,3965536	0,6034464	0,657148	0,8823131	0,1176869	7,4971238
0,4136258	0,5863742	0,7053956	0,8711926	0,1288074	6,7635276
0,3865878	0,6134122	0,6302252	0,8544725	0,1455275	5,8715538
0,4060902	0,5939098	0,6837573	0,8420669	0,1579331	5,3317935

0,496519	0,503481	0,9861723	0,784805	0,215195	3,6469484
0,6176334	0,3823666	1,6152914	0,8165132	0,1834868	4,4499843
0,4601788	0,5398212	0,8524653	0,6871251	0,3128749	2,1961653
0,5418501	0,4581499	1,1826917	0,7410792	0,2589208	2,8621853
0,619627	0,380373	1,6289985	0,849327	0,150673	5,6368877
0,5983686	0,4016314	1,4898453	0,8213288	0,1786712	4,596872
0,6634813	0,3365187	1,9716034	0,7362163	0,2637837	2,7909843
0,5944179	0,4055821	1,4655923	0,7119674	0,2880326	2,4718295
0,5428088	0,4571912	1,1872689	0,7807121	0,2192879	3,5602143
0,6959381	0,3040619	2,2888045	0,7370414	0,2629586	2,8028806

0,6505315	0,3494685	1,8614885	0,7007043	0,2992957	2,3411769
0,6723914	0,3276086	2,0524226	0,8455394	0,1544606	5,4741446
0,664373	0,335627	1,979498	0,6423408	0,3576592	1,7959575
0,6735745	0,3264255	2,0634858	0,6645392	0,3354608	1,9809741
0,6249872	0,3750128	1,6665754	0,6445578	0,3554422	1,8133966
0,5988462	0,4011538	1,4928096	0,5835311	0,4164689	1,4011397
0,391318	0,608682	0,6428941	0,5153378	0,4846622	1,0632926
0,4479074	0,5520926	0,8112904	0,5997876	0,4002124	1,4986729
0,5935466	0,4064534	1,4603065	0,7569771	0,2430229	3,1148393
0,5636729	0,4363271	1,2918583	0,7984361	0,2015639	3,961207
0,5401675	0,4598325	1,174705	0,8029853	0,1970147	4,0757641
0,5695554	0,4304446	1,3231794	0,806056	0,193944	4,1561262
0,6080842	0,3919158	1,5515684	0,8223015	0,1776985	4,6275085
0,538588	0,461412	1,1672604	0,7841964	0,2158036	3,6338423
0,5157106	0,4842894	1,0648812	0,735497	0,264503	2,7806756
0,5748187	0,4251813	1,3519381	0,7827698	0,2172302	3,603412
0,4774303	0,5225697	0,9136204	0,7392281	0,2607719	2,8347695
0,5859606	0,4140394	1,415229	0,7927493	0,2072507	3,8250737
0,5799021	0,4200979	1,3803972	0,7914725	0,2085275	3,7955307
0,5536353	0,4463647	1,2403204	0,8028556	0,1971444	4,0724244
0,5560386	0,4439614	1,2524479	0,6237182	0,3762818	1,6575826
0,5416762	0,4583238	1,1818635	0,7904178	0,2095822	3,7713977
0,5339284	0,4660716	1,1455933	0,6260151	0,3739849	1,6739048
0,476954	0,523046	0,9118777	0,4473099	0,5526901	0,8093324
0,5755695	0,4244305	1,3560984	0,8498699	0,1501301	5,6608883
0,5517738	0,4482262	1,2310165	0,844026	0,155974	5,4113255
0,5733479	0,4266521	1,34383	0,8669704	0,1330296	6,5171259
0,5929685	0,4070315	1,4568124	0,8665339	0,1334661	6,4925368
0,4689378	0,5310622	0,8830184	0,7082514	0,2917486	2,4276083
0,5839085	0,4160915	1,4033173	0,8672384	0,1327616	6,5322996
0,5866443	0,4133557	1,4192237	0,866763	0,133237	6,5054246
0,5605615	0,4394385	1,2756312	0,8274865	0,1725135	4,7966478
0,5484419	0,4515581	1,2145545	0,8589608	0,1410392	6,0902284
0,5554185	0,4445815	1,2493065	0,8371932	0,1628068	5,1422506
0,5313244	0,4686756	1,133672	0,8038528	0,1961472	4,0982131
0,5877555	0,4122445	1,425745	0,8118341	0,1881659	4,3144605
0,6080878	0,3919122	1,5515919	0,8396067	0,1603933	5,2346732
0,5382615	0,4617385	1,1657278	0,8394345	0,1605655	5,2279877
0,5661606	0,4338394	1,3050007	0,8357297	0,1642703	5,0875269
0,5506586	0,4493414	1,2254792	0,8049701	0,1950299	4,12742
0,5731697	0,4268303	1,3428512	0,8055824	0,1944176	4,1435676
0,5564019	0,4435981	1,2542928	0,756313	0,243687	3,1036251
0,5393004	0,4606996	1,1706117	0,7915895	0,2084105	3,7982227
0,6872662	0,3127338	2,1976079	0,8809211	0,1190789	7,3977932
0,5549967	0,4450033	1,2471743	0,7897882	0,2102118	3,757107
0,5523617	0,4476383	1,2339464	0,785927	0,214073	3,6713034
0,5374149	0,4625851	1,1617643	0,802657	0,197343	4,0673187
0,5327443	0,4672557	1,1401557	0,8113939	0,1886061	4,3020542
0,5385943	0,4614057	1,1672902	0,815077	0,184923	4,4076565
0,5345865	0,4654135	1,1486271	0,8090312	0,1909688	4,2364583
0,53441	0,46559	1,1478125	0,7783817	0,2216183	3,5122619
0,5107995	0,4892005	1,0441517	0,8022643	0,1977357	4,0572567

0,5500324	0,4499676	1,222382	0,7866595	0,2133405	3,6873423
0,5235929	0,4764071	1,099045	0,8039074	0,1960926	4,099631
0,5557168	0,4442832	1,2508166	0,8103633	0,1896367	4,2732405
0,5735571	0,4264429	1,34498	0,8085025	0,1914975	4,2220011
0,5634702	0,4365298	1,2907945	0,808806	0,191194	4,2302887
0,5229046	0,4770954	1,0960169	0,7970382	0,2029618	3,927035
0,5455253	0,4544747	1,2003423	0,8046915	0,1953085	4,1201046
0,5943277	0,4056723	1,465044	0,8479503	0,1520497	5,5767974
0,5965139	0,4034861	1,4784004	0,8489344	0,1510656	5,6196407
0,5750339	0,4249661	1,353129	0,845329	0,154671	5,4653365
0,5890741	0,4109259	1,4335288	0,8360148	0,1639852	5,0981104
0,4801537	0,5198463	0,9236456	0,8245182	0,1754818	4,6985981
0,5675508	0,4324492	1,3124105	0,8439263	0,1560737	5,4072299
0,5837009	0,4162991	1,4021189	0,8469636	0,1530364	5,5343941
0,5653987	0,4346013	1,3009596	0,8357426	0,1642574	5,0880058
0,4624941	0,5375059	0,8604448	0,8091922	0,1908078	4,2408759
0,5882951	0,4117049	1,4289241	0,8263049	0,1736951	4,7572156
0,639407	0,360593	1,7732093	0,8705369	0,1294631	6,7242084
0,6924418	0,3075582	2,2514171	0,7797893	0,2202107	3,5411063
0,7459446	0,2540554	2,9361488	0,8214735	0,1785265	4,601409
0,4712404	0,5287596	0,8912187	0,6189266	0,3810734	1,6241666
0,6435428	0,3564572	1,8053861	0,9261252	0,0738748	12,536419
0,5667884	0,4332116	1,3083407	0,8883341	0,1116659	7,9552865
0,5707265	0,4292735	1,3295174	0,8005836	0,1994164	4,0146337
0,5494495	0,4505505	1,2195071	0,8170104	0,1829896	4,4647908
0,4429679	0,5570321	0,7952286	0,6893987	0,3106013	2,2195613
0,5137725	0,4862275	1,0566503	0,7907377	0,2092623	3,7786906
0,5159061	0,4840939	1,0657149	0,7874328	0,2125672	3,7043944
0,5076679	0,4923321	1,0311494	0,8248159	0,1751841	4,7082807
0,4931525	0,5068475	0,9729799	0,8000537	0,1999463	4,0013437
0,5112886	0,4887114	1,0461974	0,8408796	0,1591204	5,2845481
0,7172965	0,2827035	2,537275	0,8608403	0,1391597	6,185988
0,5927422	0,4072578	1,4554471	0,7632821	0,2367179	3,2244383
0,5950334	0,4049666	1,4693396	0,8137359	0,1862641	4,3687219
0,4999683	0,5000317	0,9998731	0,8061918	0,1938082	4,1597398
0,5607558	0,4392442	1,276638	0,8530479	0,1469521	5,804939
0,6717867	0,3282133	2,0467988	0,7647939	0,2352061	3,2515905
0,5418035	0,4581965	1,1824697	0,7043138	0,2956862	2,3819632
0,6222759	0,3777241	1,6474353	0,8436473	0,1563527	5,3957963
0,6623351	0,3376649	1,961516	0,8529227	0,1470773	5,7991436
0,6487764	0,3512236	1,8471889	0,8237194	0,1762806	4,672773
0,5438386	0,4561614	1,1922065	0,7966268	0,2033732	3,9170688

0,472706	0,527294	0,8964753	0,724081	0,275919	2,6242515
0,377229	0,622771	0,6057268	0,7071747	0,2928253	2,415006
0,4218984	0,5781016	0,7297997	0,7024907	0,2975093	2,3612396
0,3928332	0,6071668	0,6469938	0,7266966	0,2733034	2,6589371
0,4576262	0,5423738	0,8437469	0,7147834	0,2852166	2,5061075
0,4222196	0,5777804	0,7307614	0,6254343	0,3745657	1,6697583
0,392382	0,607618	0,645771	0,7042859	0,2957141	2,3816446
0,4353659	0,5646341	0,7710586	0,5405317	0,4594683	1,1764289
0,5328637	0,4671363	1,1407026	0,5050804	0,4949196	1,0205302

0,5367212	0,4632788	1,1585275	0,6135601	0,3864399	1,5877247
0,6235019	0,3764981	1,6560562	0,7388707	0,2611293	2,8295198
0,5120819	0,4879181	1,0495244	0,4782024	0,5217976	0,9164518
0,5169644	0,4830356	1,0702409	0,6607063	0,3392937	1,9472994
0,4479373	0,5520627	0,8113883	0,5428279	0,4571721	1,18736
0,4499275	0,5500725	0,8179422	0,5545527	0,4454473	1,2449342
0,4587526	0,5412474	0,847584	0,7393091	0,2606909	2,83596
0,4041213	0,5958787	0,6781939	0,565772	0,434228	1,3029376
0,4226483	0,5773517	0,7320465	0,6105833	0,3894167	1,5679433
0,4857872	0,5142128	0,94472	0,5605677	0,4394323	1,2756636
0,4667625	0,5332375	0,8753368	0,5344156	0,4655844	1,1478384
0,4558129	0,5441871	0,8376033	0,691827	0,308173	2,2449305
0,3949429	0,6050571	0,6527367	0,677036	0,322964	2,0963208
0,5136906	0,4863094	1,0563042	0,6597078	0,3402922	1,9386508
0,3904989	0,6095011	0,6406862	0,7331346	0,2668654	2,7472068
0,4891118	0,5108882	0,9573754	0,7414022	0,2585978	2,8670086
0,5034028	0,4965972	1,0137046	0,7349993	0,2650007	2,7735751
0,4324369	0,5675631	0,7619187	0,6546413	0,3453587	1,8955405
0,4587968	0,5412032	0,8477347	0,6581086	0,3418914	1,9249051
0,4979107	0,5020893	0,9916774	0,4621425	0,5378575	0,8592285
0,4389288	0,5610712	0,7823049	0,5382378	0,4617622	1,1656168
0,4779528	0,5220472	0,9155357	0,5366002	0,4633998	1,1579637
0,445928	0,554072	0,8048195	0,5677811	0,4322189	1,3136424
0,4698974	0,5301026	0,8864272	0,5485289	0,4514711	1,2149811
0,4726915	0,5273085	0,8964232	0,6279645	0,3720355	1,6879158
0,5326073	0,4673927	1,1395284	0,8073408	0,1926592	4,1905139
0,5281249	0,4718751	1,119205	0,4763875	0,5236125	0,9098092
0,4277033	0,5722967	0,7473454	0,7545459	0,2454541	3,0740814
0,543867	0,456133	1,1923432	0,692762	0,307238	2,2548056
0,5671558	0,4328442	1,3102999	0,6852181	0,3147819	2,1768026
0,3275947	0,6724053	0,4871983	0,7053764	0,2946236	2,3941612
0,4541198	0,5458802	0,8319038	0,6867899	0,3132101	2,1927449
0,4849177	0,5150823	0,9414375	0,7172335	0,2827665	2,5364872
0,4055763	0,5944237	0,6823018	0,6624707	0,3375293	1,9627061
0,4941832	0,5058168	0,9770005	0,6743832	0,3256168	2,0710944
0,3846449	0,6153551	0,625078	0,746813	0,253187	2,9496497
0,4324202	0,5675798	0,7618669	0,7322732	0,2677268	2,7351504
0,4214965	0,5785035	0,728598	0,6852493	0,3147507	2,1771173
0,462491	0,537509	0,8604339	0,7650116	0,2349884	3,2555291
0,5241055	0,4758945	1,1013062	0,7372806	0,2627194	2,8063431
0,3272256	0,6727744	0,4863823	0,6112844	0,3887156	1,5725751
0,4651205	0,5348795	0,8695799	0,6296356	0,3703644	1,7000432
0,4404806	0,5595194	0,7872482	0,480822	0,519178	0,9261218
0,4540648	0,5459352	0,8317193	0,6341188	0,3658812	1,7331275
0,5455548	0,4544452	1,2004852	0,6140671	0,3859329	1,5911241
0,4329024	0,5670976	0,763365	0,6032441	0,3967559	1,5204413
0,568031	0,431969	1,3149811	0,7661912	0,2338088	3,2769986
0,492705	0,507295	0,9712394	0,6165657	0,3834343	1,608009
0,4134855	0,5865145	0,7049876	0,3818502	0,6181498	0,6177309

0,5313612	0,4686388	1,1338394	0,4489783	0,5510217	0,8148104
0,4618377	0,5381623	0,8581756	0,734945	0,265055	2,7728023
0,5032335	0,4967665	1,013018	0,2820454	0,7179546	0,3928457
0,5659677	0,4340323	1,303976	0,8819369	0,1180631	7,4700464
0,4599721	0,5400279	0,8517561	0,5348463	0,4651537	1,1498271

0,5834186	0,4165814	1,4004913	0,6937196	0,3062804	2,264982
0,564035	0,435965	1,293762	0,6682434	0,3317566	2,0142579
0,5032122	0,4967878	1,0129318	0,640335	0,359665	1,7803647
0,4783418	0,5216582	0,9169641	0,515576	0,484424	1,0643071
0,5215067	0,4784933	1,0898933	0,7666711	0,2333289	3,2857957
0,5136299	0,4863701	1,0560476	0,4428821	0,5571179	0,7949521
0,5181256	0,4818744	1,0752297	0,4473038	0,5526962	0,8093123
0,4855353	0,5144647	0,9437681	0,4701043	0,5298957	0,887164
0,4003418	0,5996582	0,6676166	0,5670214	0,4329786	1,3095831
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0,524883	0,475117	1,1047448	0,5841291	0,4158709	1,4045926
0,4938618	0,5061382	0,9757451	0,6479943	0,3520057	1,8408629
0,4538021	0,5461979	0,8308381	0,5207453	0,4792547	1,086573
0,4576753	0,5423247	0,8439136	0,5313576	0,4686424	1,1338234
0,4382743	0,5617257	0,7802284	0,4927335	0,5072665	0,9713506
0,5131232	0,4868768	1,0539076	0,4638995	0,5361005	0,8653219

0,6146864	0,3853136	1,5952889	0,4621317	0,5378683	0,859191
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0,5858279	0,4141721	1,4144551	0,519326	0,480674	1,0804122
0,6804025	0,3195975	2,128936	0,497461	0,502539	0,9898953
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0,6542817	0,3457183	1,8925288	0,5638688	0,4361312	1,2928881
0,5818043	0,4181957	1,3912249	0,3523217	0,6476783	0,5439764
0,6380608	0,3619392	1,7628954	0,695881	0,304119	2,2881869
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0,5498081	0,4501919	1,2212748	0,3698528	0,6301472	0,5869308
0,5291628	0,4708372	1,1238762	0,3577104	0,6422896	0,55693
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0,542655	0,457345	1,1865331	0,611704	0,388296	1,5753548
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0,5775916	0,4224084	1,3673772	0,5208676	0,4791324	1,0871056

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0,5971039	0,4028961	1,4820294	0,3531332	0,6468668	0,5459133
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0,6219284	0,3780716	1,6450016	0,544724	0,455276	1,19647
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0,4113472	0,5886528	0,6987943	0,3828057	0,6171943	0,6202354
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Protein#	AC	ID	Description
1	P21333	FLNA_HUM	Filamin-A (FLN-A) (ABP-280) [ISOFORM 2]
2	Q15149	PLEC_HUM	Plectin (PCN) (PLTN) (HD1)
3	P35579	MYH9_HUM	Myosin-9 (NMMHC-A) (NMMHC II-a) (NMMHC-IIA)
4	P08670	VIME_HUM	Vimentin [CHAIN 0]
5	P02545	LMNA_HUM	Prelamin-A/C [CHAIN 1]
6	Q13813	SPTA2_HL	Spectrin alpha chain, non-erythrocytic 1 [ISOFORM 3]
7	O75369	FLNB_HUM	Filamin-B (FLN-B) (Fh1) (Truncated ABP) [ISOFORM 2]
8	P02751	FN1_HUM	Fibronectin [CHAIN 0]
9	Q07065	CKAP4_HL	Cytoskeleton-associated protein 4 (p63)
10	Q00610	CLH1_HUM	Clathrin heavy chain 1 (CLH-17) [ISOFORM 2]
11	P04264	K2C1_HUM	Keratin, type II cytoskeletal 1 (CK-1) (K1) [CHAIN 0]
12	P12814	ACTN1_HL	Alpha-actinin-1
13	Q09666	AHNK_HUM	Neuroblast differentiation-associated protein AHNK
14	Q9P2E9	RRBP1_HU	Ribosome-binding protein 1 (RRp) [ISOFORM 2]
15	P08133	ANXA6_HL	Annexin A6 (CPB-II) [CHAIN 0]
16	O43707	ACTN4_HL	Alpha-actinin-4
17	P60709	ACTB_HUM	Actin, cytoplasmic 1 [CHAIN 1]
18	Q01082	SPTB2_HU	Spectrin beta chain, non-erythrocytic 1
19	P07437	TBB5_HUM	Tubulin beta chain
20	P06753	TPM3_HUM	Tropomyosin alpha-3 chain (hTM5) [ISOFORM 2]
21	P07355	ANXA2_HL	Annexin A2 (PAP-IV) [CHAIN 0]
22	P68032	ACTC_HUM	Actin, alpha cardiac muscle 1 [CHAIN 0]
23	P13645	K1C10_HL	Keratin, type I cytoskeletal 10 (CK-10) (K10)
24	P07951	TPM2_HUM	Tropomyosin beta chain
25	P07951	TPM2_HUM	Tropomyosin beta chain [ISOFORM 2]
26	P62736	ACTA_HUM	Actin, aortic smooth muscle
27	P14618	KPYM_HUM	Pyruvate kinase PKM [CHAIN 0]
28	Q9NZM1	MYOF_HUM	Myoferlin [ISOFORM 6]
29	P09493	TPM1_HUM	Tropomyosin alpha-1 chain
30	P09493	TPM1_HUM	Tropomyosin alpha-1 chain [ISOFORM 3]
31	Q9Y490	TLN1_HUM	Talin-1
32	P04843	RPN1_HUM	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1
33	P68371	TBB2C_HL	Tubulin beta-4B chain
34	P50454	SERPH_HU	Serpin H1 (AsTP3) (Colligin) [CHAIN 0]
35	P35527	K1C9_HUM	Keratin, type I cytoskeletal 9 (CK-9) (K9)
36	P67936	TPM4_HUM	Tropomyosin alpha-4 chain [ISOFORM 2]
37	P78527	PRKDC_HL	DNA-dependent protein kinase catalytic subunit (DNA-PK catalytic subunit)
38	P67936	TPM4_HUM	Tropomyosin alpha-4 chain [CHAIN 0]
39	Q13885	TBB2A_HL	Tubulin beta-2A chain
40	P07900	HS90A_HL	Heat shock protein HSP 90-alpha (HSP 86) (HSP86) [CHAIN 0]
41	P11021	GRP78_HL	78 kDa glucose-regulated protein (GRP-78) (BiP) [CHAIN 0]
42	P07237	PDIA1_HU	Protein disulfide-isomerase (PDI) [CHAIN 0]
43	P14618	KPYM_HUM	Pyruvate kinase isozymes M1/M2 (CTHBP) (OIP-3) (THBP1) [ISOFORM 1]
44	P06576	ATPB_HUM	ATP synthase subunit beta, mitochondrial [CHAIN 0]
45	P08238	HS90B_HL	Heat shock protein HSP 90-beta (HSP 90) (HSP 84) (HSP84)
46	P02452	CO1A1_HL	Collagen alpha-1(I) chain
47	P10809	CH60_HUM	60 kDa heat shock protein, mitochondrial (CPN60) (HSP-60) (Hsp60) [CHAIN 0]
48	P04083	ANXA1_HL	Annexin A1 [CHAIN 0]
49	P22626	ROA2_HUM	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)
50	Q71U36	TBA1A_HL	Tubulin alpha-1A chain
51	Q08211	DHX9_HUM	ATP-dependent RNA helicase A (NDH II)

52 P68363 TBA1B_HL Tubulin alpha-1B chain
 53 Q99715 COCA1_HL Collagen alpha-1(XII) chain [ISOFORM 4]
 54 P09651 ROA1_HU Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) [ISOFORM 2]
 55 P06733 ENOA_HU Alpha-enolase (NNE) [CHAIN 0]
 56 P04406 G3P_HUM Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [CHAIN 0]
 57 P35580 MYH10_HL Myosin-10 (NMMHC-B) (NMMHC II-b) (NMMHC-IIB)
 58 Q9BQE3 TBA1C_HL Tubulin alpha-1C chain
 59 Q14315 FLNC_HUM Filamin-C (FLN-C) (FLNc) [ISOFORM 2]
 60 P19338 NUCL_HUM Nucleolin [CHAIN 0]
 61 P35908 K22E_HUM Keratin, type II cytoskeletal 2 epidermal (CK-2e) (K2e)
 62 P61978 HNRPK_HL Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (TUNP) [ISOFO
 63 Q13509 TBB3_HUM Tubulin beta-3 chain
 64 P60174 TPIS_HUM Triosephosphate isomerase (TIM) [CHAIN 0]
 65 P06753 TPM3_HUM Tropomyosin alpha-3 chain (hTM5)
 66 P08758 ANXA5_HL Annexin A5 (CBP-I) (PP4) (PAP-I) (VAC-alpha) [CHAIN 0]
 67 P08123 CO1A2_HL Collagen alpha-2(I) chain
 68 P25705 ATPA_HUM ATP synthase subunit alpha, mitochondrial [CHAIN 0]
 69 P30101 PDIA3_HU Protein disulfide-isomerase A3 (p58) (ER protein 57) (ERp57) (ER prote
 70 P14625 ENPL_HUM Endoplasmin (GRP-94) [CHAIN 0]
 71 Q00341 VIGLN_HU Vigilin (HDL-binding protein) [CHAIN 0]
 72 P12956 XRCC6_HL X-ray repair cross-complementing protein 6 (5'-dRP lyase Ku70) (CTC7
 73 Q7KZF4_SND1_HU Staphylococcal nuclease domain-containing protein 1 [CHAIN 0]
 74 Q05682 CALD1_HL Caldesmon (CDM) [ISOFORM 5]
 75 P53621 COPA_HUM Coatamer subunit alpha
 76 Q99623 PHB2_HUM Prohibitin-2 [CHAIN 0]
 77 P13639 EF2_HUM Elongation factor 2 (EF-2) [CHAIN 0]
 78 P26641 EF1G_HUM Elongation factor 1-gamma (EF-1-gamma) [CHAIN 0]
 79 P04075 ALDOA_HL Fructose-bisphosphate aldolase A [CHAIN 0]
 80 P11142 HSP7C_HL Heat shock cognate 71 kDa protein [CHAIN 0]
 81 Q01995 TAGL_HUM Transgelin (SM22-alpha) [CHAIN 0]
 82 P35232 PHB_HUM Prohibitin
 83 P63244 GBLP_HUM Guanine nucleotide-binding protein subunit beta-2-like 1 (HLC-7) (RAC
 84 P09382 LEG1_HUM Galectin-1 (Gal-1) (HLBP14)
 85 O60506 HNRPQ_HL Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (GRY-RBP) [ISC
 86 P78371 TCPB_HUM T-complex protein 1 subunit beta (TCP-1-beta) [CHAIN 0]
 87 Q14697 GANAB_HL Neutral alpha-glucosidase AB [CHAIN 0]
 88 P15144 AMPN_HU Aminopeptidase N (AP-N) (hAPN) (AP-M) [CHAIN 0]
 89 Q13838 UAP56_HL Spliceosome RNA helicase DDX39B [CHAIN 0]
 90 P21796 VDAC1_HL Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDA
 91 Q92945 FUBP2_HU Far upstream element-binding protein 2 (FUSE-binding protein 2) (KSR
 92 P36578 RL4_HUM 60S ribosomal protein L4 [CHAIN 0]
 93 P22314 UBA1_HU Ubiquitin-like modifier-activating enzyme 1
 94 P11940 PABP1_HL Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1) [
 95 P60842 IF4A1_HU Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I)
 96 Q6S8J3 POTE_HU POTE ankyrin domain family member E (POTE-2)
 97 P04844 RPN2_HUM Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subun
 98 P68366 TBA4A_HL Tubulin alpha-4A chain
 99 P17987 TCPA_HUM T-complex protein 1 subunit alpha (TCP-1-alpha)
 100 Q02878 RL6_HUM 60S ribosomal protein L6 (TaxREB107)
 101 Q14152 EIF3A_HU Eukaryotic translation initiation factor 3 subunit A (eIF3a) [CHAIN 0]
 102 O75533 SF3B1_HU Splicing factor 3B subunit 1 (SF3b155) (SAP 155)
 103 P13010 XRCC5_HL X-ray repair cross-complementing protein 5 (CTC85) (CTCBF) (TLAA)

104 P23396_RS3_HUM/ 40S ribosomal protein S3 [CHAIN 0]
 105 P46940_IQGA1_HU Ras GTPase-activating-like protein IQGAP1 [CHAIN 0]
 106 O00571_DDX3X_HL ATP-dependent RNA helicase DDX3X (HLP2) [CHAIN 0]
 107 P62805_H4_HUM/ Histone H4 [CHAIN 0]
 108 P20700_LMN1_HL Lamin-B1 [CHAIN 0]
 109 P55072_TERA_HUM Transitional endoplasmic reticulum ATPase (TER ATPase) (VCP) [CHAIN
 110 P50990_TCPQ_HUM T-complex protein 1 subunit theta (TCP-1-theta) [CHAIN 0]
 111 Q9NQC3_RTN4_HUM Reticulon-4 (Nogo protein) (NSP) [ISOFORM 2]
 112 P08865_RSSA_HUM 40S ribosomal protein SA (37LRP) (LRP/LR) (67LR) (LamR) (LBP/p40) [C
 113 O60701_UGDH_HU/ UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH)
 114 P05556_ITB1_HUM Integrin beta-1 [CHAIN 0]
 115 P68104_EF1A1_HL Elongation factor 1-alpha 1 (EF-1-alpha-1) (EF-Tu) (eEF1A-1)
 116 P45880_VDAC2_HL Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDA
 117 P51991_ROA3_HU/ Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) [ISOFORM 2
 118 Q9NY65_TBA8_HUM Tubulin alpha-8 chain
 119 Q8WWI1_LMO7_HU/ LIM domain only protein 7 (LMO-7) [ISOFORM 3]
 120 P13489_RINI_HUM/ Ribonuclease inhibitor (Placental RNase inhibitor) (RAI) [CHAIN 0]
 121 P15880_RS2_HUM/ 40S ribosomal protein S2 [CHAIN 0]
 122 O00159_MYO1C_HL Unconventional myosin-Ic [ISOFORM 2]
 123 Q12906_ILF3_HUM/ Interleukin enhancer-binding factor 3 (DRBP76) (MPP4) (NFAR) (NF-AT
 124 P19367_HXK1_HUM Hexokinase-1 (HK I) [ISOFORM 4]
 125 Q9ULV4_COR1C_HL Coronin-1C
 126 P17844_DDX5_HU/ Probable ATP-dependent RNA helicase DDX5
 127 P48643_TCPE_HUM T-complex protein 1 subunit epsilon (TCP-1-epsilon) [CHAIN 0]
 128 Q01518_CAP1_HUM Adenyl cyclase-associated protein 1 (CAP 1) [CHAIN 0]
 129 O76021_RL1D1_HL Ribosomal L1 domain-containing protein 1
 130 P15311_EZR1_HUM/ Ezrin [CHAIN 0]
 131 Q9BUF5_TBB6_HUM Tubulin beta-6 chain
 132 P18124_RL7_HUM/ 60S ribosomal protein L7
 133 P23284_PPIB_HUM/ Peptidyl-prolyl cis-trans isomerase B (PPIase B) (SCYLP) [CHAIN 0]
 134 Q9NR30_DDX21_HL Nucleolar RNA helicase 2 [ISOFORM 2]
 135 Q96QK1_VPS35_HL Vacuolar protein sorting-associated protein 35 (hVPS35)
 136 O60814_H2B1K_HL Histone H2B type 1-K (H2B K)
 137 P06899_H2B1J_HL Histone H2B type 1-J (H2B/r) [CHAIN 0]
 138 O75643_U520_HUM U5 small nuclear ribonucleoprotein 200 kDa helicase (U5-200KD)
 139 P40926_MDHM_HU Malate dehydrogenase, mitochondrial [CHAIN 0]
 140 Q9BQG0_MBB1A_HL Myb-binding protein 1A
 141 P35609_ACTN2_HL Alpha-actinin-2
 142 P12236_ADT3_HU/ ADP/ATP translocase 3 (ANT 2) (ANT 3) [CHAIN 0]
 143 Q99832_TCPH_HUM T-complex protein 1 subunit eta (TCP-1-eta)
 144 P63104_1433Z_HL 14-3-3 protein zeta/delta (KCIP-1)
 145 Q9BSJ8_ESYT1_HU Extended synaptotagmin-1 (E-Syt1)
 146 P04792_HSPB1_HL Heat shock protein beta-1 (HspB1) (HSP 27) (SRP27)
 147 P05388_RLA0_HUM 60S acidic ribosomal protein P0
 148 Q9Y678_COPG_HUM Coatamer subunit gamma-1
 149 P61019_RAB2A_HL Ras-related protein Rab-2A [CHAIN 0]
 150 P06396_GELS_HUM Gelsolin (ADF) [ISOFORM 2]
 151 P37802_TAGL2_HL Transgelin-2 [CHAIN 0]
 152 P38646_GRP75_HL Stress-70 protein, mitochondrial (GRP-75) (MOT) (PBP74) [CHAIN 0]
 153 Q9UHB6_LIMA1_HU LIM domain and actin-binding protein 1 [ISOFORM Alpha]
 154 P04908_H2A1B_HL Histone H2A type 1-B/E [CHAIN 0]
 155 Q15365_PCBP1_HU Poly(rC)-binding protein 1 (hnRNP E1)

156 Q14247 SRC8_HUM Src substrate cortactin
157 P50995 ANX11_HL Annexin A11 (CAP-50)
158 P29692_EF1D_HUM Elongation factor 1-delta (EF-1-delta) [CHAIN 0]
159 P60660_MYL6_HUM Myosin light polypeptide 6 (LC17) (MLC-3) (Myosin light chain A3) [CH
160 O75083_WDR1_HU WD repeat-containing protein 1 (AIP1) [CHAIN 0]
161 Q8NBS9_TXND5_HL Thioredoxin domain-containing protein 5 (ER protein 46) (ERp46) [CH/
162 P00338_LDHA_HUM L-lactate dehydrogenase A chain (LDH-A) (LDH-M) [CHAIN 0]
163 P26038_MOES_HUM Moesin [CHAIN 0]
164 P00387_NB5R3_HL NADH-cytochrome b5 reductase 3 [CHAIN 1]
165 P62701_RS4X_HUM 40S ribosomal protein S4, X isoform [CHAIN 0]
166 O00148_DDX39_HL ATP-dependent RNA helicase DDX39A [CHAIN 0]
167 P23246_SFPQ_HUM Splicing factor, proline- and glutamine-rich (hPOMP100) (PSF) (PTB-as
168 Q96AG4_LRC59_HL Leucine-rich repeat-containing protein 59
169 P53618_COPB_HUM Coatamer subunit beta (Beta-COP)
170 P25398_RS12_HUM 40S ribosomal protein S12 [CHAIN 0]
171 O43852_CALU_HUM Calumenin [CHAIN 0]
172 P52272_HNRPM_HL Heterogeneous nuclear ribonucleoprotein M (hnRNP M) [ISOFORM 2]
173 P21291_CSRP1_HU Cysteine and glycine-rich protein 1 (CRP) (CRP1) [CHAIN 0]
174 P13674_P4HA1_HL Prolyl 4-hydroxylase subunit alpha-1 (4-PH alpha-1) [CHAIN 0]
175 P16403_H12_HUM Histone H1.2 [CHAIN 0]
176 Q9H0U4_RAB1B_HL Ras-related protein Rab-1B
177 Q86VP6_CAND1_HL Cullin-associated NEDD8-dissociated protein 1 (TBP-interacting proteir
178 P31949_S10AB_HL Protein S100-A11 (MLN 70)
179 P31943_HNRH1_HL Heterogeneous nuclear ribonucleoprotein H, N-terminally processed [
180 P05455_LA_HUM Lupus La protein (SS-B)
181 Q32P28_P3H1_HUM Prolyl 3-hydroxylase 1 (Leprecan-1) [CHAIN 0]
182 P51149_RAB7A_HL Ras-related protein Rab-7a
183 P62753_RS6_HUM 40S ribosomal protein S6
184 P05141_ADT2_HUM ADP/ATP translocase 2 (ANT 2) [CHAIN 0]
185 O60716_CTND1_HL Catenin delta-1 (CAS) (p120(ctn)) [ISOFORM 4]
186 Q08043_ACTN3_HL Alpha-actinin-3
187 Q9NZN4_EHD2_HUM EH domain-containing protein 2
188 P27797_CALR_HUM Calreticulin (ERp60) [CHAIN 0]
189 P26599_PTBP1_HU Polypyrimidine tract-binding protein 1 (PTB) (hnRNP I)
190 O75947_ATP5H_HL ATP synthase subunit d, mitochondrial (ATPase subunit d) [ISOFORM 2]
191 P62277_RS13_HUM 40S ribosomal protein S13 [CHAIN 0]
192 P12235_ADT1_HUM ADP/ATP translocase 1 (ANT 1) [CHAIN 0]
193 O15143_ARC1B_HL Actin-related protein 2/3 complex subunit 1B [CHAIN 0]
194 Q9BTV4_TMM43_HL Transmembrane protein 43 [CHAIN 0]
195 P35606_COPB2_HL Coatamer subunit beta' (Beta'-COP) [CHAIN 0]
196 P00558_PGK1_HUM Phosphoglycerate kinase 1 (PRP 2)
197 P0CG38_POTE1_HUM POTE ankyrin domain family member I
198 P49368_TCPG_HUM T-complex protein 1 subunit gamma (TCP-1-gamma)
199 Q02543_RL18A_HL 60S ribosomal protein L18a
200 Q15084_PDIA6_HU Protein disulfide-isomerase A6 (ER protein 5) (ERp5) [CHAIN 0]
201 P61224_RAP1B_HL Ras-related protein Rap-1b [CHAIN 0]
202 P13929_ENOB_HUM Beta-enolase (MSE) [ISOFORM 3]
203 Q9NVA2_SEP11_HU Septin-11 [CHAIN 0]
204 P62424_RL7A_HUM 60S ribosomal protein L7a [CHAIN 0]
205 P46781_RS9_HUM 40S ribosomal protein S9 [CHAIN 0]
206 P37837_TALDO_HL Transaldolase
207 Q14764_MVP_HUM Major vault protein (MVP) [CHAIN 0]

208 P39023_RL3_HUM/ 60S ribosomal protein L3 (TARBP-B) [CHAIN 0]
 209 P62258_1433E_HL 14-3-3 protein epsilon (14-3-3E) [ISOFORM SV]
 210 Q7Z406_MYH14_HL Myosin-14 (NMHC II-C) [CHAIN 0]
 211 P21964_COMT_HUI Catechol O-methyltransferase [ISOFORM Soluble]
 212 Q14974_IMB1_HUM Importin subunit beta-1 (PTAC97)
 213 Q14103_HNRPD_HL Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) [ISOFORM 4]
 214 Q16629_SRSF7_HU Serine/arginine-rich splicing factor 7 [ISOFORM 3]
 215 P0CG47_UBB_HUM/ Polyubiquitin-B [CHAIN 0]
 216 Q02809_PLOD1_HL Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 (LH1) [CHAIN 0]
 217 Q9Y224_CN166_HL UPF0568 protein C14orf166
 218 P21980_TGM2_HUI Protein-glutamine gamma-glutamyltransferase 2 (TG(C)) (TGC) (TGase)
 219 Q9NVI7_ATD3A_HL ATPase family AAA domain-containing protein 3A [ISOFORM 2]
 220 P67809_YBOX1_HL Nuclease-sensitive element-binding protein 1 (CBF-A) (DBPB) (EFI-A) (I)
 221 P69849_NOMO3_H Nodal modulator 3 [CHAIN 0]
 222 P62081_RS7_HUM/ 40S ribosomal protein S7
 223 P07910_HNRPC_HL Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2) [ISO]
 224 P35749_MYH11_HL Myosin-11
 225 P22695_QCR2_HUM Cytochrome b-c1 complex subunit 2, mitochondrial [CHAIN 0]
 226 P08134_RHOC_HUI Rho-related GTP-binding protein RhoC (h9) [CHAIN 0]
 227 Q16643_DREB_HUM Drebrin [CHAIN 0]
 228 P08107_HSP71_HL Heat shock 70 kDa protein 1A/1B (HSP70-1/HSP70-2) (HSP70.1/HSP70)
 229 P39019_RS19_HUM 40S ribosomal protein S19 [CHAIN 0]
 230 Q96D15_RCN3_HUM Reticulocalbin-3 [CHAIN 0]
 231 Q6DD88_ATLA3_HL Atlastin-3
 232 P48444_COPD_HUM Coatamer subunit delta (Delta-COP)
 233 Q14204_DYHC1_HL Cytoplasmic dynein 1 heavy chain 1
 234 P28331_NDUS1_HL NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial (CI-7)
 235 P62937_PPIA_HUM Peptidyl-prolyl cis-trans isomerase A (PPIase A) [CHAIN 0]
 236 Q99729_ROAA_HUI Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (ABBP-1) [
 237 Q13200_PSM2_HL 26S proteasome non-ATPase regulatory subunit 2
 238 O43390_HNRPR_HL Heterogeneous nuclear ribonucleoprotein R (hnRNP R) [CHAIN 0]
 239 P61026_RAB10_HL Ras-related protein Rab-10
 240 P10606_COX5B_HL Cytochrome c oxidase subunit 5B, mitochondrial [CHAIN 0]
 241 Q96AY3_FKB10_HL Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (65 kDa FK)
 242 Q07020_RL18_HUM 60S ribosomal protein L18 [CHAIN 0]
 243 P62873_GBB1_HUM Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 [CH/
 244 P08195_4F2_HUM/ 4F2 cell-surface antigen heavy chain (4F2hc) [ISOFORM 2]
 245 P54886_P5CS_HUM Delta-1-pyrroline-5-carboxylate synthase (P5CS) [ISOFORM Short]
 246 Q86UP2_KTN1_HUM Kinectin [ISOFORM 2]
 247 Q92841_DDX17_HL Probable ATP-dependent RNA helicase DDX17
 248 Q99829_CPNE1_HL Copine-1
 249 P30050_RL12_HUM 60S ribosomal protein L12
 250 P63241_IF5A1_HUI Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (eIF-5/
 251 Q02978_M2OM_HU Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) [CHAIN 0]
 252 Q9Y277_VDAC3_HL Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDA)
 253 Q12905_ILF2_HUM/ Interleukin enhancer-binding factor 2
 254 Q14980_NUMA1_HL Nuclear mitotic apparatus protein 1 (NuMA protein) [ISOFORM 2]
 255 Q15366_PCBP2_HU Poly(rC)-binding protein 2 (hnRNP E2)
 256 P29401_TKT_HUM/ Transketolase (TK)
 257 P02786_TFR1_HUM Transferrin receptor protein 1 [CHAIN 1]
 258 P05387_RLA2_HUM 60S acidic ribosomal protein P2
 259 O14979_HNRDL_HL Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRN

260 P62158 CALM_HU Calmodulin (CaM)
 261 Q96QV6 H2A1A_HL Histone H2A type 1-A [CHAIN 0]
 262 Q6NZI2 PTRF_HUM Polymerase I and transcript release factor
 263 Q15942_ZYX_HUM Zyxin [CHAIN 0]
 264 Q07954_LRP1_HUM Prolow-density lipoprotein receptor-related protein 1 [CHAIN 0]
 265 Q07955_SRSF1_HU Serine/arginine-rich splicing factor 1 (ASF-1) [ISOFORM ASF-3]
 266 P39656_OST48_HL Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kD:
 267 Q9H4M9_EHD1_HUM EH domain-containing protein 1 (hPAST1)
 268 P55209_NP1L1_HL Nucleosome assembly protein 1-like 1 (hNRP)
 269 P62241_RS8_HUM 40S ribosomal protein S8 [CHAIN 0]
 270 P27695_APEX1_HL DNA- lyase [CHAIN 1]
 271 P21589_5NTD_HU 5'-nucleotidase (5'-NT) [CHAIN 0]
 272 P41252_SYIC_HUM Isoleucyl-tRNA synthetase, cytoplasmic (IRS) (IleRS)
 273 P27348_1433T_HL 14-3-3 protein theta
 274 Q58FF8_H90B2_HL Putative heat shock protein HSP 90-beta 2 (Heat shock protein 90Bb) [
 275 Q02218_ODO1_HU 2-oxoglutarate dehydrogenase, mitochondrial (OGDC-E1) [CHAIN 0]
 276 P61106_RAB14_HL Ras-related protein Rab-14 [CHAIN 0]
 277 P61313_RL15_HUM 60S ribosomal protein L15
 278 P07195_LDHB_HUM L-lactate dehydrogenase B chain (LDH-B) (LDH-H) [CHAIN 0]
 279 Q13724_MOGS_HU Mannosyl-oligosaccharide glucosidase
 280 P30044_PRDX5_HL Peroxiredoxin-5, mitochondrial (AOEB166) (Prx-V) [CHAIN 0]
 281 P49327_FAS_HUM Fatty acid synthase
 282 P62906_RL10A_HL 60S ribosomal protein L10a (NEDD-6) [CHAIN 0]
 283 Q94925_GLSK_HUM Glutaminase kidney isoform, mitochondrial (GLS) [ISOFORM 3]
 284 P41091_IF2G_HUM Eukaryotic translation initiation factor 2 subunit 3 (eIF-2-gamma X) (eI
 285 P53396_ACLY_HUM ATP-citrate synthase
 286 Q95782_AP2A1_HL AP-2 complex subunit alpha-1 [ISOFORM B]
 287 Q16891_IMMT_HUM Mitochondrial inner membrane protein [ISOFORM 3]
 288 Q15019_SEPT2_HU Septin-2 (NEDD-5)
 289 P07737_PROF1_HL Profilin-1 [CHAIN 0]
 290 Q99613_EIF3C_HUM Eukaryotic translation initiation factor 3 subunit C (eIF3c)
 291 Q969G5_PRDBP_HU Protein kinase C delta-binding protein (hSRBC)
 292 P16188_1A30_HU HLA class I histocompatibility antigen, A-30 alpha chain [CHAIN 0]
 293 P52597_HNRPF_HL Heterogeneous nuclear ribonucleoprotein F, N-terminally processed [
 294 P27824_CALX_HUM Calnexin [CHAIN 0]
 295 Q06830_PRDX1_HL Peroxiredoxin-1 (NKEF-A) (PAG)
 296 P55769_NH2L1_HL NHP2-like protein 1 (hSNU13) [CHAIN 0]
 297 P04899_GNAI2_HU Guanine nucleotide-binding protein G subunit alpha-2 [CHAIN 0]
 298 P62491_RB11A_HL Ras-related protein Rab-11A (Rab-11) [CHAIN 0]
 299 P62280_RS11_HUM 40S ribosomal protein S11 [CHAIN 0]
 300 Q99714_HCD2_HU 3-hydroxyacyl-CoA dehydrogenase type-2 (17-beta-HSD 10) (Mitochor
 301 Q15717_ELAV1_HL ELAV-like protein 1 (HuR)
 302 O15460_P4HA2_HL Prolyl 4-hydroxylase subunit alpha-2 (4-PH alpha-2) [CHAIN 0]
 303 Q9Y3F4_STRAP_HL Serine-threonine kinase receptor-associated protein
 304 P04216_THY1_HUM Thy-1 membrane glycoprotein [CHAIN 0]
 305 Q9P258_RCC2_HUM Protein RCC2
 306 P83731_RL24_HUM 60S ribosomal protein L24
 307 Q92616_GCN1L_HL Translational activator GCN1 (HsGCN1) [CHAIN 0]
 308 P00505_AATM_HU Aspartate aminotransferase, mitochondrial (mAspAT) (FABP-1) (FABP
 309 P49756_RBM25_HL RNA-binding protein 25 (RED120)
 310 Q16658_FSCN1_HL Fascin [CHAIN 0]
 311 O75396_SC22B_HL Vesicle-trafficking protein SEC22b (ERS-24) (ERS24) [CHAIN 0]

312 P13647_K2C5_HUM Keratin, type II cytoskeletal 5 (CK-5) (K5)
 313 P59998_ARPC4_HL Actin-related protein 2/3 complex subunit 4 (p20-ARC) [CHAIN 0]
 314 Q92499_DDX1_HUM ATP-dependent RNA helicase DDX1 (DBP-RB)
 315 P62269_RS18_HUM 40S ribosomal protein S18 (Ke3) [CHAIN 0]
 316 O75367_H2AY_HUM Core histone macroH2A.1 (Histone macroH2A1) (mH2A1) (H2A/y) [ISC
 317 P61247_RS3A_HUM 40S ribosomal protein S3a (Fte-1) [CHAIN 0]
 318 P15531_NDKA_HUI Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (GAAD) [CHA
 319 Q00839_HNRPU_HL Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (SAF-A) [ISOFC
 320 Q13310_PABP4_HL Polyadenylate-binding protein 4 (PABP-4) (Poly(A)-binding protein 4) (
 321 P60900_PSA6_HUM Proteasome subunit alpha type-6 (PROS-27) (p27K)
 322 P30504_1C04_HUM HLA class I histocompatibility antigen, Cw-4 alpha chain [CHAIN 0]
 323 P32119_PRDX2_HL Peroxiredoxin-2 (NKEF-B) (TSA) [CHAIN 0]
 324 P61619_S61A1_HL Protein transport protein Sec61 subunit alpha isoform 1 (Sec61 alpha-
 325 Q9Y262_EIF3L_HUM Eukaryotic translation initiation factor 3 subunit L (eIF3L) [CHAIN 0]
 326 P62851_RS25_HUM 40S ribosomal protein S25
 327 P43243_MATR3_HL Matrin-3 [CHAIN 0]
 328 Q9UBV2_SE1L1_HU Protein sel-1 homolog 1 (Sel-1L) [CHAIN 0]
 329 P13797_PLST_HUM Plastin-3
 330 Q9UHD8_SEPT9_HU Septin-9 (MLL septin-like fusion protein) (Ov/Br septin) [ISOFORM 7]
 331 P63010_AP2B1_HL AP-2 complex subunit beta
 332 P06744_G6PI_HUM Glucose-6-phosphate isomerase (GPI) (AMF) (NLK) (PGI) (PHI) (SA-36) |
 333 P07602_SAP_HUM Proactivator polypeptide
 334 O43143_DHX15_HL Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX1.
 335 P20073_ANXA7_HL Annexin A7 [ISOFORM 2]
 336 Q86Y82_STX12_HL Syntaxin-12
 337 Q9UKM9_RALY_HUM RNA-binding protein Raly (hnRNP core protein C-like 2) [ISOFORM 1]
 338 P34931_HS71L_HL Heat shock 70 kDa protein 1-like (Heat shock 70 kDa protein 1L) (HSP7
 339 P62136_PP1A_HUM Serine/threonine-protein phosphatase PP1-alpha catalytic subunit (PP
 340 Q8NC51_PAIRB_HUI Plasminogen activator inhibitor 1 RNA-binding protein (PAI-RBP1) [ISO
 341 P11279_LAMP1_HL Lysosome-associated membrane glycoprotein 1 (LAMP-1) (Lysosome-
 342 O00469_PLOD2_HL Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 (LH2) [CHAIN 0]
 343 P40939_ECHA_HUM Trifunctional enzyme subunit alpha, mitochondrial [CHAIN 0]
 344 P16401_H15_HUM Histone H1.5 [CHAIN 0]
 345 P62140_PP1B_HUM Serine/threonine-protein phosphatase PP1-beta catalytic subunit (PP-
 346 P30153_2AAA_HUI Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A
 347 P0CG39_POTEJ_HU POTE ankyrin domain family member J
 348 P12111_CO6A3_HL Collagen alpha-3(VI) chain [ISOFORM 2]
 349 P25205_MCM3_HUI DNA replication licensing factor MCM3 [CHAIN 0]
 350 Q9Y5M8_SRPRB_HU Signal recognition particle receptor subunit beta (SR-beta)
 351 Q6P2Q9_PRP8_HUM Pre-mRNA-processing-splicing factor 8 [CHAIN 0]
 352 Q13740_CD166_HL CD166 antigen [CHAIN 0]
 353 Q13505_MTX1_HUM Metaxin-1
 354 Q16181_SEPT7_HU Septin-7 [ISOFORM 2]
 355 Q99497_PARK7_HL Protein DJ-1
 356 O15260_SURF4_HU Surfeit locus protein 4 [ISOFORM 2]
 357 P19105_ML12A_HL Myosin regulatory light chain 12A [CHAIN 0]
 358 O60568_PLOD3_HL Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (LH3) [CHAIN 0]
 359 P46777_RL5_HUM 60S ribosomal protein L5 [CHAIN 0]
 360 P12277_KCRB_HUM Creatine kinase B-type [CHAIN 0]
 361 P50914_RL14_HUM 60S ribosomal protein L14 [CHAIN 0]
 362 P62495_ERF1_HUM Eukaryotic peptide chain release factor subunit 1 (Eukaryotic release f
 363 P42704_LPPRC_HU Leucine-rich PPR motif-containing protein, mitochondrial (LRP 130) [CI

364 O00203 AP3B1_HL AP-3 complex subunit beta-1
 365 P51659_DHB4_HUM Enoyl-CoA hydratase 2 [CHAIN 0]
 366 P35637_FUS_HUM/ RNA-binding protein FUS [ISOFORM Short]
 367 P52907_CAZA1_HL F-actin-capping protein subunit alpha-1 [CHAIN 0]
 368 P60866_RS20_HUM 40S ribosomal protein S20 [CHAIN 0]
 369 Q9UBG0_MRC2_HUM C-type mannose receptor 2 (UPAR-associated protein) (Urokinase rece
 370 Q96AE4_FUBP1_HU Far upstream element-binding protein 1 (FBP) (FUSE-binding protein 1
 371 Q9UMS4_PRP19_HU Pre-mRNA-processing factor 19 (hPso4) [CHAIN 0]
 372 P16615_AT2A2_HL Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SERCA2) (SR C
 373 P61604_CH10_HUM 10 kDa heat shock protein, mitochondrial (Hsp10) (CPN10) (EPF) [CHAI
 374 P48047_ATPO_HUM ATP synthase subunit O, mitochondrial (OSCP) [CHAIN 0]
 375 P61158_ARP3_HUM Actin-related protein 3 [CHAIN 0]
 376 P99999_CYC_HUM/ Cytochrome c [CHAIN 0]
 377 P15259_PGAM2_HL Phosphoglycerate mutase 2 (PGAM-M) [CHAIN 0]
 378 P61006_RAB8A_HL Ras-related protein Rab-8A [CHAIN 0]
 379 P26640_SYVC_HUM Valine--tRNA ligase
 380 P40429_RL13A_HL 60S ribosomal protein L13a [CHAIN 0]
 381 Q02818_NUCB1_HL Nucleobindin-1 [CHAIN 0]
 382 P08648_ITA5_HUM Integrin alpha-5 [CHAIN 1]
 383 Q92520_FAM3C_HL Protein FAM3C [CHAIN 0]
 384 P62879_GBB2_HUM Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [CH
 385 O95302_FKBP9_HU Peptidyl-prolyl cis-trans isomerase FKBP9 (PPIase FKBP9) (63 kDa FKBP
 386 P17066_HSP76_HL Heat shock 70 kDa protein 6
 387 P38919_IF4A3_HUM Eukaryotic initiation factor 4A-III (eIF-4A-III) (eIF4A-III) (NMP 265) (hN
 388 P18206_VINC_HUM Vinculin [ISOFORM 1]
 389 P46459_NSF_HUM/ Vesicle-fusing ATPase (NEM-sensitive fusion protein)
 390 Q99584_S10AD_HL Protein S100-A13
 391 Q96N66_MBOA7_HL Lysophospholipid acyltransferase 7 (LPLAT 7) (LPIAT) (Lyso-PI acyltrans
 392 P61160_ARP2_HUM Actin-related protein 2
 393 Q13492_PICAL_HUM Phosphatidylinositol-binding clathrin assembly protein [ISOFORM 3]
 394 P12109_CO6A1_HL Collagen alpha-1(VI) chain
 395 P08708_RS17_HUM 40S ribosomal protein S17 [CHAIN 0]
 396 P32969_RL9_HUM/ 60S ribosomal protein L9
 397 Q14444_CAPR1_HL Caprin-1 (GPI-p137) (p137GPI) [ISOFORM 2]
 398 P51571_SSRD_HUM Translocon-associated protein subunit delta (TRAP-delta) (SSR-delta) [
 399 P60891_PRPS1_HU Ribose-phosphate pyrophosphokinase 1 (PRS-I) [CHAIN 0]
 400 P61803_DAD1_HUM Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subun
 401 P24844_MYL9_HUM Myosin regulatory light polypeptide 9 (LC20) [CHAIN 0]
 402 Q01105_SET_HUM/ Protein SET (IGAAD) (I-2PP2A) (TAF-I) [ISOFORM 2]
 403 P62829_RL23_HUM 60S ribosomal protein L23
 404 P47897_SYQ_HUM/ Glutamine--tRNA ligase [CHAIN 0]
 405 Q5SSJ5_HP1B3_HL Heterochromatin protein 1-binding protein 3 [CHAIN 0]
 406 P31930_QCR1_HUM Cytochrome b-c1 complex subunit 1, mitochondrial [CHAIN 0]
 407 P09211_GSTP1_HL Glutathione S-transferase P [CHAIN 0]
 408 P49591_SYSC_HUM Seryl-tRNA synthetase, cytoplasmic (SerRS)
 409 Q13151_ROA0_HUM Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)
 410 O00567_NOP56_HL Nucleolar protein 56
 411 Q9Y6C9_MTCH2_HL Mitochondrial carrier homolog 2 [CHAIN 0]
 412 Q9H299_SH3L3_HL SH3 domain-binding glutamic acid-rich-like protein 3 (SH3BP-1)
 413 P06756_ITAV_HUM Integrin alpha-V light chain [ISOFORM 2]
 414 Q9NSD9_SYFB_HUM Phenylalanyl-tRNA synthetase beta chain (PheRS)
 415 O43175_SERA_HUM D-3-phosphoglycerate dehydrogenase (3-PGDH) [CHAIN 0]

416 O75694_NU155_HL Nuclear pore complex protein Nup155 [ISOFORM 2]
 417 P60953_CDC42_HL Cell division control protein 42 homolog [CHAIN 0]
 418 P33993_MCM7_HU DNA replication licensing factor MCM7 [CHAIN 0]
 419 Q15233_NONO_HU Non-POU domain-containing octamer-binding protein (NonO protein)
 420 Q15286_RAB35_HL Ras-related protein Rab-35
 421 P52292_IMA2_HUM Importin subunit alpha-1 [CHAIN 0]
 422 P30041_PRDX6_HL Peroxiredoxin-6 (1-Cys PRX) (aiPLA2) (NSGPx) [CHAIN 0]
 423 P36542_ATPG_HUM ATP synthase subunit gamma, mitochondrial [CHAIN 0]
 424 A1L0T0_ILVBL_HU Acetolactate synthase-like protein
 425 P05023_AT1A1_HL Sodium/potassium-transporting ATPase subunit alpha-1 (Na⁺)/K⁺ A⁺
 426 P29590_PML_HUM Probable transcription factor PML [ISOFORM PML-9]
 427 P30086_PEBP1_HU Phosphatidylethanolamine-binding protein 1 [CHAIN 0]
 428 P06748_NPM_HUM Nucleophosmin (NPM) [ISOFORM 2]
 429 P02768_ALBU_HUM Serum albumin [ISOFORM 2]
 430 P31947_1433S_HL 14-3-3 protein sigma [ISOFORM 2]
 431 Q13247_SRSF6_HU Serine/arginine-rich splicing factor 6 [ISOFORM SRP55-3]
 432 P62910_RL32_HUM 60S ribosomal protein L32
 433 P17813_EGLN_HUM Endoglin [CHAIN 0]
 434 P36871_PGM1_HU Phosphoglucomutase-1 (PGM 1) [CHAIN 0]
 435 Q9NYL9_TM0D3_HL Tropomodulin-3 (U-Tmod)
 436 Q13263_TIF1B_HU Transcription intermediary factor 1-beta (TIF1-beta) (KAP-1) (KRIP-1) [
 437 P46977_STT3A_HL Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subun
 438 Q15185_TEBP_HUM Prostaglandin E synthase 3 (cPGES)
 439 P51114_FXR1_HUM Fragile X mental retardation syndrome-related protein 1 (hFXR1p) [ISC
 440 P08729_K2C7_HUM Keratin, type II cytoskeletal 7 (CK-7) (K7) [CHAIN 0]
 441 P35241_RADI_HUM Radixin
 442 Q9UNX3_RL26L_HU 60S ribosomal protein L26-like 1 [CHAIN 0]
 443 P50402_EMD_HUM Emerin
 444 P43304_GPDM_HU Glycerol-3-phosphate dehydrogenase, mitochondrial (GPD-M) (GPDH-
 445 Q13283_G3BP1_HL Ras GTPase-activating protein-binding protein 1 (G3BP-1) (hDH VIII) [C
 446 P18085_ARF4_HUM ADP-ribosylation factor 4 [CHAIN 0]
 447 P14923_PLAK_HUM Junction plakoglobin
 448 P49411_EFTU_HUM Elongation factor Tu, mitochondrial (EF-Tu) [CHAIN 0]
 449 Q92688_AN32B_HL Acidic leucine-rich nuclear phosphoprotein 32 family member B (PHAF
 450 P63092_GNAS2_HL Guanine nucleotide-binding protein G subunit alpha isoforms short [IS
 451 P31942_HNRH3_HL Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (hnRNP 2H9
 452 P23528_COF1_HUM Cofilin-1 (p18) [CHAIN 0]
 453 P14866_HNRPL_HL Heterogeneous nuclear ribonucleoprotein L (hnRNP L)
 454 P55010_IF5_HUM Eukaryotic translation initiation factor 5 (eIF-5)
 455 Q9Y4L1_HYOU1_HL Hypoxia up-regulated protein 1 (ORP-150) (GRP-170) [CHAIN 0]
 456 P34932_HSP74_HL Heat shock 70 kDa protein 4
 457 Q9H853_TBA4B_HL Putative tubulin-like protein alpha-4B
 458 O75390_CISY_HUM Citrate synthase, mitochondrial [CHAIN 0]
 459 O15400_STX7_HUM Syntaxin-7 [ISOFORM 2]
 460 Q03252_LMNB2_HL Lamin-B2 [CHAIN 0]
 461 P20591_MX1_HUM Interferon-induced GTP-binding protein Mx1 [CHAIN 1]
 462 P17931_LEG3_HUM Galectin-3 (Gal-3) (CBP 35) (GALBP) [CHAIN 0]
 463 O95470_SGPL1_HU Sphingosine-1-phosphate lyase 1 (SP-lyase 1) (SPL 1) (hSPL)
 464 P55084_ECHB_HUM Trifunctional enzyme subunit beta, mitochondrial [CHAIN 0]
 465 Q16531_DDB1_HU DNA damage-binding protein 1 (DDBa) (XAP-1) (UV-DDB 1) (XPE-BF) (X
 466 Q15005_SPCS2_HU Signal peptidase complex subunit 2 (SPase 25 kDa subunit) [CHAIN 0]
 467 Q96FQ6_S10AG_HL Protein S100-A16

468 Q02952_AKA12_HL A-kinase anchor protein 12 (AKAP-12) (AKAP 250) [ISOFORM 3]
 469 P16070_CD44_HU CD44 antigen (ECMR-III) (PGP-1) (PGP-I) [ISOFORM 15]
 470 P54727_RD23B_HL UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (p58)
 471 Q8NBJ5_GT251_HL Procollagen galactosyltransferase 1 [CHAIN 0]
 472 Q0ZGT2_NEXN_HU Nexilin [ISOFORM 2]
 473 P14868_SYDC_HU Aspartate--tRNA ligase, cytoplasmic
 474 P56134_ATPK_HU ATP synthase subunit f, mitochondrial [ISOFORM 2]
 475 P40227_TCPZ_HU T-complex protein 1 subunit zeta (TCP-1-zeta) [CHAIN 0]
 476 Q9BWM7_SFXN3_HL Sideroflexin-3
 477 Q14566_MCM6_HU DNA replication licensing factor MCM6
 478 Q07021_C1QBP_HL Complement component 1 Q subcomponent-binding protein, mitoch
 479 P35268_RL22_HU 60S ribosomal protein L22 (EAP) [CHAIN 0]
 480 Q15758_AAAT_HU Neutral amino acid transporter B
 481 Q01813_K6PP_HU 6-phosphofructokinase type C (PFK-C)
 482 P07996_TSP1_HU Thrombospondin-1 [CHAIN 0]
 483 P30533_AMRP_HU Alpha-2-macroglobulin receptor-associated protein (Alpha-2-MRAP) (F
 484 P50991_TCPD_HU T-complex protein 1 subunit delta (TCP-1-delta) [CHAIN 0]
 485 P34897_GLYM_HU Serine hydroxymethyltransferase, mitochondrial (SHMT) [CHAIN 0]
 486 Q16555_DPYL2_HL Dihydropyrimidinase-related protein 2 (DRP-2) (CRMP-2) (ULIP-2)
 487 P61769_B2MG_HU Beta-2-microglobulin [CHAIN 1]
 488 Q9UBQ0_VPS29_HL Vacuolar protein sorting-associated protein 29 (hVPS29)
 489 P49755_TMEDA_HL Transmembrane emp24 domain-containing protein 10 (S31125) [CHA
 490 P22087_FBRL_HU rRNA 2'-O-methyltransferase fibrillarin
 491 Q8N556_AFAP1_HL Actin filament-associated protein 1 (AFAP-110)
 492 Q14554_PDIA5_HU Protein disulfide-isomerase A5 [CHAIN 0]
 493 P12270_TPR_HU Nucleoprotein TPR [CHAIN 0]
 494 Q9HDC9_APMAP_HL Adipocyte plasma membrane-associated protein [ISOFORM 2]
 495 P24539_AT5F1_HL ATP synthase subunit b, mitochondrial (ATPase subunit b) [CHAIN 0]
 496 P38159_HNRPG_HL Heterogeneous nuclear ribonucleoprotein G, N-terminally processed [
 497 P20618_PSB1_HU Proteasome subunit beta type-1 [CHAIN 0]
 498 P07099_HYEP_HU Epoxide hydrolase 1
 499 Q9UKV3_ACINU_HU Apoptotic chromatin condensation inducer in the nucleus (Acinus)
 500 P37108_SRP14_HU Signal recognition particle 14 kDa protein (SRP14) [CHAIN 0]
 501 Q70UQ0_IKIP_HU Inhibitor of nuclear factor kappa-B kinase-interacting protein (I kappa-
 502 Q9NVD7_PARVA_HL Alpha-parvin
 503 P13987_CD59_HU CD59 glycoprotein (HRF-20) (HRF20) (MAC-IP) (MACIF) (MIRL) [CHAIN
 504 Q99439_CNN2_HU Calponin-2 [CHAIN 0]
 505 Q9Y5X1_SNX9_HU Sorting nexin-9 (Protein SDP1)
 506 O75380_NDUS6_HL NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondri
 507 P09669_COX6C_HL Cytochrome c oxidase subunit 6C [CHAIN 0]
 508 Q9Y2D5_AKAP2_HL A-kinase anchor protein 2 (AKAP-2) (PRKA2)
 509 Q13641_TPBG_HU Trophoblast glycoprotein (5T4 oncotrophoblast glycoprotein) [CHAIN 0]
 510 P09525_ANXA4_HL Annexin A4 (PAP-II) [CHAIN 0]
 511 P09661_RU2A_HU U2 small nuclear ribonucleoprotein A' (U2 snRNP A') [CHAIN 0]
 512 Q6IAA8_PDRO_HU Ragulator complex protein LAMTOR1 [CHAIN 0]
 513 P62888_RL30_HU 60S ribosomal protein L30 [CHAIN 0]
 514 P07093_GDN_HU Glia-derived nexin (GDN) (PI-7) (PN-1) [CHAIN 0]
 515 O75534_CSDE1_HL Cold shock domain-containing protein E1 [ISOFORM Short]
 516 Q10713_MPPA_HU Mitochondrial-processing peptidase subunit alpha [CHAIN 0]
 517 Q92598_HS105_HL Heat shock protein 105 kDa [ISOFORM Beta]
 518 O00231_PSD11_HL 26S proteasome non-ATPase regulatory subunit 11 [CHAIN 0]
 519 P30049_ATPD_HU ATP synthase subunit delta, mitochondrial [CHAIN 0]

520 P62913_RL11_HUM 60S ribosomal protein L11 [CHAIN 0]
521 Q15436 SC23A_HL Protein transport protein Sec23A
522 P30443_1A01_HUI HLA class I histocompatibility antigen, A-1 alpha chain [CHAIN 0]
523 Q53GQ0 DHB12_HL Estradiol 17-beta-dehydrogenase 12 (17-beta-HSD 12) (KAR)
524 Q53FA7 QORX_HUM Quinone oxidoreductase PIG3
525 P04632 CPNS1_HL Calpain small subunit 1 (CSS1) (CANP small subunit) (CDPS)
526 P41250 SYG_HUM/ Glycine--tRNA ligase
527 Q8IVL6_P3H3_HUM Prolyl 3-hydroxylase 3 [CHAIN 0]
528 P02533_K1C14_HL Keratin, type I cytoskeletal 14 (CK-14) (K14) [CHAIN 0]
529 Q8N4C6_NIN_HUMA Ninein (hNinein) (GSK3B-interacting protein) [ISOFORM 6]
530 Q96I24_FUBP3_HU Far upstream element-binding protein 3 (FUSE-binding protein 3) [CH/
531 Q70UQ0_IKIP_HUM/ Inhibitor of nuclear factor kappa-B kinase-interacting protein (I kappa-
532 Q00688_FKBP3_HU Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (25 kDa FKBP
533 Q15393_SF3B3_HU Splicing factor 3B subunit 3 (SF3b130) (SAP 130)
534 Q16630_CPSF6_HU Cleavage and polyadenylation specificity factor subunit 6 (CPSF 68 kDa
535 P49748_ACADV_HL Very long-chain specific acyl-CoA dehydrogenase, mitochondrial (VLCA
536 Q9BUJ2_HNRL1_HL Heterogeneous nuclear ribonucleoprotein U-like protein 1 (E1B-AP5) [
537 P21281_VATB2_HL V-type proton ATPase subunit B, brain isoform (V-ATPase subunit B 2)
538 Q969X5_ERG11_HU Endoplasmic reticulum-Golgi intermediate compartment protein 1 (ER
539 P08779_K1C16_HL Keratin, type I cytoskeletal 16 (CK-16) (K16) [CHAIN 0]
540 Q9UQ80_PA2G4_HL Proliferation-associated protein 2G4 (hG4-1) [CHAIN 0]
541 P60033_CD81_HU CD81 antigen (Tspan-28)
542 Q15459_SF3A1_HL Splicing factor 3A subunit 1 (SAP 114)
543 Q9Y230_RUVB2_HL RuvB-like 2 (48 kDa TBP-interacting protein) (ECP-51) (Reptin 52) (TAP
544 P62826_RAN_HUM/ GTP-binding nuclear protein Ran [CHAIN 0]
545 P09874_PARP1_HL Poly [ADP-ribose] polymerase 1 (PARP-1) (ADPRT 1) [CHAIN 0]
546 Q92791_SC65_HUM Synaptonemal complex protein SC65
547 P62917_RL8_HUM/ 60S ribosomal protein L8 [CHAIN 0]
548 P20674_COX5A_HL Cytochrome c oxidase subunit 5A, mitochondrial [CHAIN 0]
549 P24534_EF1B_HUM Elongation factor 1-beta (EF-1-beta) [CHAIN 0]
550 Q93008_USP9X_HU Probable ubiquitin carboxyl-terminal hydrolase FAF-X (hFAM) [ISOFOR
551 Q14019_COTL1_HL Coactosin-like protein [CHAIN 0]
552 O76094_SRP72_HU Signal recognition particle 72 kDa protein (SRP72) [CHAIN 0]
553 Q13423_NNTM_HUI NAD transhydrogenase, mitochondrial [CHAIN 0]
554 O14602_IF1AY_HUI Eukaryotic translation initiation factor 1A, Y-chromosomal (eIF-1A Y is
555 P46063_RECQ1_HL ATP-dependent DNA helicase Q1 (RecQ1) [CHAIN 0]
556 P54136_SYRC_HUM Arginyl-tRNA synthetase, cytoplasmic (ArgRS) [ISOFORM Monomeric]
557 Q6NYC8_PHTNS_HL Phostensin
558 Q9Y4P3_TBL2_HUM Transducin beta-like protein 2 (WS-betaTRP)
559 O94874_UFL1_HUM E3 UFM1-protein ligase 1 [ISOFORM 3]
560 P28066_PSA5_HUM Proteasome subunit alpha type-5
561 Q4VXU2_PAP1L_HL Polyadenylate-binding protein 1-like
562 P54920_SNAA_HUI Alpha-soluble NSF attachment protein (SNAP-alpha)
563 P11177_ODPB_HUM Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (I
564 Q16795_NDUA9_HL NADH dehydrogenase 1 alpha subcomplex subunit 9, mitochondrial (C
565 Q9Y3B3_TMED7_HL Transmembrane emp24 domain-containing protein 7 [CHAIN 0]
566 P09622_DLDH_HUM Dihydrolipoyl dehydrogenase, mitochondrial [CHAIN 0]
567 P04181_OAT_HUM/ Ornithine aminotransferase, renal form [CHAIN 1]
568 Q15043_S39AE_HL Zinc transporter ZIP14 (LZT-Hs4) (ZIP-14) [CHAIN 0]
569 O75131_CPNE3_HL Copine-3 [CHAIN 0]
570 O14776_TCRG1_HL Transcription elongation regulator 1 [ISOFORM 2]
571 P98179_RBM3_HUM Putative RNA-binding protein 3

572 P18621_RL17_HUM 60S ribosomal protein L17 [CHAIN 0]
573 Q08431_MFGM_HUI Lactadherin [ISOFORM 2]
574 Q04837_SSBP_HUM Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB)
575 Q16881_TRXR1_HU Thioredoxin reductase 1, cytoplasmic (TR) (GRIM-12) (Gene associated
576 P24752_THIL_HUM Acetyl-CoA acetyltransferase, mitochondrial [CHAIN 0]
577 Q14676_MDC1_HUI Mediator of DNA damage checkpoint protein 1 [ISOFORM 4]
578 P61221_ABCE1_HL ATP-binding cassette sub-family E member 1 (RNS4I)
579 Q6UVK1_CSPG4_HL Chondroitin sulfate proteoglycan 4 [CHAIN 0]
580 P08574_CY1_HUM Cytochrome c1, heme protein, mitochondrial (Cytochrome c-1) [CHAIN
581 P59190_RAB15_HL Ras-related protein Rab-15 [ISOFORM 2]
582 Q9UJZ1_STML2_HL Stomatin-like protein 2 (SLP-2)
583 Q13243_SRSF5_HU Serine/arginine-rich splicing factor 5 [ISOFORM SRP40-4]
584 P10321_1C07_HUM HLA class I histocompatibility antigen, Cw-7 alpha chain [CHAIN 0]
585 Q03135_CAV1_HUI Caveolin-1 [ISOFORM Beta]
586 Q9NX63_CHCH3_HL Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitoch
587 P42766_RL35_HUM 60S ribosomal protein L35 [CHAIN 0]
588 Q15008_PSM6_HL 26S proteasome non-ATPase regulatory subunit 6 [CHAIN 0]
589 Q9Y265_RUVB1_HL RuvB-like 1 (49 kDa TBP-interacting protein) (ECP-54) (NMP 238) (TAP
590 O75531_BAF_HUM Barrier-to-autointegration factor
591 P49257_LMAN1_HL Protein ERGIC-53 [CHAIN 0]
592 O75368_SH3L1_HL SH3 domain-binding glutamic acid-rich-like protein
593 P49773_HINT1_HU Histidine triad nucleotide-binding protein 1 (PKCI-1) [CHAIN 0]
594 P33176_KINH_HUM Kinesin-1 heavy chain (UKHC) [CHAIN 0]
595 Q15293_RCN1_HUM Reticulocalbin-1 [CHAIN 0]
596 P30084_ECHM_HUI Enoyl-CoA hydratase, mitochondrial (SCEH) [CHAIN 0]
597 P17301_ITA2_HUM Integrin alpha-2 (GPIa) [CHAIN 0]
598 O14737_PDCD5_HL Programmed cell death protein 5 (Protein TFAR19) [CHAIN 0]
599 Q14344_GNA13_HL Guanine nucleotide-binding protein subunit alpha-13 (G alpha-13) (G-
600 O14653_GOSR2_HL Golgi SNAP receptor complex member 2
601 P22102_PUR2_HUM Trifunctional purine biosynthetic protein adenosine-3
602 Q13895_BYST_HUM Bystin
603 Q16666_IFI16_HUM Gamma-interferon-inducible protein 16 (Ifi-16) [ISOFORM 4]
604 Q10567_AP1B1_HL AP-1 complex subunit beta-1 [ISOFORM C]
605 P14927_QCR7_HUM Cytochrome b-c1 complex subunit 7 [CHAIN 0]
606 Q13177_PAK2_HUM PAK-2p34 (p34) [CHAIN 1]
607 P62249_RS16_HUM 40S ribosomal protein S16 [CHAIN 0]
608 O43294_TGFI1_HUI Transforming growth factor beta-1-induced transcript 1 protein (Hic-5
609 A0FGR8_ESYT2_HU Extended synaptotagmin-2 (E-Syt2) [ISOFORM 4]
610 Q9Y512_SAM50_HL Sorting and assembly machinery component 50 homolog (TRG-3)
611 Q8WUM4_PDC6L_HUI Programmed cell death 6-interacting protein (PDCD6-interacting prote
612 P09496_CLCA_HUM Clathrin light chain A (Lca) [ISOFORM Non-brain]
613 P63000_RAC1_HUM Ras-related C3 botulinum toxin substrate 1
614 P68402_PA1B2_HL Platelet-activating factor acetylhydrolase IB subunit beta (PAF-AH 30 k
615 O15145_ARPC3_HL Actin-related protein 2/3 complex subunit 3 (p21-ARC) [CHAIN 0]
616 P26368_U2AF2_HL Splicing factor U2AF 65 kDa subunit (hU2AF(65)) (hU2AF65) [ISOFORM
617 O43684_BUB3_HUM Mitotic checkpoint protein BUB3 [ISOFORM 2]
618 P13073_COX41_HL Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (COX IV-1) [(
619 P62995_TRA2B_HL Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-beta) (hTRA2
620 P26373_RL13_HUM 60S ribosomal protein L13 [CHAIN 0]
621 O75844_FACE1_HL CAAX prenyl protease 1 homolog (FACE-1)
622 Q9UKM7_MA1B1_HL Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosid
623 P29992_GNA11_HL Guanine nucleotide-binding protein subunit alpha-11 (G alpha-11) (G-

624 P62750_RL23A_HL 60S ribosomal protein L23a [CHAIN 0]
625 P42224_STAT1_HL Signal transducer and activator of transcription 1-alpha/beta [ISOFORM 1]
626 P30837_AL1B1_HL Aldehyde dehydrogenase X, mitochondrial [CHAIN 0]
627 Q9H930_LY10L_HU Nuclear body protein SP140-like protein [ISOFORM 2]
628 Q9UHX1_PUF60_HL Poly(U)-binding-splicing factor PUF60 (FBP-interacting repressor) (RoB)
629 Q9NP72_RAB18_HL Ras-related protein Rab-18 [CHAIN 0]
630 Q9UJS0_CMC2_HU Calcium-binding mitochondrial carrier protein Aralar2
631 Q9UL25_RAB21_HL Ras-related protein Rab-21 [CHAIN 0]
632 O75915_PRAF3_HL PRA1 family protein 3 (ARL-6-interacting protein 5) (Aip-5)
633 P62244_RS15A_HL 40S ribosomal protein S15a [CHAIN 0]
634 Q9P0L0_VAPA_HU Vesicle-associated membrane protein-associated protein A (VAMP-A)
635 P14314_GLU2B_HL Glucosidase 2 subunit beta (PKCSH) [CHAIN 0]
636 P62899_RL31_HU 60S ribosomal protein L31
637 P46776_RL27A_HL 60S ribosomal protein L27a [CHAIN 0]
638 P51572_BAP31_HL B-cell receptor-associated protein 31 (BCR-associated protein 31) (Bap)
639 O75340_PDCD6_HL Programmed cell death protein 6
640 Q969H8_CS010_HL UPF0556 protein C19orf10 (IL-25) [CHAIN 0]
641 Q01844_EWS_HU RNA-binding protein EWS [ISOFORM EWS-B]
642 Q9UJ70_NAGK_HU N-acetyl-D-glucosamine kinase (N-acetylglucosamine kinase) [CHAIN 0]
643 P12004_PCNA_HU Proliferating cell nuclear antigen (PCNA)
644 P35221_CTNA1_HL Catenin alpha-1 [CHAIN 0]
645 P16152_CBR1_HU Carbonyl reductase [NADPH] 1 [CHAIN 0]
646 A2RRP1_NBAS_HU Neuroblastoma-amplified sequence [ISOFORM 2]
647 Q14498_RBM39_HL RNA-binding protein 39 [ISOFORM 2]
648 Q99805_TM9S2_HL Transmembrane 9 superfamily member 2 [CHAIN 0]
649 Q9Y2W2_WBP11_HL WW domain-binding protein 11 (WBP-11) (NpwBP)
650 P35613_BAS1_HU Basigin (EMMPRIN) (TCSF) [ISOFORM 2]
651 O75489_NDUS3_HL NADH dehydrogenase iron-sulfur protein 3, mitochondrial [CHAIN 0]
652 Q9BXP5_SRRT_HU Serrate RNA effector molecule homolog [ISOFORM 5]
653 Q8N163_K1967_HL Protein KIAA1967 (DBC-1) (DBC.1)
654 O94905_ERLN2_HU Erlin-2 (SPFH domain-containing protein 2)
655 O43747_AP1G1_HL AP-1 complex subunit gamma-1 [CHAIN 0]
656 P84103_SRSF3_HU Serine/arginine-rich splicing factor 3
657 O00629_IMA4_HU Importin subunit alpha-3 [CHAIN 0]
658 O94826_TOM70_HL Mitochondrial import receptor subunit TOM70 [CHAIN 0]
659 P60903_S10AA_HL Protein S100-A10 [CHAIN 0]
660 P10301_RRAS_HU Ras-related protein R-Ras [CHAIN 0]
661 P11387_TOP1_HU DNA topoisomerase 1 [CHAIN 0]
662 Q96CW1_AP2M1_HL AP-2 complex subunit mu
663 Q9HBRO_S38AA_HL Putative sodium-coupled neutral amino acid transporter 10 [ISOFORM 1]
664 Q16698_DECR_HU 2,4-dienoyl-CoA reductase, mitochondrial (4-enoyl-CoA reductase [NA
665 Q92804_RBP56_HL TATA-binding protein-associated factor 2N (TAF(II)68) (TAFII68)
666 P23634_AT2B4_HL Plasma membrane calcium-transporting ATPase 4 (PMCA4) [ISOFORM 1]
667 P26639_SYTC_HU Threonyl-tRNA synthetase, cytoplasmic (ThrRS)
668 O15144_ARPC2_HL Actin-related protein 2/3 complex subunit 2 (p34-ARC)
669 Q9P0K7_RAI14_HU Ankycorbin [ISOFORM 3]
670 P39687_AN32A_HL Acidic leucine-rich nuclear phosphoprotein 32 family member A (LANP)
671 P63173_RL38_HU 60S ribosomal protein L38
672 Q9H0S4_DDX47_HL Probable ATP-dependent RNA helicase DDX47 [CHAIN 0]
673 Q9Y3I0_CV028_HL UPF0027 protein C22orf28
674 P63167_DYL1_HU Dynein light chain 1, cytoplasmic (DLC8) (PIN)
675 Q12797_ASPH_HU Aspartyl/asparaginyl beta-hydroxylase (ASP beta-hydroxylase)

676 Q9Y3U8_RL36_HUMAN 60S ribosomal protein L36 [CHAIN 0]
677 Q8TAQ2_SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 [ISOFORM 2]
678 P26196_DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6
679 P16949_STMN1_HUMAN Stathmin (Op18) (pp19)
680 P36957_ODO2_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex [CHAIN 0]
681 Q02880_TOP2B_HUMAN DNA topoisomerase 2-beta [ISOFORM Beta-1]
682 P42892_ECE1_HUMAN Endothelin-converting enzyme 1 (ECE-1) [ISOFORM C]
683 P05161_ISG15_HUMAN Ubiquitin-like protein ISG15 (IP17) (hUCRP) [CHAIN 0]
684 Q15417_CNN3_HUMAN Calponin-3
685 P49821_NDUV1_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (CI-55)
686 P25786_PSA1_HUMAN Proteasome subunit alpha type-1 (PROS-30)
687 Q95816_BAG2_HUMAN BAG family molecular chaperone regulator 2 (BAG-2)
688 Q7L014_DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46
689 P46939_UTRO_HUMAN Utrophin (DRP-1)
690 Q13425_SNTB2_HUMAN Beta-2-syntrophin (SNT3) (SNTL)
691 P28370_SMCA1_HUMAN Probable global transcription activator SNF2L1 [ISOFORM 2]
692 Q8WUJ3_K1199_HUMAN Protein KIAA1199 [CHAIN 0]
693 Q9H3N1_TMX1_HUMAN Thioredoxin-related transmembrane protein 1 [CHAIN 0]
694 P62318_SMD3_HUMAN Small nuclear ribonucleoprotein Sm D3 (Sm-D3)
695 P08727_K1C19_HUMAN Keratin, type I cytoskeletal 19 (CK-19) (K19)
696 P13473_LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane glycoprotein 2)
697 Q99733_NP1L4_HUMAN Nucleosome assembly protein 1-like 4 (NAP-2) [CHAIN 0]
698 P46783_RS10_HUMAN 40S ribosomal protein S10
699 P02042_HBD_HUMAN Hemoglobin subunit delta [CHAIN 0]
700 Q13242_SRSF9_HUMAN Serine/arginine-rich splicing factor 9
701 Q6P1M0_S27A4_HUMAN Long-chain fatty acid transport protein 4 (FATP-4) (Fatty acid transport protein 4)
702 P17655_CAN2_HUMAN Calpain-2 catalytic subunit (CANP 2) (M-calpain) [CHAIN 0]
703 P23526_SAHH_HUMAN Adenosylhomocysteinase (AdoHcyase) [CHAIN 0]
704 P61353_RL27_HUMAN 60S ribosomal protein L27
705 P48735_IDHP_HUMAN Isocitrate dehydrogenase, mitochondrial [CHAIN 0]
706 Q8TCS8_PNPT1_HUMAN Polyribonucleotide nucleotidyltransferase 1, mitochondrial (PNPase 1)
707 Q08945_SSRP1_HUMAN FACT complex subunit SSRP1 (FACT 80 kDa subunit) (FACTp80) (hSSRP1)
708 O43854_EDIL3_HUMAN EGF-like repeat and discoidin I-like domain-containing protein 3 [CHAIN 0]
709 O00410_IPO5_HUMAN Importin-5 (Imp5) (RanBP5) [CHAIN 0]
710 Q12841_FSTL1_HUMAN Follistatin-related protein 1 [CHAIN 0]
711 Q00325_MPCP_HUMAN Phosphate carrier protein, mitochondrial (PTP) [CHAIN 0]
712 Q86UX6_ST32C_HUMAN Serine/threonine-protein kinase 32C (PKE)
713 P41223_BUD31_HUMAN Protein BUD31 homolog
714 P20908_CO5A1_HUMAN Collagen alpha-1(V) chain [CHAIN 0]
715 P52943_CRIP2_HUMAN Cysteine-rich protein 2 (CRP-2)
716 Q9BVK6_TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 [CHAIN 0]
717 Q12904_AIMP1_HUMAN Endothelial monocyte-activating polypeptide 2 (EMAP-2) (EMAP-II)
718 P07942_LAMB1_HUMAN Laminin subunit beta-1
719 Q07666_KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1
720 P05783_K1C18_HUMAN Keratin, type I cytoskeletal 18 (CK-18) (K18) [CHAIN 0]
721 P37235_HPCL1_HUMAN Hippocalcin-like protein 1 (VILIP-3) [CHAIN 0]
722 P55265_DSRAD_HUMAN Double-stranded RNA-specific adenosine deaminase (DRADA) (p136) (p136)
723 Q9Y2H6_FND3A_HUMAN Fibronectin type-III domain-containing protein 3A [ISOFORM 2]
724 Q9P035_HACD3_HUMAN Very-long-chain -3-hydroxyacyl-CoA dehydratase 3
725 Q9NSK0_KLC4_HUMAN Kinesin light chain 4 (KLC 4) [ISOFORM 3]
726 Q04637_IF4G1_HUMAN Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (eIF4G1)
727 P36776_LONM_HUMAN Lon protease homolog, mitochondrial (LONP) [CHAIN 0]

728 Q13561.DCTN2_HL Dynactin subunit 2 (DCTN-50) [CHAIN 0]
 729 P11413_G6PD_HUM Glucose-6-phosphate 1-dehydrogenase (G6PD) [CHAIN 0]
 730 Q9Y6M1_IF2B2_HU Insulin-like growth factor 2 mRNA-binding protein 2 (IGF2 mRNA-bindi
 731 O95573_ACSL3_HL Long-chain-fatty-acid--CoA ligase 3 (LACS 3)
 732 Q06323_PSME1_HL Proteasome activator complex subunit 1 (REG-alpha) (IGUP I-5111) (P
 733 Q13557_KCC2D_HL Calcium/calmodulin-dependent protein kinase type II subunit delta (C
 734 Q9BS26_ERP44_HU Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) [C
 735 Q96AC1_FERM2_HL Fermitin family homolog 2 (MIG-2) (PH domain-containing family C me
 736 O15042_SR140_HL U2-associated protein SR140 [ISOFORM 2]
 737 Q6NUQ4_TM214_HL Transmembrane protein 214
 738 P56385_ATP5I_HU ATP synthase subunit e, mitochondrial (ATPase subunit e) [CHAIN 0]
 739 Q14534_ERG1_HUM Squalene monooxygenase (SE)
 740 P78357_CNTP1_HL Contactin-associated protein 1 (Caspr) (Caspr1) [CHAIN 0]
 741 Q16851_UGPA_HUM UTP--glucose-1-phosphate uridylyltransferase (UDPGP) (UGPase) [ISO
 742 Q12849_GRSF1_HU G-rich sequence factor 1 (GRSF-1)
 743 Q8TF01_SFR18_HU Arginine/serine-rich protein PNISR
 744 Q07157_ZO1_HUM Tight junction protein ZO-1 [ISOFORM Short]
 745 O60762_DPM1_HU Dolichol-phosphate mannosyltransferase (DPM synthase) (MPD synth
 746 Q99459_CDC5L_HL Cell division cycle 5-like protein (Cdc5-like protein)

Score	Coverage	#Peptides	#Uniq Peptid	#Sub-protein	Sub-proteins
468,696	36,64	139	64	2	P21333_CHAIN_0,P21333
428,979	15,2	86	62	9	Q15149_ISOFORM_7,Q15149_ISOFORM_8,Q15149_ISOFORM_9
428,329	33,93	127	59	1	P35579_CHAIN_0
271,984	65,81	153	37	5	P08670,P17661_CHAIN_0,P17661,P41219,P41220
259,871	46,75	104	34	4	P02545_CHAIN_0,P02545,P02545_ISOFORM_A,P02545_ISOFORM_B
248,727	17,74	49	35	2	Q13813,Q13813_ISOFORM_2
197,486	13,89	39	27	6	O75369,O75369_ISOFORM_6,O75369_ISOFORM_7,O75369_ISOFORM_8,O75369_ISOFORM_9,O75369_ISOFORM_10
194,087	16,43	47	25	16	P02751_ISOFORM_3,P02751,P02751_ISOFORM_4,P02751_ISOFORM_5,P02751_ISOFORM_6,P02751_ISOFORM_7,P02751_ISOFORM_8,P02751_ISOFORM_9,P02751_ISOFORM_10,P02751_ISOFORM_11,P02751_ISOFORM_12,P02751_ISOFORM_13,P02751_ISOFORM_14,P02751_ISOFORM_15
193,489	52,66	57	25	1	Q07065_ISOFORM_2
189,336	19,34	39	26	4	Q00610_CHAIN_0,Q00610,P53675_ISOFORM_1,P53675_ISOFORM_2
189,155	45,57	38	23	1	P04264
188,711	35,2	53	26	0	
182,489	6,35	45	26	0	
175,875	28,25	34	23	2	Q9P2E9_ISOFORM_1,Q9P2E9
173,605	40,33	48	25	1	P08133
172,979	33,04	46	22	0	
160,12	61,5	135	20	5	P63261_CHAIN_1,P60709,P63261,Q562R1,Q9B0L1
151,737	11,17	27	21	2	Q01082_ISOFORM_2,Q01082_ISOFORM_Short
137,032	58,56	35	18	4	A6NNZ2,Q3ZCM7,A6NKZ8,Q99867
136,474	44,35	48	18	3	P06753_ISOFORM_3,A6NL28_ISOFORM_2,A6NL28
134,699	49,41	53	17	4	P07355,P07355_ISOFORM_2,A6NMY6_CHAIN_0,A6NMY6
131,813	52,8	53	17	4	P68032,P68133_CHAIN_0,P68133,Q562R1
128,762	36,99	27	17	0	
127,367	40,85	52	17	0	
127,354	42,25	52	17	1	P07951_ISOFORM_3
123,121	49,6	49	16	1	P62736_CHAIN_0
121,54	41,89	32	17	1	P14618
117,033	9,91	20	17	7	Q9NZM1,Q9NZM1_ISOFORM_3,Q9NZM1_ISOFORM_4,Q9NZM1_ISOFORM_5,Q9NZM1_ISOFORM_6,Q9NZM1_ISOFORM_7,Q9NZM1_ISOFORM_8
116,46	32,39	49	15	1	P09493_ISOFORM_5
116,283	33,45	50	15	2	P09493_ISOFORM_4,P09493_ISOFORM_2
115,934	9,21	19	16	0	
113,665	37,84	21	16	1	P04843
112,453	48,09	29	15	5	P04350,A6NNZ2,Q3ZCM7,A6NKZ8,Q99867
112,265	47	29	15	1	P50454
110,309	44,94	15	15	0	
110,26	34,51	38	16	0	
109,966	4,98	17	16	1	P78527_CHAIN_0
109,857	35,63	45	15	1	P67936
109,363	42,47	29	14	5	Q9BVA1,A6NNZ2,Q3ZCM7,A6NKZ8,Q99867
107,195	21,61	24	16	4	P07900,P07900_ISOFORM_2,Q14568,Q58FG1
106,608	26,89	43	14	1	P11021
106,453	36,86	27	17	1	P07237
105,263	35,59	26	15	0	
104,774	43,78	35	14	1	P06576
104,747	23,2	27	15	1	P08238_CHAIN_0
104,084	12,02	23	13	1	P02452_CHAIN_0
100,447	31,26	24	15	1	P10809
99,158	44,64	41	13	1	P04083
94,221	40,23	25	13	1	P22626_ISOFORM_A2
93,407	35,03	44	11	3	Q13748,Q6PEY2,Q13748_ISOFORM_2
92,436	13,23	21	14	0	

92,304	35,03	47	11	0
90,251	4,82	14	13	3 Q99715_CHAIN_0,Q99715,Q99715_ISOFORM_
86,478	48,31	21	13	6 P0C7M2_CHAIN_0,P09651_ISOFORM_A1-A,P0I
85,57	36,95	25	11	4 P06733,P06733_ISOFORM_MBP-1,P09104_CH/
85,184	44,91	44	11	1 P04406
84,692	8	15	12	1 P35580_CHAIN_0
84,39	31,4	41	10	0
83,73	5,91	19	12	1 Q14315
82,695	20,45	21	11	1 P19338
80,9	23,79	18	11	1 Q7Z794
79,881	32,5	34	11	2 P61978,P61978_ISOFORM_2
78,914	25,11	20	10	0
77,976	55,65	21	10	2 P60174,P60174_ISOFORM_2
76,047	22,54	31	11	0
75,916	39,18	24	11	1 P08758
74,846	13,03	12	10	1 P08123_CHAIN_0
74,661	25,29	23	10	1 P25705
74,543	23,91	17	11	1 P30101
73,288	13,43	14	10	1 P14625
73,06	12,08	14	11	1 Q00341
71,916	17,6	16	10	1 P12956
71,666	14,74	15	10	1 Q7KZF4
71,458	17,48	22	9	4 Q05682_ISOFORM_4,Q05682_ISOFORM_3,Q05
70,723	10,95	16	11	1 P53621_ISOFORM_2
70,551	41,95	22	10	1 Q99623
70,309	14,94	24	11	1 P13639
70,008	22,25	17	9	1 P26641
69,967	34,44	16	9	1 P04075
69,887	17,52	27	10	3 P11142,P11142_ISOFORM_2,P54652
68,399	52,5	23	10	1 Q01995
67,955	45,22	26	9	0
67,778	35,13	17	9	1 P63244
67,585	81,48	40	9	1 P09382_CHAIN_0
66,794	22,2	13	10	5 O60506_ISOFORM_3,O60506_ISOFORM_2,O60
66,084	22,47	16	9	1 P78371
66,004	14,41	17	11	2 Q14697,Q14697_ISOFORM_2
65,638	13,77	11	10	1 P15144
64,765	24,59	13	10	2 Q13838,Q13838_ISOFORM_2
64,752	33,33	16	8	1 P21796
64,65	14,79	9	8	1 Q92945
63,94	30,05	15	9	1 P36578
62,914	11,44	12	9	0
62,016	20,66	15	9	2 P11940,Q9H361
61,929	22,66	17	9	2 Q14240,Q14240_ISOFORM_2
61,848	7,81	54	7	1 Q9BYX7
61,594	16,91	18	8	1 P04844
60,809	23,21	35	7	0
60,631	21,94	11	9	0
60,413	31,25	20	9	1 Q02878_CHAIN_0
59,302	7,82	10	9	1 Q14152
59,209	8,74	10	8	0
58,219	15,03	13	9	1 P13010_CHAIN_0

57,491	41,32	16	9	1 P23396
56,774	6,04	10	8	1 P46940
56,082	14,37	10	7	2 O00571,O15523
55,944	63,73	24	8	1 P62805
55,856	11,86	15	8	1 P20700
55,816	12,8	11	7	1 P55072
55,638	15,36	10	6	1 P50990
55,377	19,3	13	6	5 Q9NQC3_ISOFORM_5,Q9NQC3,Q9NQC3_ISOFORM_5
55,13	25,51	12	7	1 P08865
54,542	22,06	9	7	0
54,408	13,88	14	7	5 P05556_ISOFORM_Beta-1B,P05556,P05556_ISOFORM_Beta-1B
54,248	25,97	23	8	2 Q5VTE0,Q05639
53,388	22,61	18	6	3 P45880_CHAIN_0,P45880,P45880_ISOFORM_1
53,059	23,88	11	7	1 P51991
52,509	19,6	26	6	0
52,403	6,89	23	8	3 Q8WWI1_ISOFORM_4,Q8WWI1_ISOFORM_2,C
52,014	25,43	8	7	1 P13489
51,891	30,48	15	7	1 P15880
51,737	8,37	10	8	2 O00159_ISOFORM_3,O00159
51,537	11,45	10	8	5 Q12906_ISOFORM_4,Q12906_ISOFORM_2,Q12906_ISOFORM_3
51,447	8,51	9	7	4 P19367_ISOFORM_2,P19367,P19367_ISOFORM_1
51,035	17,09	12	7	0
50,811	13,19	13	8	0
49,717	15,37	14	7	1 P48643
49,653	20,89	12	7	2 Q01518,Q01518_ISOFORM_2
49,338	13,27	8	6	0
49,304	11,28	12	7	1 P15311
49,262	18,61	13	7	0
48,989	17,34	11	7	0
48,602	38,8	14	7	1 P23284
48,587	12,45	10	6	1 Q9NR30
48,517	11,93	15	7	0
48,236	42,06	23	7	1 O60814_CHAIN_0
48,165	41,6	21	7	15 P23527_CHAIN_0,P33778_CHAIN_0,Q16778_CHAIN_0
48,141	4,03	8	7	1 O75643_ISOFORM_2
48,137	27,07	14	6	1 P40926
48,092	6,33	7	7	1 Q9BQG0_ISOFORM_2
48,084	8,95	13	7	0
48,057	28,28	12	7	1 P12236
47,693	13,63	9	7	0
47,064	33,47	25	7	0
46,874	8,06	8	6	1 Q9BSJ8_ISOFORM_2
46,816	49,76	13	6	0
46,795	34,07	11	6	1 Q8NHW5
46,792	10,07	9	7	1 Q9UBF2
46,763	36,49	9	7	2 P61019,Q8WUD1
46,359	14,91	9	7	2 P06396_CHAIN_0,P06396
46,284	34,85	13	6	1 P37802
46,25	9,79	14	5	1 P38646
46,133	16,53	12	8	1 Q9UHB6
45,909	36,43	36	6	24 Q7L7L0_CHAIN_0,Q93077_CHAIN_0,P04908,Q7L7L0
45,83	23,31	14	6	0

45,83	11,27	8	7	0
45,559	13,27	9	6	0
45,343	26,43	14	5	2 P29692,P29692_ISOFORM_2
45,341	48	18	6	3 P60660,P60660_ISOFORM_Smoothmuscle,P14
45,097	15,04	8	7	2 O75083,O75083_ISOFORM_2
44,964	18,5	11	6	1 Q8NBS9
44,779	23,26	11	7	2 P00338,P00338_ISOFORM_2
44,634	11,98	12	7	1 P26038
44,504	28,73	6	6	3 P00387_ISOFORM_2,P00387_CHAIN_0,P00387
44,27	24,81	13	6	5 P62701,P22090_CHAIN_0,Q8TD47_CHAIN_0,P:
44,084	16,9	10	7	1 O00148
43,94	9,76	7	6	1 P23246_ISOFORM_Short
43,765	23,13	17	6	0
43,67	7,66	11	6	0
43,505	41,22	11	7	1 P25398
43,486	25	10	6	2 O43852,O43852_ISOFORM_2
43,265	10,71	11	6	2 P52272_CHAIN_0,P52272
43,05	34,9	9	5	1 P21291
42,64	14,7	9	6	2 P13674,P13674_ISOFORM_2
42,605	23,58	11	7	9 P16403,P10412_CHAIN_0,P10412,P16402_CHA
42,605	29,85	11	6	5 P62820_CHAIN_0,P62820,Q92928,P62820_ISO
42,146	6,59	8	6	3 Q86VP6,Q86VP6_ISOFORM_2,Q86VP6_ISOFOR
42,12	46,67	17	5	0
41,754	17,19	9	5	2 P31943,P55795
41,472	13,97	7	6	0
41,39	8,26	9	5	3 Q32P28,Q32P28_ISOFORM_3,Q32P28_ISOFOR
41,34	29,47	8	5	0
41,321	17,67	10	5	0
40,96	22,9	12	6	1 P05141
40,83	12,71	5	5	31 O60716_ISOFORM_4C,O60716_ISOFORM_4A,C
40,747	7,1	11	6	0
40,683	12,52	8	6	0
40,658	14	9	5	1 P27797
40,617	16,2	12	6	6 P26599_ISOFORM_2,O95758_ISOFORM_1,O95
40,294	42,34	9	6	2 O75947_CHAIN_0,O75947
40,168	38	9	6	1 P62277
40,034	23,91	9	6	1 P12235
39,796	25,88	9	6	1 O15143
39,776	23,56	8	6	1 Q9BTV4
39,633	8,84	6	6	1 P35606
39,234	17,99	14	5	1 P00558_CHAIN_0
38,582	6,14	20	5	0
38,297	11,19	10	6	0
38,177	25,57	11	5	0
38,089	21,62	12	5	2 Q15084,Q15084_ISOFORM_2
37,853	28,18	8	5	5 P62834_CHAIN_0,P61224,P62834,A6NIZ1_CHA
37,819	17,9	11	4	5 P13929_ISOFORM_2,P13929_CHAIN_0,P13929
37,689	11,68	5	5	2 Q9NVA2,Q9NVA2_ISOFORM_2
37,682	18,49	15	5	1 P62424
37,598	24,87	7	6	1 P46781
37,535	19,58	9	6	0
36,983	8,41	6	5	1 Q14764

36,972	15,42	9	6	1 P39023
36,709	28,76	25	6	1 P62258
36,414	3,41	15	5	4 Q7Z406,Q7Z406_ISOFORM_2,Q7Z406_ISOFORI
36,365	29,86	7	5	1 P21964
36,32	8,79	7	5	0
36,222	21,25	10	6	3 Q14103_ISOFORM_3,Q14103_ISOFORM_2,Q14
35,912	38,64	8	5	2 Q16629_ISOFORM_2,Q16629
35,845	47,37	13	5	17 P0CG47_CHAIN_1,P0CG47_CHAIN_2,P0CG48_(
35,594	9,59	7	5	1 Q02809
35,582	27,05	8	5	0
35,308	10,33	8	5	1 P21980_CHAIN_0
35,301	10,75	7	5	5 Q9NVI7_CHAIN_0,Q9NVI7,Q5T2N8,Q5T9A4_ISI
35,242	19,5	12	4	5 P67809,P16989_ISOFORM_2,P16989_ISOFORM
35,218	5,12	5	5	6 Q15155_CHAIN_0,P69849,Q15155,Q5JPE7_ISO
35,161	27,32	9	5	0
35,1	18	10	5	1 P07910_ISOFORM_C1
35,056	3,19	11	5	0
34,899	14,35	6	4	1 P22695
34,879	18,95	7	5	3 P61586_CHAIN_0,P08134,P61586
34,801	11,27	6	4	2 Q16643,Q16643_ISOFORM_2
34,737	12,81	9	5	2 P08107,P48741
34,728	29,17	10	6	1 P39019
34,558	20,13	10	4	1 Q96D15
34,502	9,8	9	5	0
34,46	10,57	5	5	0
34,437	1,55	6	5	0
34,232	10,8	6	5	1 P28331
34,01	42,68	13	5	1 P62937
33,843	18,6	13	5	3 Q99729_ISOFORM_2,Q99729_ISOFORM_4,Q99
33,835	8,04	6	5	0
33,818	9,49	8	5	1 O43390
33,722	21	8	5	0
33,628	52,04	10	5	1 P10606
33,623	10,07	7	5	1 Q96AY3
33,613	25,67	9	4	1 Q07020
33,56	16,52	9	4	1 P62873
33,529	11,34	8	5	3 P08195_ISOFORM_3,P08195,P08195_ISOFORM
33,428	6,56	4	4	1 P54886
33,332	7,08	5	5	1 Q86UP2
33,014	9,38	9	5	3 Q92841_ISOFORM_2,Q92841_ISOFORM_3,Q92
33,013	12,48	6	5	0
32,912	38,18	10	4	1 P30050_ISOFORM_2
32,91	43,51	9	4	1 P63241_CHAIN_0
32,758	14,7	6	4	1 Q02978
32,723	15,19	8	4	1 Q9Y277_ISOFORM_2
32,653	17,44	6	5	0
32,445	4,09	6	5	1 Q14980
32,368	16,99	9	5	5 P57721_ISOFORM_2,P57721_ISOFORM_3,P57
32,292	11,08	5	5	0
32,21	8,33	6	5	1 P02786
31,989	69,57	17	4	0
31,903	22,13	8	5	2 O14979_ISOFORM_2,O14979

31,864	36,24	9	4	1 P62158_CHAIN_0
31,802	35,38	8	4	10 Q96QV6,P16104_CHAIN_0,P16104,Q8IUE6_CH
31,73	15,13	7	4	1 Q6NZI2_ISOFORM_2
31,712	11,91	5	5	1 Q15942
31,711	1,26	7	5	1 Q07954
31,568	23,38	12	5	3 Q07955_CHAIN_0,Q07955,Q07955_ISOFORM_
31,475	11,84	10	5	1 P39656
31,437	12,36	5	5	1 Q9NZN3
31,35	10,74	8	4	1 P55209_CHAIN_0
31,317	24,64	13	4	1 P62241
31,249	22,65	5	4	2 P27695_CHAIN_0,P27695
31,245	12,24	8	5	1 P21589
31,21	3,65	5	5	0
31,141	19,18	22	5	7 P31946_ISOFORM_Short,P31946_CHAIN_1,P31
31,029	15,79	13	5	1 Q58FF8
30,889	5,9	5	5	3 Q02218,Q9ULD0_CHAIN_0,Q9ULD0
30,82	32,71	5	4	1 P61106
30,473	24,51	7	4	1 P61313_CHAIN_0
30,401	15,02	8	4	1 P07195
30,315	7,17	7	4	0
30,144	22,22	9	4	2 P30044_ISOFORM_Cytoplasmic,P30044
30,144	3,11	4	4	0
29,886	25,46	6	4	1 P62906
29,755	11,04	4	4	3 O94925_CHAIN_0,O94925,O94925_ISOFORM_
29,745	16,77	7	5	4 P41091,Q2VIR3_CHAIN_0,Q2VIR3,Q2VIR3_ISO
29,527	5,36	6	4	0
29,354	4,82	5	5	1 O95782
29,349	11,57	5	5	2 Q16891_ISOFORM_2,Q16891
29,323	14,96	5	4	1 Q15019_ISOFORM_2
29,274	28,78	14	4	1 P07737
29,244	5,15	6	5	0
29,229	17,24	7	4	0
29,11	16,13	6	4	38 P16188,P01891_CHAIN_0,P30453_CHAIN_0,P0
29,06	12,56	8	4	1 P52597
29,047	8,92	5	4	1 P27824
29,032	19,6	6	4	0
29,001	28,35	6	4	1 P55769
28,999	14,41	7	4	9 P04899,P04899_ISOFORM_2,P08754_CHAIN_0
28,933	19,81	5	4	3 Q15907_CHAIN_0,P62491,Q15907
28,821	26,11	9	5	1 P62280
28,773	23,85	6	4	2 Q99714,Q99714_ISOFORM_2
28,77	14,11	5	4	0
28,489	11,48	5	4	2 O15460_ISOFORM_Ila,O15460
28,481	12,86	5	4	0
28,315	35,14	9	3	1 P04216
27,867	9,58	4	4	0
27,857	24,84	6	4	0
27,834	2,4	4	4	1 Q92616
27,639	12,22	4	3	1 P00505
27,47	6,76	5	4	2 P49756_ISOFORM_2,P49756_ISOFORM_3
27,452	10,77	6	4	1 Q16658
27,389	15,89	6	3	1 O75396

27,318	7,12	5	4	8 Q5XKE5,O95678,P02538_CHAIN_0,P04259_CH.
27,312	29,34	8	4	1 P59998
27,24	8,38	5	4	0
27,213	23,84	8	5	1 P62269
27,068	12,47	5	4	3 O75367_CHAIN_0,O75367_ISOFORM_3,O7536
26,895	16,73	5	4	1 P61247
26,878	31,79	7	4	1 P22392_ISOFORM_3
26,627	6,58	12	4	2 Q00839_CHAIN_0,Q00839
26,537	8,08	4	4	1 Q13310
26,534	14,63	4	3	0
26,482	10,82	4	3	26 P30504,Q29960_ISOFORM_2,P30492_CHAIN_0
26,434	24,37	7	4	1 P32119
26,193	14,89	6	4	2 P61619_CHAIN_0,P61619
26,117	7,82	4	4	1 Q9Y262
25,942	24,8	9	4	0
25,859	6,86	10	4	1 P43243
25,78	7,24	4	3	2 Q9UBV2,Q9UBV2_ISOFORM_2
25,74	10,16	6	4	1 Q14651
25,683	7,58	4	4	7 Q9UHD8_ISOFORM_2,Q9UHD8_ISOFORM_5,Q
25,565	5,76	6	4	1 P63010_ISOFORM_2
25,396	7,9	5	3	1 P06744
25,374	8,59	7	4	2 P07602_ISOFORM_Sap-mu-6,P07602_ISOFORM
25,313	5,79	4	4	0
25,282	9,01	7	4	1 P20073
25,159	16,67	5	3	0
25,157	13,1	6	4	1 Q9UKM9
25,105	6,24	9	3	0
24,918	16,72	7	4	4 P62136,P36873_CHAIN_0,P36873,P36873_ISO
24,837	15,5	4	4	4 Q8NC51_ISOFORM_3,Q8NC51_ISOFORM_2,Q8
24,695	9,25	6	3	1 P11279
24,69	5,76	5	4	2 O00469,O00469_ISOFORM_2
24,597	5,5	6	3	1 P40939
24,528	17,33	5	4	1 P16401
24,524	18,4	7	4	4 P62140,P36873_CHAIN_0,P36873,P36873_ISO
24,492	9,51	5	4	1 P30153_CHAIN_0
24,45	3,28	14	3	0
24,41	1,68	5	4	2 P12111_CHAIN_0,P12111
24,384	3,47	4	3	1 P25205
24,03	14,39	6	3	0
23,955	2,01	4	4	1 Q6P2Q9
23,899	9,35	4	4	2 Q13740_ISOFORM_2,Q13740
23,894	10,52	4	4	2 Q13505_ISOFORM_3,Q13505_ISOFORM_2
23,85	10,09	3	3	1 Q16181
23,827	28,57	4	3	0
23,788	23,27	7	3	1 O15260
23,764	27,65	4	4	3 O14950_CHAIN_0,P19105,O14950
23,725	5,6	5	3	1 O60568
23,541	13,18	4	3	1 P46777
23,428	10,79	4	3	1 P12277
23,32	16,36	8	3	1 P50914
23,144	8,03	4	3	1 P62495
22,988	2,77	3	3	1 P42704

22,947	4,2	3	3	0
22,828	5,99	4	3	2 P51659,P51659_CHAIN_1
22,8	6,29	7	3	1 P35637
22,763	15,79	4	3	1 P52907
22,762	22,88	6	3	1 P60866
22,629	2,9	8	3	1 Q9UBG0
22,423	5,6	4	3	2 Q96AE4,Q96AE4_ISOFORM_2
22,339	7,55	5	3	1 Q9UMS4
22,33	4,81	3	3	4 P16615_ISOFORM_5,P16615_ISOFORM_3,P16615_ISOFORM_4
22,288	35,64	7	3	1 P61604
22,245	18,42	4	3	1 P48047
22,193	10,79	6	3	1 P61158
22,051	22,12	4	3	1 P99999
21,903	13,89	6	3	4 P15259,P18669_CHAIN_0,P18669,Q8N0Y7
21,876	14,71	5	3	10 Q92930_CHAIN_0,P61006,Q92930,O95716_CHAIN_0
21,709	2,77	3	3	1 P26640_CHAIN_0
21,698	18,32	7	4	2 P40429,Q6NVV1
21,683	5,75	4	3	1 Q02818
21,595	5,74	4	3	2 P08648_CHAIN_0,P08648
21,568	8,37	6	2	1 Q92520
21,527	12,98	7	3	3 P62879,Q9HAV0_CHAIN_0,Q9HAV0
21,497	5,86	6	3	1 O95302
21,365	5,29	5	3	1 P48741
21,34	9,76	4	4	1 P38919
21,329	4,6	10	3	2 P18206_CHAIN_0,P18206
21,167	3,63	3	3	0
21,158	33,67	7	3	0
21,108	9,75	3	3	2 Q96N66_ISOFORM_3,Q96N66_ISOFORM_2
21,09	10,66	3	3	0
21,09	7,54	3	3	2 Q13492_ISOFORM_2,Q13492
21,066	3,79	3	3	1 P12109_CHAIN_0
21,053	32,84	11	3	1 P08708
20,982	20,83	5	3	0
20,92	5,48	5	3	1 Q14444
20,897	26,67	3	3	1 P51571
20,894	12,62	3	3	3 P60891,P21108_CHAIN_0,P21108
20,842	28,57	4	3	1 P61803
20,831	33,33	4	4	1 P24844
20,824	13,36	6	3	2 Q01105_CHAIN_0,Q01105
20,625	25,71	7	3	0
20,613	4,39	3	3	1 P47897
20,575	5,07	3	3	2 Q5SSJ5,Q5SSJ5_ISOFORM_4
20,559	6,5	3	3	1 P31930
20,537	19,62	3	3	1 P09211
20,47	7,59	3	3	1 P49591_CHAIN_0
20,435	13,44	5	3	0
20,423	5,39	3	3	0
20,327	10,93	4	3	1 Q9Y6C9
20,193	32,26	4	3	0
20,046	4,15	3	3	3 P06756_CHAIN_0,P06756,P06756_CHAIN_1
20,042	5,26	3	3	0
19,997	6,2	6	3	1 O43175

19,918	3,83	3	3	1 O75694
19,818	21,28	6	3	1 P60953
19,803	5,71	5	3	1 P33993
19,791	9,77	3	3	0
19,751	15,42	5	3	1 Q15286_CHAIN_0
19,728	7,95	3	3	1 P52292
19,725	17,04	3	3	1 P30041
19,603	12,09	5	3	2 P36542_ISOFORM_Heart,P36542
19,589	9,49	3	3	1 A1L0T0_ISOFORM_2
19,557	2,85	3	3	2 P05023,P13637
19,387	4,52	3	3	3 P29590_ISOFORM_PML-11,P29590_ISOFORM_
19,372	19,35	4	3	1 P30086
19,328	13,21	4	3	1 P06748
19,309	8,39	3	3	2 P02768_CHAIN_0,P02768
19,213	12,5	19	3	1 P31947
19,153	7,46	4	3	1 Q13247
19,148	27,41	3	3	1 P62910_CHAIN_0
19,127	6,32	4	3	2 P17813_ISOFORM_Short,P17813
19,077	6,24	3	3	2 P36871,P36871_ISOFORM_2
19,075	9,38	3	3	0
19,071	5,84	3	3	2 Q13263_CHAIN_0,Q13263
19,044	3,83	3	3	0
18,93	20	3	3	0
18,781	5,97	2	2	3 P51114_ISOFORM_2,P51114_CHAIN_0,P51114
18,771	6,41	4	3	3 P08729,P05787_CHAIN_0,P05787
18,737	3,43	7	3	0
18,694	11,81	4	3	2 P61254,Q9UNX3
18,646	12,2	4	3	0
18,563	5,82	5	3	2 P43304_CHAIN_0,P43304
18,542	6,45	2	2	1 Q13283
18,54	22,91	5	3	1 P18085
18,513	4,43	3	3	1 P35222
18,481	6,36	2	2	1 P49411
18,408	20,51	3	3	1 Q92688
18,4	7,65	6	3	5 P63092_ISOFORM_Gnas-2,P63092_CHAIN_0,Pi
18,381	19,42	3	2	1 P31942_ISOFORM_3
18,335	32,12	5	3	1 P23528
18,323	5,26	3	3	0
18,314	7,19	4	3	0
18,264	3,52	4	3	1 Q9Y4L1
18,249	3,93	3	3	0
18,189	10,79	5	2	0
18,154	7,06	5	3	1 O75390
18,126	10,04	4	2	2 O15400_CHAIN_0,O15400
18,081	4,87	3	3	1 Q03252
18,047	3,93	3	2	2 P20591,P20592
17,921	12,85	3	3	1 P17931
17,848	6,69	2	2	0
17,773	7,03	3	2	1 P55084
17,749	2,54	3	3	0
17,746	11,56	4	3	1 Q15005
17,721	40,78	5	3	0

17,708	1,85	3	2	2 Q02952_ISOFORM_2,Q02952
17,692	7,48	5	2	16 P16070_ISOFORM_12,P16070_ISOFORM_14,P:
17,675	9,29	7	3	0
17,637	4,22	3	3	1 Q8NBJS
17,565	6,95	3	3	2 Q0ZGT2,Q0ZGT2_ISOFORM_3
17,542	6,79	4	3	0
17,538	27,27	7	2	2 P56134_CHAIN_0,P56134
17,481	6,23	5	3	1 P40227
17,457	9,54	2	2	0
17,35	4,51	3	3	0
17,336	16,27	4	2	1 Q07021
17,317	18,9	4	2	1 P35268
17,309	4,44	3	2	0
17,3	4,85	4	2	0
17,272	2	3	2	1 P07996
17,244	10,22	4	3	1 P30533
17,203	4,83	5	2	1 P50991
17,096	9,47	3	3	1 P34897
17,09	4,02	2	2	0
16,997	32,65	3	2	2 P61769_CHAIN_0,P61769
16,988	17,03	3	3	1 Q9UBQ0_ISOFORM_2
16,938	16,49	3	3	1 P49755
16,918	13,4	3	3	0
16,824	5,48	3	3	0
16,739	5,42	3	3	1 Q14554
16,734	1,23	3	2	1 P12270
16,733	12,11	3	3	1 Q9HDC9
16,728	14,49	3	3	1 P24539
16,708	7,44	6	3	1 P38159
16,691	12,68	2	2	1 P20618
16,644	4,84	3	3	0
16,638	2,09	4	3	2 Q9UKV3_ISOFORM_3,Q9UKV3_ISOFORM_2
16,576	20	3	2	1 P37108
16,545	6,86	5	3	0
16,541	5,91	2	2	0
16,53	35,06	6	2	0
16,507	9,09	3	2	1 Q99439
16,421	4,2	2	2	0
16,364	31,25	4	2	1 O75380
16,3	21,62	4	3	1 P09669
16,298	3,96	2	2	4 Q9Y2D5_ISOFORM_3,Q9Y2D5_ISOFORM_5,Q9
16,291	10,28	3	3	1 Q13641
16,283	6,92	2	2	1 P09525
16,195	9,06	2	2	1 P09661
16,19	15	3	2	1 Q6IAA8
16,189	24,56	4	2	1 P62888
16,141	5,8	2	2	2 P07093_ISOFORM_2,P07093
16,099	3,52	4	3	1 O75534
16,075	7,32	3	3	1 Q10713
16,065	5,04	3	3	2 Q92598_ISOFORM_3,Q92598
16,032	6,18	3	3	1 O00231
16,017	16,44	5	2	1 P30049

15,872	12,99	8	2	2 P62913_ISOFORM_2,P62913
15,84	2,88	2	2	1 Q15437
15,81	7,33	5	2	3 P30455_CHAIN_0,P30443,P30455
15,808	9,62	3	2	0
15,743	5,12	2	2	0
15,742	11,94	3	2	0
15,732	3,52	2	2	0
15,705	3,21	2	2	1 Q8IVL6
15,694	5,1	5	2	1 P02533
15,674	2,43	3	3	7 Q8N4C6_ISOFORM_4,Q8N4C6_ISOFORM_8,Q8
15,609	5,6	2	2	1 Q96I24
15,571	7,16	3	3	0
15,57	16,14	3	3	1 Q00688
15,554	2,38	2	2	0
15,53	8,79	3	2	2 Q16630,Q16630_ISOFORM_2
15,518	4,39	2	2	2 P49748_ISOFORM_2,P49748
15,492	4,92	2	2	3 Q9BUJ2_ISOFORM_4,Q9BUJ2_ISOFORM_2,Q9E
15,453	6,65	3	2	1 P15313
15,436	19,19	2	2	1 Q969X5
15,408	4,87	3	2	1 P08779
15,299	7,12	3	2	1 Q9UQ80
15,287	16,53	3	2	0
15,264	3,91	2	2	0
15,233	5,63	2	2	1 Q9Y230
15,23	9,77	3	2	1 P62826
15,22	2,67	3	2	1 P09874
15,201	6,64	3	2	0
15,117	6,64	4	2	1 P62917
15,041	9,17	3	2	1 P20674
15,02	9,82	4	2	1 P24534
14,997	0,82	2	2	1 Q93008
14,982	15,6	3	2	1 Q14019
14,877	4,03	2	2	1 O76094
14,836	2,97	2	2	1 Q13423
14,835	10,49	2	2	3 P47813_CHAIN_0,O14602,P47813
14,834	4,94	3	2	1 P46063
14,818	4,08	2	2	1 P54136
14,797	6,53	2	2	0
14,795	5,59	2	2	0
14,706	5,3	2	2	2 O94874_ISOFORM_2,O94874
14,703	12,86	4	2	0
14,694	3,26	4	2	0
14,423	8,81	2	2	0
14,414	9,73	3	2	2 P11177_ISOFORM_2,P11177
14,412	7,31	2	2	1 Q16795
14,403	11,58	3	2	1 Q9Y3B3
14,403	6,12	3	2	1 P09622
14,403	5,2	2	2	2 P04181_CHAIN_0,P04181
14,387	6,93	2	2	0
14,376	4,66	4	2	1 O75131
14,37	2,04	2	2	1 O14776
14,354	21,02	2	2	0

14,345	16,39	3	2	1 P18621
14,318	8,97	2	2	3 Q08431_ISOFORM_3,Q08431_CHAIN_0,Q0843
14,311	22,73	3	2	0
14,284	6,81	2	2	5 Q16881_ISOFORM_2,Q16881_ISOFORM_4,Q16
14,26	6,35	3	2	1 P24752
14,253	3,75	2	2	3 Q14676_ISOFORM_3,Q14676_ISOFORM_2,Q14
14,238	4,67	3	2	0
14,21	1,66	2	2	1 Q6UVK1
14,204	11,62	2	2	1 P08574
14,184	10,58	4	2	1 P59190
14,18	7,58	3	2	0
14,177	8,55	4	2	1 Q13243
14,173	6,73	2	2	5 Q29865_CHAIN_0,Q29963_CHAIN_0,P10321,Q
14,162	21,09	3	2	2 Q03135_CHAIN_0,Q03135
14,148	6,17	2	2	0
14,131	18,85	5	2	1 P42766
14,117	6,19	2	2	1 Q15008
14,088	6,14	3	2	0
14,052	14,61	3	2	0
13,992	5,42	4	2	0
13,986	13,16	4	2	0
13,976	19,2	2	2	1 P49773
13,968	1,98	2	2	1 P33176
13,965	6,95	2	2	1 Q15293
13,962	14,83	3	2	1 P30084
13,951	2,26	2	2	1 P17301
13,949	19,35	3	2	1 O14737
13,901	5,57	4	2	0
13,895	14,62	2	2	1 O14653_ISOFORM_B
13,886	2,57	2	2	1 P22102_CHAIN_0
13,847	6,64	2	2	0
13,844	6,76	2	2	3 Q16666_ISOFORM_3,Q16666_ISOFORM_2,Q16
13,792	3,83	4	2	2 Q10567_ISOFORM_B,Q10567
13,746	19,09	3	2	1 P14927
13,734	8,96	2	2	1 Q13177
13,725	14,48	5	2	1 P62249
13,72	2,39	2	2	1 O43294_ISOFORM_2
13,718	4,55	3	2	3 A0FGR8_ISOFORM_2,A0FGR8,A0FGR8_ISOFOR
13,716	4,26	2	2	0
13,711	2,54	2	2	1 Q8WUM4
13,68	8,26	2	2	2 P09496_ISOFORM_3,P09496
13,66	11,98	2	2	1 P63000_CHAIN_0
13,631	12,66	2	2	0
13,615	10,17	3	2	1 O15145
13,614	3,82	5	2	2 P26368_CHAIN_0,P26368
13,6	7,06	2	2	1 O43684
13,554	14,29	2	2	1 P13073
13,525	12,23	2	2	1 P62995
13,5	10	4	2	1 P26373
13,491	6,74	2	2	0
13,474	3,15	2	2	0
13,473	7,8	2	2	0

13,416	15,48	3	2	1 P62750
13,402	3,93	2	2	1 P42224
13,362	4,2	3	2	1 P30837
13,331	4,96	3	2	1 P23497_ISOFORM_SpAlt-C
13,318	8,22	2	2	5 Q9UHX1_ISOFORM_6,Q9UHX1_ISOFORM_3,Q9UHX1_ISOFORM_4,Q9UHX1_ISOFORM_5
13,312	11,33	2	2	1 Q9NP72
13,273	5,63	2	2	0
13,262	9,95	3	2	1 Q9UL25
13,254	13,83	4	2	0
13,248	10,85	4	2	1 P62244
13,248	13,31	4	2	2 Q9P0L0,Q9P0L0_ISOFORM_2
13,212	7	4	2	1 P14314
13,182	17,6	5	2	0
13,169	14,29	4	2	1 P46776
13,147	9,8	4	2	1 P51572
13,141	10,99	2	2	0
13,119	17,61	3	2	1 Q969H8
13,082	4,97	4	2	1 Q01844
13,076	6,41	2	2	1 Q9UJ70
13,062	8,43	4	2	0
13,056	2,76	3	2	2 P35221,P35221_ISOFORM_2
13,056	6,88	2	2	1 P16152
13,035	0,84	2	2	1 A2RRP1
13,001	4,39	4	2	2 Q14498_CHAIN_0,Q14498
12,976	4,09	2	2	1 Q99805
12,928	4,52	2	2	0
12,914	8,55	3	2	2 P35613_CHAIN_0,P35613
12,888	12,28	2	2	1 O75489
12,874	1,67	2	2	4 Q9BXP5_ISOFORM_4,Q9BXP5_ISOFORM_2,Q9BXP5_ISOFORM_3,Q9BXP5_ISOFORM_5
12,856	2,38	2	2	1 Q8N163_ISOFORM_2
12,813	9,44	2	2	0
12,809	2,31	2	2	2 O43747,O43747_ISOFORM_2
12,685	14,02	3	2	0
12,667	5,77	2	2	1 O00629
12,649	3,29	2	2	1 O94826
12,621	28,12	6	2	1 P60903
12,59	8,84	2	2	1 P10301
12,59	3,66	2	2	1 P11387
12,586	3,91	3	2	1 Q96CW1_ISOFORM_2
12,573	3,35	2	2	1 Q9HBR0
12,556	7,97	2	2	1 Q16698
12,543	3,04	2	2	1 Q92804_ISOFORM_Short
12,532	1,34	3	2	7 P23634_ISOFORM_XK,P23634_ISOFORM_ZA,P23634_ISOFORM_ZB,P23634_ISOFORM_ZC,P23634_ISOFORM_ZD,P23634_ISOFORM_ZE,P23634_ISOFORM_ZF,P23634_ISOFORM_ZG,P23634_ISOFORM_ZH,P23634_ISOFORM_ZI,P23634_ISOFORM_ZJ,P23634_ISOFORM_ZK,P23634_ISOFORM_ZL,P23634_ISOFORM_ZM,P23634_ISOFORM_ZN,P23634_ISOFORM_ZO,P23634_ISOFORM_ZP,P23634_ISOFORM_ZQ,P23634_ISOFORM_ZR,P23634_ISOFORM_ZS,P23634_ISOFORM_ZT,P23634_ISOFORM_ZU,P23634_ISOFORM_ZV,P23634_ISOFORM_ZW,P23634_ISOFORM_ZX,P23634_ISOFORM_ZY,P23634_ISOFORM_ZZ
12,485	2,63	2	2	0
12,421	6,67	3	2	0
12,398	1,44	2	2	2 Q9P0K7,Q9P0K7_ISOFORM_2
12,341	10,84	2	2	0
12,328	28,57	4	2	1 P63173_CHAIN_0
12,327	6,17	2	2	1 Q9H0S4
12,321	7,72	2	2	0
12,3	24,72	3	2	1 Q96FJ2
12,295	3,69	2	2	0

12,234	18,27	3	2	1 Q9Y3U8
12,23	1,95	2	2	1 Q8TAQ2
12,223	5,18	3	2	0
12,222	7,38	3	2	1 P16949_CHAIN_0
12,218	5,7	2	2	1 P36957
12,187	1,17	2	2	1 Q02880
12,186	5,17	2	2	3 P42892_ISOFORM_A,P42892_ISOFORM_D,P42
12,179	14,1	3	2	1 P05161
12,168	9,12	5	2	0
12,1	3,38	2	2	2 P49821_ISOFORM_2,P49821
12,098	7,98	2	2	1 P25786_ISOFORM_Long
12,086	11,85	2	2	0
12,046	1,84	3	2	0
12,041	0,61	2	2	0
12,01	4,26	3	2	0
11,999	2,02	2	2	2 O60264,P28370
11,895	1,35	2	2	1 Q8WUJ3
11,869	8,66	2	2	1 Q9H3N1
11,858	15,08	3	2	0
11,854	4,75	3	2	0
11,815	5,5	2	2	2 P13473,P13473_ISOFORM_LAMP-2B
11,803	5,35	2	2	1 Q99733
11,789	14,55	4	2	0
11,772	13,01	2	2	1 P68871_CHAIN_0
11,746	10,41	3	2	0
11,729	3,42	2	2	0
11,638	3,82	2	2	1 P17655
11,545	3,94	2	2	1 P23526
11,54	13,24	2	2	1 P61353_CHAIN_0
11,522	5,33	2	2	1 P48735
11,514	2,98	2	2	1 Q8TCS8
11,504	2,97	2	2	1 Q08945
11,394	4,09	3	2	2 O43854_ISOFORM_2,O43854
11,371	1,55	2	2	2 O00410,O00410_ISOFORM_3
11,337	6,25	2	2	1 Q12841
11,298	6,39	3	2	2 Q00325_ISOFORM_B,Q00325
11,293	4,32	2	2	0
11,283	12,5	2	2	0
11,161	2,04	2	2	1 P20908
11,05	11,06	2	2	0
10,99	10	5	2	1 Q9BVK6
10,986	6,09	3	2	0
10,979	1,18	2	2	1 P07942_CHAIN_0
10,861	5,74	2	2	1 Q07666
10,859	3,73	2	2	1 P05783
10,811	9,38	3	2	1 P37235
10,81	3,54	2	2	4 P55265_ISOFORM_3,P55265_ISOFORM_2,P55:
10,753	1,23	2	2	1 Q9Y2H6
10,679	8,84	2	2	0
10,648	3,14	2	2	1 Q9NSK0
10,513	1,43	2	2	4 Q04637_ISOFORM_D,Q04637_ISOFORM_C,Q0:
10,477	2,8	3	2	1 P36776

10,448	4,5	2	2	3 Q13561,Q13561_ISOFORM_3,Q13561_ISOFOR
10,41	4,67	3	2	3 P11413,P11413_ISOFORM_3,P11413_ISOFORM
10,378	6,29	2	2	1 Q9Y6M1
10,339	4,03	2	2	0
10,253	6,83	3	2	0
10,241	4,22	2	2	2 Q13557,Q13557_ISOFORM_Delta
10,135	4,51	2	2	1 Q9BS26
10,101	4,58	2	2	1 Q96AC1
10,084	3,5	2	2	1 O15042
10,03	2,03	2	2	0
9,963	26,47	2	2	1 P56385
9,952	4,53	2	2	0
9,951	1,32	2	2	1 P78357
9,938	4,83	2	2	2 Q16851_CHAIN_0,Q16851
9,935	3,75	2	2	0
9,804	2,86	2	2	0
9,726	1,2	2	2	1 Q07157
9,711	6,18	2	2	1 O60762
9,653	2,37	2	2	0

5149_ISOFORM_9,Q15149_ISOFORM_4,Q15149_ISOFORM_5,Q15149_ISOFORM_6,Q15149_ISOFORM_3,C

219_ISOFORM_2
Delta10,P02545_ISOFORM_C

M_3,O75369_ISOFORM_5,O75369_ISOFORM_4,O75369_ISOFORM_7
1_7,P02751_ISOFORM_15,P02751_ISOFORM_11,P02751_ISOFORM_10,P02751_ISOFORM_9,P02751_ISOF
2,P53675

BYX7
:

IL28
_0,A6NMY6

ORM_2,Q9NZM1_ISOFORM_5,Q9NZM1_ISOFORM_8,Q9NZM1_ISOFORM_7,Q9NZM1_ISOFORM_4

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C7M2,P09651_CHAIN_0,P09651,Q32P51
AIN_0,P09104

5682_ISOFORM_2,Q05682

O506_CHAIN_0,O60506,O60506_ISOFORM_5

DRM_3,Q9NQC3_ISOFORM_4,Q9NQC3_ISOFORM_6

OFORM_Beta-1D,P05556_ISOFORM_Beta-1C-2,P05556_ISOFORM_Beta-1C

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28WWI1

2906_ISOFORM_6,Q12906_ISOFORM_3,Q12906
A_3,P52789

CHAIN_0,P06899,P23527,P33778,Q16778,Q8N257_CHAIN_0,Q8N257,Q96A08_CHAIN_0,Q96A08,Q6DRA6_

7L7L0,Q93077,Q96KK5_CHAIN_0,Q99878_CHAIN_0,Q16777_CHAIN_0,Q96KK5,Q99878,Q9BTM1_CHAIN_C

649

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22090,Q8TD47

AIN_0,P16402,Q02539_CHAIN_0,Q02539,P22492_CHAIN_0,P22492
FORM_2,P62820_ISOFORM_3
M_3

M_2

O60716_ISOFORM_4AC,O60716_ISOFORM_4B,O60716_ISOFORM_4BC,O60716_ISOFORM_4AB,O60716_IS

O95758_ISOFORM_2,O95758,O95758_ISOFORM_5,O95758_ISOFORM_4

AIN_0,A6NIZ1
,P09104_CHAIN_0,P09104

M_5,Q7Z406_ISOFORM_4

4103

CHAIN_0,POCG48_CHAIN_1,POCG48_CHAIN_3,POCG48_CHAIN_4,POCG48_CHAIN_5,POCG48_CHAIN_6,POC

OFORM_3,Q5T9A4
1_3,P16989,Q9Y2T7
OFORM_2,Q5JPE7_CHAIN_0,Q5JPE7

3729

1_4

2841_ISOFORM_4

721_ISOFORM_5,P57721_ISOFORM_4,P57721

AIN_0,Q8IUE6,Q9BTM1_ISOFORM_2,P0C0S5_CHAIN_0,Q71UI9_CHAIN_0,P0C0S5,Q71UI9

.ASF-2

I946,Q04917_CHAIN_0,P61981_CHAIN_1,Q04917,P61981

.2
FORM_2

I1891,P10316,P30453,Q29960_ISOFORM_2,P30492_CHAIN_0,P30493_CHAIN_0,Q29940_CHAIN_0,P01892

I,P63096_CHAIN_0,P08754,P63096,P09471_CHAIN_0,P09471,P09471_ISOFORM_Alpha-2

AIN_0,P48668_CHAIN_0,P02538,P04259,P48668

7

,P30493_CHAIN_0,Q29940_CHAIN_0,P01892_CHAIN_0,P10314_CHAIN_0,P16189_CHAIN_0,P16190_CHAI

9UHD8,Q9UHD8_ISOFORM_3,Q9UHD8_ISOFORM_4,Q9UHD8_ISOFORM_9,Q9UHD8_ISOFORM_8

1_Sap-mu-9

FORM_Gamma-2
;NC51_CHAIN_0,Q8NC51

FORM_Gamma-2

515,P16615_ISOFORM_4

IAIN_0,O95716,P20337,P20336,Q96E17,P51153_CHAIN_0,P51153

_PML-10,P29590

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63092,Q5JWF2_ISOFORM_XLas-2,Q5JWF2

16070_ISOFORM_13,P16070_ISOFORM_11,P16070_ISOFORM_10,P16070_ISOFORM_16,P16070_ISOFORM

Y2D5_ISOFORM_4,Q9Y2D5_ISOFORM_2

3N4C6_ISOFORM_2,Q8N4C6,Q8N4C6_ISOFORM_5,Q8N4C6_ISOFORM_3,Q8N4C6_ISOFORM_7

3UJ2

1

5881_ISOFORM_3,Q16881_ISOFORM_6,Q16881

4676

29865,Q29963

5666

M_6

9UHX1_ISOFORM_5,Q9UHX1_ISOFORM_2,Q9UHX1

BXP5_ISOFORM_3,Q9BXP5

23634_ISOFORM_XA,P23634_ISOFORM_ZB,P23634_ISOFORM_XB,P23634_ISOFORM_ZD,P23634

892

265,P55265_ISOFORM_4

4637_ISOFORM_B,Q04637

M_2
1_Long

15149_ISOFORM_2,P58107

ORM_14,P02751_ISOFORM_13,P02751_ISOFORM_8,P02751_ISOFORM_5,P02751_ISOFORM_6,P02751_IS

CHAIN_0,Q6DRA6,Q6DN03_CHAIN_0,Q6DN03

),POCOS8_CHAIN_0,P20671_CHAIN_0,Q16777,Q6FI13_CHAIN_0,Q9BTM1,POCOS8,P20671,Q6FI13,Q9BTM1.

ISOFORM_4ABC,O60716_ISOFORM_3,O60716_ISOFORM_3C,O60716_ISOFORM_3A,O60716_ISOFORM_3A

G48_CHAIN_7,POCG48_CHAIN_8,P62979_CHAIN_0,P62987_CHAIN_0,P62987,P62979,POCG47,POCG48,POC

!_CHAIN_0,P10314_CHAIN_0,P16189_CHAIN_0,P16190_CHAIN_0,P30459_CHAIN_0,P30512_CHAIN_0,P30

IN_0,P30459_CHAIN_0,P30512_CHAIN_0,P30508_CHAIN_0,P30510_CHAIN_0,Q29960_CHAIN_0,P30492,P

1_8,P16070_ISOFORM_9,P16070_ISOFORM_17,P16070_ISOFORM_4,P16070_ISOFORM_6,P16070_ISOFOF

ISOFORM_12,P02751_ISOFORM_4,P02751_ISOFORM_2,P02751_CHAIN_1

_ISOFORM_2,POC0S5_CHAIN_0,Q71UI9_CHAIN_0,POC0S5,Q71UI9

2,O60716_ISOFORM_3B,O60716_ISOFORM_3BC,O60716_ISOFORM_2,O60716_ISOFORM_3AB,O60716_IS(

CG48_CHAIN_2

508_CHAIN_0,P30510_CHAIN_0,Q29960_CHAIN_0,P30492,P30493,Q29940,P01892,P10314,P16189,P1619

30493,Q29940,P01892,P10314,P16189,P16190,P30459,P30512,P30508,P30510,Q29960

RM_3,P16070_ISOFORM_7,P16070_CHAIN_0,P16070_ISOFORM_5,P16070

IFORM_2C,O60716_ISOFORM_3ABC,O60716_ISOFORM_2A,O60716_ISOFORM_2AC,O60716_ISOFORM_2

0,P30459,P30512,P30508,P30510,Q29960,P04439_CHAIN_0,P13746_CHAIN_0,P30457_CHAIN_0,P04439,

B,O60716_ISOFORM_2BC,O60716_ISOFORM_2AB,O60716_ISOFORM_1,O60716_ISOFORM_2ABC,O60716.

P13746,P30457,P13746_ISOFORM_2

_ISOFORM_1C,O60716_ISOFORM_1A,O60716_ISOFORM_1AC,O60716_ISOFORM_1B,O60716_ISOFORM_1

IBC,O60716_ISOFORM_1AB,O60716

	<i>i</i> (114)	<i>i</i> (115)	<i>i</i> (116)	<i>i</i> (117)
#Total quantified peptides	5482	5482	5482	5482
Min	18,449089	81,681345	18,598144	13,16279
Max	29279037	19925473	7571367,6	5806150,1
Sum	1,263E+09	1,64E+09	#####	#####
Normal distribution	FALSO	FALSO	FALSO	FALSO
Normalisation factor				

	<i>i</i> (116/114)		<i>i</i> (117/115)	
	<i>log2 ratios</i>	<i>ratios</i>	<i>log2 ratios</i>	<i>ratios</i>
#Total quantified peptides	5482	5482	5482	5482
Mean	-1,267787	0,4600162	-3,664998	0,1091974
Median	-1,263303	0,4165891	-3,845107	0,0695837
std dev.	0,5913051	0,6791198	1,1182313	0,1097731
Normal distribution	FALSO	FALSO	FALSO	FALSO
CI inf 95 %	-1,283443	0,4420349	-3,694606	0,1062909
CI sup 95 %	-1,252131	0,4779975	-3,63539	0,1121039

116/114

N(114)	N(116)
5482	5482
44,643854	18,449089
18174664	29279037
1,202E+09	1,263E+09
FALSO	FALSO
2,4004467	1

N(116/114)

<i>log2 ratios</i>	<i>ratios</i>
5482	5482
-0,004484	1,1042444
-8,63E-17	1
0,5913051	1,6301909
FALSO	FALSO
-0,02014	1,0610813
0,0111722	1,1474075

117/115

N(115)	N(117)
5482	5482
189,16481	81,681345
83441223	19925473
3,349E+09	1,64E+09
FALSO	FALSO
14,371179	1

N(117/115)

<i>log2 ratios</i>	<i>ratios</i>
5482	5482
0,1801084	1,5692955
2,325E-16	1
1,1182313	1,5775695
FALSO	FALSO
0,1505006	1,5275256
0,2097162	1,6110653

Rank	Species	Accession	Description	IR.N(116)		
				#Ident	#Uniq	#Quant
1	P21333_	FLNA_HUM	Filamin-A (FLN-A) (ABP-280) [ISOFORM 2]	139	64	132
2	Q15149	PLEC_HUM	Plectin (PCN) (PLTN) (HD1)	86	62	86
3	P35579	MYH9_HUM	Myosin-9 (NMMHC-A) (NMMHC II-a) (NMMHC-IIA)	127	59	112
4	P08670_	VIME_HUM	Vimentin [CHAIN 0]	153	37	151
5	P02545_	LMNA_HUM	Prelamin-A/C [CHAIN 1]	104	34	104
6	Q13813	SPTA2_HU	Spectrin alpha chain, non-erythrocytic 1 [ISOFORM 3]	49	35	49
7	O75369	FLNB_HUM	Filamin-B (FLN-B) (Fh1) (Truncated ABP) [ISOFORM 2]	39	27	30
8	P02751_	FINC_HUM	Fibronectin [CHAIN 0]	47	25	47
9	Q07065	CKAP4_HU	Cytoskeleton-associated protein 4 (p63)	57	25	57
10	Q00610	CLH1_HUM	Clathrin heavy chain 1 (CLH-17) [ISOFORM 2]	39	26	39
11	P04264_	K2C1_HUM	Keratin, type II cytoskeletal 1 (CK-1) (K1) [CHAIN 0]	38	23	31
12	P12814	ACTN1_HL	Alpha-actinin-1	53	26	24
13	Q09666	AHNK_HUM	Neuroblast differentiation-associated protein AHNK	45	26	45
14	Q9P2E9	RRBP1_HU	Ribosome-binding protein 1 (RRp) [ISOFORM 2]	34	23	33
15	P08133_	ANXA6_HL	Annexin A6 (CPB-II) [CHAIN 0]	48	25	48
16	O43707	ACTN4_HL	Alpha-actinin-4	46	22	18
17	P60709_	ACTB_HUM	Actin, cytoplasmic 1 [CHAIN 1]	135	20	63
18	Q01082	SPTB2_HU	Spectrin beta chain, non-erythrocytic 1	27	21	27
19	P07437	TBB5_HUM	Tubulin beta chain	35	18	6
20	P06753_	TPM3_HUM	Tropomyosin alpha-3 chain (hTM5) [ISOFORM 2]	48	18	18
21	P07355_	ANXA2_HL	Annexin A2 (PAP-IV) [CHAIN 0]	53	17	53
23	P13645	K1C10_HU	Keratin, type I cytoskeletal 10 (CK-10) (K10)	27	17	25
24	P07951	TPM2_HUM	Tropomyosin beta chain	52	17	2
25	P07951_	TPM2_HUM	Tropomyosin beta chain [ISOFORM 2]	52	17	3
27	P14618_	KPYM_HUM	Pyruvate kinase PKM [CHAIN 0]	32	17	5
28	Q9NZM1	MYOF_HUM	Myoferlin [ISOFORM 6]	20	17	20
30	P09493_	TPM1_HUM	Tropomyosin alpha-1 chain [ISOFORM 3]	50	15	2
31	Q9Y490	TLN1_HUM	Talin-1	19	16	19
32	P04843_	RPN1_HUM	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	21	16	21
33	P68371	TBB2C_HU	Tubulin beta-4B chain	29	15	4
34	P50454_	SERPH_HU	Serpin H1 (AsTP3) (Colligin) [CHAIN 0]	29	15	29
35	P35527	K1C9_HUM	Keratin, type I cytoskeletal 9 (CK-9) (K9)	15	15	13
36	P67936_	TPM4_HUM	Tropomyosin alpha-4 chain [ISOFORM 2]	38	16	3
37	P78527_	PRKDC_HU	DNA-dependent protein kinase catalytic subunit (DNA-PK	17	16	17
38	P67936_	TPM4_HUM	Tropomyosin alpha-4 chain [CHAIN 0]	45	15	10
40	P07900_	HS90A_HL	Heat shock protein HSP 90-alpha (HSP 86) (HSP86) [CHAIN	24	16	12
41	P11021_	GRP78_HU	78 kDa glucose-regulated protein (GRP-78) (BiP) [CHAIN 0]	43	14	43
42	P07237_	PDIA1_HU	Protein disulfide-isomerase (PDI) [CHAIN 0]	27	17	27
44	P06576_	ATPB_HUM	ATP synthase subunit beta, mitochondrial [CHAIN 0]	35	14	35
45	P08238	HS90B_HU	Heat shock protein HSP 90-beta (HSP 90) (HSP 84) (HSP84)	27	15	7
46	P02452	CO1A1_HL	Collagen alpha-1(I) chain	23	13	23
47	P10809_	CH60_HUM	60 kDa heat shock protein, mitochondrial (CPN60) (HSP-60)	24	15	24
48	P04083_	ANXA1_HL	Annexin A1 [CHAIN 0]	41	13	40
49	P22626	ROA2_HUM	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP	25	13	25
50	Q71U36	TBA1A_HL	Tubulin alpha-1A chain	44	11	2
51	Q08211	DHX9_HUM	ATP-dependent RNA helicase A (NDH II)	21	14	21
53	Q99715	COCA1_HL	Collagen alpha-1(XII) chain [ISOFORM 4]	14	13	14
54	P09651_	ROA1_HUM	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1)	21	13	19
55	P06733_	ENOA_HUM	Alpha-enolase (NNE) [CHAIN 0]	25	11	19
56	P04406_	G3P_HUM	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [CH	44	11	44

57	P35580	MYH10_HL	Myosin-10 (NMMHC-B) (NMMHC II-b) (NMMHC-IIB)	15	12	6
59	Q14315	FLNC_HUM	Filamin-C (FLN-C) (FLNc) [ISOFORM 2]	19	12	9
60	P19338	NUCL_HUM	Nucleolin [CHAIN 0]	21	11	21
61	P35908	K22E_HUM	Keratin, type II cytoskeletal 2 epidermal (CK-2e) (K2e)	18	11	8
62	P61978	HNRPK_HU	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (TL	34	11	34
64	P60174	TPIS_HUM	Triosephosphate isomerase (TIM) [CHAIN 0]	21	10	21
66	P08758	ANXA5_HL	Annexin A5 (CBP-I) (PP4) (PAP-I) (VAC-alpha) [CHAIN 0]	24	11	24
67	P08123	CO1A2_HL	Collagen alpha-2(I) chain	12	10	12
68	P25705	ATPA_HUM	ATP synthase subunit alpha, mitochondrial [CHAIN 0]	23	10	23
69	P30101	PDIA3_HU	Protein disulfide-isomerase A3 (p58) (ER protein 57) (ERp5	17	11	17
70	P14625	ENPL_HUM	Endoplasmin (GRP-94) [CHAIN 0]	14	10	9
71	Q00341	VIGLN_HU	Vigilin (HDL-binding protein) [CHAIN 0]	14	11	14
72	P12956	XRCC6_HU	X-ray repair cross-complementing protein 6 (5'-dRP lyase I	16	10	16
73	Q7KZF4	SND1_HUM	Staphylococcal nuclease domain-containing protein 1 [CH	15	10	15
74	Q05682	CALD1_HU	Caldesmon (CDM) [ISOFORM 5]	22	9	22
75	P53621	COPA_HUM	Coatomer subunit alpha	16	11	16
76	Q99623	PHB2_HUM	Prohibitin-2 [CHAIN 0]	22	10	22
77	P13639	EF2_HUMA	Elongation factor 2 (EF-2) [CHAIN 0]	24	11	24
78	P26641	EF1G_HUM	Elongation factor 1-gamma (EF-1-gamma) [CHAIN 0]	17	9	17
79	P04075	ALDOA_HL	Fructose-bisphosphate aldolase A [CHAIN 0]	16	9	16
80	P11142	HSP7C_HU	Heat shock cognate 71 kDa protein [CHAIN 0]	27	10	23
81	Q01995	TAGL_HUM	Transgelin (SM22-alpha) [CHAIN 0]	23	10	23
82	P35232	PHB_HUMA	Prohibitin	26	9	26
83	P63244	GBLP_HUM	Guanine nucleotide-binding protein subunit beta-2-like 1 (17	9	17
84	P09382	LEG1_HUM	Galectin-1 (Gal-1) (HLBP14)	40	9	40
85	O60506	HNRPQ_HU	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (G	13	10	8
86	P78371	TCPB_HUM	T-complex protein 1 subunit beta (TCP-1-beta) [CHAIN 0]	16	9	16
87	Q14697	GANAB_HL	Neutral alpha-glucosidase AB [CHAIN 0]	17	11	17
88	P15144	AMPN_HUM	Aminopeptidase N (AP-N) (hAPN) (AP-M) [CHAIN 0]	11	10	11
89	Q13838	UAP56_HU	Spliceosome RNA helicase DDX39B [CHAIN 0]	13	10	5
90	P21796	VDAC1_HL	Voltage-dependent anion-selective channel protein 1 (VD	16	8	16
91	Q92945	FUBP2_HU	Far upstream element-binding protein 2 (FUSE-binding pr	9	8	9
92	P36578	RL4_HUMA	60S ribosomal protein L4 [CHAIN 0]	15	9	15
93	P22314	UBA1_HUM	Ubiquitin-like modifier-activating enzyme 1	12	9	12
94	P11940	PABP1_HU	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding	15	9	9
95	P60842	IF4A1_HUM	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I)	17	9	16
97	P04844	RPN2_HUM	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	18	8	18
99	P17987	TCPA_HUM	T-complex protein 1 subunit alpha (TCP-1-alpha)	11	9	11
100	Q02878	RL6_HUMA	60S ribosomal protein L6 (TaxREB107)	20	9	20
101	Q14152	EIF3A_HUM	Eukaryotic translation initiation factor 3 subunit A (eIF3a)	10	9	10
102	O75533	SF3B1_HU	Splicing factor 3B subunit 1 (SF3b155) (SAP 155)	10	8	10
103	P13010	XRCC5_HU	X-ray repair cross-complementing protein 5 (CTC85) (CTCE	13	9	13
104	P23396	RS3_HUMA	40S ribosomal protein S3 [CHAIN 0]	16	9	16
105	P46940	IQGA1_HU	Ras GTPase-activating-like protein IQGAP1 [CHAIN 0]	10	8	10
106	O00571	DDX3X_HU	ATP-dependent RNA helicase DDX3X (HLP2) [CHAIN 0]	10	7	10
107	P62805	H4_HUMA	Histone H4 [CHAIN 0]	24	8	24
108	P20700	LMNB1_HL	Lamin-B1 [CHAIN 0]	15	8	15
109	P55072	TERA_HUM	Transitional endoplasmic reticulum ATPase (TER ATPase) (11	7	11
110	P50990	TCPQ_HUM	T-complex protein 1 subunit theta (TCP-1-theta) [CHAIN 0]	10	6	10
111	Q9NQC3	RTN4_HUM	Reticulon-4 (Nogo protein) (NSP) [ISOFORM 2]	13	6	13
112	P08865	RSSA_HUM	40S ribosomal protein SA (37LRP) (LRP/LR) (67LR) (LamR) (12	7	12
113	O60701	UGDH_HUM	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (9	7	9

114	P05556_	ITB1_HUM	Integrin beta-1 [CHAIN 0]	14	7	14
115	P68104_	EF1A1_HU	Elongation factor 1-alpha 1 (EF-1-alpha-1) (EF-Tu) (eEF1A-1)	23	8	23
116	P45880_	VDAC2_HL	Voltage-dependent anion-selective channel protein 2 (VDAC2)	18	6	18
117	P51991_	ROA3_HUM	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	11	7	9
119	Q8WWI1	LMO7_HUM	LIM domain only protein 7 (LMO-7) [ISOFORM 3]	23	8	23
120	P13489_	RINI_HUMA	Ribonuclease inhibitor (Placental RNase inhibitor) (RAI) [CHAIN 0]	8	7	8
121	P15880_	RS2_HUMA	40S ribosomal protein S2 [CHAIN 0]	15	7	15
122	O00159_	MYO1C_HL	Unconventional myosin-Ic [ISOFORM 2]	10	8	10
123	Q12906_	ILF3_HUM	Interleukin enhancer-binding factor 3 (DRBP76) (MPP4) (NFI-B)	10	8	10
124	P19367_	HXK1_HUM	Hexokinase-1 (HK I) [ISOFORM 4]	9	7	9
125	Q9ULV4	COR1C_HU	Coronin-1C	12	7	12
126	P17844_	DDX5_HUM	Probable ATP-dependent RNA helicase DDX5	13	8	8
127	P48643_	TCPE_HUM	T-complex protein 1 subunit epsilon (TCP-1-epsilon) [CHAIN 0]	14	7	14
128	Q01518_	CAP1_HUM	Adenylyl cyclase-associated protein 1 (CAP 1) [CHAIN 0]	12	7	12
129	O76021	RL1D1_HU	Ribosomal L1 domain-containing protein 1	8	6	8
130	P15311_	EZR1_HUM	Ezrin [CHAIN 0]	12	7	5
132	P18124	RL7_HUMA	60S ribosomal protein L7	11	7	11
133	P23284_	PPIB_HUM	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (SCYLP) [CHAIN 0]	14	7	14
134	Q9NR30_	DDX21_HL	Nucleolar RNA helicase 2 [ISOFORM 2]	10	6	10
135	Q96QK1	VPS35_HU	Vacuolar protein sorting-associated protein 35 (hVPS35)	15	7	15
136	O60814	H2B1K_HU	Histone H2B type 1-K (H2B K)	23	7	5
137	P06899_	H2B1J_HU	Histone H2B type 1-J (H2B/r) [CHAIN 0]	21	7	3
138	O75643	U520_HUM	U5 small nuclear ribonucleoprotein 200 kDa helicase (U5-200)	8	7	8
139	P40926_	MDHM_HU	Malate dehydrogenase, mitochondrial [CHAIN 0]	14	6	14
140	Q9BQG0	MBB1A_HL	Myb-binding protein 1A	7	7	7
142	P12236_	ADT3_HUM	ADP/ATP translocase 3 (ANT 2) (ANT 3) [CHAIN 0]	12	7	4
143	Q99832	TCPE_HUM	T-complex protein 1 subunit eta (TCP-1-eta)	9	7	9
144	P63104_	1433Z_HU	14-3-3 protein zeta/delta (KCIP-1)	25	7	7
145	Q9BSJ8	ESYT1_HU	Extended synaptotagmin-1 (E-Syt1)	8	6	7
146	P04792	HSPB1_HU	Heat shock protein beta-1 (HspB1) (HSP 27) (SRP27)	13	6	13
147	P05388	RLA0_HUM	60S acidic ribosomal protein P0	11	6	11
148	Q9Y678	COPG_HUM	Coatomer subunit gamma-1	9	7	9
149	P61019_	RAB2A_HL	Ras-related protein Rab-2A [CHAIN 0]	9	7	9
150	P06396_	GELS_HUM	Gelsolin (ADF) [ISOFORM 2]	9	7	9
151	P37802_	TAGL2_HU	Transgelin-2 [CHAIN 0]	13	6	13
152	P38646_	GRP75_HU	Stress-70 protein, mitochondrial (GRP-75) (MOT) (PBP74)	14	5	14
153	Q9UHB6	LIMA1_HU	LIM domain and actin-binding protein 1 [ISOFORM Alpha]	12	8	12
154	P04908_	H2A1B_HL	Histone H2A type 1-B/E [CHAIN 0]	36	6	30
155	Q15365	PCBP1_HU	Poly(rC)-binding protein 1 (hnRNP E1)	14	6	11
156	Q14247	SRC8_HUM	Src substrate cortactin	8	7	8
157	P50995	ANX11_HL	Annexin A11 (CAP-50)	9	6	9
158	P29692_	EF1D_HUM	Elongation factor 1-delta (EF-1-delta) [CHAIN 0]	14	5	14
159	P60660_	MYL6_HUM	Myosin light polypeptide 6 (LC17) (MLC-3) (Myosin light chain 6)	18	6	18
160	O75083_	WDR1_HU	WD repeat-containing protein 1 (AIP1) [CHAIN 0]	8	7	8
161	Q8NBS9_	TXND5_HU	Thioredoxin domain-containing protein 5 (ER protein 46) (TXND5)	11	6	11
162	P00338_	LDHA_HUM	L-lactate dehydrogenase A chain (LDH-A) (LDH-M) [CHAIN 0]	11	7	7
163	P26038_	MOES_HUM	Moesin [CHAIN 0]	12	7	5
164	P00387_	NB5R3_HU	NADH-cytochrome b5 reductase 3 [CHAIN 1]	6	6	6
165	P62701_	RS4X_HUM	40S ribosomal protein S4, X isoform [CHAIN 0]	13	6	13
166	O00148_	DDX39_HL	ATP-dependent RNA helicase DDX39A [CHAIN 0]	10	7	2
167	P23246	SFPQ_HUM	Splicing factor, proline- and glutamine-rich (hPOMP100) (FUS)	7	6	7
168	Q96AG4	LRC59_HU	Leucine-rich repeat-containing protein 59	17	6	17

169	P53618	COPB_HUM	Coatomer subunit beta (Beta-COP)	11	6	11
170	P25398	RS12_HUM	40S ribosomal protein S12 [CHAIN 0]	11	7	11
171	O43852	CALU_HUM	Calumenin [CHAIN 0]	10	6	10
172	P52272	HNRPM_HL	Heterogeneous nuclear ribonucleoprotein M (hnRNP M) [I	11	6	11
173	P21291	CSRP1_HU	Cysteine and glycine-rich protein 1 (CRP) (CRP1) [CHAIN 0]	9	5	9
174	P13674	P4HA1_HU	Prolyl 4-hydroxylase subunit alpha-1 (4-PH alpha-1) [CHAIN	9	6	9
175	P16403	H12_HUM	Histone H1.2 [CHAIN 0]	11	7	9
176	Q9H0U4	RAB1B_HU	Ras-related protein Rab-1B	11	6	7
177	Q86VP6	CAND1_HL	Cullin-associated NEDD8-dissociated protein 1 (TBP-intera	8	6	8
178	P31949	S10AB_HU	Protein S100-A11 (MLN 70)	17	5	17
179	P31943	HNRH1_HL	Heterogeneous nuclear ribonucleoprotein H, N-terminally	9	5	5
180	P05455	LA_HUMAN	Lupus La protein (SS-B)	7	6	7
181	Q32P28	P3H1_HUM	Prolyl 3-hydroxylase 1 (Leprecan-1) [CHAIN 0]	9	5	9
182	P51149	RAB7A_HL	Ras-related protein Rab-7a	8	5	8
183	P62753	RS6_HUMA	40S ribosomal protein S6	10	5	10
184	P05141	ADT2_HUM	ADP/ATP translocase 2 (ANT 2) [CHAIN 0]	12	6	5
185	O60716	CTND1_HL	Catenin delta-1 (CAS) (p120(ctn)) [ISOFORM 4]	5	5	5
187	Q9NZN4	EHD2_HUM	EH domain-containing protein 2	8	6	7
188	P27797	CALR_HUM	Calreticulin (ERp60) [CHAIN 0]	9	5	9
189	P26599	PTBP1_HU	Polypyrimidine tract-binding protein 1 (PTB) (hnRNP I)	12	6	12
190	O75947	ATP5H_HU	ATP synthase subunit d, mitochondrial (ATPase subunit d)	9	6	9
191	P62277	RS13_HUM	40S ribosomal protein S13 [CHAIN 0]	9	6	9
193	O15143	ARC1B_HU	Actin-related protein 2/3 complex subunit 1B [CHAIN 0]	9	6	9
194	Q9BTV4	TMM43_HL	Transmembrane protein 43 [CHAIN 0]	8	6	8
195	P35606	COPB2_HU	Coatomer subunit beta' (Beta'-COP) [CHAIN 0]	6	6	6
196	P00558	PGK1_HUM	Phosphoglycerate kinase 1 (PRP 2)	14	5	14
198	P49368	TCPG_HUM	T-complex protein 1 subunit gamma (TCP-1-gamma)	10	6	10
199	Q02543	RL18A_HU	60S ribosomal protein L18a	11	5	11
200	Q15084	PDIA6_HU	Protein disulfide-isomerase A6 (ER protein 5) (ERp5) [CHAI	12	5	12
201	P61224	RAP1B_HU	Ras-related protein Rap-1b [CHAIN 0]	8	5	8
202	P13929	ENOB_HUM	Beta-enolase (MSE) [ISOFORM 3]	11	4	5
203	Q9NVA2	SEP11_HU	Septin-11 [CHAIN 0]	5	5	5
204	P62424	RL7A_HUM	60S ribosomal protein L7a [CHAIN 0]	15	5	15
205	P46781	RS9_HUMA	40S ribosomal protein S9 [CHAIN 0]	7	6	7
206	P37837	TALDO_HL	Transaldolase	9	6	9
207	Q14764	MVP_HUM	Major vault protein (MVP) [CHAIN 0]	6	5	6
208	P39023	RL3_HUMA	60S ribosomal protein L3 (TARBP-B) [CHAIN 0]	9	6	9
209	P62258	1433E_HU	14-3-3 protein epsilon (14-3-3E) [ISOFORM SV]	25	6	8
210	Q7Z406	MYH14_HL	Myosin-14 (NMHC II-C) [CHAIN 0]	15	5	5
211	P21964	COMT_HUM	Catechol O-methyltransferase [ISOFORM Soluble]	7	5	7
212	Q14974	IMB1_HUM	Importin subunit beta-1 (PTAC97)	7	5	7
213	Q14103	HNRPD_HU	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0)	10	6	9
214	Q16629	SRSF7_HU	Serine/arginine-rich splicing factor 7 [ISOFORM 3]	8	5	6
215	POCG47	UBB_HUMA	Polyubiquitin-B [CHAIN 0]	13	5	13
216	Q02809	PLOD1_HU	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 (LH1) (7	5	7
217	Q9Y224	CN166_HL	UPF0568 protein C14orf166	8	5	8
218	P21980	TGM2_HUM	Protein-glutamine gamma-glutamyltransferase 2 (TG(C)) (8	5	8
219	Q9NVI7	ATD3A_HL	ATPase family AAA domain-containing protein 3A [ISOFOR	7	5	7
220	P67809	YBOX1_HU	Nuclease-sensitive element-binding protein 1 (CBF-A) (DBI	12	4	12
221	P69849	NOMO3_HL	Nodal modulator 3 [CHAIN 0]	5	5	5
222	P62081	RS7_HUMA	40S ribosomal protein S7	9	5	9
223	P07910	HNRPC_HU	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP	10	5	10

225	P22695_QCR2_HUM	Cytochrome b-c1 complex subunit 2, mitochondrial [CHAIN	6	4	6
226	P08134_RHOC_HUM	Rho-related GTP-binding protein RhoC (h9) [CHAIN 0]	7	5	7
227	Q16643_DREB_HUM	Drebrin [CHAIN 0]	6	4	6
228	P08107_HSP71_HU	Heat shock 70 kDa protein 1A/1B (HSP70-1/HSP70-2) (HSP	9	5	2
229	P39019_RS19_HUM	40S ribosomal protein S19 [CHAIN 0]	10	6	10
230	Q96D15_RCN3_HUM	Reticulocalbin-3 [CHAIN 0]	10	4	10
231	Q6DD88_ATLA3_HL	Atlastin-3	9	5	9
232	P48444_COPD_HUM	Coatomer subunit delta (Delta-COP)	5	5	5
233	Q14204_DYHC1_HU	Cytoplasmic dynein 1 heavy chain 1	6	5	6
234	P28331_NDUS1_HL	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitoch	6	5	6
235	P62937_PPIA_HUM	Peptidyl-prolyl cis-trans isomerase A (PPIase A) [CHAIN 0]	13	5	13
236	Q99729_ROAA_HUM	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B	13	5	10
237	Q13200_PSM2_HU	26S proteasome non-ATPase regulatory subunit 2	6	5	6
238	O43390_HNRPR_HU	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) [Ch	8	5	2
239	P61026_RAB10_HU	Ras-related protein Rab-10	8	5	4
240	P10606_COX5B_HU	Cytochrome c oxidase subunit 5B, mitochondrial [CHAIN 0	10	5	10
241	Q96AY3_FKB10_HU	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10	7	5	7
242	Q07020_RL18_HUM	60S ribosomal protein L18 [CHAIN 0]	9	4	9
243	P62873_GBB1_HUM	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit	9	4	4
244	P08195_4F2_HUMA	4F2 cell-surface antigen heavy chain (4F2hc) [ISOFORM 2]	8	5	8
245	P54886_P5CS_HUM	Delta-1-pyrroline-5-carboxylate synthase (P5CS) [ISOFORM	4	4	4
246	Q86UP2_KTN1_HUM	Kinectin [ISOFORM 2]	5	5	5
247	Q92841_DDX17_HL	Probable ATP-dependent RNA helicase DDX17	9	5	4
248	Q99829_CPNE1_HU	Copine-1	6	5	6
249	P30050_RL12_HUM	60S ribosomal protein L12	10	4	10
250	P63241_IF5A1_HUM	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF	9	4	9
251	Q02978_M2OM_HU	Mitochondrial 2-oxoglutarate/malate carrier protein (OGC	6	4	6
252	Q9Y277_VDAC3_HL	Voltage-dependent anion-selective channel protein 3 (VDAC	8	4	8
253	Q12905_ILF2_HUM	Interleukin enhancer-binding factor 2	6	5	6
254	Q14980_NUMA1_HL	Nuclear mitotic apparatus protein 1 (NuMA protein) [ISO	6	5	6
255	Q15366_PCBP2_HU	Poly(rC)-binding protein 2 (hnRNP E2)	9	5	6
256	P29401_TKT_HUMA	Transketolase (TK)	5	5	5
257	P02786_TFR1_HUM	Transferrin receptor protein 1 [CHAIN 1]	6	5	6
258	P05387_RLA2_HUM	60S acidic ribosomal protein P2	17	4	17
259	O14979_HNRDL_HU	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D	8	5	4
260	P62158_CALM_HUM	Calmodulin (CaM)	9	4	9
261	Q96QV6_H2A1A_HL	Histone H2A type 1-A [CHAIN 0]	8	4	2
262	Q6NZI2_PTRF_HUM	Polymerase I and transcript release factor	7	4	7
263	Q15942_ZYX_HUMA	Zyxin [CHAIN 0]	5	5	5
264	Q07954_LRP1_HUM	Prolow-density lipoprotein receptor-related protein 1 [CH	7	5	7
265	Q07955_SRSF1_HU	Serine/arginine-rich splicing factor 1 (ASF-1) [ISOFORM AS	12	5	12
266	P39656_OST48_HU	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	10	5	10
267	Q9H4M9_EHD1_HUM	EH domain-containing protein 1 (hPAST1)	5	5	4
268	P55209_NP1L1_HU	Nucleosome assembly protein 1-like 1 (hNRP)	8	4	8
269	P62241_RS8_HUMA	40S ribosomal protein S8 [CHAIN 0]	13	4	13
270	P27695_APEX1_HU	DNA- lyase [CHAIN 1]	5	4	5
271	P21589_5NTD_HUM	5'-nucleotidase (5'-NT) [CHAIN 0]	8	5	8
272	P41252_SYIC_HUM	Isoleucyl-tRNA synthetase, cytoplasmic (IRS) (IleRS)	5	5	5
273	P27348_1433T_HU	14-3-3 protein theta	22	5	4
274	Q58FF8_H90B2_HU	Putative heat shock protein HSP 90-beta 2 (Heat shock pr	13	5	2
275	Q02218_ODO1_HUM	2-oxoglutarate dehydrogenase, mitochondrial (OGDC-E1)	5	5	5
276	P61106_RAB14_HU	Ras-related protein Rab-14 [CHAIN 0]	5	4	4

277	P61313	RL15_HUM	60S ribosomal protein L15	7	4	7
278	P07195	LDHB_HUM	L-lactate dehydrogenase B chain (LDH-B) (LDH-H) [CHAIN 0]	8	4	4
279	Q13724	MOGS_HUM	Mannosyl-oligosaccharide glucosidase	7	4	7
280	P30044	PRDX5_HU	Peroxiredoxin-5, mitochondrial (AOEB166) (Prx-V) [CHAIN 0]	9	4	9
281	P49327	FAS_HUMA	Fatty acid synthase	4	4	4
282	P62906	RL10A_HU	60S ribosomal protein L10a (NEDD-6) [CHAIN 0]	6	4	6
283	O94925	GLSK_HUM	Glutaminase kidney isoform, mitochondrial (GLS) [ISOFORM 0]	4	4	4
284	P41091	IF2G_HUM	Eukaryotic translation initiation factor 2 subunit 3 (eIF-2-gamma) [CHAIN 0]	7	5	7
285	P53396	ACLY_HUM	ATP-citrate synthase	6	4	6
286	O95782	AP2A1_HL	AP-2 complex subunit alpha-1 [ISOFORM B]	5	5	5
287	Q16891	IMMT_HUM	Mitochondrial inner membrane protein [ISOFORM 3]	5	5	5
288	Q15019	SEPT2_HU	Septin-2 (NEDD-5)	5	4	5
289	P07737	PROF1_HU	Profilin-1 [CHAIN 0]	14	4	14
290	Q99613	EIF3C_HUM	Eukaryotic translation initiation factor 3 subunit C (eIF3c)	6	5	6
291	Q969G5	PRDBP_HU	Protein kinase C delta-binding protein (hSRBC)	7	4	7
292	P16188	1A30_HUM	HLA class I histocompatibility antigen, A-30 alpha chain [CHAIN 0]	6	4	3
293	P52597	HNRPF_HU	Heterogeneous nuclear ribonucleoprotein F, N-terminally truncated	8	4	4
294	P27824	CALX_HUM	Calnexin [CHAIN 0]	5	4	5
295	Q06830	PRDX1_HU	Peroxiredoxin-1 (NKEF-A) (PAG)	6	4	4
296	P55769	NH2L1_HU	NHP2-like protein 1 (hSNU13) [CHAIN 0]	6	4	6
297	P04899	GNAI2_HU	Guanine nucleotide-binding protein G subunit alpha-2 [CHAIN 0]	7	4	4
298	P62491	RB11A_HU	Ras-related protein Rab-11A (Rab-11) [CHAIN 0]	5	4	5
299	P62280	RS11_HUM	40S ribosomal protein S11 [CHAIN 0]	9	5	9
300	Q99714	HCD2_HUM	3-hydroxyacyl-CoA dehydrogenase type-2 (17-beta-HSD 1C) [CHAIN 0]	6	4	6
301	Q15717	ELAV1_HU	ELAV-like protein 1 (HuR)	5	4	5
302	O15460	P4HA2_HU	Prolyl 4-hydroxylase subunit alpha-2 (4-PH alpha-2) [CHAIN 0]	5	4	5
303	Q9Y3F4	STRAP_HU	Serine-threonine kinase receptor-associated protein	5	4	5
304	P04216	THY1_HUM	Thy-1 membrane glycoprotein [CHAIN 0]	9	3	9
305	Q9P258	RCC2_HUM	Protein RCC2	4	4	4
306	P83731	RL24_HUM	60S ribosomal protein L24	6	4	6
307	Q92616	GCN1L_HU	Translational activator GCN1 (HsGCN1) [CHAIN 0]	4	4	4
308	P00505	AATM_HUM	Aspartate aminotransferase, mitochondrial (mAspAT) (FAE)	4	3	4
309	P49756	RBM25_HL	RNA-binding protein 25 (RED120)	5	4	5
310	Q16658	FSCN1_HU	Fascin [CHAIN 0]	6	4	6
311	O75396	SC22B_HU	Vesicle-trafficking protein SEC22b (ERS-24) (ERS24) [CHAIN 0]	6	3	6
312	P13647	K2C5_HUM	Keratin, type II cytoskeletal 5 (CK-5) (K5)	5	4	2
313	P59998	ARPC4_HU	Actin-related protein 2/3 complex subunit 4 (p20-ARC) [CHAIN 0]	8	4	8
314	Q92499	DDX1_HUM	ATP-dependent RNA helicase DDX1 (DBP-RB)	5	4	5
315	P62269	RS18_HUM	40S ribosomal protein S18 (Ke3) [CHAIN 0]	8	5	8
316	O75367	H2AY_HUM	Core histone macro-H2A.1 (Histone macroH2A1) (mH2A1)	5	4	5
317	P61247	RS3A_HUM	40S ribosomal protein S3a (Fte-1) [CHAIN 0]	5	4	5
318	P15531	NDKA_HUM	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (NDPK A) [CHAIN 0]	7	4	7
319	Q00839	HNRPU_HU	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (S) [CHAIN 0]	12	4	12
320	Q13310	PABP4_HU	Polyadenylate-binding protein 4 (PABP-4) (Poly(A)-binding protein 4) [CHAIN 0]	4	4	2
321	P60900	PSA6_HUM	Proteasome subunit alpha type-6 (PROS-27) (p27K)	4	3	4
323	P32119	PRDX2_HU	Peroxiredoxin-2 (NKEF-B) (TSA) [CHAIN 0]	7	4	5
324	P61619	S61A1_HU	Protein transport protein Sec61 subunit alpha isoform 1 (S) [CHAIN 0]	6	4	6
325	Q9Y262	EIF3L_HUM	Eukaryotic translation initiation factor 3 subunit L (eIF3L) (eIF3L1) [CHAIN 0]	4	4	4
326	P62851	RS25_HUM	40S ribosomal protein S25	9	4	9
327	P43243	MATR3_HL	Matrin-3 [CHAIN 0]	10	4	10
328	Q9UBV2	SE1L1_HU	Protein sel-1 homolog 1 (Sel-1L) [CHAIN 0]	4	3	4
329	P13797	PLST_HUM	Plastin-3	6	4	6

330	Q9UHD8	SEPT9_HU	Septin-9 (MLL septin-like fusion protein) (Ov/Br septin) [IS	4	4	4
331	P63010	AP2B1_HU	AP-2 complex subunit beta	6	4	3
332	P06744	G6PI_HUM	Glucose-6-phosphate isomerase (GPI) (AMF) (NLK) (PGI) (F	5	3	5
333	P07602	SAP_HUMA	Proactivator polypeptide	7	4	7
334	O43143	DHX15_HU	Putative pre-mRNA-splicing factor ATP-dependent RNA he	4	4	4
335	P20073	ANXA7_HL	Annexin A7 [ISOFORM 2]	7	4	7
336	Q86Y82	STX12_HU	Syntaxin-12	5	3	5
337	Q9UKM9	RALY_HUM	RNA-binding protein Raly (hnRNP core protein C-like 2) [IS	6	4	6
338	P34931	HS71L_HU	Heat shock 70 kDa protein 1-like (Heat shock 70 kDa prote	9	3	3
340	Q8NC51	PAIRB_HUM	Plasminogen activator inhibitor 1 RNA-binding protein (PA	4	4	4
341	P11279	LAMP1_HL	Lysosome-associated membrane glycoprotein 1 (LAMP-1)	6	3	6
342	O00469	PLOD2_HU	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 (LH2) [(5	4	5
343	P40939	ECHA_HUM	Trifunctional enzyme subunit alpha, mitochondrial [CHAIN	6	3	6
344	P16401	H15_HUM	Histone H1.5 [CHAIN 0]	5	4	3
346	P30153	2AAA_HUM	Serine/threonine-protein phosphatase 2A 65 kDa regulato	5	4	5
348	P12111	CO6A3_HL	Collagen alpha-3(VI) chain [ISOFORM 2]	5	4	5
349	P25205	MCM3_HUM	DNA replication licensing factor MCM3 [CHAIN 0]	4	3	4
350	Q9Y5M8	SRPRB_HU	Signal recognition particle receptor subunit beta (SR-beta)	6	3	6
351	Q6P2Q9	PRP8_HUM	Pre-mRNA-processing-splicing factor 8 [CHAIN 0]	4	4	4
352	Q13740	CD166_HL	CD166 antigen [CHAIN 0]	4	4	4
353	Q13505	MTX1_HUM	Metaxin-1	4	4	4
354	Q16181	SEPT7_HU	Septin-7 [ISOFORM 2]	3	3	3
355	Q99497	PARK7_HU	Protein DJ-1	4	3	4
356	O15260	SURF4_HU	Surfeit locus protein 4 [ISOFORM 2]	7	3	7
358	O60568	PLOD3_HU	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (LH3) [(5	3	5
359	P46777	RL5_HUMA	60S ribosomal protein L5 [CHAIN 0]	4	3	4
360	P12277	KCRB_HUM	Creatine kinase B-type [CHAIN 0]	4	3	4
361	P50914	RL14_HUM	60S ribosomal protein L14 [CHAIN 0]	8	3	8
362	P62495	ERF1_HUM	Eukaryotic peptide chain release factor subunit 1 (Eukaryo	4	3	4
363	P42704	LPPRC_HU	Leucine-rich PPR motif-containing protein, mitochondrial (3	3	3
364	O00203	AP3B1_HU	AP-3 complex subunit beta-1	3	3	3
365	P51659	DHB4_HUM	Enoyl-CoA hydratase 2 [CHAIN 0]	4	3	4
366	P35637	FUS_HUMA	RNA-binding protein FUS [ISOFORM Short]	7	3	6
367	P52907	CAZA1_HL	F-actin-capping protein subunit alpha-1 [CHAIN 0]	4	3	4
368	P60866	RS20_HUM	40S ribosomal protein S20 [CHAIN 0]	6	3	6
369	Q9UBG0	MRC2_HUM	C-type mannose receptor 2 (UPAR-associated protein) (Ur	8	3	8
370	Q96AE4	FUBP1_HU	Far upstream element-binding protein 1 (FBP) (FUSE-bindi	4	3	4
371	Q9UMS4	PRP19_HU	Pre-mRNA-processing factor 19 (hPso4) [CHAIN 0]	5	3	5
372	P16615	AT2A2_HL	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (SE	3	3	3
373	P61604	CH10_HUM	10 kDa heat shock protein, mitochondrial (Hsp10) (CPN10)	7	3	7
374	P48047	ATPO_HUM	ATP synthase subunit O, mitochondrial (OSCP) [CHAIN 0]	4	3	4
375	P61158	ARP3_HUM	Actin-related protein 3 [CHAIN 0]	6	3	6
376	P99999	CYC_HUMA	Cytochrome c [CHAIN 0]	4	3	4
377	P15259	PGAM2_HL	Phosphoglycerate mutase 2 (PGAM-M) [CHAIN 0]	6	3	6
379	P26640	SYVC_HUM	Valine--tRNA ligase	3	3	3
380	P40429	RL13A_HU	60S ribosomal protein L13a [CHAIN 0]	7	4	7
381	Q02818	NUCB1_HU	Nucleobindin-1 [CHAIN 0]	4	3	4
382	P08648	ITA5_HUM	Integrin alpha-5 [CHAIN 1]	4	3	4
383	Q92520	FAM3C_HL	Protein FAM3C [CHAIN 0]	6	2	6
384	P62879	GBB2_HUM	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit	7	3	2
385	O95302	FKBP9_HU	Peptidyl-prolyl cis-trans isomerase FKBP9 (PPIase FKBP9) (6	3	6
387	P38919	IF4A3_HUM	Eukaryotic initiation factor 4A-III (eIF4A-III) (eIF4A-III) (NM	4	4	3

388	P18206_VINC_HUM	Vinculin [ISOFORM 1]	10	3	10
389	P46459_NSF_HUMA	Vesicle-fusing ATPase (NEM-sensitive fusion protein)	3	3	3
390	Q99584_S10AD_HL	Protein S100-A13	7	3	7
391	Q96N66_MBOA7_HL	Lysophospholipid acyltransferase 7 (LPLAT 7) (LPIAT) (Lyso	3	3	3
392	P61160_ARP2_HUM	Actin-related protein 2	3	3	3
393	Q13492_PICAL_HUM	Phosphatidylinositol-binding clathrin assembly protein [IS	3	3	3
394	P12109_CO6A1_HL	Collagen alpha-1(VI) chain	3	3	3
395	P08708_RS17_HUM	40S ribosomal protein S17 [CHAIN 0]	11	3	11
396	P32969_RL9_HUMA	60S ribosomal protein L9	5	3	5
397	Q14444_CAPR1_HU	Caprin-1 (GPI-p137) (p137GPI) [ISOFORM 2]	5	3	5
398	P51571_SSRD_HUM	Translocon-associated protein subunit delta (TRAP-delta) (3	3	3
399	P60891_PRPS1_HUI	Ribose-phosphate pyrophosphokinase 1 (PRS-I) [CHAIN 0]	3	3	3
400	P61803_DAD1_HUM	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	4	3	4
402	Q01105_SET_HUMA	Protein SET (IGAAD) (I-2PP2A) (TAF-I) [ISOFORM 2]	6	3	6
403	P62829_RL23_HUM	60S ribosomal protein L23	7	3	7
404	P47897_SYQ_HUMA	Glutamine--tRNA ligase [CHAIN 0]	3	3	3
405	Q5SSJ5_HP1B3_HU	Heterochromatin protein 1-binding protein 3 [CHAIN 0]	3	3	3
406	P31930_QCR1_HUM	Cytochrome b-c1 complex subunit 1, mitochondrial [CHAI	3	3	3
407	P09211_GSTP1_HU	Glutathione S-transferase P [CHAIN 0]	3	3	3
408	P49591_SYSC_HUM	Seryl-tRNA synthetase, cytoplasmic (SerRS)	3	3	3
409	Q13151_ROAO_HUM	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	5	3	5
410	O00567_NOP56_HL	Nucleolar protein 56	3	3	3
411	Q9Y6C9_MTCH2_HL	Mitochondrial carrier homolog 2 [CHAIN 0]	4	3	4
412	Q9H299_SH3L3_HU	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3	4	3	4
413	P06756_ITAV_HUM	Integrin alpha-V light chain [ISOFORM 2]	3	3	3
414	Q9NSD9_SYFB_HUM	Phenylalanyl-tRNA synthetase beta chain (PheRS)	3	3	3
415	O43175_SERA_HUM	D-3-phosphoglycerate dehydrogenase (3-PGDH) [CHAIN 0]	6	3	6
416	O75694_NU155_HL	Nuclear pore complex protein Nup155 [ISOFORM 2]	3	3	3
417	P60953_CDC42_HU	Cell division control protein 42 homolog [CHAIN 0]	6	3	5
418	P33993_MCM7_HUM	DNA replication licensing factor MCM7 [CHAIN 0]	5	3	5
419	Q15233_NONO_HUM	Non-POU domain-containing octamer-binding protein (No	3	3	3
420	Q15286_RAB35_HU	Ras-related protein Rab-35	5	3	4
421	P52292_IMA2_HUM	Importin subunit alpha-1 [CHAIN 0]	3	3	3
422	P30041_PRDX6_HU	Peroxiredoxin-6 (1-Cys PRX) (aiPLA2) (NSGPx) [CHAIN 0]	3	3	3
423	P36542_ATPG_HUM	ATP synthase subunit gamma, mitochondrial [CHAIN 0]	5	3	5
424	A1LOT0_ILVBL_HUM	Acetolactate synthase-like protein	3	3	3
425	P05023_AT1A1_HL	Sodium/potassium-transporting ATPase subunit alpha-1 (f	3	3	3
426	P29590_PML_HUMA	Probable transcription factor PML [ISOFORM PML-9]	3	3	3
427	P30086_PEBP1_HUI	Phosphatidylethanolamine-binding protein 1 [CHAIN 0]	4	3	4
428	P06748_NPM_HUM	Nucleophosmin (NPM) [ISOFORM 2]	4	3	4
429	P02768_ALBU_HUM	Serum albumin [ISOFORM 2]	3	3	3
430	P31947_1433S_HU	14-3-3 protein sigma [ISOFORM 2]	19	3	2
431	Q13247_SRSF6_HUI	Serine/arginine-rich splicing factor 6 [ISOFORM SRP55-3]	4	3	2
432	P62910_RL32_HUM	60S ribosomal protein L32	3	3	3
433	P17813_EGLN_HUM	Endoglin [CHAIN 0]	4	3	4
434	P36871_PGM1_HUM	Phosphoglucomutase-1 (PGM 1) [CHAIN 0]	3	3	3
435	Q9NYL9_TMOD3_HL	Tropomodulin-3 (U-Tmod)	3	3	3
436	Q13263_TIF1B_HUM	Transcription intermediary factor 1-beta (TIF1-beta) (KAP-	3	3	3
437	P46977_STT3A_HU	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	3	3	3
438	Q15185_TEBP_HUM	Prostaglandin E synthase 3 (cPGES)	3	3	3
439	P51114_FXR1_HUM	Fragile X mental retardation syndrome-related protein 1 (f	2	2	2
442	Q9UNX3_RL26L_HU	60S ribosomal protein L26-like 1 [CHAIN 0]	4	3	4

443	P50402	EMD_HUM	Emerin	4	3	4
444	P43304	GPDM_HUM	Glycerol-3-phosphate dehydrogenase, mitochondrial (GPC	5	3	5
445	Q13283	G3BP1_HU	Ras GTPase-activating protein-binding protein 1 (G3BP-1)	2	2	2
446	P18085	ARF4_HUM	ADP-ribosylation factor 4 [CHAIN 0]	5	3	5
447	P14923	PLAK_HUM	Junction plakoglobin	3	3	3
448	P49411	EFTU_HUM	Elongation factor Tu, mitochondrial (EF-Tu) [CHAIN 0]	2	2	2
449	Q92688	AN32B_HL	Acidic leucine-rich nuclear phosphoprotein 32 family mem	3	3	2
450	P63092	GNAS2_HL	Guanine nucleotide-binding protein G subunit alpha isofo	6	3	3
451	P31942	HNRH3_HL	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3)	3	2	3
452	P23528	COF1_HUM	Cofilin-1 (p18) [CHAIN 0]	5	3	5
453	P14866	HNRPL_HU	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	3	3	3
454	P55010	IF5_HUMA	Eukaryotic translation initiation factor 5 (eIF-5)	4	3	4
455	Q9Y4L1	HYOU1_HL	Hypoxia up-regulated protein 1 (ORP-150) (GRP-170) [CHA	4	3	4
456	P34932	HSP74_HU	Heat shock 70 kDa protein 4	3	3	2
457	Q9H853	TBA4B_HU	Putative tubulin-like protein alpha-4B	5	2	3
458	O75390	CISY_HUM	Citrate synthase, mitochondrial [CHAIN 0]	5	3	5
459	O15400	STX7_HUM	Syntaxin-7 [ISOFORM 2]	4	2	4
460	Q03252	LMNB2_HL	Lamin-B2 [CHAIN 0]	3	3	3
461	P20591	MX1_HUM	Interferon-induced GTP-binding protein Mx1 [CHAIN 1]	3	2	3
462	P17931	LEG3_HUM	Galectin-3 (Gal-3) (CBP 35) (GALBP) [CHAIN 0]	3	3	3
463	O95470	SGPL1_HU	Sphingosine-1-phosphate lyase 1 (SP-lyase 1) (SPL 1) (hSPL	2	2	2
464	P55084	ECHB_HUM	Trifunctional enzyme subunit beta, mitochondrial [CHAIN	3	2	3
465	Q16531	DDB1_HUM	DNA damage-binding protein 1 (DDBa) (XAP-1) (UV-DDB 1	3	3	3
466	Q15005	SPCS2_HU	Signal peptidase complex subunit 2 (SPase 25 kDa subunit	4	3	4
467	Q96FQ6	S10AG_HU	Protein S100-A16	5	3	5
468	Q02952	AKA12_HL	A-kinase anchor protein 12 (AKAP-12) (AKAP 250) [ISOFOR	3	2	3
469	P16070	CD44_HUM	CD44 antigen (ECMR-III) (PGP-1) (PGP-I) [ISOFORM 15]	5	2	5
470	P54727	RD23B_HU	UV excision repair protein RAD23 homolog B (HR23B) (hHI	7	3	7
471	Q8NBJS	GT251_HU	Procollagen galactosyltransferase 1 [CHAIN 0]	3	3	3
472	Q0ZGT2	NEXN_HUM	Nexilin [ISOFORM 2]	3	3	3
473	P14868	SYDC_HUM	Aspartate--tRNA ligase, cytoplasmic	4	3	4
474	P56134	ATPK_HUM	ATP synthase subunit f, mitochondrial [ISOFORM 2]	7	2	7
475	P40227	TCPZ_HUM	T-complex protein 1 subunit zeta (TCP-1-zeta) [CHAIN 0]	5	3	5
476	Q9BWM7	SFXN3_HU	Sideroflexin-3	2	2	2
477	Q14566	MCM6_HU	DNA replication licensing factor MCM6	3	3	3
478	Q07021	C1QBP_HU	Complement component 1 Q subcomponent-binding prot	4	2	4
479	P35268	RL22_HUM	60S ribosomal protein L22 (EAP) [CHAIN 0]	4	2	4
480	Q15758	AAAT_HUM	Neutral amino acid transporter B	3	2	3
481	Q01813	K6PP_HUM	6-phosphofructokinase type C (PFK-C)	4	2	4
482	P07996	TSP1_HUM	Thrombospondin-1 [CHAIN 0]	3	2	3
483	P30533	AMRP_HUM	Alpha-2-macroglobulin receptor-associated protein (Alpha	4	3	4
484	P50991	TCPD_HUM	T-complex protein 1 subunit delta (TCP-1-delta) [CHAIN 0]	5	2	5
485	P34897	GLYM_HUM	Serine hydroxymethyltransferase, mitochondrial (SHMT) [I	3	3	3
486	Q16555	DPYL2_HU	Dihydropyrimidinase-related protein 2 (DRP-2) (CRMP-2) (2	2	2
487	P61769	B2MG_HUM	Beta-2-microglobulin [CHAIN 1]	3	2	3
488	Q9UBQ0	VPS29_HU	Vacuolar protein sorting-associated protein 29 (hVPS29)	3	3	3
489	P49755	TMEDA_HL	Transmembrane emp24 domain-containing protein 10 (S3	3	3	3
490	P22087	FBRL_HUM	rRNA 2'-O-methyltransferase fibrillarin	3	3	3
491	Q8N556	AFAP1_HU	Actin filament-associated protein 1 (AFAP-110)	3	3	3
492	Q14554	PDIA5_HU	Protein disulfide-isomerase A5 [CHAIN 0]	3	3	3
493	P12270	TPR_HUMA	Nucleoprotein TPR [CHAIN 0]	3	2	3
494	Q9HDC9	APMAP_HL	Adipocyte plasma membrane-associated protein [ISOFOR	3	3	3

495	P24539_	AT5F1_HU	ATP synthase subunit b, mitochondrial (ATPase subunit b)	3	3	3
496	P38159_	HNRPG_HU	Heterogeneous nuclear ribonucleoprotein G, N-terminally	6	3	6
497	P20618_	PSB1_HUM	Proteasome subunit beta type-1 [CHAIN 0]	2	2	2
498	P07099_	HYEP_HUM	Epoxide hydrolase 1	3	3	3
499	Q9UKV3_	ACINU_HUI	Apoptotic chromatin condensation inducer in the nucleus	4	3	4
500	P37108_	SRP14_HU	Signal recognition particle 14 kDa protein (SRP14) [CHAIN	3	2	3
501	Q70UQ0_	IKIP_HUMA	Inhibitor of nuclear factor kappa-B kinase-interacting prot	5	3	3
502	Q9NVD7_	PARVA_HL	Alpha-parvin	2	2	2
503	P13987_	CD59_HUM	CD59 glycoprotein (HRF-20) (HRF20) (MAC-IP) (MACIF) (M	6	2	6
504	Q99439_	CNN2_HUM	Calponin-2 [CHAIN 0]	3	2	3
505	Q9Y5X1_	SNX9_HUM	Sorting nexin-9 (Protein SDP1)	2	2	2
506	O75380_	NDUS6_HL	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, r	4	2	4
507	P09669_	COX6C_HU	Cytochrome c oxidase subunit 6C [CHAIN 0]	4	3	4
508	Q9Y2D5_	AKAP2_HL	A-kinase anchor protein 2 (AKAP-2) (PRKA2)	2	2	2
509	Q13641_	TPBG_HUM	Trophoblast glycoprotein (5T4 oncotrophoblast glycoprote	3	3	3
510	P09525_	ANXA4_HL	Annexin A4 (PAP-II) [CHAIN 0]	2	2	2
511	P09661_	RU2A_HUM	U2 small nuclear ribonucleoprotein A' (U2 snRNP A') [CHA	2	2	2
512	Q6IAA8_	PDRO_HUM	Ragulator complex protein LAMTOR1 [CHAIN 0]	3	2	3
513	P62888_	RL30_HUM	60S ribosomal protein L30 [CHAIN 0]	4	2	4
514	P07093_	GDN_HUM	Glia-derived nexin (GDN) (PI-7) (PN-1) [CHAIN 0]	2	2	2
515	O75534_	CSDE1_HU	Cold shock domain-containing protein E1 [ISOFORM Short	4	3	4
516	Q10713_	MPPA_HUM	Mitochondrial-processing peptidase subunit alpha [CHAIN	3	3	3
517	Q92598_	HS105_HU	Heat shock protein 105 kDa [ISOFORM Beta]	3	3	2
518	O00231_	PSD11_HU	26S proteasome non-ATPase regulatory subunit 11 [CHAIN	3	3	3
519	P30049_	ATPD_HUM	ATP synthase subunit delta, mitochondrial [CHAIN 0]	5	2	5
520	P62913_	RL11_HUM	60S ribosomal protein L11 [CHAIN 0]	8	2	8
521	Q15436_	SC23A_HU	Protein transport protein Sec23A	2	2	2
522	P30443_	1A01_HUM	HLA class I histocompatibility antigen, A-1 alpha chain [CH	5	2	3
523	Q53GQ0_	DHB12_HL	Estradiol 17-beta-dehydrogenase 12 (17-beta-HSD 12) (KA	3	2	3
524	Q53FA7_	QORX_HUM	Quinone oxidoreductase PIG3	2	2	2
525	P04632_	CPNS1_HU	Calpain small subunit 1 (CSS1) (CANP small subunit) (CDPS	3	2	3
526	P41250_	SYG_HUMA	Glycine--tRNA ligase	2	2	2
527	Q8IVL6_	P3H3_HUM	Prolyl 3-hydroxylase 3 [CHAIN 0]	2	2	2
528	P02533_	K1C14_HU	Keratin, type I cytoskeletal 14 (CK-14) (K14) [CHAIN 0]	5	2	3
529	Q8N4C6_	NIN_HUMA	Ninein (hNinein) (GSK3B-interacting protein) [ISOFORM 6]	3	3	2
530	Q96I24_	FUBP3_HUI	Far upstream element-binding protein 3 (FUSE-binding pr	2	2	2
532	Q00688_	FKBP3_HUI	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (3	3	3
533	Q15393_	SF3B3_HU	Splicing factor 3B subunit 3 (SF3b130) (SAP 130)	2	2	2
534	Q16630_	CPSF6_HUI	Cleavage and polyadenylation specificity factor subunit 6 (3	2	3
536	Q9BUJ2_	HNRL1_HU	Heterogeneous nuclear ribonucleoprotein U-like protein 1	2	2	2
537	P21281_	VATB2_HL	V-type proton ATPase subunit B, brain isoform (V-ATPase :	3	2	3
538	Q969X5_	ERGI1_HUM	Endoplasmic reticulum-Golgi intermediate compartment p	2	2	2
540	Q9UQ80_	PA2G4_HU	Proliferation-associated protein 2G4 (hG4-1) [CHAIN 0]	3	2	3
541	P60033_	CD81_HUM	CD81 antigen (Tspan-28)	3	2	3
542	Q15459_	SF3A1_HU	Splicing factor 3A subunit 1 (SAP 114)	2	2	2
543	Q9Y230_	RUVB2_HU	RuvB-like 2 (48 kDa TBP-interacting protein) (ECP-51) (Rep	2	2	2
544	P62826_	RAN_HUM	GTP-binding nuclear protein Ran [CHAIN 0]	3	2	3
545	P09874_	PARP1_HU	Poly [ADP-ribose] polymerase 1 (PARP-1) (ADPRT 1) [CHAI	3	2	3
546	Q92791_	SC65_HUM	Synaptonemal complex protein SC65	3	2	3
547	P62917_	RL8_HUMA	60S ribosomal protein L8 [CHAIN 0]	4	2	4
548	P20674_	COX5A_HL	Cytochrome c oxidase subunit 5A, mitochondrial [CHAIN 0	3	2	3
549	P24534_	EF1B_HUM	Elongation factor 1-beta (EF-1-beta) [CHAIN 0]	4	2	4

550	Q93008.	USP9X_HU	Probable ubiquitin carboxyl-terminal hydrolase FAF-X (hFA	2	2	2
551	Q14019.	COTL1_HU	Coactosin-like protein [CHAIN 0]	3	2	3
552	O76094.	SRP72_HU	Signal recognition particle 72 kDa protein (SRP72) [CHAIN	2	2	2
553	Q13423.	NNTM_HUM	NAD transhydrogenase, mitochondrial [CHAIN 0]	2	2	2
554	O14602.	IF1AY_HUM	Eukaryotic translation initiation factor 1A, Y-chromosomal	2	2	2
555	P46063.	RECQ1_HU	ATP-dependent DNA helicase Q1 (RecQ1) [CHAIN 0]	3	2	3
556	P54136.	SYRC_HUM	Arginyl-tRNA synthetase, cytoplasmic (ArgRS) [ISOFORM N	2	2	2
557	Q6NYC8	PHTNS_HU	Phostensin	2	2	2
558	Q9Y4P3	TBL2_HUM	Transducin beta-like protein 2 (WS-betaTRP)	2	2	2
559	O94874.	UFL1_HUM	E3 UFM1-protein ligase 1 [ISOFORM 3]	2	2	2
560	P28066	PSA5_HUM	Proteasome subunit alpha type-5	4	2	4
562	P54920	SNAAL_HUM	Alpha-soluble NSF attachment protein (SNAP-alpha)	2	2	2
563	P11177.	ODPB_HUM	Pyruvate dehydrogenase E1 component subunit beta, mit	3	2	3
564	Q16795.	NDUA9_HL	NADH dehydrogenase 1 alpha subcomplex subunit 9, mit	2	2	2
565	Q9Y3B3.	TMED7_HL	Transmembrane emp24 domain-containing protein 7 [CH/	3	2	3
566	P09622.	DLDH_HUM	Dihydrolipoyl dehydrogenase, mitochondrial [CHAIN 0]	3	2	3
567	P04181.	OAT_HUM	Ornithine aminotransferase, renal form [CHAIN 1]	2	2	2
568	Q15043.	S39AE_HU	Zinc transporter ZIP14 (LZT-Hs4) (ZIP-14) [CHAIN 0]	2	2	2
569	O75131.	CPNE3_HU	Copine-3 [CHAIN 0]	4	2	4
570	O14776.	TCRG1_HU	Transcription elongation regulator 1 [ISOFORM 2]	2	2	2
571	P98179	RBM3_HUM	Putative RNA-binding protein 3	2	2	2
572	P18621.	RL17_HUM	60S ribosomal protein L17 [CHAIN 0]	3	2	3
573	Q08431.	MFGM_HUM	Lactadherin [ISOFORM 2]	2	2	2
574	Q04837.	SSBP_HUM	Single-stranded DNA-binding protein, mitochondrial (Mt-S	3	2	3
575	Q16881.	TRXR1_HU	Thioredoxin reductase 1, cytoplasmic (TR) (GRIM-12) (Gen	2	2	2
576	P24752.	THIL_HUM	Acetyl-CoA acetyltransferase, mitochondrial [CHAIN 0]	3	2	3
577	Q14676.	MDC1_HUM	Mediator of DNA damage checkpoint protein 1 [ISOFORM	2	2	2
578	P61221	ABCE1_HU	ATP-binding cassette sub-family E member 1 (RNS4I)	3	2	3
579	Q6UVK1.	CSPG4_HU	Chondroitin sulfate proteoglycan 4 [CHAIN 0]	2	2	2
580	P08574.	CY1_HUM	Cytochrome c1, heme protein, mitochondrial (Cytochrome	2	2	2
582	Q9UJZ1	STML2_HU	Stomatin-like protein 2 (SLP-2)	3	2	3
583	Q13243.	SRSF5_HU	Serine/arginine-rich splicing factor 5 [ISOFORM SRP40-4]	4	2	2
585	Q03135.	CAV1_HUM	Caveolin-1 [ISOFORM Beta]	3	2	3
586	Q9NX63	CHCH3_HL	Coiled-coil-helix-coiled-coil-helix domain-containing prote	2	2	2
587	P42766.	RL35_HUM	60S ribosomal protein L35 [CHAIN 0]	5	2	5
588	Q15008.	PSMD6_HL	26S proteasome non-ATPase regulatory subunit 6 [CHAIN	2	2	2
589	Q9Y265	RUVB1_HU	RuvB-like 1 (49 kDa TBP-interacting protein) (ECP-54) (NM	3	2	3
590	O75531	BAF_HUM	Barrier-to-autointegration factor	3	2	3
591	P49257.	LMAN1_HL	Protein ERGIC-53 [CHAIN 0]	4	2	4
592	O75368	SH3L1_HU	SH3 domain-binding glutamic acid-rich-like protein	4	2	4
593	P49773.	HINT1_HU	Histidine triad nucleotide-binding protein 1 (PKCI-1) [CHAI	2	2	2
595	Q15293.	RCN1_HUM	Reticulocalbin-1 [CHAIN 0]	2	2	2
596	P30084.	ECHM_HUM	Enoyl-CoA hydratase, mitochondrial (SCEH) [CHAIN 0]	3	2	3
597	P17301.	ITA2_HUM	Integrin alpha-2 (GPIa) [CHAIN 0]	2	2	2
598	O14737.	PDCD5_HU	Programmed cell death protein 5 (Protein TFAR19) [CHAIN	3	2	3
599	Q14344	GNA13_HL	Guanine nucleotide-binding protein subunit alpha-13 (G al	4	2	4
600	O14653	GOSR2_HU	Golgi SNAP receptor complex member 2	2	2	2
601	P22102	PUR2_HUM	Trifunctional purine biosynthetic protein adenosine-3	2	2	2
602	Q13895	BYST_HUM	Bystin	2	2	2
603	Q16666.	IF16_HUM	Gamma-interferon-inducible protein 16 (Ifi-16) [ISOFORM	2	2	2
605	P14927.	QCR7_HUM	Cytochrome b-c1 complex subunit 7 [CHAIN 0]	3	2	3
606	Q13177.	PAK2_HUM	PAK-2p34 (p34) [CHAIN 1]	2	2	2

607	P62249_RS16_HUM	40S ribosomal protein S16 [CHAIN 0]	5	2	5	
608	O43294	TGFI1_HUM	Transforming growth factor beta-1-induced transcript 1 pr	2	2	2
609	A0FGR8	ESYT2_HU	Extended synaptotagmin-2 (E-Syt2) [ISOFORM 4]	3	2	3
610	Q9Y512	SAM50_HL	Sorting and assembly machinery component 50 homolog (2	2	2
611	Q8WUM4	PDC6L_HUM	Programmed cell death 6-interacting protein (PDCD6-inter	2	2	2
612	P09496	CLCA_HUM	Clathrin light chain A (Lca) [ISOFORM Non-brain]	2	2	2
613	P63000	RAC1_HUM	Ras-related C3 botulinum toxin substrate 1	2	2	2
614	P68402	PA1B2_HU	Platelet-activating factor acetylhydrolase IB subunit beta (2	2	2
615	O15145	ARPC3_HU	Actin-related protein 2/3 complex subunit 3 (p21-ARC) [Ch	3	2	3
616	P26368	U2AF2_HU	Splicing factor U2AF 65 kDa subunit (hU2AF(65)) (hU2AF65	5	2	5
617	O43684	BUB3_HUM	Mitotic checkpoint protein BUB3 [ISOFORM 2]	2	2	2
618	P13073	COX41_HU	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (2	2	2
619	P62995	TRA2B_HU	Transformer-2 protein homolog beta (TRA-2 beta) (TRA2-k	2	2	2
620	P26373	RL13_HUM	60S ribosomal protein L13 [CHAIN 0]	4	2	4
621	O75844	FACE1_HU	CAAX prenyl protease 1 homolog (FACE-1)	2	2	2
622	Q9UKM7	MA1B1_HL	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha	2	2	2
623	P29992	GNA11_HL	Guanine nucleotide-binding protein subunit alpha-11 (G al	2	2	2
624	P62750	RL23A_HU	60S ribosomal protein L23a [CHAIN 0]	3	2	3
625	P42224	STAT1_HU	Signal transducer and activator of transcription 1-alpha/be	2	2	2
626	P30837	AL1B1_HU	Aldehyde dehydrogenase X, mitochondrial [CHAIN 0]	3	2	3
627	Q9H930	LY10L_HU	Nuclear body protein SP140-like protein [ISOFORM 2]	3	2	3
628	Q9UHX1	PUF60_HU	Poly(U)-binding-splicing factor PUF60 (FBP-interacting rep	2	2	2
629	Q9NP72	RAB18_HU	Ras-related protein Rab-18 [CHAIN 0]	2	2	2
630	Q9UJS0	CMC2_HUM	Calcium-binding mitochondrial carrier protein Aralar2	2	2	2
631	Q9UL25	RAB21_HU	Ras-related protein Rab-21 [CHAIN 0]	3	2	3
632	O75915	PRAF3_HU	PRA1 family protein 3 (ARL-6-interacting protein 5) (Aip-5)	4	2	4
633	P62244	RS15A_HU	40S ribosomal protein S15a [CHAIN 0]	4	2	4
634	Q9POL0	VAPA_HUM	Vesicle-associated membrane protein-associated protein /	4	2	4
635	P14314	GLU2B_HU	Glucosidase 2 subunit beta (PKCSH) [CHAIN 0]	4	2	4
636	P62899	RL31_HUM	60S ribosomal protein L31	5	2	5
637	P46776	RL27A_HU	60S ribosomal protein L27a [CHAIN 0]	4	2	4
638	P51572	BAP31_HU	B-cell receptor-associated protein 31 (BCR-associated prot	4	2	4
639	O75340	PDCD6_HU	Programmed cell death protein 6	2	2	2
640	Q969H8	CS010_HU	UPF0556 protein C19orf10 (IL-25) [CHAIN 0]	3	2	3
641	Q01844	EWS_HUM	RNA-binding protein EWS [ISOFORM EWS-B]	4	2	4
642	Q9UJ70	NAGK_HUM	N-acetyl-D-glucosamine kinase (N-acetylglucosamine kina	2	2	2
643	P12004	PCNA_HUM	Proliferating cell nuclear antigen (PCNA)	4	2	4
644	P35221	CTNA1_HL	Catenin alpha-1 [CHAIN 0]	3	2	3
645	P16152	CBR1_HUM	Carbonyl reductase [NADPH] 1 [CHAIN 0]	2	2	2
646	A2RRP1	NBAS_HUM	Neuroblastoma-amplified sequence [ISOFORM 2]	2	2	2
647	Q14498	RBM39_HL	RNA-binding protein 39 [ISOFORM 2]	4	2	4
648	Q99805	TM9S2_HL	Transmembrane 9 superfamily member 2 [CHAIN 0]	2	2	2
649	Q9Y2W2	WBP11_HL	WW domain-binding protein 11 (WBP-11) (NpwBP)	2	2	2
650	P35613	BASI_HUM	Basigin (EMMPRIN) (TCSF) [ISOFORM 2]	3	2	3
651	O75489	NDUS3_HU	NADH dehydrogenase iron-sulfur protein 3, mitochondria	2	2	2
652	Q9BXP5	SRRT_HUM	Serrate RNA effector molecule homolog [ISOFORM 5]	2	2	2
653	Q8N163	K1967_HU	Protein KIAA1967 (DBC-1) (DBC.1)	2	2	2
654	O94905	ERLN2_HU	Erlin-2 (SPFH domain-containing protein 2)	2	2	2
655	O43747	AP1G1_HU	AP-1 complex subunit gamma-1 [CHAIN 0]	2	2	2
657	O00629	IMA4_HUM	Importin subunit alpha-3 [CHAIN 0]	2	2	2
658	O94826	TOM70_HL	Mitochondrial import receptor subunit TOM70 [CHAIN 0]	2	2	2
659	P60903	S10AA_HL	Protein S100-A10 [CHAIN 0]	6	2	6

660	P10301_RRAS_HUM	Ras-related protein R-Ras [CHAIN 0]	2	2	2
661	P11387_TOP1_HUM	DNA topoisomerase 1 [CHAIN 0]	2	2	2
662	Q96CW1_AP2M1_HL	AP-2 complex subunit mu	3	2	3
663	Q9HBR0_S38AA_HL	Putative sodium-coupled neutral amino acid transporter 1	2	2	2
664	Q16698_DECR_HUM	2,4-dienoyl-CoA reductase, mitochondrial (4-enoyl-CoA reductase)	2	2	2
666	P23634_AT2B4_HU	Plasma membrane calcium-transporting ATPase 4 (PMCA4)	3	2	3
667	P26639_SYTC_HUM	Threonyl-tRNA synthetase, cytoplasmic (ThrRS)	2	2	2
668	O15144_ARPC2_HU	Actin-related protein 2/3 complex subunit 2 (p34-ARC)	3	2	3
669	Q9P0K7_RAI14_HU	Ankycorbin [ISOFORM 3]	2	2	2
671	P63173_RL38_HUM	60S ribosomal protein L38	4	2	4
672	Q9H0S4_DDX47_HL	Probable ATP-dependent RNA helicase DDX47 [CHAIN 0]	2	2	2
673	Q9Y3I0_CV028_HL	UPF0027 protein C22orf28	2	2	2
674	P63167_DYL1_HUM	Dynein light chain 1, cytoplasmic (DLC8) (PIN)	3	2	3
675	Q12797_ASPH_HUM	Aspartyl/asparaginyl beta-hydroxylase (ASP beta-hydroxylase)	2	2	2
676	Q9Y3U8_RL36_HUM	60S ribosomal protein L36 [CHAIN 0]	3	2	3
677	Q8TAQ2_SMRC2_HU	SWI/SNF complex subunit SMARCC2 [ISOFORM 2]	2	2	2
678	P26196_DDX6_HUM	Probable ATP-dependent RNA helicase DDX6	3	2	3
679	P16949_STMN1_HL	Stathmin (Op18) (pp19)	3	2	3
680	P36957_ODO2_HUM	Dihydrolipoyllysine-residue succinyltransferase component 2	2	2	2
681	Q02880_TOP2B_HU	DNA topoisomerase 2-beta [ISOFORM Beta-1]	2	2	2
682	P42892_ECE1_HUM	Endothelin-converting enzyme 1 (ECE-1) [ISOFORM C]	2	2	2
683	P05161_ISG15_HUM	Ubiquitin-like protein ISG15 (IP17) (hUCRP) [CHAIN 0]	3	2	3
684	Q15417_CNN3_HUM	Calponin-3	5	2	5
685	P49821_NDUV1_HL	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	2	2	2
686	P25786_PSA1_HUM	Proteasome subunit alpha type-1 (PROS-30)	2	2	2
687	O95816_BAG2_HUM	BAG family molecular chaperone regulator 2 (BAG-2)	2	2	2
688	Q7L014_DDX46_HL	Probable ATP-dependent RNA helicase DDX46	3	2	3
689	P46939_UTRO_HUM	Utrophin (DRP-1)	2	2	2
690	Q13425_SNTB2_HU	Beta-2-syntrophin (SNT3) (SNTL)	3	2	3
691	P28370_SMCA1_HL	Probable global transcription activator SNF2L1 [ISOFORM 1]	2	2	2
692	Q8WUJ3_K1199_HU	Protein KIAA1199 [CHAIN 0]	2	2	2
693	Q9H3N1_TMX1_HUM	Thioredoxin-related transmembrane protein 1 [CHAIN 0]	2	2	2
694	P62318_SMD3_HUM	Small nuclear ribonucleoprotein Sm D3 (Sm-D3)	3	2	3
696	P13473_LAMP2_HL	Lysosome-associated membrane glycoprotein 2 (LAMP-2)	2	2	2
697	Q99733_NP1L4_HU	Nucleosome assembly protein 1-like 4 (NAP-2) [CHAIN 0]	2	2	2
698	P46783_RS10_HUM	40S ribosomal protein S10	4	2	4
699	P02042_HBD_HUM	Hemoglobin subunit delta [CHAIN 0]	2	2	2
700	Q13242_SRSF9_HU	Serine/arginine-rich splicing factor 9	3	2	3
701	Q6P1M0_S27A4_HU	Long-chain fatty acid transport protein 4 (FATP-4) (Fatty acid transport protein 4)	2	2	2
702	P17655_CAN2_HUM	Calpain-2 catalytic subunit (CANP 2) (M-calpain) [CHAIN 0]	2	2	2
703	P23526_SAHH_HUM	Adenosylhomocysteinase (AdoHcyase) [CHAIN 0]	2	2	2
704	P61353_RL27_HUM	60S ribosomal protein L27	2	2	2
705	P48735_IDHP_HUM	Isocitrate dehydrogenase, mitochondrial [CHAIN 0]	2	2	2
706	Q8TCS8_PNPT1_HU	Polyribonucleotide nucleotidyltransferase 1, mitochondria	2	2	2
707	Q08945_SSRP1_HU	FACT complex subunit SSRP1 (FACT 80 kDa subunit) (FACT)	2	2	2
708	O43854_EDIL3_HUM	EGF-like repeat and discoidin I-like domain-containing protein 3	3	2	3
709	O00410_IPO5_HUM	Importin-5 (Imp5) (RanBP5) [CHAIN 0]	2	2	2
710	Q12841_FSTL1_HU	Follistatin-related protein 1 [CHAIN 0]	2	2	2
711	Q00325_MPCP_HUM	Phosphate carrier protein, mitochondrial (PTP) [CHAIN 0]	3	2	3
712	Q86UX6_ST32C_HU	Serine/threonine-protein kinase 32C (PKE)	2	2	2
713	P41223_BUD31_HU	Protein BUD31 homolog	2	2	2
714	P20908_CO5A1_HL	Collagen alpha-1(V) chain [CHAIN 0]	2	2	2

715	P52943	CRIP2_HU	Cysteine-rich protein 2 (CRP-2)	2	2	2
716	Q9BVK6	TMED9_HL	Transmembrane emp24 domain-containing protein 9 [CH	5	2	5
717	Q12904	AIMP1_HU	Endothelial monocyte-activating polypeptide 2 (EMAP-2) (3	2	3
718	P07942	LAMB1_HL	Laminin subunit beta-1	2	2	2
719	Q07666	KHDR1_HU	KH domain-containing, RNA-binding, signal transduction-a	2	2	2
721	P37235	HPCL1_HU	Hippocalcin-like protein 1 (VILIP-3) [CHAIN 0]	3	2	3
722	P55265	DSRAD_HU	Double-stranded RNA-specific adenosine deaminase (DRA	2	2	2
723	Q9Y2H6	FND3A_HL	Fibronectin type-III domain-containing protein 3A [ISOFOR	2	2	2
724	Q9P035	HACD3_HL	Very-long-chain -3-hydroxyacyl- dehydratase 3	2	2	2
725	Q9NSK0	KLC4_HU	Kinesin light chain 4 (KLC 4) [ISOFORM 3]	2	2	2
726	Q04637	IF4G1_HU	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-g	2	2	2
727	P36776	LONM_HU	Lon protease homolog, mitochondrial (LONP) [CHAIN 0]	3	2	3
728	Q13561	DCTN2_HL	Dynactin subunit 2 (DCTN-50) [CHAIN 0]	2	2	2
729	P11413	G6PD_HU	Glucose-6-phosphate 1-dehydrogenase (G6PD) [CHAIN 0]	3	2	3
730	Q9Y6M1	IF2B2_HU	Insulin-like growth factor 2 mRNA-binding protein 2 (IGF2	2	2	2
731	O95573	ACSL3_HU	Long-chain-fatty-acid--CoA ligase 3 (LACS 3)	2	2	2
732	Q06323	PSME1_HU	Proteasome activator complex subunit 1 (REG-alpha) (IGU	3	2	3
733	Q13557	KCC2D_HU	Calcium/calmodulin-dependent protein kinase type II sub	2	2	2
734	Q9BS26	ERP44_HU	Endoplasmic reticulum resident protein 44 (ER protein 44)	2	2	2
735	Q96AC1	FERM2_HU	Fermitin family homolog 2 (MIG-2) (PH domain-containing	2	2	2
736	O15042	SR140_HU	U2-associated protein SR140 [ISOFORM 2]	2	2	2
737	Q6NUQ4	TM214_HL	Transmembrane protein 214	2	2	2
738	P56385	ATP5I_HU	ATP synthase subunit e, mitochondrial (ATPase subunit e)	2	2	2
739	Q14534	ERG1_HU	Squalene monooxygenase (SE)	2	2	2
741	Q16851	UGPA_HU	UTP--glucose-1-phosphate uridylyltransferase (UDPGP) (U	2	2	2
742	Q12849	GRSF1_HU	G-rich sequence factor 1 (GRSF-1)	2	2	2
743	Q8TF01	SFR18_HU	Arginine/serine-rich protein PNISR	2	2	2
744	Q07157	ZO1_HU	Tight junction protein ZO-1 [ISOFORM Short]	2	2	2
745	O60762	DPM1_HU	Dolichol-phosphate mannosyltransferase (DPM synthase)	2	2	2
746	Q99459	CDC5L_HU	Cell division cycle 5-like protein (Cdc5-like protein)	2	2	2

IR.N(114)					IR.N(117)				
Mean	Median	Std	CV (%)	#Quant	Mean	Median	Std	CV (%)	
0,4610229	0,4706432	0,0754028	16,355536	132	0,5389771	0,5293568	0,0754028	13,989977	
0,421334	0,4241288	0,0580967	13,78876	86	0,578666	0,5758712	0,0580967	10,03977	
0,4483823	0,4432899	0,0834613	18,61386	112	0,5516177	0,5567101	0,0834613	15,130273	
0,3944528	0,397315	0,0568174	14,404099	151	0,6055472	0,602685	0,0568174	9,3828162	
0,5668706	0,562113	0,0616428	10,87423	104	0,4331294	0,437887	0,0616428	14,23196	
0,4625172	0,4587526	0,05601	12,109827	49	0,5374828	0,5412474	0,05601	10,420803	
0,4869507	0,4932834	0,0557057	11,43971	30	0,5130493	0,5067166	0,0557057	10,857777	
0,6096388	0,6146864	0,0744797	12,217017	47	0,3903612	0,3853136	0,0744797	19,079685	
0,4264737	0,4223471	0,0632315	14,82659	57	0,5735263	0,5776529	0,0632315	11,025042	
0,5348841	0,5402128	0,0439048	8,2082737	39	0,4651159	0,4597872	0,0439048	9,439531	
0,3643434	0,3671256	0,0664083	18,226834	31	0,6356566	0,6328744	0,0664083	10,447194	
0,4649528	0,4670744	0,0415341	8,9329622	24	0,5350472	0,5329256	0,0415341	7,7626915	
0,3885892	0,3932588	0,0818195	21,05553	45	0,6114108	0,6067412	0,0818195	13,382084	
0,6007645	0,6104666	0,0733476	12,209043	33	0,3992355	0,3895334	0,0733476	18,37201	
0,4957467	0,5062565	0,0641896	12,94807	48	0,5042533	0,4937435	0,0641896	12,729642	
0,4290239	0,4492477	0,0640188	14,92197	18	0,5709761	0,5507523	0,0640188	11,21217	
0,5130141	0,5122964	0,0519881	10,133858	63	0,4869859	0,4877036	0,0519881	10,675487	
0,4848399	0,4673866	0,0912628	18,823296	27	0,5151601	0,5326134	0,0912628	17,715432	
0,5084613	0,5033148	0,0413401	8,1304272	6	0,4915387	0,4966852	0,0413401	8,4103409	
0,4917383	0,4985482	0,0562486	11,438736	18	0,5082617	0,5014518	0,0562486	11,066865	
0,4285059	0,4374761	0,0778757	18,17377	53	0,5714941	0,5625239	0,0778757	13,626682	
0,4033625	0,4154539	0,0863099	21,397601	25	0,5966375	0,5845461	0,0863099	14,466055	
0,6987167	0,6987167	0,0247129	3,5369035	2	0,3012833	0,3012833	0,0247129	8,2025564	
0,6942872	0,713419	0,0875634	12,611987	3	0,3057128	0,286581	0,0875634	28,642379	
0,576911	0,558548	0,0553832	9,5999537	5	0,423089	0,441452	0,0553832	13,0902	
0,4900941	0,5011481	0,0426555	8,7035285	20	0,5099059	0,4988519	0,0426555	8,3653624	
0,7299914	0,7299914	0,0159086	2,1792803	2	0,2700086	0,2700086	0,0159086	5,8918725	
0,5221026	0,5379108	0,0877009	16,797628	19	0,4778974	0,4620892	0,0877009	18,3514	
0,4413532	0,44924	0,059657	13,516839	21	0,5586468	0,55076	0,059657	10,67884	
0,4659453	0,4484961	0,0566595	12,160118	4	0,5340547	0,5515039	0,0566595	10,609307	
0,6487244	0,6475567	0,0768205	11,841777	29	0,3512756	0,3524433	0,0768205	21,869013	
0,3544093	0,3291741	0,1060629	29,926661	13	0,6455907	0,6708259	0,1060629	16,428811	
0,5645589	0,551961	0,0717117	12,70226	3	0,4354411	0,448039	0,0717117	16,468755	
0,4176319	0,4198987	0,0785663	18,812333	17	0,5823681	0,5801013	0,0785663	13,490831	
0,5499811	0,5282961	0,0829523	15,082752	10	0,4500189	0,4717039	0,0829523	18,433068	
0,5046151	0,4972199	0,0463902	9,19318	12	0,4953849	0,5027801	0,0463902	9,3644707	
0,513586	0,5265897	0,0684169	13,321421	43	0,486414	0,4734103	0,0684169	14,065578	
0,548197	0,5579421	0,0740828	13,513911	27	0,451803	0,4420579	0,0740828	16,397155	
0,4845175	0,4864402	0,0393711	8,125844	35	0,5154825	0,5135598	0,0393711	7,6377257	
0,5378398	0,4975997	0,0778906	14,482125	7	0,4621602	0,5024003	0,0778906	16,853598	
0,6950253	0,7222037	0,1244108	17,900176	23	0,3049747	0,2777963	0,1244108	40,7938	
0,4666263	0,4814186	0,0787107	16,868035	24	0,5333737	0,5185814	0,0787107	14,757137	
0,4231603	0,4121393	0,0696236	16,453234	40	0,5768397	0,5878607	0,0696236	12,069829	
0,5628913	0,5806793	0,0896094	15,919484	25	0,4371087	0,4193207	0,0896094	20,500479	
0,6630131	0,6630131	0,0029019	0,4376766	2	0,3369869	0,3369869	0,0029019	0,8611175	
0,4929669	0,4944103	0,0552847	11,214677	21	0,5070331	0,5055897	0,0552847	10,90356	
0,508325	0,5291935	0,1424949	28,032242	14	0,491675	0,4708065	0,1424949	28,981517	
0,584179	0,5654919	0,0604628	10,35005	19	0,415821	0,4345081	0,0604628	14,540591	
0,5504182	0,5584084	0,0613473	11,145572	19	0,4495818	0,4415916	0,0613473	13,645403	
0,5653675	0,5753385	0,0860019	15,21169	44	0,4346325	0,4246615	0,0860019	19,787277	

0,3747614	0,3354611	0,0752633	20,082998	6	0,6252386	0,6645389	0,0752633	12,037538
0,4049556	0,3699973	0,0921839	22,763949	9	0,5950444	0,6300027	0,0921839	15,491934
0,5205836	0,5199004	0,0574836	11,042141	21	0,4794164	0,4800996	0,0574836	11,990323
0,3736164	0,371908	0,0543051	14,535	8	0,6263836	0,628092	0,0543051	8,6696293
0,5809597	0,5643539	0,0656762	11,304769	34	0,4190403	0,4356461	0,0656762	15,672992
0,5480151	0,5483064	0,0307687	5,6145703	21	0,4519849	0,4516936	0,0307687	6,8074604
0,4708377	0,4775095	0,1000922	21,258318	24	0,5291623	0,5224905	0,1000922	18,915216
0,6058054	0,6088387	0,1417557	23,399544	12	0,3941946	0,3911613	0,1417557	35,960847
0,4331655	0,4458196	0,0578944	13,365426	23	0,5668345	0,5541804	0,0578944	10,213637
0,534935	0,5453074	0,0611599	11,433152	17	0,465065	0,4546926	0,0611599	13,150833
0,5520393	0,5437336	0,0576711	10,446911	9	0,4479607	0,4562664	0,0576711	12,874134
0,5609194	0,5693821	0,0578635	10,315823	14	0,4390806	0,4306179	0,0578635	13,178324
0,4834922	0,4976448	0,0761667	15,753458	16	0,5165078	0,5023552	0,0761667	14,746481
0,4849045	0,479543	0,0560048	11,54965	15	0,5150955	0,520457	0,0560048	10,872695
0,5834534	0,6073874	0,0896016	15,357109	22	0,4165466	0,3926126	0,0896016	21,510579
0,4642348	0,4672445	0,0523639	11,279615	16	0,5357652	0,5327555	0,0523639	9,7736638
0,4047224	0,4159489	0,0522463	12,909165	22	0,5952776	0,5840511	0,0522463	8,776792
0,4837399	0,5194562	0,0843056	17,427882	24	0,5162601	0,4805438	0,0843056	16,330069
0,5054718	0,5128248	0,0476779	9,4323514	17	0,4945282	0,4871752	0,0476779	9,6410835
0,5419923	0,5217967	0,0805135	14,855097	16	0,4580077	0,4782033	0,0805135	17,579069
0,4546785	0,4767928	0,0522869	11,499747	23	0,5453215	0,5232072	0,0522869	9,5882676
0,6038503	0,6465661	0,1023044	16,942009	23	0,3961497	0,3534339	0,1023044	25,824675
0,3962752	0,4043888	0,0889981	22,458647	26	0,6037248	0,5956112	0,0889981	14,741494
0,5110836	0,5136232	0,0588672	11,518125	17	0,4889164	0,4863768	0,0588672	12,040351
0,5075706	0,5111226	0,0949635	18,709416	40	0,4924294	0,4888774	0,0949635	19,284695
0,5397653	0,5594152	0,0700096	12,970374	8	0,4602347	0,4405848	0,0700096	15,211714
0,4830963	0,4831247	0,0579302	11,991444	16	0,5169037	0,5168753	0,0579302	11,20716
0,496622	0,5328921	0,1312231	26,423132	17	0,503378	0,4671079	0,1312231	26,068498
0,4730507	0,4547683	0,0684033	14,460041	11	0,5269493	0,5452317	0,0684033	12,981005
0,4995864	0,5099671	0,0619305	12,396345	5	0,5004136	0,4900329	0,0619305	12,375855
0,4597809	0,4808847	0,0770305	16,753748	16	0,5402191	0,5191153	0,0770305	14,259126
0,6151953	0,6200533	0,0382236	6,2132536	9	0,3848047	0,3799467	0,0382236	9,9332568
0,4720563	0,4789239	0,0619652	13,126664	15	0,5279437	0,5210761	0,0619652	11,737095
0,5907929	0,6100947	0,0629276	10,651376	12	0,4092071	0,3899053	0,0629276	15,377929
0,4270747	0,4006805	0,0689495	16,14461	9	0,5729253	0,5993195	0,0689495	12,03465
0,4635784	0,4764482	0,0598074	12,901236	16	0,5364216	0,5235518	0,0598074	11,149319
0,4986942	0,5018616	0,0453626	9,0962705	18	0,5013058	0,4981384	0,0453626	9,0488834
0,4521868	0,4480426	0,047581	10,522423	11	0,5478132	0,5519574	0,047581	8,6856255
0,4997244	0,4987762	0,0446985	8,9446227	20	0,5002756	0,5012238	0,0446985	8,9347682
0,4377295	0,44909	0,0368292	8,4136859	10	0,5622705	0,55091	0,0368292	6,5500834
0,481715	0,47269	0,0296482	6,1547249	10	0,518285	0,52731	0,0296482	5,7204508
0,5035522	0,525669	0,0582755	11,572884	13	0,4964478	0,474331	0,0582755	11,738498
0,5149732	0,5204407	0,0631022	12,253493	16	0,4850268	0,4795593	0,0631022	13,010045
0,4261178	0,4414928	0,0557346	13,079615	10	0,5738822	0,5585072	0,0557346	9,7118469
0,4723875	0,4556406	0,0469098	9,9303701	10	0,5276125	0,5443594	0,0469098	8,8909604
0,3023277	0,2935706	0,0570424	18,867745	24	0,6976723	0,7064294	0,0570424	8,176105
0,3763365	0,3830219	0,0545265	14,488755	15	0,6236635	0,6169781	0,0545265	8,7429309
0,5667809	0,5704998	0,0417953	7,3741618	11	0,4332191	0,4295002	0,0417953	9,6476206
0,4785239	0,4874963	0,0482756	10,088439	10	0,5214761	0,5125037	0,0482756	9,2574878
0,5162098	0,5002965	0,0417181	8,081618	13	0,4837902	0,4997035	0,0417181	8,6231802
0,477144	0,505754	0,0783133	16,412932	12	0,522856	0,494246	0,0783133	14,977987
0,4754151	0,4825677	0,1075423	22,620708	9	0,5245849	0,5174323	0,1075423	20,500453

0,5678701	0,5737494	0,0439473	7,7389757	14	0,4321299	0,4262506	0,0439473	10,169933
0,4939281	0,498647	0,0456813	9,248569	23	0,5060719	0,501353	0,0456813	9,0266401
0,4855475	0,4866641	0,0348226	7,1718264	18	0,5144525	0,5133359	0,0348226	6,7688695
0,6465945	0,6059458	0,1390269	21,501408	9	0,3534055	0,3940542	0,1390269	39,339212
0,5505323	0,5444091	0,0708092	12,861949	23	0,4494677	0,4555909	0,0708092	15,754007
0,5578361	0,5407015	0,0388023	6,9558685	8	0,4421639	0,4592985	0,0388023	8,7755587
0,4967875	0,5122721	0,0726337	14,62068	15	0,5032125	0,4877279	0,0726337	14,434001
0,4380129	0,4231398	0,072097	16,460027	10	0,5619871	0,5768602	0,072097	12,828949
0,6071864	0,5976538	0,04962	8,1721118	10	0,3928136	0,4023462	0,04962	12,631932
0,4846969	0,482758	0,0269517	5,560517	9	0,5153031	0,517242	0,0269517	5,2302515
0,4491072	0,4373942	0,0716645	15,957092	12	0,5508928	0,5626058	0,0716645	13,008785
0,4096732	0,4330576	0,0597568	14,58645	8	0,5903268	0,5669424	0,0597568	10,122662
0,4727596	0,4639228	0,0399645	8,4534519	14	0,5272404	0,5360772	0,0399645	7,5799395
0,6202785	0,6307402	0,1015648	16,374058	12	0,3797215	0,3692598	0,1015648	26,747175
0,450651	0,4472548	0,0431131	9,5668406	8	0,549349	0,5527452	0,0431131	7,8480283
0,4749707	0,4851627	0,0320537	6,7485545	5	0,5250293	0,5148373	0,0320537	6,1051186
0,5161085	0,5190199	0,0450883	8,7361984	11	0,4838915	0,4809801	0,0450883	9,3178472
0,491028	0,485523	0,0580688	11,825965	14	0,508972	0,514477	0,0580688	11,409037
0,3116489	0,314944	0,0679684	21,809299	10	0,6883511	0,685056	0,0679684	9,8740966
0,5375575	0,5305447	0,05651	10,51237	15	0,4624425	0,4694553	0,05651	12,219904
0,4171349	0,3958806	0,0686808	16,464879	5	0,5828651	0,6041194	0,0686808	11,783305
0,3903976	0,4067897	0,0299442	7,6701738	3	0,6096024	0,5932103	0,0299442	4,9120836
0,4539603	0,4554823	0,0478926	10,54995	8	0,5460397	0,5445177	0,0478926	8,7708984
0,619957	0,6170886	0,0669913	10,805801	14	0,380043	0,3829114	0,0669913	17,627301
0,3372844	0,3292232	0,031531	9,3484837	7	0,6627156	0,6707768	0,031531	4,7578448
0,5145025	0,5185825	0,0361015	7,0167699	4	0,4854975	0,4814175	0,0361015	7,4359716
0,5048068	0,5107483	0,0445061	8,8164548	9	0,4951932	0,4892517	0,0445061	8,9876161
0,6513823	0,6720197	0,0564682	8,6689836	7	0,3486177	0,3279803	0,0564682	16,197749
0,4610797	0,5064261	0,0843895	18,302577	7	0,5389203	0,4935739	0,0843895	15,658991
0,5905429	0,641794	0,134114	22,710283	13	0,4094571	0,358206	0,134114	32,754098
0,4281354	0,4530969	0,1243824	29,052113	11	0,5718646	0,5469031	0,1243824	21,750316
0,4980066	0,5009518	0,1178504	23,664421	9	0,5019934	0,4990482	0,1178504	23,476482
0,4984533	0,5058564	0,0259516	5,2064347	9	0,5015467	0,4941436	0,0259516	5,1743233
0,543034	0,5624078	0,0651111	11,990236	9	0,456966	0,4375922	0,0651111	14,248559
0,6182771	0,6460757	0,0807315	13,057488	13	0,3817229	0,3539243	0,0807315	21,14923
0,5675358	0,5680527	0,0424403	7,4779972	14	0,4324642	0,4319473	0,0424403	9,813602
0,4832362	0,5171229	0,0864085	17,881218	12	0,5167638	0,4828771	0,0864085	16,721085
0,3627767	0,3044997	0,1805915	49,780346	30	0,6372233	0,6955003	0,1805915	28,340378
0,5749325	0,575455	0,0909209	15,814192	11	0,4250675	0,424545	0,0909209	21,389764
0,3899305	0,40963	0,0832752	21,356411	8	0,6100695	0,59037	0,0832752	13,650112
0,4964584	0,4814057	0,0584729	11,778007	9	0,5035416	0,5185943	0,0584729	11,612327
0,4578953	0,4628445	0,0485221	10,59677	14	0,5421047	0,5371555	0,0485221	8,9506902
0,5351877	0,5367879	0,0465811	8,7036875	18	0,4648123	0,4632121	0,0465811	10,021479
0,5223875	0,5280221	0,0423358	8,1042914	8	0,4776125	0,4719779	0,0423358	8,86405
0,5797444	0,5979985	0,0454106	7,8328721	11	0,4202556	0,4020015	0,0454106	10,80548
0,5353887	0,5379287	0,0854905	15,967926	7	0,4646113	0,4620713	0,0854905	18,400426
0,4856324	0,4834452	0,050786	10,457698	5	0,5143676	0,5165548	0,050786	9,8734791
0,4585239	0,4522465	0,0346396	7,5545791	6	0,5414761	0,5477535	0,0346396	6,3972452
0,4432414	0,4306289	0,0618608	13,956453	13	0,5567586	0,5693711	0,0618608	11,11088
0,4402099	0,4402099	0,0061301	1,392543	2	0,5597901	0,5597901	0,0061301	1,0950732
0,4668159	0,4894315	0,107107	22,944166	7	0,5331841	0,5105685	0,107107	20,088186
0,4216219	0,4240044	0,0486226	11,532281	17	0,5783781	0,5759956	0,0486226	8,4067183

0,4863743	0,4999559	0,0804995	16,550932	11	0,5136257	0,5000441	0,0804995	15,672794
0,4632285	0,4723588	0,0462317	9,9803264	11	0,5367715	0,5276412	0,0462317	8,6129238
0,6822822	0,684913	0,0765191	11,215174	10	0,3177178	0,315087	0,0765191	24,08399
0,5358909	0,5314045	0,0552046	10,301468	11	0,4641091	0,4685955	0,0552046	11,894752
0,6005393	0,602369	0,0540507	9,0003683	9	0,3994607	0,397631	0,0540507	13,530928
0,5188307	0,5088813	0,0434186	8,368543	9	0,4811693	0,4911187	0,0434186	9,0235528
0,522634	0,5163539	0,0509701	9,7525496	9	0,477366	0,4836461	0,0509701	10,677372
0,4930096	0,4968126	0,0433164	8,7861248	7	0,5069904	0,5031874	0,0433164	8,5438369
0,5386569	0,5439584	0,0694435	12,891977	8	0,4613431	0,4560416	0,0694435	15,052467
0,5297753	0,5268517	0,0421093	7,9485127	17	0,4702247	0,4731483	0,0421093	8,9551356
0,5259528	0,5289616	0,0467242	8,8837259	5	0,4740472	0,4710384	0,0467242	9,8564454
0,6495181	0,6621656	0,0628271	9,6728822	7	0,3504819	0,3378344	0,0628271	17,925926
0,5523641	0,5474969	0,0441661	7,9958303	9	0,4476359	0,4525031	0,0441661	9,8665227
0,4927668	0,4985179	0,0495857	10,06272	8	0,5072332	0,5014821	0,0495857	9,7757272
0,5192201	0,484481	0,0888403	17,110336	10	0,4807799	0,515519	0,0888403	18,47837
0,4557528	0,4644556	0,0174342	3,8253605	5	0,5442472	0,5355444	0,0174342	3,203358
0,4790239	0,4758983	0,0901355	18,8165	5	0,5209761	0,5241017	0,0901355	17,301278
0,5554424	0,5464247	0,0547808	9,8625565	7	0,4445576	0,4535753	0,0547808	12,322546
0,5541628	0,5678025	0,07592	13,69995	9	0,4458372	0,4321975	0,07592	17,028643
0,5196105	0,5294842	0,0442884	8,5233896	12	0,4803895	0,4705158	0,0442884	9,2192764
0,3947113	0,4142987	0,0753175	19,081667	9	0,6052887	0,5857013	0,0753175	12,443233
0,4921211	0,5021288	0,0454279	9,2310354	9	0,5078789	0,4978712	0,0454279	8,9446281
0,5215664	0,5267598	0,0286514	5,4933298	9	0,4784336	0,4732402	0,0286514	5,9885763
0,4347947	0,4324555	0,0356186	8,1920437	8	0,5652053	0,5675445	0,0356186	6,3018809
0,4993592	0,5079882	0,0205136	4,1079933	6	0,5006408	0,4920118	0,0205136	4,0974765
0,5776196	0,5929183	0,0622694	10,780345	14	0,4223804	0,4070817	0,0622694	14,742492
0,4635424	0,4669644	0,0559573	12,07168	10	0,5364576	0,5330356	0,0559573	10,430898
0,4657904	0,4656222	0,0509305	10,934201	11	0,5342096	0,5343778	0,0509305	9,5337983
0,5649233	0,5716857	0,0591988	10,479081	12	0,4350767	0,4283143	0,0591988	13,606513
0,5717703	0,5665139	0,038318	6,7016459	8	0,4282297	0,4334861	0,038318	8,9480056
0,5478531	0,5584084	0,0610522	11,143906	5	0,4521469	0,4415916	0,0610522	13,502744
0,4995475	0,5032523	0,0676179	13,535838	5	0,5004525	0,4967477	0,0676179	13,511359
0,50895	0,4954876	0,0509717	10,015064	15	0,49105	0,5045124	0,0509717	10,380139
0,5100198	0,5015738	0,0322579	6,3248363	7	0,4899802	0,4984262	0,0322579	6,5835143
0,675486	0,691106	0,1061655	15,716904	9	0,324514	0,308894	0,1061655	32,715227
0,5502558	0,5482154	0,0697973	12,684526	6	0,4497442	0,4517846	0,0697973	15,519341
0,4563142	0,4412557	0,087053	19,077429	9	0,5436858	0,5587443	0,087053	16,011639
0,6044344	0,6115513	0,0506944	8,3870766	8	0,3955656	0,3884487	0,0506944	12,815669
0,5210374	0,5238207	0,0819404	15,726395	5	0,4789626	0,4761793	0,0819404	17,107893
0,5325526	0,5161228	0,0965285	18,12563	7	0,4674474	0,4838772	0,0965285	20,650132
0,4607468	0,5075126	0,0890099	19,318623	7	0,5392532	0,4924874	0,0890099	16,506151
0,581747	0,5950814	0,0708056	12,171196	9	0,418253	0,4049186	0,0708056	16,928886
0,4417555	0,4352583	0,0215501	4,8782917	6	0,5582445	0,5647417	0,0215501	3,8603377
0,6384592	0,6040233	0,1090467	17,079661	13	0,3615408	0,3959767	0,1090467	30,161649
0,5137283	0,5128633	0,0560231	10,905208	7	0,4862717	0,4871367	0,0560231	11,520952
0,5539657	0,5779868	0,0661175	11,935305	8	0,4460343	0,4220132	0,0661175	14,823412
0,6028667	0,5782763	0,0648715	10,76051	8	0,3971333	0,4217237	0,0648715	16,334954
0,3763578	0,3810036	0,0437632	11,628074	7	0,6236422	0,6189964	0,0437632	7,0173517
0,6336418	0,6363473	0,028823	4,5487841	12	0,3663582	0,3636527	0,028823	7,8674375
0,4358934	0,4434898	0,0328762	7,5422595	5	0,5641066	0,5565102	0,0328762	5,8280141
0,5151675	0,520253	0,0835003	16,208389	9	0,4848325	0,479747	0,0835003	17,222512
0,4475328	0,467759	0,054111	12,090947	10	0,5524672	0,532241	0,054111	9,7944199

0,4429895	0,4579923	0,0571966	12,911509	6	0,5570105	0,5420077	0,0571966	10,268501
0,5262981	0,5093227	0,0446086	8,4759153	7	0,4737019	0,4906773	0,0446086	9,417014
0,4909442	0,5025553	0,0809111	16,480721	6	0,5090558	0,4974447	0,0809111	15,894356
0,5885167	0,5885167	0,0482945	8,2061335	2	0,4114833	0,4114833	0,0482945	11,736678
0,5239881	0,5487786	0,0552557	10,545213	10	0,4760119	0,4512214	0,0552557	11,60804
0,6562942	0,6580858	0,0666549	10,156245	10	0,3437058	0,3419142	0,0666549	19,392996
0,5590722	0,5804652	0,0428482	7,6641701	9	0,4409278	0,4195348	0,0428482	9,7177467
0,5045638	0,5004285	0,0400755	7,942604	5	0,4954362	0,4995715	0,0400755	8,088935
0,5105851	0,5100455	0,0355668	6,9658967	6	0,4894149	0,4899545	0,0355668	7,2672145
0,4968669	0,4964069	0,0390613	7,8615269	6	0,5031331	0,5035931	0,0390613	7,7636179
0,4803579	0,480685	0,0298705	6,2183845	13	0,5196421	0,519315	0,0298705	5,7482832
0,5622997	0,593121	0,0775811	13,797103	10	0,4377003	0,406879	0,0775811	17,724702
0,5945067	0,6029094	0,0301112	5,0649022	6	0,4054933	0,3970906	0,0301112	7,425815
0,5615403	0,5615403	0,002209	0,3933867	2	0,4384597	0,4384597	0,002209	0,5038149
0,5284539	0,537343	0,0235098	4,4487974	4	0,4715461	0,462657	0,0235098	4,9856938
0,5665107	0,5921288	0,0434374	7,667539	10	0,4334893	0,4078712	0,0434374	10,020413
0,5799087	0,6147785	0,0858576	14,805365	7	0,4200913	0,3852215	0,0858576	20,437846
0,4923452	0,4905513	0,0845025	17,163263	9	0,5076548	0,5094487	0,0845025	16,645659
0,5531135	0,5353574	0,0994115	17,973079	4	0,4468865	0,4646426	0,0994115	22,245366
0,4740235	0,4828248	0,0535287	11,29242	8	0,5259765	0,5171752	0,0535287	10,17702
0,4620983	0,4662325	0,0446178	9,6554785	4	0,5379017	0,5337675	0,0446178	8,2947884
0,4078704	0,3764036	0,0720414	17,662817	5	0,5921296	0,6235964	0,0720414	12,166495
0,3382943	0,3345627	0,0620729	18,348801	4	0,6617057	0,6654373	0,0620729	9,3807483
0,4415223	0,4383697	0,0257255	5,8265406	6	0,5584777	0,5616303	0,0257255	4,6063561
0,5007233	0,507911	0,0388096	7,7507153	10	0,4992767	0,492089	0,0388096	7,7731723
0,5072586	0,5064898	0,0286869	5,6552858	9	0,4927414	0,4935102	0,0286869	5,8219029
0,4493505	0,446122	0,040255	8,9584939	6	0,5506495	0,553878	0,040255	7,3104641
0,4870753	0,4823553	0,0583586	11,98143	8	0,5129247	0,5176447	0,0583586	11,377613
0,5688295	0,6066041	0,1004736	17,663218	6	0,4311705	0,3933959	0,1004736	23,302518
0,4308541	0,4263337	0,0391215	9,0799818	6	0,5691459	0,5736663	0,0391215	6,873717
0,5631295	0,5492282	0,0645452	11,461877	6	0,4368705	0,4507718	0,0645452	14,774451
0,6057305	0,6001132	0,0413017	6,8184919	5	0,3942695	0,3998868	0,0413017	10,475495
0,4292952	0,4196465	0,0241628	5,6284863	6	0,5707048	0,5803535	0,0241628	4,2338569
0,4963834	0,4761968	0,0963069	19,401716	17	0,5036166	0,5238032	0,0963069	19,123061
0,5018196	0,5026344	0,0628996	12,534295	4	0,4981804	0,4973656	0,0628996	12,625859
0,5883651	0,5887554	0,0537888	9,1420709	9	0,4116349	0,4112446	0,0537888	13,067102
0,2905594	0,2905594	0,0412384	14,192763	2	0,7094406	0,7094406	0,0412384	5,8128059
0,4934303	0,5274069	0,0846895	17,163414	7	0,5065697	0,4725931	0,0846895	16,718227
0,5083167	0,5207847	0,0410658	8,0787845	5	0,4916833	0,4792153	0,0410658	8,3520855
0,5455273	0,5582176	0,0520606	9,5431719	7	0,4544727	0,4417824	0,0520606	11,455165
0,4756919	0,4735343	0,0305605	6,4244252	12	0,5243081	0,5264657	0,0305605	5,8287244
0,4985973	0,5026694	0,0350088	7,0214617	10	0,5014027	0,4973306	0,0350088	6,9821772
0,4884903	0,5145079	0,055296	11,319778	4	0,5115097	0,4854921	0,055296	10,810358
0,3417026	0,3370948	0,0548511	16,052277	8	0,6582974	0,6629052	0,0548511	8,3322607
0,4489104	0,4636127	0,0790593	17,611381	13	0,5510896	0,5363873	0,0790593	14,346001
0,4581834	0,4486187	0,0228461	4,9862399	5	0,5418166	0,5513813	0,0228461	4,2165782
0,6037771	0,6154446	0,0666445	11,037928	8	0,3962229	0,3845554	0,0666445	16,819944
0,5112086	0,5081297	0,0412438	8,0679019	5	0,4887914	0,4918703	0,0412438	8,4379159
0,6622502	0,6819145	0,0526374	7,9482669	4	0,3377498	0,3180855	0,0526374	15,584738
0,4749823	0,4749823	0,0143921	3,0300233	2	0,5250177	0,5250177	0,0143921	2,7412555
0,4919612	0,5128349	0,054553	11,088886	5	0,5080388	0,4871651	0,054553	10,737962
0,428446	0,4300239	0,0276605	6,456014	4	0,571554	0,5699761	0,0276605	4,8395308

0,4611529	0,4882527	0,0941481	20,415803	7	0,5388471	0,5117473	0,0941481	17,472129
0,5965971	0,6078241	0,0624925	10,47483	4	0,4034029	0,3921759	0,0624925	15,491346
0,4338099	0,4504407	0,054093	12,46929	7	0,5661901	0,5495593	0,054093	9,5538589
0,6321962	0,6284391	0,0449706	7,1133969	9	0,3678038	0,3715609	0,0449706	12,226797
0,4218447	0,423855	0,0453034	10,739353	4	0,5781553	0,576145	0,0453034	7,8358535
0,4859568	0,4927454	0,0454211	9,3467366	6	0,5140432	0,5072546	0,0454211	8,8360468
0,5280641	0,5279047	0,0655714	12,417325	4	0,4719359	0,4720953	0,0655714	13,89414
0,417129	0,4369588	0,0771134	18,486701	7	0,582871	0,5630412	0,0771134	13,229926
0,5542088	0,5385856	0,0348851	6,2945758	6	0,4457912	0,4614144	0,0348851	7,8254343
0,4822793	0,5002945	0,0524267	10,870617	5	0,5177207	0,4997055	0,0524267	10,126451
0,4074832	0,3962849	0,0896223	21,994116	5	0,5925168	0,6037151	0,0896223	15,125704
0,5013371	0,5343318	0,0645449	12,874552	5	0,4986629	0,4656682	0,0645449	12,943593
0,5719485	0,5799954	0,0495754	8,6678151	14	0,4280515	0,4200046	0,0495754	11,581653
0,4658433	0,4597999	0,033682	7,2303275	6	0,5341567	0,5402001	0,033682	6,3056385
0,489051	0,4893352	0,0291892	5,9685456	7	0,510949	0,5106648	0,0291892	5,7127479
0,5294003	0,5572947	0,0483452	9,1320658	3	0,4705997	0,4427053	0,0483452	10,2731
0,5056406	0,5070511	0,0955435	18,895532	4	0,4943594	0,4929489	0,0955435	19,326725
0,4515221	0,4729523	0,0592132	13,114134	5	0,5484779	0,5270477	0,0592132	10,795916
0,476927	0,4942781	0,0420382	8,8143906	4	0,523073	0,5057219	0,0420382	8,0367757
0,4285312	0,4291357	0,051398	11,994	6	0,5714688	0,5708643	0,051398	8,9940221
0,5869795	0,5757718	0,0476253	8,1136304	4	0,4130205	0,4242282	0,0476253	11,53099
0,5179179	0,52682	0,0309439	5,9746726	5	0,4820821	0,47318	0,0309439	6,4188027
0,5039354	0,5092567	0,0748508	14,853254	9	0,4960646	0,4907433	0,0748508	15,088923
0,5429056	0,5593467	0,0478636	8,8161901	6	0,4570944	0,4406533	0,0478636	10,471268
0,5815175	0,6016445	0,0613225	10,545247	5	0,4184825	0,3983555	0,0613225	14,65353
0,5990213	0,6057186	0,0769001	12,837624	5	0,4009787	0,3942814	0,0769001	19,178105
0,5170125	0,5045653	0,0307809	5,9536034	5	0,4829875	0,4954347	0,0307809	6,373017
0,5508381	0,5304966	0,0398813	7,2401113	9	0,4491619	0,4695034	0,0398813	8,8790468
0,4720157	0,4727656	0,0506491	10,730375	4	0,5279843	0,5272344	0,0506491	9,5929096
0,5007261	0,5049335	0,0455204	9,0908804	6	0,4992739	0,4950665	0,0455204	9,1173235
0,4988405	0,4932988	0,0544739	10,920099	4	0,5011595	0,5067012	0,0544739	10,86957
0,5999965	0,5865579	0,058389	9,7315545	4	0,4000035	0,4134421	0,058389	14,597117
0,4021108	0,3983852	0,0376399	9,3605697	5	0,5978892	0,6016148	0,0376399	6,2954575
0,5065056	0,5042664	0,021215	4,1885034	6	0,4934944	0,4957336	0,021215	4,2989352
0,520391	0,5059475	0,06106	11,733485	6	0,479609	0,4940525	0,06106	12,731206
0,4675294	0,4675294	0,0722405	15,451537	2	0,5324706	0,5324706	0,0722405	13,567036
0,5253938	0,5298592	0,0451836	8,5999422	8	0,4746062	0,4701408	0,0451836	9,520223
0,5361351	0,5226847	0,044435	8,2880186	5	0,4638649	0,4773153	0,044435	9,5792917
0,5245499	0,5156868	0,0312993	5,96689	8	0,4754501	0,4843132	0,0312993	6,5830913
0,2034101	0,2009642	0,0440276	21,644755	5	0,7965899	0,7990358	0,0440276	5,5270123
0,444203	0,4803669	0,0752764	16,946399	5	0,555797	0,5196331	0,0752764	13,543868
0,5401256	0,5704482	0,0564107	10,443993	7	0,4598744	0,4295518	0,0564107	12,266543
0,5243272	0,5141469	0,0722818	13,785624	12	0,4756728	0,4858531	0,0722818	15,195692
0,4665164	0,4665164	0,0038977	0,8354945	2	0,5334836	0,5334836	0,0038977	0,7306164
0,6369603	0,6276484	0,0561288	8,8119759	4	0,3630397	0,3723516	0,0561288	15,460786
0,5314215	0,5263847	0,0357159	6,7208331	5	0,4685785	0,4736153	0,0357159	7,6221904
0,5015931	0,498049	0,0544427	10,853948	6	0,4984069	0,501951	0,0544427	10,923336
0,4653196	0,4586872	0,0369663	7,9442756	4	0,5346804	0,5413128	0,0369663	6,9137145
0,4968584	0,5114618	0,0611278	12,30287	9	0,5031416	0,4885382	0,0611278	12,149233
0,4935901	0,490526	0,0558632	11,317724	10	0,5064099	0,509474	0,0558632	11,031217
0,4464169	0,4468347	0,0421901	9,4508299	4	0,5535831	0,5531653	0,0421901	7,6212761
0,5060474	0,4880364	0,1272703	25,149873	6	0,4939526	0,5119636	0,1272703	25,76569

0,5372154	0,5516113	0,0387397	7,2112053	4	0,4627846	0,4483887	0,0387397	8,3710026
0,446319	0,4401431	0,0564126	12,639515	3	0,553681	0,5598569	0,0564126	10,18864
0,5596524	0,5616755	0,0281899	5,0370415	5	0,4403476	0,4383245	0,0281899	6,4017437
0,6465194	0,632071	0,0819982	12,683028	7	0,3534806	0,367929	0,0819982	23,19738
0,467711	0,4794513	0,031068	6,6425694	4	0,532289	0,5205487	0,031068	5,8366834
0,4821937	0,5121243	0,0669105	13,87628	7	0,5178063	0,4878757	0,0669105	12,921924
0,4679647	0,4448793	0,0694888	14,849153	5	0,5320353	0,5551207	0,0694888	13,060935
0,540948	0,5654251	0,0556817	10,293361	6	0,459052	0,4345749	0,0556817	12,129722
0,486019	0,4759253	0,0990151	20,372685	3	0,513981	0,5240747	0,0990151	19,264355
0,4638937	0,4600388	0,1042931	22,482102	4	0,5361063	0,5399612	0,1042931	19,453801
0,5696773	0,5896762	0,0585013	10,269194	6	0,4303227	0,4103238	0,0585013	13,594742
0,5921666	0,635672	0,0958133	16,180122	5	0,4078334	0,364328	0,0958133	23,493236
0,4692835	0,5063955	0,1393287	29,689655	6	0,5307165	0,4936045	0,1393287	26,252939
0,5330123	0,5257538	0,0829439	15,561344	3	0,4669877	0,4742462	0,0829439	17,761467
0,5108247	0,5070141	0,0536798	10,508453	5	0,4891753	0,4929859	0,0536798	10,973525
0,6264538	0,6843683	0,0963924	15,386988	5	0,3735462	0,3156317	0,0963924	25,804674
0,4421662	0,4543328	0,037289	8,4332541	4	0,5578338	0,5456672	0,037289	6,6846083
0,4228836	0,4189395	0,0642625	15,196268	6	0,5771164	0,5810605	0,0642625	11,135105
0,4553017	0,4624295	0,0480634	10,556387	4	0,5446983	0,5375705	0,0480634	8,8238598
0,6203006	0,6662331	0,1130708	18,228381	4	0,3796994	0,3337669	0,1130708	29,779016
0,4813156	0,4409749	0,1068607	22,201786	4	0,5186844	0,5590251	0,1068607	20,602248
0,5119856	0,5297161	0,0953584	18,625207	3	0,4880144	0,4702839	0,0953584	19,540077
0,5371105	0,5395021	0,0332929	6,198526	4	0,4628895	0,4604979	0,0332929	7,1924152
0,5235233	0,4974829	0,0497685	9,5064621	7	0,4764767	0,5025171	0,0497685	10,445117
0,5396058	0,5347127	0,0637622	11,816448	5	0,4603942	0,4652873	0,0637622	13,849487
0,4664683	0,4474367	0,1189589	25,502025	4	0,5335317	0,5525633	0,1189589	22,296495
0,4340326	0,4467824	0,0438079	10,093234	4	0,5659674	0,5532176	0,0438079	7,7403625
0,4950726	0,5366381	0,093195	18,824518	8	0,5049274	0,4633619	0,093195	18,457115
0,5219224	0,5286687	0,0189889	3,6382534	4	0,4780776	0,4713313	0,0189889	3,9719201
0,464481	0,4771654	0,0598324	12,881558	3	0,535519	0,5228346	0,0598324	11,172786
0,4681251	0,4887223	0,0380884	8,1363731	3	0,5318749	0,5112777	0,0380884	7,1611598
0,5104911	0,518263	0,0432208	8,4665223	4	0,4895089	0,481737	0,0432208	8,8294284
0,566908	0,5721427	0,0339717	5,9924524	6	0,433092	0,4278573	0,0339717	7,8439891
0,4834672	0,4845859	0,0821812	16,998308	4	0,5165328	0,5154141	0,0821812	15,91017
0,4686345	0,4597069	0,0425035	9,0696413	6	0,5313655	0,5402931	0,0425035	7,9989134
0,593985	0,6090294	0,0442559	7,4506798	8	0,406015	0,3909706	0,0442559	10,90007
0,7129594	0,7003613	0,043808	6,1445243	4	0,2870406	0,2996387	0,043808	15,26194
0,3971743	0,377319	0,0535018	13,470603	5	0,6028257	0,622681	0,0535018	8,8751661
0,4866284	0,5009305	0,0399674	8,2131262	3	0,5133716	0,4990695	0,0399674	7,7852772
0,570325	0,5704394	0,0342301	6,0018624	7	0,429675	0,4295606	0,0342301	7,9665134
0,4051697	0,4088576	0,0209658	5,1745707	4	0,5948303	0,5911424	0,0209658	3,5246685
0,5294866	0,5346946	0,0256713	4,8483473	6	0,4705134	0,4653054	0,0256713	5,4560292
0,5829318	0,5819534	0,0314207	5,3901103	4	0,4170682	0,4180466	0,0314207	7,5337
0,5635703	0,5709094	0,0379648	6,7364774	6	0,4364297	0,4290906	0,0379648	8,6989474
0,5227975	0,5280009	0,0857632	16,404679	3	0,4772025	0,4719991	0,0857632	17,972086
0,4916968	0,4906517	0,034097	6,9345556	7	0,5083032	0,5093483	0,034097	6,708002
0,648506	0,6519431	0,0244115	3,764262	4	0,351494	0,3480569	0,0244115	6,9450582
0,6082751	0,5971532	0,0659742	10,846113	4	0,3917249	0,4028468	0,0659742	16,841976
0,5300171	0,5320887	0,0485414	9,158454	6	0,4699829	0,4679113	0,0485414	10,328325
0,4653723	0,4653723	0,054501	11,711277	2	0,5346277	0,5346277	0,054501	10,194206
0,5980088	0,6037646	0,0443978	7,4242802	6	0,4019912	0,3962354	0,0443978	11,044481
0,4658055	0,4549267	0,0798635	17,145237	3	0,5341945	0,5450733	0,0798635	14,950259

0,6219805	0,6271244	0,0282452	4,5411687	10	0,3780195	0,3728756	0,0282452	7,4718849
0,4799496	0,4765193	0,0179165	3,7329942	3	0,5200504	0,5234807	0,0179165	3,4451448
0,4440447	0,4435015	0,0457805	10,309893	7	0,5559553	0,5564985	0,0457805	8,2345712
0,5493078	0,5445919	0,0457668	8,3317168	3	0,4506922	0,4554081	0,0457668	10,154771
0,4664777	0,444561	0,0904096	19,381331	3	0,5335223	0,555439	0,0904096	16,945795
0,5886036	0,5872329	0,0570934	9,699811	3	0,4113964	0,4127671	0,0570934	13,877961
0,5321901	0,572718	0,0716385	13,461068	3	0,4678099	0,427282	0,0716385	15,313583
0,5041353	0,5181954	0,0506372	10,044376	11	0,4958647	0,4818046	0,0506372	10,211908
0,5087612	0,5013479	0,0633199	12,445902	5	0,4912388	0,4986521	0,0633199	12,889846
0,5015582	0,4923404	0,025454	5,0749853	5	0,4984418	0,5076596	0,025454	5,1067164
0,3856866	0,3616592	0,0669964	17,370679	3	0,6143134	0,6383408	0,0669964	10,905895
0,4638097	0,4804307	0,0363226	7,8313551	3	0,5361903	0,5195693	0,0363226	6,7741971
0,503057	0,5165293	0,0277166	5,5096335	4	0,496943	0,4834707	0,0277166	5,5774188
0,6524062	0,6545176	0,0299573	4,5918248	6	0,3475938	0,3454824	0,0299573	8,618493
0,4650021	0,4861234	0,072562	15,604653	7	0,5349979	0,5138766	0,072562	13,563037
0,4459361	0,4324925	0,0875173	19,625516	3	0,5540639	0,5675075	0,0875173	15,795517
0,4332397	0,4210013	0,042992	9,9233811	3	0,5667603	0,5789987	0,042992	7,5855761
0,4495432	0,4435602	0,0447365	9,9515473	3	0,5504568	0,5564398	0,0447365	8,1271592
0,5860506	0,5566834	0,1052319	17,956113	3	0,4139494	0,4433166	0,1052319	25,42144
0,5011004	0,5336378	0,0973892	19,435061	3	0,4988996	0,4663622	0,0973892	19,520795
0,5851641	0,6028554	0,0672682	11,495618	5	0,4148359	0,3971446	0,0672682	16,215621
0,3809188	0,3696826	0,0240725	6,3195891	3	0,6190812	0,6303174	0,0240725	3,8884243
0,4277669	0,4273317	0,0244849	5,7238948	4	0,5722331	0,5726683	0,0244849	4,2788379
0,6479118	0,6699573	0,0559766	8,6395394	4	0,3520882	0,3300427	0,0559766	15,898461
0,5614648	0,516376	0,0826061	14,712607	3	0,4385352	0,483624	0,0826061	18,836829
0,4932866	0,5110207	0,0643409	13,043304	3	0,5067134	0,4889793	0,0643409	12,697686
0,5472991	0,5592499	0,0360848	6,5932533	6	0,4527009	0,4407501	0,0360848	7,9710063
0,45119	0,4678938	0,0370377	8,2088869	3	0,54881	0,5321062	0,0370377	6,7487245
0,5297085	0,5330559	0,0267005	5,0406073	5	0,4702915	0,4669441	0,0267005	5,677442
0,4301829	0,4412589	0,0396848	9,2251034	5	0,5698171	0,5587411	0,0396848	6,9644825
0,3922858	0,4030964	0,0245929	6,2691191	3	0,6077142	0,5969036	0,0245929	4,0467814
0,5022834	0,4894583	0,0658393	13,107997	4	0,4977166	0,5105417	0,0658393	13,228271
0,3249986	0,3285372	0,0162796	5,0091202	3	0,6750014	0,6714628	0,0162796	2,4117834
0,5378505	0,5162131	0,0703757	13,084628	3	0,4621495	0,4837869	0,0703757	15,227917
0,4639357	0,4623872	0,0357078	7,6967065	5	0,5360643	0,5376128	0,0357078	6,6610979
0,4239197	0,4314686	0,0521789	12,308683	3	0,5760803	0,5685314	0,0521789	9,0575808
0,5300904	0,5500585	0,0363666	6,8604551	3	0,4699096	0,4499415	0,0363666	7,7390645
0,525494	0,5219531	0,0294157	5,5977315	3	0,474506	0,4780469	0,0294157	6,1992359
0,5299973	0,5272734	0,0217269	4,0994279	4	0,4700027	0,4727266	0,0217269	4,6227092
0,507177	0,5081848	0,0765812	15,099506	4	0,492823	0,4918152	0,0765812	15,539296
0,5203437	0,5265744	0,0270146	5,1916765	3	0,4796563	0,4734256	0,0270146	5,6320664
0,6952354	0,6952354	0,0069273	0,9963918	2	0,3047646	0,3047646	0,0069273	2,2729904
0,4186467	0,4186467	0,0535416	12,789219	2	0,5813533	0,5813533	0,0535416	9,2098305
0,4625486	0,4808623	0,0369958	7,998247	3	0,5374514	0,5191377	0,0369958	6,8835568
0,535397	0,5384392	0,0388058	7,2480331	4	0,464603	0,4615608	0,0388058	8,3524543
0,5692907	0,5533359	0,0313003	5,4981149	3	0,4307093	0,4466641	0,0313003	7,2671408
0,5471376	0,5506159	0,0087457	1,5984467	3	0,4528624	0,4493841	0,0087457	1,9312057
0,6697888	0,6669678	0,0089626	1,3381269	3	0,3302112	0,3330322	0,0089626	2,7142093
0,4755244	0,4818344	0,0526764	11,077537	3	0,5244756	0,5181656	0,0526764	10,043629
0,5337215	0,5231458	0,0324014	6,0708378	3	0,4662785	0,4768542	0,0324014	6,9489289
0,5157333	0,5157333	0,0559021	10,839333	2	0,4842667	0,4842667	0,0559021	11,54365
0,5290606	0,5091396	0,0756592	14,300667	4	0,4709394	0,4908604	0,0756592	16,065593

0,4885982	0,5044653	0,0418838	8,5722298	4	0,5114018	0,4955347	0,0418838	8,1899913
0,4871408	0,4890443	0,0478055	9,8134863	5	0,5128592	0,5109557	0,0478055	9,3213672
0,4477487	0,4477487	0,0346607	7,7411011	2	0,5522513	0,5522513	0,0346607	6,2762503
0,5668432	0,5778289	0,052222	9,2127692	5	0,4331568	0,4221711	0,052222	12,056131
0,5045013	0,5301947	0,1474367	29,224255	3	0,4954987	0,4698053	0,1474367	29,755222
0,4905847	0,4905847	0,088754	18,091473	2	0,5094153	0,5094153	0,088754	17,422722
0,5785723	0,5785723	0,0902016	15,590385	2	0,4214277	0,4214277	0,0902016	21,403824
0,5356208	0,558059	0,0535492	9,9975884	3	0,4643792	0,441941	0,0535492	11,531342
0,6494329	0,6561881	0,070909	10,918595	3	0,3505671	0,3438119	0,070909	20,226927
0,5752031	0,5764958	0,028777	5,0029341	5	0,4247969	0,4235042	0,028777	6,7743025
0,4893382	0,4881567	0,0250835	5,1260137	3	0,5106618	0,5118433	0,0250835	4,9119683
0,4904685	0,4891831	0,0147805	3,0135386	4	0,5095315	0,5108169	0,0147805	2,9007942
0,5695086	0,5703694	0,0138567	2,4330944	4	0,4304914	0,4296306	0,0138567	3,2188062
0,5909651	0,5909651	0,035118	5,9424812	2	0,4090349	0,4090349	0,035118	8,5855726
0,432337	0,4200707	0,0213114	4,9293439	3	0,567663	0,5799293	0,0213114	3,7542305
0,530154	0,5288256	0,0171035	3,2261324	5	0,469846	0,4711744	0,0171035	3,6402286
0,517289	0,5174085	0,0453958	8,7757035	4	0,482711	0,4825915	0,0453958	9,4043341
0,4769856	0,4722149	0,0447254	9,3766745	3	0,5230144	0,5277851	0,0447254	8,5514621
0,5708907	0,5782254	0,0425433	7,4520952	3	0,4291093	0,4217746	0,0425433	9,9143313
0,4490499	0,4256134	0,0445527	9,921546	3	0,5509501	0,5743866	0,0445527	8,0865212
0,4216031	0,4216031	0,1095587	25,986228	2	0,5783969	0,5783969	0,1095587	18,941791
0,4472022	0,4529493	0,0480949	10,754622	3	0,5527978	0,5470507	0,0480949	8,7002729
0,5599208	0,5479217	0,0322629	5,762038	3	0,4400792	0,4520783	0,0322629	7,3311474
0,5205696	0,5199457	0,0094448	1,8143279	4	0,4794304	0,4800543	0,0094448	1,9700124
0,4601545	0,4580807	0,0504153	10,956159	5	0,5398455	0,5419193	0,0504153	9,3388296
0,630041	0,6156599	0,0342691	5,4391805	3	0,369959	0,3843401	0,0342691	9,2629364
0,4951701	0,4565776	0,0681616	13,765296	5	0,5048299	0,5434224	0,0681616	13,501899
0,6391614	0,6490003	0,02774	4,3400662	7	0,3608386	0,3509997	0,02774	7,687654
0,5068879	0,5124813	0,0585001	11,541039	3	0,4931121	0,4875187	0,0585001	11,863453
0,5460224	0,5708089	0,1501349	27,496111	3	0,4539776	0,4291911	0,1501349	33,071004
0,4332961	0,4391164	0,0235439	5,4336728	4	0,5667039	0,5608836	0,0235439	4,1545311
0,490966	0,4873225	0,0393344	8,0116433	7	0,509034	0,5126775	0,0393344	7,7272723
0,4635572	0,4438193	0,0501944	10,828082	5	0,5364428	0,5561807	0,0501944	9,3568894
0,4679014	0,4679014	0,0179729	3,8411746	2	0,5320986	0,5320986	0,0179729	3,37774
0,4809404	0,4470166	0,070246	14,605963	3	0,5190596	0,5529834	0,070246	13,533315
0,4445155	0,4471247	0,060815	13,681186	4	0,5554845	0,5528753	0,060815	10,9481
0,5399615	0,5549999	0,0716851	13,275971	4	0,4600385	0,4450001	0,0716851	15,582418
0,5014927	0,5205785	0,0352189	7,0228046	3	0,4985073	0,4794215	0,0352189	7,0648632
0,5076458	0,4915043	0,0509308	10,032733	4	0,4923542	0,5084957	0,0509308	10,344333
0,6488914	0,6376611	0,0406076	6,258004	3	0,3511086	0,3623389	0,0406076	11,565551
0,4804364	0,4812322	0,012886	2,6821418	4	0,5195636	0,5187678	0,012886	2,4801556
0,503577	0,4603308	0,0818519	16,254092	5	0,496423	0,5396692	0,0818519	16,488333
0,4539055	0,4346365	0,0529555	11,666643	3	0,5460945	0,5653635	0,0529555	9,6971362
0,5807249	0,5807249	0,0148664	2,5599736	2	0,4192751	0,4192751	0,0148664	3,5457395
0,6095846	0,5959107	0,02705	4,437453	3	0,3904154	0,4040893	0,02705	6,9285264
0,5389982	0,5436643	0,0348586	6,4673026	3	0,4610018	0,4563357	0,0348586	7,5614979
0,4639836	0,4466321	0,0490235	10,565784	3	0,5360164	0,5533679	0,0490235	9,1458955
0,3909981	0,4150392	0,0440455	11,264889	3	0,6090019	0,5849608	0,0440455	7,2324068
0,4906233	0,5043548	0,0557178	11,356541	3	0,5093767	0,4956452	0,0557178	10,938434
0,5296698	0,5430774	0,0343087	6,477384	3	0,4703302	0,4569226	0,0343087	7,2946085
0,3483076	0,3518224	0,0702405	20,166232	3	0,6516924	0,6481776	0,0702405	10,778172
0,5879269	0,589012	0,0561291	9,5469544	3	0,4120731	0,410988	0,0561291	13,621156

0,4425444	0,4429468	0,0311799	7,0456037	3	0,5574556	0,5570532	0,0311799	5,5932566
0,571201	0,6036233	0,1390893	24,350328	6	0,428799	0,3963767	0,1390893	32,436947
0,5214777	0,5214777	0,1183336	22,691971	2	0,4785223	0,4785223	0,1183336	24,728959
0,5109132	0,5390602	0,0836743	16,377409	3	0,4890868	0,4609398	0,0836743	17,108282
0,4248265	0,4252627	0,0729838	17,179666	4	0,5751735	0,5747373	0,0729838	12,689004
0,5142928	0,5251411	0,0252209	4,9039899	3	0,4857072	0,4748589	0,0252209	5,1926081
0,5914539	0,6072959	0,030004	5,0729236	3	0,4085461	0,3927041	0,030004	7,3440921
0,6174542	0,6174542	0,0665077	10,771281	2	0,3825458	0,3825458	0,0665077	17,38556
0,5844457	0,5772843	0,0316823	5,4209214	6	0,4155543	0,4227157	0,0316823	7,6241163
0,4857487	0,511149	0,0584582	12,034649	3	0,5142513	0,488851	0,0584582	11,367625
0,4042234	0,4042234	0,0402226	9,9505757	2	0,5957766	0,5957766	0,0402226	6,7512806
0,5441128	0,5436385	0,0270021	4,9625977	4	0,4558872	0,4563615	0,0270021	5,9229845
0,375028	0,3673441	0,0371066	9,8943603	4	0,624972	0,6326559	0,0371066	5,9373258
0,4919524	0,4919524	0,0504963	10,264476	2	0,5080476	0,5080476	0,0504963	9,9392911
0,633003	0,6257059	0,0173917	2,7474853	3	0,366997	0,3742941	0,0173917	4,7389121
0,3469166	0,3469166	0,0226445	6,5273646	2	0,6530834	0,6530834	0,0226445	3,4673232
0,4815653	0,4815653	0,0048714	1,0115812	2	0,5184347	0,5184347	0,0048714	0,9396409
0,431985	0,4267465	0,0155487	3,5993516	3	0,568015	0,5732535	0,0155487	2,7373676
0,5953888	0,5969823	0,0424275	7,1260096	4	0,4046112	0,4030177	0,0424275	10,485985
0,7160932	0,7160932	0,0738233	10,309169	2	0,2839068	0,2839068	0,0738233	26,002634
0,5610925	0,5641876	0,0268984	4,7939421	4	0,4389075	0,4358124	0,0268984	6,1284996
0,6707455	0,6723632	0,0097662	1,4560235	3	0,3292545	0,3276368	0,0097662	2,9661585
0,5171621	0,5171621	0,0978934	18,928953	2	0,4828379	0,4828379	0,0978934	20,274582
0,5606974	0,5542937	0,0395236	7,0489998	3	0,4393026	0,4457063	0,0395236	8,9968879
0,4925778	0,4943396	0,0380322	7,7210597	5	0,5074222	0,5056604	0,0380322	7,4951823
0,5138285	0,5015852	0,0346413	6,7417984	8	0,4861715	0,4984148	0,0346413	7,1253215
0,4930702	0,4930702	0,0049445	1,0027914	2	0,5069298	0,5069298	0,0049445	0,975375
0,4185798	0,4123969	0,0202219	4,8310844	3	0,5814202	0,5876031	0,0202219	3,4780253
0,5309853	0,5619446	0,0590993	11,130114	3	0,4690147	0,4380554	0,0590993	12,600731
0,4662357	0,4662357	0,1816122	38,952862	2	0,5337643	0,5337643	0,1816122	34,024788
0,5411646	0,5351574	0,0337609	6,2385576	3	0,4588354	0,4648426	0,0337609	7,3579482
0,5842259	0,5842259	0,0451965	7,736129	2	0,4157741	0,4157741	0,0451965	10,870439
0,4910015	0,4910015	0,015171	3,0898023	2	0,5089985	0,5089985	0,015171	2,9805543
0,4560356	0,4590954	0,0498964	10,941347	3	0,5439644	0,5409046	0,0498964	9,1727394
0,3401043	0,3401043	0,3020139	88,800378	2	0,6598957	0,6598957	0,3020139	45,766924
0,5011541	0,5011541	0,0507182	10,12029	2	0,4988459	0,4988459	0,0507182	10,167117
0,5047365	0,5464923	0,0853318	16,906199	3	0,4952635	0,4535077	0,0853318	17,229569
0,4614707	0,4614707	0,0917395	19,879812	2	0,5385293	0,5385293	0,0917395	17,035193
0,6619168	0,690871	0,059532	8,9938743	3	0,3380832	0,309129	0,059532	17,608676
0,4442513	0,4442513	0,0156822	3,5300339	2	0,5557487	0,5557487	0,0156822	2,8218186
0,4801257	0,473139	0,0499881	10,41147	3	0,5198743	0,526861	0,0499881	9,6154286
0,4918996	0,4918996	0,0295758	6,0125603	2	0,5081004	0,5081004	0,0295758	5,8208502
0,4674153	0,4653274	0,0199474	4,2675861	3	0,5325847	0,5346726	0,0199474	3,7453861
0,5247341	0,517881	0,0280503	5,3456129	3	0,4752659	0,482119	0,0280503	5,902012
0,4119097	0,4119097	0,0321519	7,8055797	2	0,5880903	0,5880903	0,0321519	5,4671777
0,5312261	0,5312261	0,0056369	1,0611113	2	0,4687739	0,4687739	0,0056369	1,2024775
0,5483207	0,5620066	0,0412953	7,5312258	3	0,4516793	0,4379934	0,0412953	9,1426073
0,3000275	0,314238	0,0469606	15,652105	3	0,6999725	0,685762	0,0469606	6,7089234
0,5255761	0,5261909	0,0111236	2,1164567	3	0,4744239	0,4738091	0,0111236	2,3446524
0,4964647	0,5166155	0,0537338	10,823286	4	0,5035353	0,4833845	0,0537338	10,671307
0,4851867	0,4612114	0,0463905	9,5613703	3	0,5148133	0,5387886	0,0463905	9,0111288
0,439182	0,4437294	0,0315261	7,1783634	4	0,560818	0,5562706	0,0315261	5,6214462

0,5486517	0,5486517	0,0226904	4,1356674	2	0,4513483	0,4513483	0,0226904	5,0272506
0,5865321	0,5732158	0,046233	7,8824368	3	0,4134679	0,4267842	0,046233	11,18177
0,4046424	0,4046424	0,0652472	16,12466	2	0,5953576	0,5953576	0,0652472	10,959332
0,420644	0,420644	0,1150548	27,352068	2	0,579356	0,579356	0,1150548	19,85909
0,5929378	0,5929378	0,0179354	3,0248342	2	0,4070622	0,4070622	0,0179354	4,4060547
0,3856584	0,3804259	0,0600482	15,570302	3	0,6143416	0,6195741	0,0600482	9,7743931
0,4727046	0,4727046	0,0255978	5,4151877	2	0,5272954	0,5272954	0,0255978	4,8545549
0,4322962	0,4322962	0,0703465	16,272744	2	0,5677038	0,5677038	0,0703465	12,391402
0,481335	0,481335	0,0276989	5,7545958	2	0,518665	0,518665	0,0276989	5,3404181
0,5025272	0,5025272	0,0339457	6,7550005	2	0,4974728	0,4974728	0,0339457	6,8236314
0,6700759	0,6706364	0,0238346	3,5570039	4	0,3299241	0,3293636	0,0238346	7,2242771
0,4871837	0,4871837	0,0600686	12,329764	2	0,5128163	0,5128163	0,0600686	11,713474
0,4182404	0,4183848	0,0030927	0,7394551	3	0,5817596	0,5816152	0,0030927	0,5316112
0,5074957	0,5074957	0,0282449	5,5655458	2	0,4925043	0,4925043	0,0282449	5,7349572
0,43627	0,4392039	0,0278228	6,3774383	3	0,56373	0,5607961	0,0278228	4,9354913
0,442581	0,4545221	0,033515	7,5726192	3	0,557419	0,5454779	0,033515	6,0125275
0,659298	0,659298	0,1764011	26,755904	2	0,340702	0,340702	0,1764011	51,775788
0,3241646	0,3241646	0,1296402	39,992095	2	0,6758354	0,6758354	0,1296402	19,182221
0,3801412	0,3655148	0,0384029	10,102266	4	0,6198588	0,6344852	0,0384029	6,195423
0,5012282	0,5012282	0,0193281	3,8561545	2	0,4987718	0,4987718	0,0193281	3,875146
0,5300709	0,5300709	0,0714952	13,487856	2	0,4699291	0,4699291	0,0714952	15,214039
0,485278	0,4626358	0,0830664	17,117276	3	0,514722	0,5373642	0,0830664	16,138104
0,5259142	0,5259142	0,0511897	9,733461	2	0,4740858	0,4740858	0,0511897	10,79755
0,5964768	0,5879683	0,0217626	3,6485303	3	0,4035232	0,4120317	0,0217626	5,3931566
0,5680508	0,5680508	0,0860781	15,153248	2	0,4319492	0,4319492	0,0860781	19,927841
0,4665448	0,4907114	0,0427139	9,1553698	3	0,5334552	0,5092886	0,0427139	8,0070268
0,4324858	0,4324858	0,0919477	21,26027	2	0,5675142	0,5675142	0,0919477	16,201824
0,4578059	0,4720754	0,0387426	8,4626799	3	0,5421941	0,5279246	0,0387426	7,1455311
0,5831526	0,5831526	0,0428198	7,3428065	2	0,4168474	0,4168474	0,0428198	10,272289
0,4565246	0,4565246	0,05445	11,92706	2	0,5434754	0,5434754	0,05445	10,018848
0,4403453	0,4154505	0,0458726	10,417423	3	0,5596547	0,5845495	0,0458726	8,1965967
0,4056754	0,4056754	0,0021322	0,5255894	2	0,5943246	0,5943246	0,0021322	0,358758
0,5519079	0,576759	0,0520181	9,4251433	3	0,4480921	0,423241	0,0520181	11,608798
0,3894184	0,3894184	0,0085692	2,2005069	2	0,6105816	0,6105816	0,0085692	1,403445
0,5304159	0,5134707	0,0783211	14,765976	5	0,4695841	0,4865293	0,0783211	16,678817
0,4980551	0,4980551	0,0561296	11,269748	2	0,5019449	0,5019449	0,0561296	11,182415
0,4863243	0,4699645	0,0448418	9,2205487	3	0,5136757	0,5300355	0,0448418	8,7295857
0,4432604	0,4465895	0,017657	3,9834331	3	0,5567396	0,5534105	0,017657	3,1714972
0,4725073	0,4482522	0,0555141	11,748839	4	0,5274927	0,5517478	0,0555141	10,524149
0,6188564	0,6051449	0,0765303	12,366405	4	0,3811436	0,3948551	0,0765303	20,079119
0,508008	0,508008	0,0384271	7,5642657	2	0,491992	0,491992	0,0384271	7,8105065
0,7288782	0,7288782	0,0518653	7,1157711	2	0,2711218	0,2711218	0,0518653	19,129886
0,6254153	0,5956785	0,1134084	18,133299	3	0,3745847	0,4043215	0,1134084	30,275771
0,6312892	0,6312892	0,0098001	1,5523995	2	0,3687108	0,3687108	0,0098001	2,6579455
0,4238672	0,4219179	0,0127047	2,9973191	3	0,5761328	0,5780821	0,0127047	2,2051603
0,5599055	0,5228578	0,0825712	14,747342	4	0,4400945	0,4771422	0,0825712	18,762146
0,4725063	0,4725063	0,0830622	17,579065	2	0,5274937	0,5274937	0,0830622	15,746577
0,4843607	0,4843607	0,0744169	15,363945	2	0,5156393	0,5156393	0,0744169	14,431969
0,4455481	0,4455481	0,0704317	15,80788	2	0,5544519	0,5544519	0,0704317	12,702942
0,5767078	0,5767078	0,0534545	9,2688983	2	0,4232922	0,4232922	0,0534545	12,628262
0,4278832	0,421094	0,0354969	8,2959392	3	0,5721168	0,578906	0,0354969	6,2044894
0,4983054	0,4983054	0,0449294	9,0164421	2	0,5016946	0,5016946	0,0449294	8,9555305

0,5066011	0,4972072	0,0434675	8,5802293	5	0,4933989	0,5027928	0,0434675	8,8098177
0,5395637	0,5395637	0,0365445	6,7729689	2	0,4604363	0,4604363	0,0365445	7,9369258
0,4935304	0,4928172	0,0125657	2,5460819	3	0,5064696	0,5071828	0,0125657	2,4810348
0,4520819	0,4520819	0,0854196	18,894722	2	0,5479181	0,5479181	0,0854196	15,589849
0,5609425	0,5609425	0,0253597	4,5209038	2	0,4390575	0,4390575	0,0253597	5,7759346
0,6069435	0,6069435	0,0397345	6,546653	2	0,3930565	0,3930565	0,0397345	10,109101
0,5007211	0,5007211	0,086559	17,286858	2	0,4992789	0,4992789	0,086559	17,336796
0,557241	0,557241	0,0022259	0,3994546	2	0,442759	0,442759	0,0022259	0,5027396
0,5048907	0,5069236	0,0048968	0,9698806	3	0,4951093	0,4930764	0,0048968	0,9890415
0,4424138	0,4456846	0,0448902	10,14666	5	0,5575862	0,5543154	0,0448902	8,0508131
0,5023778	0,5023778	0,0440951	8,777288	2	0,4976222	0,4976222	0,0440951	8,8611691
0,4165689	0,4165689	0,0434106	10,421	2	0,5834311	0,5834311	0,0434106	7,4405787
0,4417417	0,4417417	0,0363206	8,2221397	2	0,5582583	0,5582583	0,0363206	6,5060587
0,4722139	0,457608	0,0781282	16,545095	4	0,5277861	0,542392	0,0781282	14,803008
0,4572421	0,4572421	0,0653853	14,299938	2	0,5427579	0,5427579	0,0653853	12,046871
0,6716849	0,6716849	0,0028937	0,4308193	2	0,3283151	0,3283151	0,0028937	0,8813936
0,3893205	0,3893205	0,0367153	9,4306188	2	0,6106795	0,6106795	0,0367153	6,0122105
0,558258	0,5586048	0,0496545	8,8945465	3	0,441742	0,4413952	0,0496545	11,240615
0,5866837	0,5866837	0,0891092	15,188621	2	0,4133163	0,4133163	0,0891092	21,559557
0,8045777	0,8377703	0,0832598	10,348261	3	0,1954223	0,1622297	0,0832598	42,605068
0,5072798	0,5075424	0,0413893	8,1590598	3	0,4927202	0,4924576	0,0413893	8,4001549
0,4588119	0,4588119	0,0251306	5,4773145	2	0,5411881	0,5411881	0,0251306	4,6435929
0,5271726	0,5271726	0,0097986	1,8587015	2	0,4728274	0,4728274	0,0097986	2,0723344
0,4555692	0,4555692	0,097747	21,456025	2	0,5444308	0,5444308	0,097747	17,953989
0,4476647	0,4546913	0,0235242	5,2548617	3	0,5523353	0,5453087	0,0235242	4,2590362
0,5294763	0,5131199	0,0401487	7,5827238	4	0,4705237	0,4868801	0,0401487	8,5327729
0,5584925	0,5346779	0,0508494	9,1047692	4	0,4415075	0,4653221	0,0508494	11,517233
0,3471618	0,3578098	0,0246605	7,1034643	4	0,6528382	0,6421902	0,0246605	3,7774319
0,4788902	0,4865441	0,0714405	14,917924	4	0,5211098	0,5134559	0,0714405	13,709296
0,5513749	0,5787498	0,0489301	8,8741891	5	0,4486251	0,4212502	0,0489301	10,906669
0,4923781	0,4965636	0,0217892	4,4252924	4	0,5076219	0,5034364	0,0217892	4,2924023
0,4759656	0,4946745	0,0438133	9,205142	4	0,5240344	0,5053255	0,0438133	8,3607696
0,54398	0,54398	0,0053853	0,9899737	2	0,45602	0,45602	0,0053853	1,1809259
0,5848304	0,5881884	0,0293368	5,0162932	3	0,4151696	0,4118116	0,0293368	7,0662225
0,5646097	0,5750811	0,1022481	18,109527	4	0,4353903	0,4249189	0,1022481	23,484246
0,6175465	0,6175465	0,0291527	4,720726	2	0,3824535	0,3824535	0,0291527	7,6225426
0,495451	0,4892017	0,0262731	5,3028615	4	0,504549	0,5107983	0,0262731	5,2072416
0,5082001	0,470519	0,0875114	17,21988	3	0,4917999	0,529481	0,0875114	17,794118
0,5787476	0,5787476	0,0364026	6,289887	2	0,4212524	0,4212524	0,0364026	8,64151
0,4923941	0,4923941	0,0323866	6,5773657	2	0,5076059	0,5076059	0,0323866	6,3802572
0,3980487	0,3856135	0,0311654	7,8295543	4	0,6019513	0,6143865	0,0311654	5,1774018
0,3727089	0,3727089	0,0202011	5,4200872	2	0,6272911	0,6272911	0,0202011	3,2203786
0,5222567	0,5222567	0,1636123	31,327952	2	0,4777433	0,4777433	0,1636123	34,246906
0,4806848	0,4715874	0,0479332	9,9718587	3	0,5193152	0,5284126	0,0479332	9,2300818
0,4948395	0,4948395	0,0211128	4,2665914	2	0,5051605	0,5051605	0,0211128	4,1794208
0,4394652	0,4394652	0,0474244	10,791392	2	0,5605348	0,5605348	0,0474244	8,4605652
0,4244419	0,4244419	0,0522196	12,303131	2	0,5755581	0,5755581	0,0522196	9,072872
0,4007861	0,4007861	0,0569259	14,203558	2	0,5992139	0,5992139	0,0569259	9,500093
0,5694597	0,5694597	0,0680525	11,950364	2	0,4305403	0,4305403	0,0680525	15,806303
0,4892272	0,4892272	0,0924302	18,893094	2	0,5107728	0,5107728	0,0924302	18,096138
0,4882435	0,4882435	0,0483846	9,9099399	2	0,5117565	0,5117565	0,0483846	9,4546224
0,5808394	0,5768604	0,1028062	17,699591	6	0,4191606	0,4231396	0,1028062	24,526686

0,5461878	0,5461878	0,0363635	6,657692	2	0,4538122	0,4538122	0,0363635	8,0128951
0,4030485	0,4030485	0,0450188	11,169568	2	0,5969515	0,5969515	0,0450188	7,5414472
0,502469	0,4865058	0,0289777	5,7670558	3	0,497531	0,5134942	0,0289777	5,824294
0,6600837	0,6600837	0,0753024	11,408009	2	0,3399163	0,3399163	0,0753024	22,153222
0,5383564	0,5383564	0,0265114	4,9245102	2	0,4616436	0,4616436	0,0265114	5,7428309
0,5848283	0,5708638	0,0309224	5,2874289	3	0,4151717	0,4291362	0,0309224	7,4480936
0,5312037	0,5312037	0,0362177	6,8180402	2	0,4687963	0,4687963	0,0362177	7,7256747
0,4824921	0,5060006	0,0418572	8,6752114	3	0,5175079	0,4939994	0,0418572	8,0882268
0,488084	0,488084	0,0005193	0,1064008	2	0,511916	0,511916	0,0005193	0,1014473
0,4298067	0,4262276	0,0324735	7,5553838	4	0,5701933	0,5737724	0,0324735	5,695181
0,4267844	0,4267844	0,078758	18,453818	2	0,5732156	0,5732156	0,078758	13,739684
0,5678108	0,5678108	0,0826894	14,562836	2	0,4321892	0,4321892	0,0826894	19,132674
0,3776169	0,3896582	0,0361168	9,5643898	3	0,6223831	0,6103418	0,0361168	5,8029772
0,5358796	0,5358796	0,0973959	18,17496	2	0,4641204	0,4641204	0,0973959	20,985052
0,4811405	0,4886968	0,0197221	4,0990295	3	0,5188595	0,5113032	0,0197221	3,8010469
0,4927204	0,4927204	0,1218533	24,730727	2	0,5072796	0,5072796	0,1218533	24,020943
0,4730515	0,4534735	0,0358923	7,5873963	3	0,5269485	0,5465265	0,0358923	6,8113472
0,5049221	0,5412345	0,0740333	14,662316	3	0,4950779	0,4587655	0,0740333	14,953864
0,4482279	0,4482279	0,0246324	5,4955059	2	0,5517721	0,5517721	0,0246324	4,464233
0,4417534	0,4417534	0,2101897	47,580791	2	0,5582466	0,5582466	0,2101897	37,651769
0,5713278	0,5713278	0,039103	6,8442267	2	0,4286722	0,4286722	0,039103	9,1218798
0,6176854	0,6349615	0,0647829	10,488009	3	0,3823146	0,3650385	0,0647829	16,944922
0,6437918	0,6600367	0,0859585	13,351916	5	0,3562082	0,3399633	0,0859585	24,131549
0,555026	0,555026	0,000262	0,047204	2	0,444974	0,444974	0,000262	0,0588786
0,5808564	0,5808564	0,0695542	11,974418	2	0,4191436	0,4191436	0,0695542	16,594352
0,4020099	0,4020099	0,0121939	3,0332408	2	0,5979901	0,5979901	0,0121939	2,0391526
0,4332632	0,4355274	0,0314414	7,256882	3	0,5667368	0,5644726	0,0314414	5,5477964
0,4586477	0,4586477	0,0640786	13,971211	2	0,5413523	0,5413523	0,0640786	11,836771
0,490614	0,4974683	0,0236056	4,8114429	3	0,509386	0,5025317	0,0236056	4,6341307
0,4293248	0,4293248	0,0221166	5,1514736	2	0,5706752	0,5706752	0,0221166	3,8755061
0,6613487	0,6613487	0,111618	16,877323	2	0,3386513	0,3386513	0,111618	32,959551
0,4358515	0,4358515	0,056911	13,057437	2	0,5641485	0,5641485	0,056911	10,087954
0,5140903	0,541702	0,0512207	9,9633663	3	0,4859097	0,458298	0,0512207	10,541196
0,573642	0,573642	0,1131987	19,733334	2	0,426358	0,426358	0,1131987	26,550153
0,2652446	0,2652446	0,0084739	3,194761	2	0,7347554	0,7347554	0,0084739	1,1532998
0,5253207	0,5270209	0,0280921	5,3476076	4	0,4746793	0,4729791	0,0280921	5,9181201
0,619789	0,619789	0,0865064	13,957397	2	0,380211	0,380211	0,0865064	22,752215
0,3699518	0,4101028	0,0877228	23,711946	3	0,6300482	0,5898972	0,0877228	13,923186
0,4660926	0,4660926	0,11217	24,066026	2	0,5339074	0,5339074	0,11217	21,009257
0,513054	0,513054	0,0236604	4,6116862	2	0,486946	0,486946	0,0236604	4,8589455
0,5075551	0,5075551	0,0067207	1,324127	2	0,4924449	0,4924449	0,0067207	1,3647565
0,4670528	0,4670528	0,0869725	18,621547	2	0,5329472	0,5329472	0,0869725	16,319152
0,6560221	0,6560221	0,0007154	0,1090527	2	0,3439779	0,3439779	0,0007154	0,2079813
0,4474574	0,4474574	0,0084248	1,882809	2	0,5525426	0,5525426	0,0084248	1,5247277
0,2724082	0,2724082	0,0391651	14,377369	2	0,7275918	0,7275918	0,0391651	5,3828441
0,6211818	0,6175211	0,0075188	1,2103991	3	0,3788182	0,3824789	0,0075188	1,9847984
0,5423405	0,5423405	0,0429355	7,9166955	2	0,4576595	0,4576595	0,0429355	9,3815281
0,732668	0,732668	0,0490813	6,6989863	2	0,267332	0,267332	0,0490813	18,359695
0,4719225	0,474833	0,0128731	2,7277915	3	0,5280775	0,525167	0,0128731	2,4377217
0,5466402	0,5466402	0,0199882	3,6565635	2	0,4533598	0,4533598	0,0199882	4,4089152
0,4621699	0,4621699	0,0369759	8,0004901	2	0,5378301	0,5378301	0,0369759	6,8750079
0,6594907	0,6594907	0,1679021	25,459356	2	0,3405093	0,3405093	0,1679021	49,309095

0,5235263	0,5235263	0,0045911	0,8769525	2	0,4764737	0,4764737	0,0045911	0,9635531
0,4379242	0,4293311	0,0473435	10,810886	5	0,5620758	0,5706689	0,0473435	8,422972
0,4745917	0,4864825	0,0388854	8,1934371	3	0,5254083	0,5135175	0,0388854	7,4009826
0,5452957	0,5452957	0,0252166	4,6243888	2	0,4547043	0,4547043	0,0252166	5,5457116
0,4550605	0,4550605	0,1346153	29,581837	2	0,5449395	0,5449395	0,1346153	24,702792
0,4976003	0,5112037	0,0536318	10,778079	3	0,5023997	0,4887963	0,0536318	10,675118
0,5050078	0,5050078	0,0676663	13,39907	2	0,4949922	0,4949922	0,0676663	13,670186
0,4860986	0,4860986	0,068014	13,991813	2	0,5139014	0,5139014	0,068014	13,234839
0,4098545	0,4098545	0,016113	3,9313946	2	0,5901455	0,5901455	0,016113	2,7303438
0,6103087	0,6103087	0,124143	20,341011	2	0,3896913	0,3896913	0,124143	31,856739
0,5058553	0,5058553	0,0129759	2,5651364	2	0,4941447	0,4941447	0,0129759	2,6259266
0,5608273	0,5670802	0,0524795	9,3575113	3	0,4391727	0,4329198	0,0524795	11,949623
0,4485551	0,4485551	0,030751	6,8555586	2	0,5514449	0,5514449	0,030751	5,5764341
0,6272053	0,6199838	0,0203308	3,2414831	3	0,3727947	0,3800162	0,0203308	5,4536058
0,5148908	0,5148908	0,0565067	10,974503	2	0,4851092	0,4851092	0,0565067	11,648246
0,5736128	0,5736128	0,0523228	9,1216309	2	0,4263872	0,4263872	0,0523228	12,271206
0,6218696	0,613566	0,0191327	3,0766413	3	0,3781304	0,386434	0,0191327	5,0598138
0,4878551	0,4878551	0,0403247	8,265721	2	0,5121449	0,5121449	0,0403247	7,8736991
0,5378711	0,5378711	0,0483638	8,9917096	2	0,4621289	0,4621289	0,0483638	10,465435
0,5777146	0,5777146	0,009442	1,6343784	2	0,4222854	0,4222854	0,009442	2,235939
0,4617584	0,4617584	0,086325	18,694831	2	0,5382416	0,5382416	0,086325	16,03833
0,523248	0,523248	0,0083145	1,5890119	2	0,476752	0,476752	0,0083145	1,7439831
0,4821812	0,4821812	0,0002379	0,0493373	2	0,5178188	0,5178188	0,0002379	0,0459418
0,5367458	0,5367458	0,1734533	32,315722	2	0,4632542	0,4632542	0,1734533	37,442351
0,5967326	0,5967326	0,0089419	1,4984833	2	0,4032674	0,4032674	0,0089419	2,2173717
0,6130241	0,6130241	0,0072751	1,1867629	2	0,3869759	0,3869759	0,0072751	1,8799989
0,5149539	0,5149539	0,1030573	20,012923	2	0,4850461	0,4850461	0,1030573	21,246914
0,5036613	0,5036613	0,1296296	25,737462	2	0,4963387	0,4963387	0,1296296	26,11717
0,5080074	0,5080074	0,078607	15,473583	2	0,4919926	0,4919926	0,078607	15,977264
0,3996453	0,3996453	0,0726622	18,181681	2	0,6003547	0,6003547	0,0726622	12,103219

IR.N(115)								
#Qual	Mean	Median	Std	CV (%)	#Quant	Mean	Median	Std
132	0,5799301	0,5875167	0,1209818	20,861437	132	0,4200699	0,4124833	0,1209818
86	0,6330957	0,6006031	0,1731429	27,348622	86	0,3669043	0,3993969	0,1731429
112	0,5881067	0,6623716	0,181608	30,880109	112	0,4118933	0,3376284	0,181608
151	0,8205332	0,8305019	0,0543992	6,6297344	151	0,1794668	0,1694981	0,0543992
104	0,7869918	0,8048308	0,0781698	9,9327339	104	0,2130082	0,1951692	0,0781698
49	0,6512484	0,677036	0,0884632	13,583627	49	0,3487516	0,322964	0,0884632
30	0,5791144	0,5936866	0,1278976	22,085034	30	0,4208856	0,4063134	0,1278976
47	0,5173059	0,497461	0,1113105	21,517352	47	0,4826941	0,502539	0,1113105
57	0,7116385	0,7419118	0,113371	15,930977	57	0,2883615	0,2580882	0,113371
39	0,4099014	0,3757164	0,137864	33,633461	39	0,5900986	0,6242836	0,137864
31	0,7009867	0,7082714	0,0888949	12,681402	31	0,2990133	0,2917286	0,0888949
24	0,3987689	0,38817	0,1071964	26,881829	24	0,6012311	0,61183	0,1071964
45	0,7138259	0,724859	0,0863968	12,103344	45	0,2861741	0,275141	0,0863968
33	0,7581684	0,7598644	0,0701753	9,2558944	33	0,2418316	0,2401356	0,0701753
48	0,3628386	0,3474391	0,0912499	25,148905	48	0,6371614	0,6525609	0,0912499
18	0,4734487	0,5000851	0,1212692	25,614011	18	0,5265513	0,4999149	0,1212692
63	0,3894217	0,3737685	0,1056262	27,123849	63	0,6105783	0,6262315	0,1056262
27	0,6251836	0,6346075	0,1438787	23,01383	27	0,3748164	0,3653925	0,1438787
6	0,5037894	0,5377306	0,1416665	28,120195	6	0,4962106	0,4622694	0,1416665
18	0,8126471	0,8370692	0,0625034	7,6913294	18	0,1873529	0,1629308	0,0625034
53	0,3567258	0,335372	0,1193647	33,4612	53	0,6432742	0,664628	0,1193647
25	0,6314041	0,6325663	0,0638934	10,119256	25	0,3685959	0,3674337	0,0638934
2	0,7746469	0,7746469	0,0200813	2,5923131	2	0,2253531	0,2253531	0,0200813
3	0,7647329	0,7904592	0,0610341	7,9811033	3	0,2352671	0,2095408	0,0610341
5	0,3944869	0,3892687	0,0425966	10,79798	5	0,6055131	0,6107313	0,0425966
20	0,3977821	0,4007234	0,0847913	21,316018	20	0,6022179	0,5992766	0,0847913
2	0,7838109	0,7838109	0,0421082	5,3722364	2	0,2161891	0,2161891	0,0421082
19	0,5046829	0,5130312	0,0826313	16,372907	19	0,4953171	0,4869688	0,0826313
21	0,408302	0,3899664	0,0947632	23,209097	21	0,591698	0,6100336	0,0947632
4	0,6840524	0,6772198	0,0590577	8,6335044	4	0,3159476	0,3227802	0,0590577
29	0,4567915	0,4603256	0,1491329	32,647918	29	0,5432085	0,5396744	0,1491329
13	0,7181641	0,7207557	0,0638585	8,8919053	13	0,2818359	0,2792443	0,0638585
3	0,7327542	0,7341827	0,0266036	3,6306295	3	0,2672458	0,2658173	0,0266036
17	0,4065594	0,3956287	0,1390766	34,208192	17	0,5934406	0,6043713	0,1390766
10	0,8279513	0,8390527	0,0241404	2,9156792	10	0,1720487	0,1609473	0,0241404
12	0,4403199	0,4153602	0,1050132	23,849292	12	0,5596801	0,5846398	0,1050132
43	0,5026163	0,5088735	0,0906698	18,039559	43	0,4973837	0,4911265	0,0906698
27	0,6244318	0,637718	0,0888645	14,23125	27	0,3755682	0,362282	0,0888645
35	0,5414444	0,5669145	0,0947923	17,507302	35	0,4585556	0,4330855	0,0947923
7	0,4689031	0,4423792	0,0812742	17,332826	7	0,5310969	0,5576208	0,0812742
23	0,5467207	0,5475819	0,112119	20,507554	23	0,4532793	0,4524181	0,112119
24	0,7047143	0,7013748	0,1098972	15,59457	24	0,2952857	0,2986252	0,1098972
40	0,4519234	0,4093775	0,1389833	30,753733	40	0,5480766	0,5906225	0,1389833
25	0,6564448	0,6943641	0,0959268	14,613073	25	0,3435552	0,3056359	0,0959268
2	0,511339	0,511339	0,3475673	67,971994	2	0,488661	0,488661	0,3475673
21	0,4545388	0,4852098	0,1099984	24,199997	21	0,5454612	0,5147902	0,1099984
14	0,4108137	0,3992393	0,1166792	28,401968	14	0,5891863	0,6007607	0,1166792
19	0,6558133	0,6955175	0,0875057	13,343086	19	0,3441867	0,3044825	0,0875057
19	0,4246629	0,3928896	0,1263318	29,748732	19	0,5753371	0,6071104	0,1263318
44	0,4333228	0,4436373	0,1256167	28,989173	44	0,5666772	0,5563627	0,1256167

6	0,6471786	0,7149472	0,1892427	29,241194	6	0,3528214	0,2850528	0,1892427
9	0,6210432	0,6462274	0,1665499	26,817768	9	0,3789568	0,3537726	0,1665499
21	0,6945144	0,6834697	0,0955369	13,755931	21	0,3054856	0,3165303	0,0955369
8	0,532591	0,5408816	0,0570053	10,703398	8	0,467409	0,4591184	0,0570053
34	0,5990397	0,6139804	0,1014561	16,936458	34	0,4009603	0,3860196	0,1014561
21	0,4260084	0,4290432	0,0634552	14,895306	21	0,5739916	0,5709568	0,0634552
24	0,309522	0,2909246	0,092984	30,041156	24	0,690478	0,7090754	0,092984
12	0,5459474	0,5631936	0,0721563	13,216709	12	0,4540526	0,4368064	0,0721563
23	0,5359211	0,4833432	0,1367533	25,51743	23	0,4640789	0,5166568	0,1367533
17	0,4507281	0,4608494	0,0855986	18,991181	17	0,5492719	0,5391506	0,0855986
9	0,4256234	0,4309632	0,0908193	21,337943	9	0,5743766	0,5690368	0,0908193
14	0,4762891	0,498288	0,0731151	15,351001	14	0,5237109	0,501712	0,0731151
16	0,4048605	0,405544	0,1222368	30,192334	16	0,5951395	0,594456	0,1222368
15	0,4340983	0,3959961	0,1331804	30,679771	15	0,5659017	0,6040039	0,1331804
22	0,689915	0,734932	0,1250376	18,123625	22	0,310085	0,265068	0,1250376
16	0,3486988	0,3663241	0,0791324	22,693636	16	0,6513012	0,6336759	0,0791324
22	0,4094373	0,4307555	0,1205523	29,443411	22	0,5905627	0,5692445	0,1205523
24	0,4446985	0,4582482	0,1157342	26,025331	24	0,5553015	0,5417518	0,1157342
17	0,4238174	0,4020649	0,088773	20,946055	17	0,5761826	0,5979351	0,088773
16	0,4424362	0,4764271	0,1183617	26,75227	16	0,5575638	0,5235729	0,1183617
23	0,4160052	0,4248074	0,1369875	32,92928	23	0,5839948	0,5751926	0,1369875
23	0,4001006	0,4236906	0,1410935	35,264514	23	0,5998994	0,5763094	0,1410935
26	0,5797118	0,5757445	0,1079078	18,614049	26	0,4202882	0,4242555	0,1079078
17	0,4401242	0,3969144	0,1716544	39,001355	17	0,5598758	0,6030856	0,1716544
40	0,5955949	0,5984654	0,098317	16,507362	40	0,4044051	0,4015346	0,098317
8	0,6071137	0,5999683	0,1263308	20,808428	8	0,3928863	0,4000317	0,1263308
16	0,5221824	0,526597	0,1674697	32,071103	16	0,4778176	0,473403	0,1674697
17	0,3888657	0,3702635	0,1135828	29,208744	17	0,6111343	0,6297365	0,1135828
11	0,415681	0,3961546	0,1309829	31,51044	11	0,584319	0,6038454	0,1309829
5	0,3146142	0,253619	0,0978256	31,093836	5	0,6853858	0,746381	0,0978256
16	0,3622906	0,3524632	0,0874974	24,15116	16	0,6377094	0,6475368	0,0874974
9	0,6602843	0,6492486	0,0938793	14,218012	9	0,3397157	0,3507514	0,0938793
15	0,3880708	0,3844444	0,0915555	23,592472	15	0,6119292	0,6155556	0,0915555
12	0,3448527	0,3278773	0,0874901	25,37028	12	0,6551473	0,6721227	0,0874901
9	0,6385317	0,6093642	0,1107836	17,349737	9	0,3614683	0,3906358	0,1107836
16	0,39302	0,4003712	0,1040357	26,47085	16	0,60698	0,5996288	0,1040357
18	0,3510813	0,3399511	0,1073702	30,582702	18	0,6489187	0,6600489	0,1073702
11	0,4256197	0,4360722	0,0875384	20,567279	11	0,5743803	0,5639278	0,0875384
20	0,3776722	0,3796839	0,1211412	32,075746	20	0,6223278	0,6203161	0,1211412
10	0,4506882	0,4133057	0,1712505	37,997559	10	0,5493118	0,5866943	0,1712505
10	0,5595554	0,5969437	0,1699755	30,376888	10	0,4404446	0,4030563	0,1699755
13	0,4038113	0,4648911	0,1110848	27,509082	13	0,5961887	0,5351089	0,1110848
16	0,3731775	0,3647529	0,0889299	23,830451	16	0,6268225	0,6352471	0,0889299
10	0,4582511	0,4638767	0,0979396	21,37248	10	0,5417489	0,5361233	0,0979396
10	0,3637921	0,3587848	0,053311	14,654255	10	0,6362079	0,6412152	0,053311
24	0,5067027	0,4986646	0,055468	10,946847	24	0,4932973	0,5013354	0,055468
15	0,7701681	0,7879271	0,051133	6,6392015	15	0,2298319	0,2120729	0,051133
11	0,4439493	0,4212693	0,1050702	23,667167	11	0,5560507	0,5787307	0,1050702
10	0,4570346	0,4475909	0,0923453	20,205309	10	0,5429654	0,5524091	0,0923453
13	0,3904358	0,3539199	0,1180439	30,23387	13	0,6095642	0,6460801	0,1180439
12	0,3592133	0,3689072	0,1175962	32,737138	12	0,6407867	0,6310928	0,1175962
9	0,4637141	0,4461198	0,0934283	20,147829	9	0,5362859	0,5538802	0,0934283

14	0,3985014	0,3772819	0,0626817	15,729359	14	0,6014986	0,6227181	0,0626817
23	0,4813305	0,477586	0,1213143	25,203949	23	0,5186695	0,522414	0,1213143
18	0,4091833	0,3786427	0,0950885	23,238619	18	0,5908167	0,6213573	0,0950885
9	0,614224	0,6387338	0,1122889	18,281433	9	0,385776	0,3612662	0,1122889
23	0,5483616	0,4802513	0,1622997	29,597209	23	0,4516384	0,5197487	0,1622997
8	0,4644154	0,4662822	0,0727685	15,668847	8	0,5355846	0,5337178	0,0727685
15	0,3986081	0,3873006	0,0692531	17,373721	15	0,6013919	0,6126994	0,0692531
10	0,4001295	0,3654876	0,1378738	34,457304	10	0,5998705	0,6345124	0,1378738
10	0,5276867	0,4628422	0,1834692	34,768593	10	0,4723133	0,5371578	0,1834692
9	0,3099227	0,3014608	0,0881086	28,429217	9	0,6900773	0,6985392	0,0881086
12	0,4631114	0,4112181	0,2135033	46,101937	12	0,5368886	0,5887819	0,2135033
8	0,4959207	0,5019957	0,0682956	13,771479	8	0,5040793	0,4980043	0,0682956
14	0,4465055	0,4079435	0,152787	34,218387	14	0,5534945	0,5920565	0,152787
12	0,5011543	0,4806525	0,106411	21,233176	12	0,4988457	0,5193475	0,106411
8	0,3965212	0,3856371	0,0869063	21,917181	8	0,6034788	0,6143629	0,0869063
5	0,7245193	0,8359043	0,2266469	31,282387	5	0,2754807	0,1640957	0,2266469
11	0,3593881	0,3334946	0,0867517	24,138711	11	0,6406119	0,6665054	0,0867517
14	0,3840652	0,4016032	0,0638583	16,626937	14	0,6159348	0,5983968	0,0638583
10	0,5380869	0,5600168	0,0873226	16,228352	10	0,4619131	0,4399832	0,0873226
15	0,3884493	0,3397941	0,1311775	33,769534	15	0,6115507	0,6602059	0,1311775
5	0,3059121	0,2862114	0,0525926	17,192075	5	0,6940879	0,7137886	0,0525926
3	0,3596248	0,3748686	0,0532508	14,807313	3	0,6403752	0,6251314	0,0532508
8	0,5080459	0,4279794	0,1654639	32,568681	8	0,4919541	0,5720206	0,1654639
14	0,311933	0,3179392	0,0761948	24,426652	14	0,688067	0,6820608	0,0761948
7	0,3587456	0,3520539	0,0416252	11,602977	7	0,6412544	0,6479461	0,0416252
4	0,4516012	0,4554604	0,0121608	2,6928159	4	0,5483988	0,5445396	0,0121608
9	0,491039	0,4400265	0,1264927	25,760218	9	0,508961	0,5599735	0,1264927
7	0,4971987	0,4825322	0,0705499	14,18948	7	0,5028013	0,5174678	0,0705499
7	0,3525306	0,3531844	0,1247155	35,377221	7	0,6474694	0,6468156	0,1247155
13	0,7037221	0,7964637	0,1761057	25,024889	13	0,2962779	0,2035363	0,1761057
11	0,3848812	0,3158502	0,149616	38,873296	11	0,6151188	0,6841498	0,149616
9	0,3631636	0,3379385	0,091339	25,150923	9	0,6368364	0,6620615	0,091339
9	0,3892112	0,3601871	0,0829717	21,317925	9	0,6107888	0,6398129	0,0829717
9	0,504746	0,5087552	0,1152005	22,823465	9	0,495254	0,4912448	0,1152005
13	0,5101203	0,4984005	0,0682247	13,374245	13	0,4898797	0,5015995	0,0682247
14	0,4288302	0,4059072	0,0766241	17,868174	14	0,5711698	0,5940928	0,0766241
12	0,7059616	0,728326	0,1360916	19,277485	12	0,2940384	0,271674	0,1360916
30	0,4079779	0,4050688	0,0677286	16,60105	30	0,5920221	0,5949312	0,0677286
11	0,4734063	0,4253787	0,1288416	27,215853	11	0,5265937	0,5746213	0,1288416
8	0,719754	0,7455261	0,0927851	12,891224	8	0,280246	0,2544739	0,0927851
9	0,3561591	0,3855448	0,0834638	23,434404	9	0,6438409	0,6144552	0,0834638
14	0,7130331	0,7422998	0,0698546	9,7968185	14	0,2869669	0,2577002	0,0698546
18	0,7757245	0,7826011	0,0297617	3,8366283	18	0,2242755	0,2173989	0,0297617
8	0,3787106	0,3757572	0,0759109	20,044553	8	0,6212894	0,6242428	0,0759109
11	0,6871194	0,6779569	0,0405548	5,9021494	11	0,3128806	0,3220431	0,0405548
7	0,3594367	0,352167	0,1103926	30,712656	7	0,6405633	0,647833	0,1103926
5	0,7422211	0,7346656	0,047331	6,3769416	5	0,2577789	0,2653344	0,047331
6	0,3687573	0,356476	0,1312332	35,587945	6	0,6312427	0,643524	0,1312332
13	0,342469	0,2524896	0,1889145	55,162509	13	0,657531	0,7475104	0,1889145
2	0,3253966	0,3253966	0,0194454	5,9759074	2	0,6746034	0,6746034	0,0194454
7	0,5821544	0,5743233	0,1447289	24,860917	7	0,4178456	0,4256767	0,1447289
17	0,3582779	0,3451113	0,0694502	19,384448	17	0,6417221	0,6548887	0,0694502

11	0,4450134	0,4125357	0,0887355	19,939959	11	0,5549866	0,5874643	0,0887355
11	0,6588	0,6509576	0,0514081	7,803301	11	0,3412	0,3490424	0,0514081
10	0,7992322	0,7976048	0,0665849	8,3311079	10	0,2007678	0,2023952	0,0665849
11	0,4921713	0,4855417	0,0421527	8,5646422	11	0,5078287	0,5144583	0,0421527
9	0,5702816	0,585092	0,0631526	11,073942	9	0,4297184	0,414908	0,0631526
9	0,4688177	0,4555881	0,1241044	26,47178	9	0,5311823	0,5444119	0,1241044
9	0,713414	0,7075802	0,0436432	6,1175123	9	0,286586	0,2924198	0,0436432
7	0,3820936	0,3948158	0,0397838	10,412054	7	0,6179064	0,6051842	0,0397838
8	0,3956214	0,3894279	0,0590916	14,9364	8	0,6043786	0,6105721	0,0590916
17	0,6447667	0,6312172	0,0851264	13,202671	17	0,3552333	0,3687828	0,0851264
5	0,5403695	0,5523517	0,0769148	14,233739	5	0,4596305	0,4476483	0,0769148
7	0,5331539	0,4531537	0,131769	24,715011	7	0,4668461	0,5468463	0,131769
9	0,4430109	0,5079973	0,1339172	30,228866	9	0,5569891	0,4920027	0,1339172
8	0,4213974	0,425278	0,1084401	25,733457	8	0,5786026	0,574722	0,1084401
10	0,604368	0,4805608	0,2132048	35,277315	10	0,395632	0,5194392	0,2132048
5	0,4793992	0,5036607	0,0810977	16,916519	5	0,5206008	0,4963393	0,0810977
5	0,420283	0,4717708	0,1495347	35,579523	5	0,579717	0,5282292	0,1495347
7	0,4436904	0,3653055	0,1748233	39,402096	7	0,5563096	0,6346945	0,1748233
9	0,5618218	0,5749732	0,1551756	27,620081	9	0,4381782	0,4250268	0,1551756
12	0,4647009	0,4648473	0,1589659	34,20823	12	0,5352991	0,5351527	0,1589659
9	0,764395	0,8307094	0,1036564	13,560585	9	0,235605	0,1692906	0,1036564
9	0,3841768	0,3666589	0,1045478	27,213461	9	0,6158232	0,6333411	0,1045478
9	0,4805314	0,5067041	0,0907192	18,878941	9	0,5194686	0,4932959	0,0907192
8	0,3930751	0,3827796	0,0411816	10,476779	8	0,6069249	0,6172204	0,0411816
6	0,4756713	0,468003	0,1398885	29,408655	6	0,5243287	0,531997	0,1398885
14	0,4149584	0,4112764	0,1077728	25,971963	14	0,5850416	0,5887236	0,1077728
10	0,5156386	0,5153597	0,0686563	13,314808	10	0,4843614	0,4846403	0,0686563
11	0,3982295	0,3730763	0,1607607	40,368854	11	0,6017705	0,6269237	0,1607607
12	0,4687697	0,4357316	0,0846926	18,067007	12	0,5312303	0,5642684	0,0846926
8	0,3777504	0,3639403	0,110619	29,283615	8	0,6222496	0,6360597	0,110619
5	0,3991347	0,3928896	0,0894207	22,403631	5	0,6008653	0,6071104	0,0894207
5	0,5448402	0,6074913	0,1424877	26,152207	5	0,4551598	0,3925087	0,1424877
15	0,4028867	0,3740021	0,0931977	23,13248	15	0,5971133	0,6259979	0,0931977
7	0,4009811	0,4111773	0,0493418	12,305278	7	0,5990189	0,5888227	0,0493418
9	0,3853172	0,3662758	0,1068449	27,729063	9	0,6146828	0,6337242	0,1068449
6	0,6391805	0,639442	0,04076	6,3769116	6	0,3608195	0,360558	0,04076
9	0,4687454	0,4931967	0,0886592	18,914155	9	0,5312546	0,5068033	0,0886592
8	0,4986237	0,4939886	0,0977341	19,600773	8	0,5013763	0,5060114	0,0977341
5	0,4035008	0,3395231	0,1306872	32,388322	5	0,5964992	0,6604769	0,1306872
7	0,4473974	0,3553113	0,1764053	39,429221	7	0,5526026	0,6446887	0,1764053
7	0,4463791	0,4811402	0,1979589	44,347702	7	0,5536209	0,5188598	0,1979589
9	0,5897067	0,5642638	0,1139143	19,317106	9	0,4102933	0,4357362	0,1139143
6	0,6741644	0,72054	0,0798222	11,840161	6	0,3258356	0,27946	0,0798222
13	0,8340517	0,7952427	0,0850084	10,192224	13	0,1659483	0,2047573	0,0850084
7	0,3834556	0,3640545	0,1217341	31,746592	7	0,6165444	0,6359455	0,1217341
8	0,5731928	0,5694624	0,070091	12,228169	8	0,4268072	0,4305376	0,070091
8	0,3542601	0,3270561	0,1101818	31,101959	8	0,6457399	0,6729439	0,1101818
7	0,4744194	0,4449465	0,14766	31,124357	7	0,5255806	0,5550535	0,14766
12	0,7811364	0,7931252	0,0381061	4,878292	12	0,2188636	0,2068748	0,0381061
5	0,3884875	0,3905491	0,1054005	27,130988	5	0,6115125	0,6094509	0,1054005
9	0,4440973	0,398361	0,1377089	31,008735	9	0,5559027	0,601639	0,1377089
10	0,5137997	0,406241	0,180071	35,046924	10	0,4862003	0,593759	0,180071

6	0,5607304	0,6162753	0,1165081	20,777915	6	0,4392696	0,3837247	0,1165081
7	0,4904457	0,4957017	0,07163	14,605087	7	0,5095543	0,5042983	0,07163
6	0,6662601	0,6950807	0,084853	12,735714	6	0,3337399	0,3049193	0,084853
2	0,4598274	0,4598274	0,0886628	19,281758	2	0,5401726	0,5401726	0,0886628
10	0,5317603	0,5930102	0,1291616	24,289434	10	0,4682397	0,4069898	0,1291616
10	0,7929303	0,8155443	0,0613596	7,7383371	10	0,2070697	0,1844557	0,0613596
9	0,3551522	0,342731	0,0456611	12,856757	9	0,6448478	0,657269	0,0456611
5	0,4073224	0,367953	0,064934	15,941673	5	0,5926776	0,632047	0,064934
6	0,3536246	0,3778179	0,1155795	32,684237	6	0,6463754	0,6221821	0,1155795
6	0,5283863	0,5225862	0,171167	32,3943	6	0,4716137	0,4774138	0,171167
13	0,4312726	0,4313594	0,0415087	9,6246955	13	0,5687274	0,5686406	0,0415087
10	0,7286889	0,7397932	0,0621516	8,5292329	10	0,2713111	0,2602068	0,0621516
6	0,4631501	0,4734742	0,067675	14,611885	6	0,5368499	0,5265258	0,067675
2	0,452953	0,452953	0,1358982	30,002706	2	0,547047	0,547047	0,1358982
4	0,3841896	0,3446641	0,0922044	23,999713	4	0,6158104	0,6553359	0,0922044
10	0,7231478	0,7386321	0,0644087	8,9067066	10	0,2768522	0,2613679	0,0644087
7	0,5884358	0,5631829	0,1033293	17,559995	7	0,4115642	0,4368171	0,1033293
9	0,4350733	0,4562902	0,0678964	15,605746	9	0,5649267	0,5437098	0,0678964
4	0,4294876	0,4348043	0,0565514	13,167185	4	0,5705124	0,5651957	0,0565514
8	0,3827537	0,3300527	0,1016841	26,566452	8	0,6172463	0,6699473	0,1016841
4	0,3896789	0,3746444	0,0468695	12,02772	4	0,6103211	0,6253556	0,0468695
5	0,7206695	0,7264307	0,0623044	8,6453545	5	0,2793305	0,2735693	0,0623044
4	0,450087	0,4544483	0,0783407	17,405671	4	0,549913	0,5455517	0,0783407
6	0,3081832	0,294125	0,0536429	17,406171	6	0,6918168	0,705875	0,0536429
10	0,5366907	0,5489771	0,0970219	18,077815	10	0,4633093	0,4510229	0,0970219
9	0,6863981	0,6865176	0,058904	8,5816044	9	0,3136019	0,3134824	0,058904
6	0,4114598	0,4372464	0,0964943	23,451685	6	0,5885402	0,5627536	0,0964943
8	0,4001694	0,3973627	0,063013	15,746586	8	0,5998306	0,6026373	0,063013
6	0,3576663	0,3478736	0,0797472	22,296538	6	0,6423337	0,6521264	0,0797472
6	0,7814857	0,775742	0,0192311	2,4608433	6	0,2185143	0,224258	0,0192311
6	0,4543764	0,4076921	0,145382	31,995931	6	0,5456236	0,5923079	0,145382
5	0,3651962	0,3935234	0,086776	23,761471	5	0,6348038	0,6064766	0,086776
6	0,3843445	0,3981159	0,0553999	14,414137	6	0,6156555	0,6018841	0,0553999
17	0,6806306	0,6902697	0,0849958	12,487801	17	0,3193694	0,3097303	0,0849958
4	0,7617483	0,7642164	0,092919	12,198117	4	0,2382517	0,2357836	0,092919
9	0,8195139	0,8407986	0,0570004	6,9553917	9	0,1804861	0,1592014	0,0570004
2	0,4093393	0,4093393	0,0159684	3,9010282	2	0,5906607	0,5906607	0,0159684
7	0,6121268	0,6238554	0,0482753	7,8864913	7	0,3878732	0,3761446	0,0482753
5	0,7068349	0,7427858	0,0681424	9,6405004	5	0,2931651	0,2572142	0,0681424
7	0,4633377	0,4369568	0,0810804	17,499195	7	0,5366623	0,5630432	0,0810804
12	0,7044418	0,6883223	0,0644967	9,1557134	12	0,2955582	0,3116777	0,0644967
10	0,4515148	0,4570323	0,0637966	14,129469	10	0,5484852	0,5429677	0,0637966
4	0,5783428	0,6061177	0,1765401	30,525166	4	0,4216572	0,3938823	0,1765401
8	0,5169367	0,4883807	0,0749522	14,4993	8	0,4830633	0,5116193	0,0749522
13	0,473441	0,4837286	0,1127309	23,810973	13	0,526559	0,5162714	0,1127309
5	0,3255289	0,2626804	0,1272553	39,091849	5	0,6744711	0,7373196	0,1272553
8	0,3629865	0,3571607	0,0935893	25,783122	8	0,6370135	0,6428393	0,0935893
5	0,4517149	0,4513819	0,1134799	25,122011	5	0,5482851	0,5486181	0,1134799
4	0,4622794	0,5017021	0,0868638	18,790323	4	0,5377206	0,4982979	0,0868638
2	0,4605468	0,4605468	0,0256928	5,578762	2	0,5394532	0,5394532	0,0256928
5	0,4084135	0,3078273	0,1860223	45,547534	5	0,5915865	0,6921727	0,1860223
4	0,4385088	0,4456991	0,0453279	10,336825	4	0,5614912	0,5543009	0,0453279

7	0,3242178	0,3577544	0,0818661	25,250331	7	0,6757822	0,6422456	0,0818661
4	0,5281751	0,55825	0,0841233	15,927161	4	0,4718249	0,44175	0,0841233
7	0,3661802	0,3950625	0,0691101	18,873243	7	0,6338198	0,6049375	0,0691101
9	0,4546337	0,4470248	0,0409646	9,0104543	9	0,5453663	0,5529752	0,0409646
4	0,4563044	0,4330001	0,1048184	22,971154	4	0,5436956	0,5669999	0,1048184
6	0,4545203	0,4248484	0,073094	16,081577	6	0,5454797	0,5751516	0,073094
4	0,3509712	0,3258593	0,1202394	34,259036	4	0,6490288	0,6741407	0,1202394
7	0,4006615	0,3553784	0,0905706	22,605262	7	0,5993385	0,6446216	0,0905706
6	0,3925665	0,3447781	0,1399016	35,637697	6	0,6074335	0,6552219	0,1399016
5	0,4059241	0,3772428	0,0864963	21,308484	5	0,5940759	0,6227572	0,0864963
5	0,706226	0,7002993	0,060018	8,4984072	5	0,293774	0,2997007	0,060018
5	0,3774761	0,400595	0,0894814	23,70517	5	0,6225239	0,599405	0,0894814
14	0,4266611	0,4185145	0,0880124	20,628166	14	0,5733389	0,5814855	0,0880124
6	0,4452194	0,471963	0,0648586	14,567794	6	0,5547806	0,528037	0,0648586
7	0,5573006	0,5420804	0,0881115	15,810411	7	0,4426994	0,4579196	0,0881115
3	0,5353676	0,5035038	0,0568844	10,625303	3	0,4646324	0,4964962	0,0568844
4	0,5771855	0,5972121	0,1100556	19,067632	4	0,4228145	0,4027879	0,1100556
5	0,3993672	0,3693518	0,12412	31,079173	5	0,6006328	0,6306482	0,12412
4	0,4236336	0,4362325	0,1044184	24,648283	4	0,5763664	0,5637675	0,1044184
6	0,5298073	0,5689129	0,0883599	16,677742	6	0,4701927	0,4310871	0,0883599
4	0,3685041	0,3619578	0,0661401	17,948275	4	0,6314959	0,6380422	0,0661401
5	0,4449399	0,4530455	0,114292	25,687058	5	0,5550601	0,5469545	0,114292
9	0,4667495	0,4283442	0,0775963	16,62484	9	0,5332505	0,5716558	0,0775963
6	0,3527935	0,3495524	0,1498008	42,461317	6	0,6472065	0,6504476	0,1498008
5	0,5252922	0,5448284	0,0936096	17,820487	5	0,4747078	0,4551716	0,0936096
5	0,5207053	0,5356977	0,1158159	22,242129	5	0,4792947	0,4643023	0,1158159
5	0,4778207	0,4175665	0,1313666	27,492869	5	0,5221793	0,5824335	0,1313666
9	0,350483	0,3336164	0,0762853	21,765758	9	0,649517	0,6663836	0,0762853
4	0,4443971	0,4857418	0,1237366	27,843711	4	0,5556029	0,5142582	0,1237366
6	0,4424386	0,4122311	0,1293755	29,241454	6	0,5575614	0,5877689	0,1293755
4	0,4428857	0,3524843	0,2010655	45,398951	4	0,5571143	0,6475157	0,2010655
4	0,3620905	0,3748618	0,0630357	17,408813	4	0,6379095	0,6251382	0,0630357
5	0,7647153	0,7535607	0,0576804	7,5427335	5	0,2352847	0,2464393	0,0576804
6	0,3832675	0,3658764	0,0673967	17,584762	6	0,6167325	0,6341236	0,0673967
6	0,6468205	0,6519874	0,095933	14,831476	6	0,3531795	0,3480126	0,095933
2	0,6669785	0,6669785	0,0901382	13,514416	2	0,3330215	0,3330215	0,0901382
8	0,4030277	0,3967673	0,1120703	27,807103	8	0,5969723	0,6032327	0,1120703
5	0,4543048	0,4247877	0,1261022	27,757178	5	0,5456952	0,5752123	0,1261022
8	0,440981	0,4238589	0,0964587	21,873657	8	0,559019	0,5761411	0,0964587
5	0,4106951	0,4078095	0,0323741	7,8827572	5	0,5893049	0,5921905	0,0323741
5	0,4947383	0,502618	0,0276629	5,591418	5	0,5052617	0,497382	0,0276629
7	0,4669261	0,4807321	0,0481649	10,315307	7	0,5330739	0,5192679	0,0481649
12	0,4545987	0,4515619	0,127568	28,061664	12	0,5454013	0,5484381	0,127568
2	0,5262102	0,5262102	0,0773698	14,703213	2	0,4737898	0,4737898	0,0773698
4	0,3834205	0,3840781	0,0325174	8,4808621	4	0,6165795	0,6159219	0,0325174
5	0,4744182	0,4641419	0,0708885	14,942193	5	0,5255818	0,5358581	0,0708885
6	0,4616675	0,4176238	0,116453	25,224438	6	0,5383325	0,5823762	0,116453
4	0,3199002	0,3198921	0,0089726	2,8048033	4	0,6800998	0,6801079	0,0089726
9	0,4087406	0,4154895	0,0299642	7,3308622	9	0,5912594	0,5845105	0,0299642
10	0,6265659	0,6485809	0,1079225	17,22445	10	0,3734341	0,3514191	0,1079225
4	0,6551748	0,6712737	0,1891933	28,876766	4	0,3448252	0,3287263	0,1891933
6	0,3264665	0,2986133	0,1447383	44,334815	6	0,6735335	0,7013867	0,1447383

4	0,3883033	0,3914547	0,0721288	18,575368	4	0,6116967	0,6085453	0,0721288
3	0,3415382	0,3423609	0,0886117	25,944896	3	0,6584618	0,6576391	0,0886117
5	0,3333318	0,305322	0,0694557	20,836809	5	0,6666682	0,694678	0,0694557
7	0,7633603	0,7769169	0,0502394	6,5813496	7	0,2366397	0,2230831	0,0502394
4	0,4895901	0,4165072	0,1990589	40,658282	4	0,5104099	0,5834928	0,1990589
7	0,3393193	0,3449732	0,0773262	22,788609	7	0,6606807	0,6550268	0,0773262
5	0,6205106	0,6534565	0,0744443	11,997261	5	0,3794894	0,3465435	0,0744443
6	0,5988431	0,596635	0,159842	26,691794	6	0,4011569	0,403365	0,159842
3	0,4135187	0,4271857	0,0831682	20,112325	3	0,5864813	0,5728143	0,0831682
4	0,7012989	0,7201482	0,0590174	8,4154438	4	0,2987011	0,2798518	0,0590174
6	0,5086359	0,4929929	0,0594492	11,687966	6	0,4913641	0,5070071	0,0594492
5	0,3436359	0,3379044	0,0758741	22,079781	5	0,6563641	0,6620956	0,0758741
6	0,4119929	0,3786392	0,1015986	24,660275	6	0,5880071	0,6213608	0,1015986
3	0,7092626	0,7400506	0,0600145	8,4615325	3	0,2907374	0,2599494	0,0600145
5	0,4156904	0,4117931	0,0611659	14,714281	5	0,5843096	0,5882069	0,0611659
5	0,4200484	0,4289589	0,0683796	16,278984	5	0,5799516	0,5710411	0,0683796
4	0,4897311	0,4669602	0,1834966	37,468849	4	0,5102689	0,5330398	0,1834966
6	0,4897491	0,503586	0,0387802	7,9183882	6	0,5102509	0,496414	0,0387802
4	0,4037994	0,3643696	0,1152718	28,546794	4	0,5962006	0,6356304	0,1152718
4	0,5445192	0,5515784	0,045718	8,396037	4	0,4554808	0,4484216	0,045718
4	0,4974412	0,5083189	0,1209224	24,308894	4	0,5025588	0,4916811	0,1209224
3	0,3593233	0,3518993	0,1242436	34,577099	3	0,6406767	0,6481007	0,1242436
4	0,5060545	0,5190642	0,1273137	25,158106	4	0,4939455	0,4809358	0,1273137
7	0,4505456	0,4764581	0,0922237	20,46933	7	0,5494544	0,5235419	0,0922237
5	0,5123979	0,5136664	0,1518779	29,640609	5	0,4876021	0,4863336	0,1518779
4	0,4539084	0,4397638	0,0935403	20,60774	4	0,5460916	0,5602362	0,0935403
4	0,501364	0,4937505	0,04416	8,8079692	4	0,498636	0,5062495	0,04416
8	0,4272034	0,4312293	0,0843044	19,734023	8	0,5727966	0,5687707	0,0843044
4	0,4273427	0,4223864	0,0966649	22,619996	4	0,5726573	0,5776136	0,0966649
3	0,3639977	0,3294128	0,0671962	18,46062	3	0,6360023	0,6705872	0,0671962
3	0,3926073	0,3994864	0,067012	17,06845	3	0,6073927	0,6005136	0,067012
4	0,4581787	0,417137	0,1265142	27,612418	4	0,5418213	0,582863	0,1265142
6	0,8357162	0,8377429	0,0116488	1,3938682	6	0,1642838	0,1622571	0,0116488
4	0,4880125	0,4566552	0,0746983	15,306631	4	0,5119875	0,5433448	0,0746983
6	0,469628	0,4616345	0,0703539	14,980781	6	0,530372	0,5383655	0,0703539
8	0,5708312	0,5558265	0,039209	6,8687633	8	0,4291688	0,4441735	0,039209
4	0,6548052	0,6552495	0,0230095	3,5139501	4	0,3451948	0,3447505	0,0230095
5	0,3677567	0,3619911	0,0575082	15,637559	5	0,6322433	0,6380089	0,0575082
3	0,526427	0,4869071	0,1369292	26,011051	3	0,473573	0,5130929	0,1369292
7	0,7177627	0,733442	0,0655441	9,1317231	7	0,2822373	0,266558	0,0655441
4	0,3342325	0,3339654	0,0469056	14,033809	4	0,6657675	0,6660346	0,0469056
6	0,4822978	0,5196707	0,1419465	29,431298	6	0,5177022	0,4803293	0,1419465
4	0,4951669	0,4934942	0,0559401	11,297216	4	0,5048331	0,5065058	0,0559401
6	0,451927	0,4320179	0,0621097	13,743308	6	0,548073	0,5679821	0,0621097
3	0,3537843	0,3404373	0,0903667	25,542869	3	0,6462157	0,6595627	0,0903667
7	0,4666824	0,4940462	0,1180642	25,298612	7	0,5333176	0,5059538	0,1180642
4	0,7543813	0,7487283	0,0387268	5,1335883	4	0,2456187	0,2512717	0,0387268
4	0,5599756	0,552676	0,0261664	4,6727712	4	0,4400244	0,447324	0,0261664
6	0,5219617	0,5310253	0,0529295	10,140491	6	0,4780383	0,4689747	0,0529295
2	0,3826826	0,3826826	0,1035508	27,059196	2	0,6173174	0,6173174	0,1035508
6	0,4918753	0,4924125	0,0409609	8,3274995	6	0,5081247	0,5075875	0,0409609
3	0,4590213	0,4566567	0,032611	7,1044707	3	0,5409787	0,5433433	0,032611

10	0,5913373	0,5923577	0,0174957	2,9586678	10	0,4086627	0,4076423	0,0174957
3	0,3992021	0,3754694	0,0792457	19,851022	3	0,6007979	0,6245306	0,0792457
7	0,7633394	0,7933442	0,0990309	12,973373	7	0,2366606	0,2066558	0,0990309
3	0,4755579	0,4876162	0,0687341	14,453359	3	0,5244421	0,5123838	0,0687341
3	0,4632686	0,4702436	0,1226146	26,467277	3	0,5367314	0,5297564	0,1226146
3	0,5814233	0,5986321	0,1845444	31,740114	3	0,4185767	0,4013679	0,1845444
3	0,5611396	0,5122463	0,1311364	23,36966	3	0,4388604	0,4877537	0,1311364
11	0,5951378	0,6923208	0,1623033	27,27155	11	0,4048622	0,3076792	0,1623033
5	0,5138092	0,4704056	0,1114875	21,698238	5	0,4861908	0,5295944	0,1114875
5	0,7389858	0,7620011	0,0663582	8,9796279	5	0,2610142	0,2379989	0,0663582
3	0,3182052	0,3418408	0,0679725	21,361224	3	0,6817948	0,6581592	0,0679725
3	0,3853241	0,372984	0,079648	20,670379	3	0,6146759	0,627016	0,079648
4	0,5386244	0,5193309	0,1174647	21,80828	4	0,4613756	0,4806691	0,1174647
6	0,7542619	0,7599175	0,0477773	6,3343057	6	0,2457381	0,2400825	0,0477773
7	0,4121186	0,4096934	0,0736533	17,871869	7	0,5878814	0,5903066	0,0736533
3	0,3874031	0,360218	0,0598872	15,458633	3	0,6125969	0,639782	0,0598872
3	0,7248306	0,8417427	0,2208218	30,46529	3	0,2751694	0,1582573	0,2208218
3	0,4795928	0,4435523	0,0841194	17,539764	3	0,5204072	0,5564477	0,0841194
3	0,3295532	0,3466622	0,039081	11,85879	3	0,6704468	0,6533378	0,039081
3	0,4792835	0,4642435	0,0910349	18,993949	3	0,5207165	0,5357565	0,0910349
5	0,6313213	0,6913352	0,1319161	20,895244	5	0,3686787	0,3086648	0,1319161
3	0,4151224	0,3820903	0,1050345	25,30205	3	0,5848776	0,6179097	0,1050345
4	0,3840692	0,3740776	0,0281388	7,3264922	4	0,6159308	0,6259224	0,0281388
4	0,7500149	0,7842769	0,0765286	10,203615	4	0,2499851	0,2157231	0,0765286
3	0,5143255	0,4426754	0,1379132	26,81439	3	0,4856745	0,5573246	0,1379132
3	0,4290758	0,3982302	0,1592483	37,11425	3	0,5709242	0,6017698	0,1592483
6	0,3859043	0,3820999	0,0364833	9,4539825	6	0,6140957	0,6179001	0,0364833
3	0,4173479	0,4218752	0,042699	10,23103	3	0,5826521	0,5781248	0,042699
5	0,3983684	0,3771026	0,084619	21,241386	5	0,6016316	0,6228974	0,084619
5	0,462335	0,439114	0,0569171	12,310792	5	0,537665	0,560886	0,0569171
3	0,4206173	0,4217579	0,0428455	10,186342	3	0,5793827	0,5782421	0,0428455
4	0,3868266	0,3936962	0,022737	5,8778379	4	0,6131734	0,6063038	0,022737
3	0,4618283	0,4109522	0,0942219	20,401937	3	0,5381717	0,5890478	0,0942219
3	0,3963606	0,3379692	0,1917425	48,37576	3	0,6036394	0,6620308	0,1917425
5	0,4668705	0,4575962	0,0357561	7,6586683	5	0,5331295	0,5424038	0,0357561
3	0,3791204	0,3782703	0,1103145	29,097489	3	0,6208796	0,6217297	0,1103145
3	0,4927186	0,4987212	0,0220953	4,4843742	3	0,5072814	0,5012788	0,0220953
3	0,5145889	0,5431729	0,0960384	18,66313	3	0,4854111	0,4568271	0,0960384
4	0,5436622	0,5511021	0,082347	15,146725	4	0,4563378	0,4488979	0,082347
4	0,791467	0,8223175	0,1431835	18,090895	4	0,208533	0,1776825	0,1431835
3	0,8133761	0,8244334	0,029604	3,6396408	3	0,1866239	0,1755666	0,029604
2	0,5087936	0,5087936	0,0065576	1,2888621	2	0,4912064	0,4912064	0,0065576
2	0,727952	0,727952	0,0443546	6,0930693	2	0,272048	0,272048	0,0443546
3	0,4146676	0,4373927	0,1176532	28,372886	3	0,5853324	0,5626073	0,1176532
4	0,5123114	0,5002952	0,0961693	18,771644	4	0,4876886	0,4997048	0,0961693
3	0,348002	0,3541577	0,0305479	8,7780881	3	0,651998	0,6458423	0,0305479
3	0,709961	0,8148952	0,192393	27,099098	3	0,290039	0,1851048	0,192393
3	0,5322955	0,4774887	0,1602749	30,110139	3	0,4677045	0,5225113	0,1602749
3	0,4102123	0,3897612	0,0803307	19,582721	3	0,5897877	0,6102388	0,0803307
3	0,5937254	0,5986949	0,0719342	12,115736	3	0,4062746	0,4013051	0,0719342
2	0,5901483	0,5901483	0,1490115	25,249838	2	0,4098517	0,4098517	0,1490115
4	0,3647	0,3577868	0,0450733	12,359016	4	0,6353	0,6422132	0,0450733

4	0,7405025	0,7518416	0,056922	7,6869442	4	0,2594975	0,2481584	0,056922
5	0,3806907	0,3491816	0,114701	30,129708	5	0,6193093	0,6508184	0,114701
2	0,6063356	0,6063356	0,0288533	4,7586334	2	0,3936644	0,3936644	0,0288533
5	0,3615283	0,3598125	0,0387637	10,72217	5	0,6384717	0,6401875	0,0387637
3	0,4736671	0,4268274	0,1400738	29,572205	3	0,5263329	0,5731726	0,1400738
2	0,6284754	0,6284754	0,1063948	16,929036	2	0,3715246	0,3715246	0,1063948
2	0,5288283	0,5288283	0,1895612	35,845502	2	0,4711717	0,4711717	0,1895612
3	0,3722152	0,3591885	0,0372494	10,007489	3	0,6277848	0,6408115	0,0372494
3	0,7336665	0,7668228	0,0794076	10,823396	3	0,2663335	0,2331772	0,0794076
5	0,6451399	0,6462935	0,0561217	8,6991455	5	0,3548601	0,3537065	0,0561217
3	0,4941767	0,4788032	0,0272641	5,5170774	3	0,5058233	0,5211968	0,0272641
4	0,4952084	0,4811748	0,0766081	15,469871	4	0,5047916	0,5188252	0,0766081
4	0,6303828	0,6684928	0,1335041	21,178252	4	0,3696172	0,3315072	0,1335041
2	0,3195239	0,3195239	0,0985578	30,845199	2	0,6804761	0,6804761	0,0985578
3	0,3203539	0,3136868	0,0416622	13,005055	3	0,6796461	0,6863132	0,0416622
5	0,3536914	0,3496158	0,0177138	5,0082534	5	0,6463086	0,6503842	0,0177138
4	0,6770173	0,7118558	0,0952866	14,074465	4	0,3229827	0,2881442	0,0952866
3	0,8003071	0,8233952	0,0488069	6,0985223	3	0,1996929	0,1766048	0,0488069
3	0,777213	0,8602597	0,1608628	20,69739	3	0,222787	0,1397403	0,1608628
3	0,364749	0,3932785	0,0596482	16,353208	3	0,635251	0,6067215	0,0596482
2	0,2256494	0,2256494	0,221615	98,212097	2	0,7743506	0,7743506	0,221615
3	0,4176838	0,3723606	0,1056932	25,304586	3	0,5823162	0,6276394	0,1056932
3	0,327785	0,3413787	0,033383	10,184422	3	0,672215	0,6586213	0,033383
4	0,4846589	0,4888634	0,0651072	13,433615	4	0,5153411	0,5111366	0,0651072
5	0,4688394	0,4688285	0,0264623	5,6442156	5	0,5311606	0,5311715	0,0264623
3	0,8557003	0,8602811	0,0296919	3,4698934	3	0,1442997	0,1397189	0,0296919
5	0,663837	0,7152491	0,1177474	17,737393	5	0,336163	0,2847509	0,1177474
7	0,7847486	0,7715363	0,0572364	7,2936025	7	0,2152514	0,2284637	0,0572364
3	0,3525366	0,3483468	0,0487932	13,840617	3	0,6474634	0,6516532	0,0487932
3	0,8260503	0,8130739	0,0270778	3,2779842	3	0,1739497	0,1869261	0,0270778
4	0,5420289	0,5435655	0,2103478	38,807498	4	0,4579711	0,4564345	0,2103478
7	0,3932457	0,360234	0,1170112	29,755253	7	0,6067543	0,639766	0,1170112
5	0,4857408	0,4569953	0,0708051	14,576727	5	0,5142592	0,5430047	0,0708051
2	0,317303	0,317303	0,17844	56,236452	2	0,682697	0,682697	0,17844
3	0,5393108	0,5791277	0,0977089	18,11736	3	0,4606892	0,4208723	0,0977089
4	0,7026398	0,7015382	0,0502888	7,1571215	4	0,2973602	0,2984618	0,0502888
4	0,5173599	0,4925496	0,136983	26,477308	4	0,4826401	0,5074504	0,136983
3	0,3346211	0,3369467	0,0215119	6,4287338	3	0,6653789	0,6630533	0,0215119
4	0,5138107	0,4761955	0,1224547	23,832654	4	0,4861893	0,5238045	0,1224547
3	0,5040215	0,5793711	0,1393006	27,637838	3	0,4959785	0,4206289	0,1393006
4	0,7230605	0,7998643	0,1772807	24,518094	4	0,2769395	0,2001357	0,1772807
5	0,5238608	0,3706992	0,2642023	50,433677	5	0,4761392	0,6293008	0,2642023
3	0,3935406	0,4008325	0,0904971	22,995628	3	0,6064594	0,5991675	0,0904971
2	0,4863432	0,4863432	0,009667	1,9876904	2	0,5136568	0,5136568	0,009667
3	0,8119544	0,8069452	0,0294369	3,6254392	3	0,1880456	0,1930548	0,0294369
3	0,4493598	0,4431053	0,0415872	9,2547648	3	0,5506402	0,5568947	0,0415872
3	0,449064	0,4324282	0,0540756	12,041847	3	0,550936	0,5675718	0,0540756
3	0,4630586	0,3984054	0,1262726	27,269238	3	0,5369414	0,6015946	0,1262726
3	0,4731882	0,4830624	0,0518288	10,953104	3	0,5268118	0,5169376	0,0518288
3	0,4868391	0,4413985	0,1928581	39,61435	3	0,5131609	0,5586015	0,1928581
3	0,652981	0,6008082	0,0933531	14,296455	3	0,347019	0,3991918	0,0933531
3	0,3878482	0,4347318	0,0990488	25,538027	3	0,6121518	0,5652682	0,0990488

3	0,3981425	0,4184565	0,0864407	21,710985	3	0,6018575	0,5815435	0,0864407
6	0,7450398	0,7523779	0,0814164	10,927792	6	0,2549602	0,2476221	0,0814164
2	0,3302837	0,3302837	0,0362516	10,975893	2	0,6697163	0,6697163	0,0362516
3	0,3380524	0,3482958	0,0523327	15,480642	3	0,6619476	0,6517042	0,0523327
4	0,6908732	0,6952294	0,0673186	9,7439822	4	0,3091268	0,3047706	0,0673186
3	0,4754409	0,46151	0,0882391	18,559426	3	0,5245591	0,53849	0,0882391
3	0,5382287	0,5771717	0,0925765	17,200214	3	0,4617713	0,4228283	0,0925765
2	0,3143356	0,3143356	0,042041	13,374552	2	0,6856644	0,6856644	0,042041
6	0,4474684	0,4294683	0,0538841	12,041989	6	0,5525316	0,5705317	0,0538841
3	0,5152728	0,5446805	0,187119	36,314559	3	0,4847272	0,4553195	0,187119
2	0,5739146	0,5739146	0,0943617	16,441771	2	0,4260854	0,4260854	0,0943617
4	0,7954878	0,7922778	0,026636	3,3483915	4	0,2045122	0,2077222	0,026636
4	0,4989633	0,5168213	0,06723	13,473936	4	0,5010367	0,4831787	0,06723
2	0,7080469	0,7080469	0,0499909	7,0603896	2	0,2919531	0,2919531	0,0499909
3	0,6255405	0,6249503	0,0794525	12,701414	3	0,3744595	0,3750497	0,0794525
2	0,3680915	0,3680915	0,2175845	59,111517	2	0,6319085	0,6319085	0,2175845
2	0,6173093	0,6173093	0,2976406	48,215805	2	0,3826907	0,3826907	0,2976406
3	0,5376281	0,5967051	0,1256468	23,370572	3	0,4623719	0,4032949	0,1256468
4	0,5699675	0,5274505	0,1955398	34,307189	4	0,4300325	0,4725495	0,1955398
2	0,4930647	0,4930647	0,1891657	38,365289	2	0,5069353	0,5069353	0,1891657
4	0,3778028	0,371613	0,0306095	8,1019666	4	0,6221972	0,628387	0,0306095
3	0,3325959	0,3525023	0,060948	18,32495	3	0,6674041	0,6474977	0,060948
2	0,549557	0,549557	0,2992561	54,454063	2	0,450443	0,450443	0,2992561
3	0,5396495	0,554786	0,1083103	20,070491	3	0,4603505	0,445214	0,1083103
5	0,7097073	0,7525667	0,1080111	15,219104	5	0,2902927	0,2474333	0,1080111
8	0,4204728	0,4016203	0,0805271	19,151563	8	0,5795272	0,5983797	0,0805271
2	0,3914326	0,3914326	0,0754731	19,281243	2	0,6085674	0,6085674	0,0754731
3	0,4009634	0,4030033	0,0064468	1,6078197	3	0,5990366	0,5969967	0,0064468
3	0,3570236	0,3655734	0,0212915	5,963623	3	0,6429764	0,6344266	0,0212915
2	0,4273673	0,4273673	0,2580626	60,384254	2	0,5726327	0,5726327	0,2580626
3	0,5361879	0,537333	0,0045343	0,8456592	3	0,4638121	0,462667	0,0045343
2	0,2555712	0,2555712	0,022467	8,7908949	2	0,7444288	0,7444288	0,022467
2	0,383461	0,383461	0,0068405	1,7838738	2	0,616539	0,616539	0,0068405
3	0,681015	0,653759	0,0546988	8,0319572	3	0,318985	0,346241	0,0546988
2	0,5484225	0,5484225	0,1476231	26,917771	2	0,4515775	0,4515775	0,1476231
2	0,5829257	0,5829257	0,0368408	6,3199792	2	0,4170743	0,4170743	0,0368408
3	0,7122207	0,7282105	0,0471393	6,618633	3	0,2877793	0,2717895	0,0471393
2	0,3461576	0,3461576	0,0970819	28,045571	2	0,6538424	0,6538424	0,0970819
3	0,7850098	0,7946237	0,0228808	2,9147174	3	0,2149902	0,2053763	0,0228808
2	0,273502	0,273502	0,0788562	28,832045	2	0,726498	0,726498	0,0788562
3	0,4200999	0,42221	0,1434938	34,15707	3	0,5799001	0,57779	0,1434938
2	0,363331	0,363331	0,1464363	40,303837	2	0,636669	0,636669	0,1464363
3	0,4671131	0,4307524	0,0812072	17,384903	3	0,5328869	0,5692476	0,0812072
3	0,3744749	0,3809851	0,0820996	21,923924	3	0,6255251	0,6190149	0,0820996
2	0,6797185	0,6797185	0,0860407	12,658292	2	0,3202815	0,3202815	0,0860407
2	0,5208674	0,5208674	0,2088449	40,09559	2	0,4791326	0,4791326	0,2088449
3	0,4104822	0,4094548	0,0068373	1,6656699	3	0,5895178	0,5905452	0,0068373
3	0,4618976	0,462838	0,0024339	0,5269289	3	0,5381024	0,537162	0,0024339
3	0,4098866	0,394422	0,084396	20,590081	3	0,5901134	0,605578	0,084396
4	0,4521206	0,4149807	0,1007608	22,286268	4	0,5478794	0,5850193	0,1007608
3	0,6996678	0,6848073	0,0265132	3,7894025	3	0,3003322	0,3151927	0,0265132
4	0,6789695	0,6764029	0,0870188	12,816303	4	0,3210305	0,3235971	0,0870188

2	0,3720141	0,3720141	0,0086552	2,3265873	2	0,6279859	0,6279859	0,0086552
3	0,4350743	0,4013195	0,060814	13,977842	3	0,5649257	0,5986805	0,060814
2	0,3651919	0,3651919	0,0845992	23,165673	2	0,6348081	0,6348081	0,0845992
2	0,3938301	0,3938301	0,0417557	10,602467	2	0,6061699	0,6061699	0,0417557
2	0,7006014	0,7006014	0,0678648	9,6866435	2	0,2993986	0,2993986	0,0678648
3	0,3436207	0,3114682	0,1145768	33,343964	3	0,6563793	0,6885318	0,1145768
2	0,6049353	0,6049353	0,137739	22,769216	2	0,3950647	0,3950647	0,137739
2	0,8126442	0,8126442	0,0147581	1,816057	2	0,1873558	0,1873558	0,0147581
2	0,3947256	0,3947256	0,0797451	20,202672	2	0,6052744	0,6052744	0,0797451
2	0,4705446	0,4705446	0,0298283	6,3391016	2	0,5294554	0,5294554	0,0298283
4	0,418699	0,4209118	0,0195693	4,673841	4	0,581301	0,5790882	0,0195693
2	0,4723696	0,4723696	0,0775931	16,426352	2	0,5276304	0,5276304	0,0775931
3	0,470896	0,4368997	0,1900535	40,359977	3	0,529104	0,5631003	0,1900535
2	0,3326496	0,3326496	0,0157559	4,7364957	2	0,6673504	0,6673504	0,0157559
3	0,42843	0,435913	0,0442058	10,318101	3	0,57157	0,564087	0,0442058
3	0,5382651	0,5999317	0,1454639	27,02459	3	0,4617349	0,4000683	0,1454639
2	0,3989948	0,3989948	0,1115753	27,964089	2	0,6010052	0,6010052	0,1115753
2	0,5000282	0,5000282	0,0315347	6,3065934	2	0,4999718	0,4999718	0,0315347
4	0,3449255	0,3496728	0,0479205	13,892989	4	0,6550745	0,6503272	0,0479205
2	0,7442101	0,7442101	0,096663	12,988667	2	0,2557899	0,2557899	0,096663
2	0,6670056	0,6670056	0,0696098	10,436162	2	0,3329944	0,3329944	0,0696098
3	0,5163588	0,5380376	0,096699	18,727089	3	0,4836412	0,4619624	0,096699
2	0,3635763	0,3635763	0,0121181	3,3330189	2	0,6364237	0,6364237	0,0121181
3	0,5524389	0,5603033	0,1311129	23,733458	3	0,4475611	0,4396967	0,1311129
2	0,3123199	0,3123199	0,0855123	27,379713	2	0,6876801	0,6876801	0,0855123
3	0,2987841	0,3194516	0,0997717	33,392586	3	0,7012159	0,6805484	0,0997717
2	0,4965007	0,4965007	0,0887533	17,875765	2	0,5034993	0,5034993	0,0887533
3	0,469743	0,471987	0,0059521	1,2671056	3	0,530257	0,528013	0,0059521
2	0,515535	0,515535	0,0077783	1,5087845	2	0,484465	0,484465	0,0077783
2	0,3943872	0,3943872	0,0020046	0,5082869	2	0,6056128	0,6056128	0,0020046
3	0,7177799	0,6969917	0,049337	6,8735522	3	0,2822201	0,3030083	0,049337
2	0,7468367	0,7468367	0,0228205	3,0556209	2	0,2531633	0,2531633	0,0228205
3	0,5010564	0,5025348	0,0130637	2,6072262	3	0,4989436	0,4974652	0,0130637
2	0,8264172	0,8264172	0,0114017	1,3796553	2	0,1735828	0,1735828	0,0114017
5	0,4965308	0,3598267	0,2044835	41,182434	5	0,5034692	0,6401733	0,2044835
2	0,5595242	0,5595242	0,080806	14,441915	2	0,4404758	0,4404758	0,080806
3	0,4985084	0,4452093	0,100282	20,116402	3	0,5014916	0,5547907	0,100282
3	0,5838311	0,5968523	0,0372893	6,3870051	3	0,4161689	0,4031477	0,0372893
4	0,4509945	0,4266438	0,0650456	14,422702	4	0,5490055	0,5733562	0,0650456
4	0,7184103	0,7046803	0,0448271	6,2397651	4	0,2815897	0,2953197	0,0448271
2	0,5814288	0,5814288	0,0402423	6,9212747	2	0,4185712	0,4185712	0,0402423
2	0,8441253	0,8441253	0,0203208	2,4073154	2	0,1558747	0,1558747	0,0203208
3	0,4036118	0,4024974	0,0283626	7,0271895	3	0,5963882	0,5975026	0,0283626
2	0,4793021	0,4793021	0,0044238	0,9229719	2	0,5206979	0,5206979	0,0044238
3	0,7529242	0,767067	0,0422318	5,6090402	3	0,2470758	0,232933	0,0422318
4	0,4986805	0,4726381	0,0970327	19,457897	4	0,5013195	0,5273619	0,0970327
2	0,5860002	0,5860002	0,0112074	1,9125232	2	0,4139998	0,4139998	0,0112074
2	0,4343997	0,4343997	0,0675636	15,553318	2	0,5656003	0,5656003	0,0675636
2	0,5728732	0,5728732	0,1979262	34,549749	2	0,4271268	0,4271268	0,1979262
2	0,5868894	0,5868894	0,1380417	23,520913	2	0,4131106	0,4131106	0,1380417
3	0,614756	0,6152594	0,0337435	5,4889204	3	0,385244	0,3847406	0,0337435
2	0,6350889	0,6350889	0,0864715	13,615659	2	0,3649111	0,3649111	0,0864715

5	0,3451464	0,3173327	0,0450494	13,052245	5	0,6548536	0,6826673	0,0450494
2	0,5046462	0,5046462	0,0689347	13,660005	2	0,4953538	0,4953538	0,0689347
3	0,4026041	0,4708432	0,1324948	32,909449	3	0,5973959	0,5291568	0,1324948
2	0,6023662	0,6023662	0,1094188	18,16484	2	0,3976338	0,3976338	0,1094188
2	0,5378077	0,5378077	0,1171842	21,78924	2	0,4621923	0,4621923	0,1171842
2	0,7243946	0,7243946	0,171139	23,625106	2	0,2756054	0,2756054	0,171139
2	0,3518935	0,3518935	0,0679029	19,296439	2	0,6481065	0,6481065	0,0679029
2	0,4201511	0,4201511	0,0268849	6,3988749	2	0,5798489	0,5798489	0,0268849
3	0,4759263	0,4667651	0,0970737	20,396789	3	0,5240737	0,5332349	0,0970737
5	0,3803661	0,3789243	0,0758616	19,944355	5	0,6196339	0,6210757	0,0758616
2	0,4733747	0,4733747	0,1367673	28,891973	2	0,5266253	0,5266253	0,1367673
2	0,4723224	0,4723224	0,0481873	10,202207	2	0,5276776	0,5276776	0,0481873
2	0,6104758	0,6104758	0,0038539	0,6312937	2	0,3895242	0,3895242	0,0038539
4	0,4196031	0,4343043	0,052864	12,598576	4	0,5803969	0,5656957	0,052864
2	0,388492	0,388492	0,069691	17,938845	2	0,611508	0,611508	0,069691
2	0,342801	0,342801	0,0061878	1,8050666	2	0,657199	0,657199	0,0061878
2	0,3953482	0,3953482	0,1634008	41,330841	2	0,6046518	0,6046518	0,1634008
3	0,590215	0,607234	0,0586055	9,9295228	3	0,409785	0,392766	0,0586055
2	0,7381415	0,7381415	0,0753326	10,205709	2	0,2618585	0,2618585	0,0753326
3	0,3287499	0,3046971	0,0418191	12,720649	3	0,6712501	0,6953029	0,0418191
3	0,6354392	0,6185445	0,0301216	4,74028	3	0,3645608	0,3814555	0,0301216
2	0,4090818	0,4090818	0,0375133	9,1701218	2	0,5909182	0,5909182	0,0375133
2	0,4859975	0,4859975	0,1417567	29,168191	2	0,5140025	0,5140025	0,1417567
2	0,4376234	0,4376234	0,0674037	15,402228	2	0,5623766	0,5623766	0,0674037
3	0,3966868	0,3862025	0,0193153	4,8691443	3	0,6033132	0,6137975	0,0193153
4	0,5738257	0,5614483	0,0415525	7,2413092	4	0,4261743	0,4385517	0,0415525
4	0,4404688	0,3218517	0,2701474	61,331781	4	0,5595312	0,6781483	0,2701474
4	0,6420649	0,6164381	0,0744476	11,595027	4	0,3579351	0,3835619	0,0744476
4	0,6642261	0,6578687	0,0531228	7,9977039	4	0,3357739	0,3421313	0,0531228
5	0,4618967	0,4004313	0,1082697	23,440249	5	0,5381033	0,5995687	0,1082697
4	0,4200664	0,4224046	0,0076286	1,8160555	4	0,5799336	0,5775954	0,0076286
4	0,6389884	0,6460491	0,0304544	4,7660349	4	0,3610116	0,3539509	0,0304544
2	0,3533199	0,3533199	0,024951	7,0618812	2	0,6466801	0,6466801	0,024951
3	0,4577962	0,4707195	0,0497083	10,858176	3	0,5422038	0,5292805	0,0497083
4	0,7877957	0,786647	0,0402403	5,1079614	4	0,2122043	0,213353	0,0402403
2	0,2676867	0,2676867	0,0746068	27,870936	2	0,7323133	0,7323133	0,0746068
4	0,4913525	0,493203	0,0891964	18,153233	4	0,5086475	0,506797	0,0891964
3	0,5642242	0,6130689	0,0924417	16,383851	3	0,4357758	0,3869311	0,0924417
2	0,4320834	0,4320834	0,0225469	5,2181871	2	0,5679166	0,5679166	0,0225469
2	0,3853319	0,3853319	0,0285487	7,4088536	2	0,6146681	0,6146681	0,0285487
4	0,5186177	0,5315664	0,0456996	8,8118111	4	0,4813823	0,4684336	0,0456996
2	0,3324024	0,3324024	0,1189809	35,79424	2	0,6675976	0,6675976	0,1189809
2	0,6856992	0,6856992	0,0028753	0,4193191	2	0,3143008	0,3143008	0,0028753
3	0,6226718	0,6765054	0,1132254	18,183805	3	0,3773282	0,3234946	0,1132254
2	0,3891998	0,3891998	0,0227693	5,8502896	2	0,6108002	0,6108002	0,0227693
2	0,4176926	0,4176926	0,0933763	22,355279	2	0,5823074	0,5823074	0,0933763
2	0,4301455	0,4301455	0,0795399	18,491383	2	0,5698545	0,5698545	0,0795399
2	0,436113	0,436113	0,0168489	3,8634331	2	0,563887	0,563887	0,0168489
2	0,3359297	0,3359297	0,0636909	18,959581	2	0,6640703	0,6640703	0,0636909
2	0,3630626	0,3630626	0,0628659	17,315449	2	0,6369374	0,6369374	0,0628659
2	0,4734985	0,4734985	0,0262161	5,5366848	2	0,5265015	0,5265015	0,0262161
6	0,5221986	0,515203	0,1035431	19,828308	6	0,4778014	0,484797	0,1035431

2	0,2961457	0,2961457	0,0067248	2,2707747	2	0,7038543	0,7038543	0,0067248
2	0,490789	0,490789	0,0962295	19,607095	2	0,509211	0,509211	0,0962295
3	0,334551	0,3395282	0,0350724	10,483414	3	0,665449	0,6604718	0,0350724
2	0,7483061	0,7483061	0,0306018	4,089476	2	0,2516939	0,2516939	0,0306018
2	0,3513683	0,3513683	0,1335968	38,02187	2	0,6486317	0,6486317	0,1335968
3	0,4170261	0,396933	0,0599064	14,365148	3	0,5829739	0,603067	0,0599064
2	0,368117	0,368117	0,0922459	25,058866	2	0,631883	0,631883	0,0922459
3	0,5333727	0,4602386	0,127822	23,964859	3	0,4666273	0,5397614	0,127822
2	0,8016946	0,8016946	0,0933329	11,641951	2	0,1983054	0,1983054	0,0933329
4	0,5216567	0,5206042	0,0387643	7,4309907	4	0,4783433	0,4793958	0,0387643
2	0,3990244	0,3990244	0,1691908	42,40112	2	0,6009756	0,6009756	0,1691908
2	0,5265929	0,5265929	0,0292609	5,5566537	2	0,4734071	0,4734071	0,0292609
3	0,4336436	0,3983049	0,0650717	15,005793	3	0,5663564	0,6016951	0,0650717
2	0,3342079	0,3342079	0,0285582	8,5450356	2	0,6657921	0,6657921	0,0285582
3	0,4828867	0,4790673	0,084709	17,542219	3	0,5171133	0,5209327	0,084709
2	0,6183622	0,6183622	0,0118167	1,9109624	2	0,3816378	0,3816378	0,0118167
3	0,4446322	0,4265205	0,055523	12,48739	3	0,5553678	0,5734795	0,055523
3	0,7852044	0,8202174	0,0850334	10,829455	3	0,2147956	0,1797826	0,0850334
2	0,4374679	0,4374679	0,2529479	57,820901	2	0,5625321	0,5625321	0,2529479
2	0,5334444	0,5334444	0,0801558	15,026076	2	0,4665556	0,4665556	0,0801558
2	0,5216688	0,5216688	0,0499387	9,5728716	2	0,4783312	0,4783312	0,0499387
3	0,5800259	0,5729065	0,0227555	3,9231954	3	0,4199741	0,4270935	0,0227555
5	0,3892462	0,371846	0,0452036	11,613101	5	0,6107538	0,628154	0,0452036
2	0,4420702	0,4420702	0,0608779	13,771094	2	0,5579298	0,5579298	0,0608779
2	0,4650476	0,4650476	0,0832381	17,898832	2	0,5349524	0,5349524	0,0832381
2	0,630082	0,630082	0,0167479	2,6580472	2	0,369918	0,369918	0,0167479
3	0,6425166	0,738265	0,1915633	29,814527	3	0,3574834	0,261735	0,1915633
2	0,4039791	0,4039791	0,0567412	14,045574	2	0,5960209	0,5960209	0,0567412
3	0,4271158	0,4394558	0,0468914	10,978628	3	0,5728842	0,5605442	0,0468914
2	0,4834231	0,4834231	0,0287427	5,9456633	2	0,5165769	0,5165769	0,0287427
2	0,3291117	0,3291117	0,0052494	1,5950165	2	0,6708883	0,6708883	0,0052494
2	0,4761213	0,4761213	0,10904	22,901737	2	0,5238787	0,5238787	0,10904
3	0,3797556	0,3887324	0,0389319	10,251823	3	0,6202444	0,6112676	0,0389319
2	0,5397977	0,5397977	0,1518013	28,121882	2	0,4602023	0,4602023	0,1518013
2	0,6190865	0,6190865	0,0498547	8,0529518	2	0,3809135	0,3809135	0,0498547
4	0,4890031	0,4964955	0,0384035	7,8534229	4	0,5109969	0,5035045	0,0384035
2	0,6107673	0,6107673	0,1805044	29,553704	2	0,3892327	0,3892327	0,1805044
3	0,6539884	0,6563567	0,0611702	9,3534012	3	0,3460116	0,3436433	0,0611702
2	0,5346548	0,5346548	0,2784833	52,086564	2	0,4653452	0,4653452	0,2784833
2	0,5500304	0,5500304	0,1341746	24,39404	2	0,4499696	0,4499696	0,1341746
2	0,3332103	0,3332103	0,0336881	10,110174	2	0,6667897	0,6667897	0,0336881
2	0,4033602	0,4033602	0,0328546	8,145234	2	0,5966398	0,5966398	0,0328546
2	0,37112	0,37112	0,0259688	6,9974052	2	0,62888	0,62888	0,0259688
2	0,3958665	0,3958665	0,0007546	0,1906127	2	0,6041335	0,6041335	0,0007546
2	0,5763957	0,5763957	0,2012337	34,912426	2	0,4236043	0,4236043	0,2012337
3	0,2523688	0,2451987	0,0344049	13,632799	3	0,7476312	0,7548013	0,0344049
2	0,490853	0,490853	0,2295891	46,773483	2	0,509147	0,509147	0,2295891
2	0,737163	0,737163	0,0307425	4,1703836	2	0,262837	0,262837	0,0307425
3	0,3814924	0,3721437	0,0231602	6,0709501	3	0,6185076	0,6278563	0,0231602
2	0,5252248	0,5252248	0,0213625	4,0673109	2	0,4747752	0,4747752	0,0213625
2	0,3593997	0,3593997	0,0352413	9,8056124	2	0,6406003	0,6406003	0,0352413
2	0,5779429	0,5779429	0,0819305	14,176227	2	0,4220571	0,4220571	0,0819305

2	0,5610146	0,5610146	0,0393816	7,0197023	2	0,4389854	0,4389854	0,0393816
5	0,4144991	0,3959923	0,0756436	18,249392	5	0,5855009	0,6040077	0,0756436
3	0,6304326	0,7425846	0,197829	31,37988	3	0,3695674	0,2574154	0,197829
2	0,4429141	0,4429141	0,0772593	17,443402	2	0,5570859	0,5570859	0,0772593
2	0,5087724	0,5087724	0,061299	12,048416	2	0,4912276	0,4912276	0,061299
3	0,5437967	0,5647831	0,0471535	8,6711687	3	0,4562033	0,4352169	0,0471535
2	0,6258889	0,6258889	0,0108959	1,7408655	2	0,3741111	0,3741111	0,0108959
2	0,4649024	0,4649024	0,0646496	13,906048	2	0,5350976	0,5350976	0,0646496
2	0,4291651	0,4291651	0,0248493	5,7901591	2	0,5708349	0,5708349	0,0248493
2	0,4306637	0,4306637	0,1851791	42,998549	2	0,5693363	0,5693363	0,1851791
2	0,4993997	0,4993997	0,0690415	13,824905	2	0,5006003	0,5006003	0,0690415
3	0,5276834	0,5424543	0,0273236	5,1780198	3	0,4723166	0,4575457	0,0273236
2	0,6307113	0,6307113	0,0318248	5,0458641	2	0,3692887	0,3692887	0,0318248
3	0,5254458	0,5733916	0,0974505	18,546245	3	0,4745542	0,4266084	0,0974505
2	0,5790946	0,5790946	0,1046641	18,073741	2	0,4209054	0,4209054	0,1046641
2	0,5338588	0,5338588	0,1530593	28,670377	2	0,4661412	0,4661412	0,1530593
3	0,5425345	0,5399515	0,0404201	7,4502409	3	0,4574655	0,4600485	0,0404201
2	0,4166547	0,4166547	0,1430113	34,323698	2	0,5833453	0,5833453	0,1430113
2	0,4205105	0,4205105	0,0678349	16,131561	2	0,5794895	0,5794895	0,0678349
2	0,5407803	0,5407803	0,0418723	7,7429493	2	0,4592197	0,4592197	0,0418723
2	0,7681544	0,7681544	0,0165481	2,1542625	2	0,2318456	0,2318456	0,0165481
2	0,3715187	0,3715187	0,0683891	18,407983	2	0,6284813	0,6284813	0,0683891
2	0,4786399	0,4786399	0,0248897	5,2000921	2	0,5213601	0,5213601	0,0248897
2	0,50004	0,50004	0,2131283	42,622251	2	0,49996	0,49996	0,2131283
2	0,361441	0,361441	0,1241126	34,338269	2	0,638559	0,638559	0,1241126
2	0,6237265	0,6237265	0,0384164	6,1591781	2	0,3762735	0,3762735	0,0384164
2	0,5852145	0,5852145	0,0386553	6,6053147	2	0,4147855	0,4147855	0,0386553
2	0,4931655	0,4931655	0,230227	46,683528	2	0,5068345	0,5068345	0,230227
2	0,5601288	0,5601288	0,1235015	22,048763	2	0,4398712	0,4398712	0,1235015
2	0,6271257	0,6271257	0,1707503	27,227446	2	0,3728743	0,3728743	0,1707503

CV (%)	IR.N(116/114_UP/CMV)				IR.N(117/115_SI/CTRL)			
	#Quantif	Mean	Median	tTest (pValue	#Quanti	Mean	Median	tTest (nr
28,800389	132/132	0,85536645	0,88908517	***	2,8756E-15	132/132	1,38055634	1,424340789 ***
47,190217	86/86	0,72811262	0,73649941	***	1,4174E-40	86/86	1,72550618	1,503775344 ***
44,091024	112/112	0,81284981	0,79626695	***	1,8505E-17	112/112	1,42781309	1,961836423 ***
30,311542	151/151	0,65139905	0,65924166	***	1,302E-99	151/151	4,57205982	4,899772705 ***
36,698034	104/104	1,30877871	1,28369432	***	7,0099E-37	104/104	3,69465587	4,123759712 ***
25,365668	49/49	0,86052455	0,84758396	***	2,0115E-09	49/49	1,86737075	2,096320794 ***
30,387733	30/30	0,9491304	0,9734897		0,0747696	30/30	1,37594233	1,461154432 ***
23,060264	47/47	1,5617302	1,59528892	***	4,7112E-25	47/47	1,0717055	0,989895304 NS
39,31557	57/57	0,74359934	0,73114327	***	8,7506E-23	57/57	2,4678693	2,874644969 ***
23,362882	39/39	1,15000197	1,17491911	***	8,1496E-10	39/39	0,6946321	0,60183609 ***
29,729432	31/31	0,57317655	0,58009238	***	1,9816E-23	31/31	2,34433331	2,427843735 ***
17,829478	24/24	0,8689941	0,87643446	***	4,9221E-07	24/24	0,66325391	0,634441023 ***
30,190302	45/45	0,6355615	0,6481491	***	4,9772E-22	45/45	2,49437684	2,634500082 ***
29,018229	33/33	1,50478704	1,56717426	***	1,167E-16	33/33	3,13510807	3,164313292 ***
14,321325	48/48	0,9831304	1,0253431		0,5177782	48/48	0,56946117	0,532423982 ***
23,030841	18/18	0,7513867	0,81569839	***	1,2413E-07	18/18	0,8991501	1,000340349 NS
17,299365	63/63	1,05344745	1,05042564	**	0,00576018	63/63	0,63779168	0,596853642 ***
38,386445	27/27	0,941144	0,8775345		0,2277093	27/27	1,6679729	1,736783355 ***
28,54968	6/6	1,0344279	1,0133478		0,4945104	6/6	1,0152732	1,163240811 NS
33,361309	18/18	0,9674903	0,9942097		0,3843584	18/18	4,33752186	5,137575763 ***
18,555808	53/53	0,74979939	0,77770231	***	1,1284E-15	53/53	0,554547	0,504601139 ***
17,334269	25/25	0,67605964	0,71072904	***	2,9382E-10	25/25	1,71299831	1,721579709 ***
8,9110258	2/2	2,31913491	2,31913491	**	0,00384424	2/2	3,43748057	3,437480569 **
25,942479	3/3	2,27104404	2,4894146	**	0,00556153	3/3	3,25048781	3,772339817 ***
7,0347957	5/5	1,36356903	1,26525178	**	0,00231297	5/5	0,65149185	0,637381198 ***
14,079835	20/20	0,9611461	1,0046031		0,150129	20/20	0,66052839	0,668678515 ***
19,477474	2/2	2,70358637	2,70358637	**	0,00119399	2/2	3,62558018	3,625580182 **
16,682498	19/19	1,09249949	1,16408424		0,1290343	19/19	1,0189088	1,053519689 NS
16,015466	21/21	0,79003972	0,81567304	***	1,4225E-07	21/21	0,69005124	0,639254024 ***
18,692245	4/4	0,8724674	0,8132237		0,1400396	4/4	2,16508203	2,098083878 ***
27,454088	29/29	1,84676785	1,83733587	***	6,2108E-21	29/29	0,84091391	0,852969202 *
22,658034	13/13	0,54896905	0,49069964	***	3,0857E-07	13/13	2,54816408	2,581093862 ***
9,9547284	3/3	1,2965217	1,2319486		0,0921207	3/3	2,74187397	2,76198218 ***
23,43564	17/17	0,71712697	0,72383686	***	7,8267E-07	17/17	0,68508853	0,654612069 ***
14,031141	10/10	1,22212896	1,11997385	*	0,01482096	10/10	4,81230619	5,213213614 ***
18,763072	12/12	1,0186324	0,988941		0,630816	12/12	0,78673495	0,710454998 *
18,229336	43/43	1,05586171	1,11233271		0,0690753	43/43	1,0105201	1,036135098 NS
23,661338	27/27	1,21335381	1,26214708	***	1,4755E-05	27/27	1,66263241	1,760280847 ***
20,671936	35/35	0,93993014	0,94719296	**	0,00158909	35/35	1,18076076	1,309013044 ***
15,303073	7/7	1,1637517	0,9904445		0,0941436	7/7	0,8828955	0,793333445 NS
24,735092	23/23	2,27896087	2,59976051	***	9,7587E-14	23/23	1,20614542	1,210344836 **
37,217236	24/24	0,8748581	0,92833754	**	0,00515402	24/24	2,38655104	2,34867959 ***
25,358377	40/40	0,73358398	0,70108316	***	2,2304E-15	40/40	0,82456256	0,693128967 **
27,921788	25/25	1,28776026	1,38480955	***	9,1513E-06	25/25	1,91074033	2,271866839 ***
71,126469	2/2	1,96747447	1,96747447	***	7,9213E-05	2/2	1,0464084	1,046408445 NS
20,166125	21/21	0,972258	0,9778885		0,4145734	21/21	0,83331103	0,942539068 *
19,803442	14/14	1,0338637	1,124015		0,7596753	14/14	0,69725598	0,664556281 ***
25,423915	19/19	1,40488116	1,30145302	***	3,1228E-10	19/19	1,90539996	2,284261272 ***
21,957883	19/19	1,22428919	1,26453572	***	1,227E-05	19/19	0,73811158	0,647146856 ***
22,167242	44/44	1,30079412	1,35481689	***	2,9308E-10	44/44	0,76467313	0,79738855 ***

53,636979 6/6	0,59938951	0,50480273 ***	0,00018159 6/6	1,83429511	2,508122312 *
43,949574 9/9	0,68054686	0,5872948 ***	0,00047177 9/9	1,63882295	1,826674511 **
31,273783 21/21	1,08586934	1,08290108 *	0,02549132 21/21	2,27347626	2,159255146 ***
12,196029 8/8	0,59646574	0,59212351 ***	2,2503E-07 8/8	1,13945402	1,178087523 *
25,30328 34/34	1,38640536	1,29544136 ***	3,8942E-15 34/34	1,49401255	1,590541789 ***
11,055082 21/21	1,21246328	1,21389005 ***	1,3941E-12 21/21	0,74218564	0,751445866 ***
13,466613 24/24	0,88977953	0,9139105 *	0,04938505 24/24	0,44827213	0,41028717 ***
15,89161 12/12	1,5368183	1,5564902 **	0,00138847 12/12	1,20238781	1,289343904 **
29,467685 23/23	0,76418339	0,80446656 ***	7,0941E-10 23/23	1,1548061	0,935520986 NS
15,584008 17/17	1,15023683	1,1992881 **	0,00219324 17/17	0,82059182	0,854769411 **
15,811798 9/9	1,23233886	1,19170182 **	0,00148148 9/9	0,74101791	0,757355733 **
13,960974 14/14	1,27748642	1,32224464 ***	7,4985E-06 14/14	0,9094504	0,993175474 NS
20,539186 16/16	0,936079	0,9906233	0,2297256 16/16	0,68027818	0,682210264 ***
23,534187 15/15	0,9413875	0,9213882	0,1510138 15/15	0,76709135	0,655618466 *
40,323655 22/22	1,40069198	1,54704027 ***	2,2014E-07 22/22	2,22492221	2,772616375 ***
12,149897 16/16	0,86648912	0,87703374 ***	0,00055456 16/16	0,53538787	0,57809387 ***
20,413123 22/22	0,67988842	0,71217907 ***	2,8498E-15 22/22	0,69330021	0,756714241 ***
20,841693 24/24	0,9370082	1,0809758	0,1880417 24/24	0,80082337	0,845863709 **
15,407098 17/17	1,0221294	1,0526495	0,5081706 17/17	0,73556084	0,672422306 ***
21,228375 16/16	1,18336951	1,09116088 **	0,00610419 16/16	0,79351679	0,909953563 **
23,456977 23/23	0,83378077	0,91128873 ***	5,084E-07 23/23	0,71234406	0,738548019 ***
23,519536 23/23	1,52429823	1,82938364 ***	1,6866E-08 23/23	0,66694626	0,73517903 ***
25,674728 26/26	0,65638392	0,6789475 ***	3,9663E-11 26/26	1,37931993	1,357070217 ***
30,659375 17/17	1,0453395	1,0560191	0,2804576 17/17	0,78611051	0,658139453 NS
24,31151 40/40	1,0307481	1,0455026	0,4779422 40/40	1,47276773	1,490445304 ***
32,154548 8/8	1,17280459	1,26971054 *	0,03938413 8/8	1,54526562	1,499801741 **
35,048866 16/16	0,93459635	0,93470245	0,109245 16/16	1,0928488	1,112365314 NS
18,585569 17/17	0,9865787	1,1408331	0,8816254 17/17	0,63630155	0,587965779 ***
22,416338 11/11	0,8977156	0,8340827	0,0794587 11/11	0,71139399	0,656052988 **
14,273074 5/5	0,9983471	1,0406795	0,9836689 5/5	0,45903228	0,339798297 ***
13,72057 16/16	0,85110067	0,9263545 **	0,00605578 16/16	0,56811228	0,544313886 ***
27,634666 9/9	1,59872063	1,63194823 ***	8,1616E-10 9/9	1,94363776	1,851022143 ***
14,961781 15/15	0,89414154	0,91910534 *	0,01987022 15/15	0,63417608	0,624548492 ***
13,354263 12/12	1,44375043	1,56472537 ***	4,3245E-07 12/12	0,52637426	0,487823503 ***
30,648207 9/9	0,74542836	0,66855907 ***	0,00037323 9/9	1,76649406	1,559929091 ***
17,139891 16/16	0,86420549	0,91003065 **	0,00170876 16/16	0,64750061	0,667698477 ***
16,546013 18/18	0,9947905	1,0074741	0,8639017 18/18	0,5410252	0,515039179 ***
15,240493 11/11	0,82543968	0,81173415 ***	0,00013325 11/11	0,74100677	0,773276768 ***
19,465812 20/20	0,9988983	0,9951169	0,9690998 20/20	0,6068701	0,612081387 ***
31,175462 10/10	0,77850344	0,81517866 ***	5,4183E-07 10/10	0,8204596	0,704465192 NS
38,591797 10/10	0,92944053	0,89641766 *	0,01294656 10/10	1,2704329	1,481043169 NS
18,632489 13/13	1,0143105	1,1082327	0,7586259 13/13	0,67732138	0,868778351 ***
14,187408 16/16	1,0617417	1,0852477	0,1895738 16/16	0,59534788	0,574190557 ***
18,078415 10/10	0,7425178	0,79048718 ***	1,3057E-05 10/10	0,84587354	0,865242508 NS
8,3794965 10/10	0,89533022	0,83702166 *	0,01690434 10/10	0,57181319	0,559538894 ***
11,244327 24/24	0,4333377	0,41556958 ***	1,158E-27 24/24	1,027175	0,994672498 NS
22,248008 15/15	0,60342874	0,62080313 ***	6,5618E-13 15/15	3,35100656	3,715360028 ***
18,895799 11/11	1,30830063	1,32828785 ***	3,1482E-07 11/11	0,79839718	0,727919363 *
17,007579 10/10	0,9176333	0,9512052	0,0620608 10/10	0,8417381	0,810252522 NS
19,365287 13/13	1,0670116	1,0011865	0,0591319 13/13	0,64051633	0,547795677 ***
18,351845 12/12	0,9125723	1,0232839	0,1668269 12/12	0,56058182	0,584552982 ***
17,421366 9/9	0,9062693	0,93262	0,3465332 9/9	0,8646771	0,805444501 NS

10,420924	14/14	1,31411879	1,34603749	***	1,1845E-08	14/14	0,66251424	0,605863157	***
23,389513	23/23	0,976004	0,9946025		0,3722348	23/23	0,9280099	0,914190793	NS
16,094422	18/18	0,94381391	0,94804216	*	0,01781587	18/18	0,69257221	0,609380011	***
29,10729	9/9	1,82961092	1,53772228	***	0,00038397	9/9	1,5921777	1,768042099	***
35,935771	23/23	1,22485383	1,19495188	***	1,6318E-05	23/23	1,2141608	0,924006808	*
13,586747	8/8	1,26160502	1,17723338	***	3,4741E-05	8/8	0,8671185	0,87364916	NS
11,515463	15/15	0,9872319	1,0503234		0,8103486	15/15	0,66280922	0,632121855	***
22,983935	10/10	0,77940025	0,73352219	**	0,0011862	10/10	0,6670265	0,576013372	**
38,844819	10/10	1,54573661	1,48542173	***	1,5157E-08	10/10	1,1172388	0,861650185	NS
12,767932	9/9	0,94060526	0,93333088	*	0,02840725	9/9	0,44911304	0,431558896	***
39,766778	12/12	0,81523532	0,77744357	**	0,00212849	12/12	0,8625837	0,698421657	NS
13,548587	8/8	0,69397704	0,76384755	***	3,0062E-05	8/8	0,983815	1,008014725	NS
27,604065	14/14	0,89666796	0,86540281	**	0,001292	14/14	0,8067027	0,689027912	NS
21,331439	12/12	1,63350931	1,70812054	***	7,7554E-06	12/12	1,0046278	0,925493161	NS
14,400879	8/8	0,82033648	0,80915169	***	0,00042965	8/8	0,65705891	0,627702503	***
82,273269	5/5	0,90465575	0,94236128	*	0,0387539	5/5	2,63001893	5,094005063	*
13,542001	11/11	1,0665792	1,0790881		0,1093554	11/11	0,56100762	0,500362852	***
10,367702	14/14	0,9647447	0,9437216		0,4210333	14/14	0,6235485	0,671131869	***
18,904561	10/10	0,45274709	0,45973475	***	2,9988E-10	10/10	1,1649094	1,272814122	NS
21,449983	15/15	1,16243094	1,13012816	**	0,00109256	15/15	0,63518743	0,51467901	***
7,5772289	5/5	0,71566297	0,65530181	**	0,00512336	5/5	0,44073965	0,400974986	***
8,3155593	3/3	0,6404136	0,68574287	***	0,00085631	3/3	0,56158461	0,599663789	**
33,634006	8/8	0,83136868	0,83648774	**	0,00178419	8/8	1,0327101	0,748188854	NS
11,073745	14/14	1,63128123	1,61156988	***	6,4359E-10	14/14	0,45334683	0,466145011	***
6,4912084	7/7	0,50894295	0,49080885	***	2,1022E-10	7/7	0,55944338	0,543338208	***
2,2175086	4/4	1,0597428	1,077199		0,2992001	4/4	0,82349061	0,83641376	***
24,853127	9/9	1,0194138	1,0439376		0,652957	9/9	0,9647871	0,785798644	NS
14,031371	7/7	1,86847158	2,04896353	***	3,4643E-07	7/7	0,9888573	0,932487259	NS
19,261997	7/7	0,8555621	1,026039		0,1100437	7/7	0,54447458	0,546035636	***
59,439358	13/13	1,44225847	1,79168938	**	0,00212371	13/13	2,37520963	3,9131286	***
24,323109	11/11	0,74866555	0,82847751	*	0,01347987	11/11	0,62570227	0,461668128	**
14,342617	9/9	0,9920582	1,0038146		0,9436807	9/9	0,57026204	0,510433786	***
13,58436	9/9	0,9938324	1,0237031		0,8036004	9/9	0,63722709	0,562956831	***
23,260896	9/9	1,18834682	1,2852326	*	0,01273318	9/9	1,0191658	1,035644781	NS
13,926837	13/13	1,61970125	1,82546282	***	1,0378E-07	13/13	1,0413176	0,99362227	NS
13,415299	14/14	1,31233027	1,31509699	***	6,6806E-09	14/14	0,75079293	0,683238713	***
46,283617	12/12	0,93512	1,0709202		0,3522174	12/12	2,40091577	2,680881819	***
11,440219	30/30	0,56930858	0,43781397	***	2,1011E-07	30/30	0,68912627	0,680866717	***
24,466979	11/11	1,35256757	1,35546283	***	0,00096312	11/11	0,89899731	0,740276455	NS
33,108444	8/8	0,6391576	0,69385304	***	0,00011484	8/8	2,5682933	2,929675831	***
12,963414	9/9	0,985933	0,9282898		0,8004751	9/9	0,55317876	0,627458053	***
24,34237	14/14	0,8446621	0,86165835	***	9,8773E-05	14/14	2,48472197	2,880477492	***
13,270138	18/18	1,15140607	1,15883826	***	6,8779E-05	18/18	3,45880198	3,599838834	***
12,218276	8/8	1,0937477	1,1187431		0,0528217	8/8	0,60955594	0,601940741	***
12,961754	11/11	1,37950418	1,48755305	***	7,4072E-08	11/11	2,19610735	2,105174201	***
17,233668	7/7	1,1523367	1,1641681		0,1473752	7/7	0,56112594	0,543607762	***
18,361085	5/5	0,944135	0,935903		0,3971058	5/5	2,87929319	2,768829204	***
20,789652	6/6	0,84680365	0,82563887	**	0,00198703	6/6	0,58417681	0,553943615	**
28,730885	13/13	0,79611057	0,7563238	***	9,4059E-05	13/13	0,5208408	0,337773954	***
2,8824941	2/2	0,78638376	0,78638376	**	0,00261764	2/2	0,48235254	0,482352542	**
34,636942	7/7	0,8755248	0,9586011		0,268903	7/7	1,3932287	1,349200597	NS
10,822471	17/17	0,72897271	0,73612451	***	1,0093E-10	17/17	0,5583069	0,526976912	***

15,988762	11/11	0,9469433	0,9998235	0,4365625	11/11	0,8018453	0,702231183	**	
15,066864	11/11	0,86299019	0,8952273	**	0,00131961	11/11	1,93083215	1,864981313	***
33,165119	10/10	2,14744682	2,17372627	***	3,3428E-09	10/10	3,9808774	3,940827878	***
8,3005783	11/11	1,15466576	1,13403682	**	0,00632933	11/11	0,9691681	0,943792202	NS
14,696285	9/9	1,50337496	1,51489436	***	6,6152E-07	9/9	1,32710512	1,410173049	***
23,363801	9/9	1,0782705	1,0361677		0,0843887	9/9	0,8825927	0,836844509	NS
15,228653	9/9	1,0948288	1,0676274		0,0778676	9/9	2,48935391	2,419740837	***
6,4384822	7/7	0,9724238	0,9873312		0,5571987	7/7	0,61836813	0,652389487	***
9,7772478	8/8	1,16758409	1,19278219	*	0,04289798	8/8	0,65459199	0,63780809	***
23,963528	17/17	1,12664293	1,11350239	***	0,00024756	17/17	1,8150515	1,711622859	***
16,734051	5/5	1,1094945	1,1229694		0,1170733	5/5	1,1756609	1,233896499	NS
28,225367	7/7	1,85321454	1,96003038	***	1,2355E-06	7/7	1,1420333	0,828667382	NS
24,043055	9/9	1,23395849	1,20992974	***	0,00012315	9/9	0,7953674	1,032509168	NS
18,74173	8/8	0,9714796	0,9940891		0,5688429	8/8	0,72830205	0,739971765	*
53,88968	10/10	1,0799537	0,9397929		0,3461053	10/10	1,5276015	0,925153161	*
15,577703	5/5	0,8374003	0,86725876	***	4,267E-05	5/5	0,9208575	1,01475091	NS
25,794425	5/5	0,9194737	0,9080266		0,4827975	5/5	0,7249795	0,893117464	NS
31,425549	7/7	1,24942721	1,20470551	**	0,0025911	7/7	0,7975603	0,575561075	NS
35,41382	9/9	1,24297116	1,31375723	**	0,00801851	9/9	1,2821766	1,352792635	NS
29,696657	12/12	1,08164436	1,12532712	*	0,04114562	12/12	0,8681144	0,868625682	NS
43,995855	9/9	0,65210408	0,70735494	***	2,1112E-05	9/9	3,24439209	4,907003007	***
16,976922	9/9	0,9689734	1,0085517		0,4724843	9/9	0,62384282	0,578928111	***
17,463857	9/9	1,09015416	1,11309177	**	0,00565428	9/9	0,9250444	1,027180912	NS
6,7852881	8/8	0,76926847	0,76197651	***	3,7756E-06	8/8	0,64765024	0,620166789	***
26,679545	6/6	0,9974399	1,0324717		0,9159641	6/6	0,9072005	0,879709997	NS
18,421398	14/14	1,36753436	1,45650917	***	5,3889E-07	14/14	0,70928018	0,698589998	***
14,174599	10/10	0,86408007	0,87604721	**	0,00926674	10/10	1,064574	1,063386018	NS
26,71462	11/11	0,87192458	0,87133507	**	0,00503297	11/11	0,66176315	0,595090416	**
15,942736	12/12	1,29844528	1,33473405	***	2,1471E-05	12/12	0,8824226	0,772206162	NS
17,777266	8/8	1,33519523	1,30687889	***	2,9137E-06	8/8	0,6070721	0,572179578	***
14,881982	5/5	1,21167063	1,26453572	*	0,03819419	5/5	0,66426653	0,647146856	**
31,304987	5/5	0,9981915	1,0130943		0,9836334	5/5	1,1970304	1,547714246	NS
15,608043	15/15	1,0364525	0,9821119		0,3444153	15/15	0,67472414	0,597449424	***
8,2371098	7/7	1,0408988	1,006315		0,2677419	7/7	0,66939649	0,698304199	***
17,382113	9/9	2,08153122	2,23735698	***	2,9291E-06	9/9	0,62685542	0,577973544	***
11,296502	6/6	1,22348606	1,2134444	*	0,03175884	6/6	1,77146916	1,773478945	***
16,688654	9/9	0,8392975	0,78972729	*	0,04912763	9/9	0,8823367	0,973152077	NS
19,49316	8/8	1,52802575	1,57434221	***	9,687E-07	8/8	0,9945097	0,976240214	NS
21,909026	5/5	1,0878458	1,1000491		0,4403443	5/5	0,6764483	0,514057557	*
31,92263	7/7	1,139278	1,0666402		0,2309925	7/7	0,8096186	0,551136251	NS
35,757115	7/7	0,8544165	1,0305089		0,1248406	7/7	0,8062902	0,927303022	NS
27,76411	9/9	1,39089748	1,46963188	***	0,00016077	9/9	1,43728105	1,294966451	**
24,497676	6/6	0,79132982	0,77072089	***	2,8971E-06	6/6	2,06903226	2,578329013	***
51,225826	13/13	1,76593951	1,52540101	***	1,0741E-06	13/13	5,0259714	3,883831226	***
19,744578	7/7	1,0564633	1,0528118		0,3772652	7/7	0,62194324	0,572461708	**
16,422166	8/8	1,24198017	1,36959414	**	0,00564362	8/8	1,34297832	1,32267736	***
17,062879	8/8	1,51804651	1,3712205	***	1,8201E-05	8/8	0,54861105	0,486008052	***
28,094644	7/7	0,60348358	0,61551823	***	1,9589E-07	7/7	0,9026578	0,80162828	NS
17,410898	12/12	1,72956933	1,74987649	***	9,1722E-17	12/12	3,56905621	3,83384079	***
17,236036	5/5	0,77271461	0,79691225	***	0,00026917	5/5	0,63528965	0,640821341	*
24,772131	9/9	1,0625678	1,0844322		0,4521413	9/9	0,7988759	0,662126332	NS
37,036383	10/10	0,81006225	0,87884811	***	0,00039779	10/10	1,0567656	0,684184967	NS

26,523137 6/6	0,79529825	0,84499229 **	0,00619673 6/6	1,2765062	1,606035249 NS
14,057385 7/7	1,1110321	1,03799945 *	0,04763693 7/7	0,9624992	0,982953209 NS
25,42488 6/6	0,9644212	1,0102738	0,7063538 6/6	1,99634514	2,279555841 ***
16,413789 2/2	1,4302324	1,4302324	0,0670238 2/2	0,85126	0,851259978 NS
27,584495 10/10	1,10078761	1,21620707	0,0680204 10/10	1,1356582	1,457064243 NS
29,63236 10/10	1,90946515	1,92471028 ***	4,2791E-09 10/10	3,82929292	4,421357229 ***
7,0809032 9/9	1,26794506	1,38359262 ***	2,4674E-05 9/9	0,55075345	0,521446999 ***
10,956041 5/5	1,0184236	1,0017156	0,7280767 5/5	0,68725787	0,582160804 **
17,881172 6/6	1,0432561	1,0410058	0,326851 6/6	0,54708855	0,607246554 **
36,293903 6/6	0,9875458	0,9857303	0,7867865 6/6	1,1203793	1,094618826 NS
7,2985189 13/13	0,92440137	0,92561371 **	0,00264586 13/13	0,75831167	0,758579894 ***
22,907859 10/10	1,28466839	1,45773326 **	0,00208745 10/10	2,68580534	2,843096596 ***
12,605938 6/6	1,46613196	1,51831692 ***	7,3472E-07 6/6	0,8627181	0,899242329 NS
24,842133 2/2	1,28071158	1,28071158 ***	0,00032197 2/2	0,8279964	0,827996418 NS
14,972855 4/4	1,12068349	1,16142849 *	0,01408759 4/4	0,62387642	0,525935012 *
23,264637 10/10	1,30686175	1,45175421 ***	2,0828E-06 10/10	2,61203585	2,826024042 ***
25,10648 7/7	1,38043512	1,59590908 **	0,00452624 7/7	1,42975444	1,28928745 **
12,018626 9/9	0,9698424	0,9629061	0,7057951 9/9	0,77014107	0,83921631 ***
9,9123926 4/4	1,2377047	1,1521916	0,1814957 4/4	0,7528103	0,769298587 *
16,473827 8/8	0,9012258	0,9335807	0,0726487 8/8	0,62009886	0,492654724 ***
7,6794808 4/4	0,8590759	0,873475	0,053101 4/4	0,63848184	0,599090147 ***
22,304916 5/5	0,6888196	0,60360119 **	0,00371477 5/5	2,57998864	2,655381089 ***
14,246009 4/4	0,51124586	0,50277108 ***	0,00032021 4/4	0,8184694	0,833006853 NS
7,7539161 6/6	0,79058166	0,78053075 ***	1,3522E-05 6/6	0,44546938	0,416681396 ***
20,941072 10/10	1,0028974	1,0321525	0,9344943 10/10	1,1583852	1,217182434 NS
18,783037 9/9	1,0294622	1,0263006	0,2989666 9/9	2,18875585	2,189971792 ***
16,395526 6/6	0,81603719	0,80545163 **	0,0014243 6/6	0,69911934	0,776976545 **
10,505138 8/8	0,9496039	0,931827	0,3906442 8/8	0,66713747	0,659372848 ***
12,415227 6/6	1,319268	1,54196883 *	0,039071 6/6	0,55682308	0,533445042 ***
8,8008606 6/6	0,75701881	0,74317373 ***	0,00011228 6/6	3,57635961	3,459149927 ***
26,645105 6/6	1,289008	1,21841728 **	0,0069076 6/6	0,8327654	0,688311146 NS
13,669732 5/5	1,536336	1,50070783 ***	4,0096E-05 5/5	0,57528982	0,648868313 **
8,9985293 6/6	0,75221946	0,72308774 ***	1,4035E-06 6/6	0,62428501	0,66144932 ***
26,613637 17/17	0,9856376	0,9091141	0,8280659 17/17	2,13117075	2,228614924 ***
39,000334 4/4	1,0073051	1,0105934	0,937448 4/4	3,19724205	3,241176711 ***
31,581604 9/9	1,42933719	1,43164297 ***	3,1585E-06 9/9	4,54059317	5,281349834 ***
2,7034883 2/2	0,40956125	0,40956125 **	0,00955352 2/2	0,69301942	0,693019418 **
12,446164 7/7	0,9740618	1,1159853	0,7765743 7/7	1,57816236	1,658552329 ***
23,243696 5/5	1,0338295	1,0867448	0,5398004 5/5	2,41104666	2,887809889 ***
15,108265 7/7	1,20035197	1,26355796 **	0,0066772 7/7	0,8633691	0,77606277 NS
21,821989 12/12	0,90727562	0,8994588 ***	0,00077567 12/12	2,38342858	2,208442386 ***
11,631424 10/10	0,9944051	1,010735	0,8597981 10/10	0,82320318	0,841730138 **
41,868158 4/4	0,9549973	1,0597659	0,5775201 4/4	1,3715947	1,53882961 NS
15,516022 8/8	0,51907032	0,5085114 ***	1,5358E-08 8/8	1,0701222	0,954578208 NS
21,408976 13/13	0,81458699	0,86432464 **	0,00304827 13/13	0,8991222	0,93696581 NS
18,867413 5/5	0,84564288	0,81362691 ***	0,0004107 5/5	0,48264316	0,356263984 **
14,691879 8/8	1,52383169	1,60040546 ***	2,2046E-05 8/8	0,56982545	0,555598833 ***
20,697233 5/5	1,0458625	1,0330562	0,4151312 5/5	0,8238685	0,822761713 NS
16,154073 4/4	1,9607719	2,14380839 ***	0,00012589 4/4	0,8597017	1,006831846 NS
4,76275 2/2	0,9046979	0,9046979	0,0737054 2/2	0,8537288	0,853728842 NS
31,444648 5/5	0,9683535	1,052692	0,6536495 5/5	0,6903699	0,444726185 NS
8,0727693 4/4	0,7496159	0,75445946 ***	0,00033276 4/4	0,78097181	0,804074134 **

12,114267 7/7	0,8558139	0,9540893	0,1485702 7/7	0,47976666	0,557036779 ***
17,829349 4/4	1,47891138	1,54987652 **	0,00470877 4/4	1,1194305	1,263723873 NS
10,903745 7/7	0,76619111	0,81963991 ***	0,00063416 7/7	0,57773562	0,653063347 ***
7,5113851 9/9	1,71884085	1,69134865 ***	1,1745E-09 9/9	0,83363001	0,808399411 ***
19,278871 4/4	0,72963922	0,73567404 **	0,00276772 4/4	0,8392643	0,763668759 NS
13,399953 6/6	0,9453617	0,9713966	0,3093261 6/6	0,8332487	0,738671889 NS
18,526043 4/4	1,1189318	1,1182164	0,2715873 4/4	0,5407637	0,483369879 *
15,111757 7/7	0,71564559	0,77606908 **	0,00169634 7/7	0,66850619	0,55129766 **
23,031597 6/6	1,24320282	1,16724913 ***	0,00030879 6/6	0,64627063	0,526200565 *
14,559802 5/5	0,9315434	1,0011786	0,3163128 5/5	0,68328661	0,605762189 **
20,429978 5/5	0,68771593	0,65641053 *	0,01145157 5/5	2,40397725	2,336662272 ***
14,373962 5/5	1,0053626	1,1474517	0,9493777 5/5	0,60636402	0,668320993 **
15,350844 14/14	1,33616753	1,38092654 ***	3,7744E-08 14/14	0,74416915	0,719733301 ***
11,690862 6/6	0,87210968	0,85116572 **	0,00560419 6/6	0,80251425	0,893806558 *
19,903239 7/7	0,9571424	0,9582316	0,1858078 7/7	1,25886918	1,183789506 *
12,242889 3/3	1,1249481	1,258839	0,2105684 3/3	1,1522391	1,014114168 NS
26,029284 4/4	1,0228198	1,0286078	0,8728698 4/4	1,3651032	1,482696485 NS
20,664872 5/5	0,82322753	0,89736162 *	0,03216514 5/5	0,66491063	0,585670004 *
18,116674 4/4	0,9117789	0,9773712	0,1715523 4/4	0,7350076	0,773780881 NS
18,792272 6/6	0,74987679	0,75172964 ***	0,00070558 6/6	1,1267875	1,31971674 NS
10,473566 4/4	1,42118744	1,3572218 **	0,00208325 4/4	0,58354166	0,567294518 **
20,590916 5/5	1,0743355	1,1133605	0,1044609 5/5	0,8016066	0,828305483 NS
14,551574 9/9	1,0158664	1,0377251	0,8263093 9/9	0,8752911	0,749304397 NS
23,145745 6/6	1,18773169	1,26935779 *	0,01115019 6/6	0,5451019	0,537402873 **
19,719417 5/5	1,38958627	1,51032044 **	0,00298142 5/5	1,1065588	1,196973744 NS
24,16383 5/5	1,4938983	1,53625977 **	0,00357378 5/5	1,0863992	1,153769401 NS
25,157379 5/5	1,070447	1,0184294	0,1186322 5/5	0,9150511	0,7169341 NS
11,744922 9/9	1,22636883	1,12991013 ***	5,8012E-05 9/9	0,53960547	0,500637103 ***
22,270695 4/4	0,8939958	0,8966897	0,1691414 4/4	0,7998465	0,944548625 NS
23,203807 6/6	1,0029088	1,0199308	0,9570208 6/6	0,7935244	0,701349061 NS
36,090529 4/4	0,9953728	0,9735497	0,9539486 4/4	0,7949639	0,544364031 NS
9,8815972 4/4	1,49997788	1,41871864 **	0,00286927 4/4	0,5676204	0,599646168 ***
24,515167 5/5	0,67255068	0,66219321 ***	3,5775E-05 5/5	3,25017005	3,057794915 ***
10,928025 6/6	1,0263655	1,0172125	0,3130928 6/6	0,62144858	0,57697974 ***
27,162679 6/6	1,0850319	1,0240762	0,274225 6/6	1,83142108	1,87345959 ***
27,066792 2/2	0,878038	0,878038	0,4635474 2/2	2,0028089	2,002808873 NS
18,77312 8/8	1,10701011	1,12702227 *	0,04120442 8/8	0,67511959	0,657735142 **
23,108542 5/5	1,15579998	1,09505102 *	0,03304504 5/5	0,8325249	0,738488504 NS
17,254993 8/8	1,10327011	1,06477973 **	0,00727097 8/8	0,7888481	0,735685863 *
5,4936081 5/5	0,25535111	0,25150842 ***	2,48E-08 5/5	0,69691454	0,688645779 ***
5,4749619 5/5	0,79921806	0,9244346 *	0,04712279 5/5	0,9791723	1,01052715 NS
9,0353081 7/7	1,174507	1,32800792 *	0,02073429 7/7	0,87591268	0,925788239 *
23,389745 12/12	1,1022854	1,0582353	0,1133961 12/12	0,8335124	0,823359806 NS
16,329986 2/2	0,87447182	0,87447182 **	0,00337052 2/2	1,1106406	1,110640615 NS
5,2738317 4/4	1,75451981	1,68563337 ***	0,00045722 4/4	0,6218509	0,623582401 ***
13,487623 5/5	1,13411392	1,11141814 *	0,02384921 5/5	0,9026536	0,866165563 NS
21,632175 6/6	1,0063929	0,9922262	0,9212618 6/6	0,857588	0,717103005 NS
1,3193023 4/4	0,87027628	0,84736071 *	0,03785 4/4	0,47037249	0,470354916 ***
5,0678617 9/9	0,9875121	1,046923	0,8301507 9/9	0,691305	0,710833235 ***
28,900017 10/10	0,9746851	0,9628086	0,6140925 10/10	1,67784849	1,845604813 ***
54,86643 4/4	0,80641342	0,80777791 *	0,01147327 4/4	1,9000199	2,04204466 NS
21,4894 6/6	1,0244859	0,953264	0,8725371 6/6	0,4847071	0,425747049 **

11,791588 4/4	1,16083266	1,23020777 *	0,03477468 4/4	0,63479702	0,643262958 **
13,457384 3/3	0,8060942	0,7861709	0,0801746 3/3	0,51869099	0,520590925 *
10,418333 5/5	1,27093328	1,28141492 ***	0,00015402 5/5	0,49999658	0,439515789 ***
21,230335 7/7	1,82900964	1,71791545 ***	2,2414E-05 7/7	3,22583305	3,482635369 ***
38,999819 4/4	0,87867858	0,92104998 *	0,02596157 4/4	0,9592097	0,71381726 NS
11,704014 7/7	0,931224	1,0497026	0,3390339 7/7	0,51359056	0,526655046 ***
19,616959 5/5	0,8795744	0,8014099	0,1829891 5/5	1,63511981	1,885640334 ***
39,845249 6/6	1,1784024	1,30109922 *	0,02898904 6/6	1,4927902	1,479144079 NS
14,180885 3/3	0,9455972	0,9081248	0,7468661 3/3	0,7050843	0,745766489 NS
19,758015 4/4	0,8653017	0,8519848	0,3652959 4/4	2,34782809	2,573319785 ***
12,098804 6/6	1,32383722	1,43709943 **	0,00205768 6/6	1,0351505	0,972359005 NS
11,559752 5/5	1,45198144	1,74477914 *	0,01601648 5/5	0,5235447	0,510355946 ***
17,27846 6/6	0,8842453	1,0259136	0,4626854 6/6	0,70065967	0,60937097 *
20,642159 3/3	1,1413839	1,1086095	0,3848061 3/3	2,4395296	2,84690211 **
10,468055 5/5	1,0442569	1,0284555	0,541497 5/5	0,71142144	0,700081989 **
11,790573 5/5	1,67704515	2,16824942 **	0,00321567 5/5	0,72428186	0,751187323 **
35,960768 4/4	0,79264875	0,83261884 **	0,00463409 4/4	0,9597511	0,876032442 NS
7,6002299 6/6	0,7327526	0,72099126 **	0,00195807 6/6	0,9598203	1,014447722 NS
19,334398 4/4	0,83587878	0,86022116 *	0,03903891 4/4	0,6772879	0,573241327 NS
10,037311 4/4	1,6336622	1,99610328 *	0,02372256 4/4	1,19548203	1,230044232 *
24,06135 4/4	0,9279546	0,7888285	0,6385044 4/4	0,9898167	1,033838448 NS
19,392554 3/3	1,04912	1,126375	0,7735414 3/3	0,5608497	0,542970169 NS
25,774851 4/4	1,16034283	1,17156259 *	0,01974566 4/4	1,0245148	1,079279552 NS
16,784592 7/7	1,0987386	0,989982	0,1023642 7/7	0,8199874	0,91006688 NS
31,147908 5/5	1,1720516	1,1492097	0,085098 5/5	1,0508525	1,056201797 NS
17,129039 4/4	0,8743029	0,8097474	0,4556796 4/4	0,8311945	0,784961433 NS
8,8561583 4/4	0,76688624	0,80760683 **	0,0053263 4/4	1,0054711	0,975310687 NS
14,718036 8/8	0,9804828	1,1581404	0,8355546 8/8	0,74582038	0,758177844 **
16,880062 4/4	1,09171067	1,12165001 *	0,01713289 4/4	0,7462451	0,73126127 NS
10,565408 3/3	0,8673475	0,9126508	0,2195911 3/3	0,57232141	0,491230289 **
11,032728 3/3	0,8801415	0,9558841	0,1097037 3/3	0,64638137	0,66524114 *
23,349808 4/4	1,0428637	1,0758215	0,5180055 4/4	0,8456271	0,715669127 NS
7,0906432 6/6	1,30897813	1,33722806 ***	4,6106E-05 6/6	5,08702569	5,163059351 ***
14,589863 4/4	0,9359855	0,9401874	0,5899988 4/4	0,9531727	0,840451903 NS
13,26502 6/6	0,88194374	0,85084728 *	0,02855183 6/6	0,8854692	0,857474251 NS
9,1360439 8/8	1,46296314	1,55773737 ***	6,765E-07 8/8	1,33008571	1,251372665 ***
6,6656637 4/4	2,48382769	2,33735301 ***	9,2032E-06 4/4	1,89691475	1,900648196 ***
9,0958915 5/5	0,65885441	0,60595884 ***	0,00029671 5/5	0,58166952	0,56737614 ***
28,914067 3/3	0,9479067	1,003729	0,4585161 3/3	1,111607	0,948964941 NS
23,223047 7/7	1,32734023	1,32796037 ***	5,6428E-06 7/7	2,54311778	2,751528518 ***
7,0453356 4/4	0,68115187	0,69163979 ***	1,4007E-05 4/4	0,5020259	0,501423427 ***
27,418564 6/6	1,12533796	1,14912634 **	0,00260545 6/6	0,9316125	1,081905031 NS
11,080905 4/4	1,39768941	1,39207777 ***	0,00029805 4/4	0,9808527	0,974311157 NS
11,332383 6/6	1,29131991	1,3305103 ***	0,00017284 6/6	0,8245746	0,760618985 *
13,98398 3/3	1,0955463	1,1186479	0,5504817 3/3	0,547471	0,516156193 *
22,137684 7/7	0,9673298	0,9632929	0,3801521 7/7	0,8750553	0,976465034 NS
15,767056 4/4	1,84499864	1,87309367 ***	2,4675E-06 4/4	3,07135187	2,979756125 ***
5,9465757 4/4	1,55281214	1,48233339 **	0,00353331 4/4	1,27260149	1,235516086 ***
11,072227 6/6	1,1277368	1,1371571	0,0578265 6/6	1,0918827	1,132311002 NS
16,774323 2/2	0,8704606	0,8704606	0,3316389 2/2	0,6199121	0,619912094 NS
8,0611918 6/6	1,48761646	1,52375245 ***	1,7443E-05 6/6	0,9680207	0,970103601 NS
6,0281542 3/3	0,8719774	0,8346156	0,3534665 3/3	0,84850153	0,840456953 *

4,2812087 10/10	1,64536608	1,68185964 ***	1,7588E-13 10/10	1,44700555	1,453131083 ***
13,190077 3/3	0,9228905	0,9102901	0,0518396 3/3	0,66445331	0,601202502 *
41,845094 7/7	0,7987058	0,79694989 ***	0,00063987 7/7	3,22546002	3,838963745 ***
13,106134 3/3	1,218809	1,1958329	0,0576402 3/3	0,9067881	0,95166203 NS
22,844679 3/3	0,8743359	0,8003776	0,4151289 3/3	0,8631292	0,887660212 NS
44,088558 3/3	1,43074548	1,42267352 *	0,01908108 3/3	1,3890485	1,491479803 NS
29,881126 3/3	1,1376202	1,3403749	0,3328302 3/3	1,2786291	1,050215279 NS
40,088533 11/11	1,0166791	1,0755303	0,705729 11/11	1,46997634	2,250138186 *
22,930822 5/5	1,0356699	1,0054061	0,6732868 5/5	1,0568057	0,888237383 NS
25,423208 5/5	1,0062524	0,9698239	0,8513235 5/5	2,83120955	3,201699446 ***
9,9696454 3/3	0,62783353	0,56656127 *	0,01392422 3/3	0,46671697	0,519389218 **
12,957715 3/3	0,8650096	0,9246709	0,0711649 3/3	0,62687361	0,594855647 *
25,459673 4/4	1,012303	1,0683778	0,7656295 4/4	1,1674315	1,080433295 NS
19,442347 6/6	1,87692114	1,89450323 ***	7,364E-09 6/6	3,06937306	3,165235704 ***
12,528596 7/7	0,8691662	0,9459925	0,0962641 7/7	0,70102329	0,694034932 ***
9,7759606 3/3	0,804846	0,7620911	0,2047874 3/3	0,63239488	0,563032356 **
80,249394 3/3	0,76441448	0,72711949 *	0,01904305 3/3	2,6341254	5,318824021 NS
16,164156 3/3	0,8166729	0,7971395	0,0507091 3/3	0,9215721	0,79711424 NS
5,8291 3/3	1,4157541	1,2557241	0,1157189 3/3	0,49154257	0,530601776 ***
17,482614 3/3	1,0044113	1,1442561	0,9792457 3/3	0,9204307	0,866519542 NS
35,780782 5/5	1,41059147	1,51797449 **	0,0039302 5/5	1,71238876	2,239760257 *
17,958368 3/3	0,61529701	0,58650236 ***	0,00026613 3/3	0,7097594	0,618359376 NS
4,5685006 4/4	0,74753958	0,74621168 ***	0,00016094 4/4	0,62355906	0,597642259 ***
30,613275 4/4	1,84019774	2,02991071 ***	0,0002962 4/4	3,00023803	3,635571663 ***
28,396228 3/3	1,2803189	1,067722	0,142447 3/3	1,0589921	0,794286626 NS
27,893064 3/3	0,9735022	1,0450764	0,8108781 3/3	0,7515459	0,661765067 NS
5,9409828 6/6	1,20896407	1,26885926 **	0,00107361 6/6	0,6284106	0,618384506 ***
7,3283846 3/3	0,82212418	0,87932408 *	0,03203461 3/3	0,71629003	0,729730211 **
14,064912 5/5	1,12634086	1,14158417 **	0,00786281 5/5	0,66214662	0,605400727 **
10,585979 5/5	0,75494899	0,78973762 ***	0,00053257 5/5	0,8598942	0,782893399 NS
7,3950273 3/3	0,64551037	0,67531241 ***	0,00042781 3/3	0,72597479	0,729379352 *
3,7080936 4/4	1,0091757	0,9587038	0,9250513 4/4	0,63086013	0,649338206 ***
17,507779 3/3	0,48147844	0,48928577 ***	1,2362E-05 3/3	0,858143	0,697655153 NS
31,764409 3/3	1,163802	1,0670257	0,2580916 3/3	0,6566183	0,510503849 NS
6,7068254 5/5	0,86544783	0,86007477 *	0,01272943 5/5	0,87571692	0,84364498 *
17,76746 3/3	0,73586918	0,75891765 *	0,02334408 3/3	0,6106183	0,608416039 NS
4,3556393 3/3	1,1280687	1,2225113	0,1126286 3/3	0,9712926	0,994897966 NS
19,784961 3/3	1,107455	1,0918452	0,1010091 3/3	1,0601095	1,189011862 NS
18,04519 4/4	1,1276474	1,11538755 **	0,00793727 4/4	1,1913592	1,227678006 NS
68,66225 4/4	1,0291261	1,033284	0,7998245 4/4	3,79540376	4,628015069 **
15,862907 3/3	1,0848262	1,1122642	0,1388521 3/3	4,35837171	4,695844765 ***
1,3350084 2/2	2,28122143	2,28122143 ***	0,00031459 2/2	1,0358039	1,035803924 NS
16,30397 2/2	0,7201245	0,7201245	0,0933681 2/2	2,67582213	2,675822129 **
20,100228 3/3	0,8606332	0,9262713	0,068236 3/3	0,7084309	0,777438754 NS
19,719398 4/4	1,15237529	1,16656161 *	0,04177088 4/4	1,0504886	1,001181446 NS
4,6852777 3/3	1,32175134	1,23881864 **	0,00560757 3/3	0,53374694	0,54836548 ***
66,333504 3/3	1,20817642	1,22526783 ***	0,00019016 3/3	2,4478123	4,402345911 NS
34,26842 3/3	2,02836465	2,00271289 ***	1,2901E-06 3/3	1,1381023	0,913834091 NS
13,620279 3/3	0,9066663	0,929885	0,318607 3/3	0,6955253	0,638702769 NS
17,70581 3/3	1,1446408	1,0970768	0,0633533 3/3	1,46138952	1,49186945 *
36,357421 2/2	1,0649779	1,0649779	0,6301941 2/2	1,4399071	1,439907105 NS
7,0948093 4/4	1,1234157	1,0372393	0,3190102 4/4	0,57405939	0,557115393 ***

21,935478 4/4	0,9554097	1,0180223	0,4705378 4/4	2,85360179	3,029683833 ***
18,520796 5/5	0,9498528	0,9571169	0,4197079 5/5	0,61470212	0,536527026 *
7,3294124 2/2	0,8107697	0,8107697	0,0946475 2/2	1,54023473	1,540234735 *
6,071322 5/5	1,30863274	1,36870788 **	0,0036962 5/5	0,56624007	0,562042281 ***
26,613154 3/3	1,0181687	1,1285414	0,9439775 3/3	0,8999381	0,744675012 NS
28,63736 2/2	0,963035	0,963035	0,8516368 2/2	1,691612	1,691611972 NS
40,231861 2/2	1,3728861	1,3728861	0,2236067 2/2	1,1223685	1,122368457 NS
5,9334651 3/3	1,1534124	1,2627453	0,1785622 3/3	0,59290249	0,560521231 **
29,815111 3/3	1,85252104	1,90856701 **	0,00668863 3/3	2,75469088	3,288584276 **
15,815151 5/5	1,3540659	1,36125161 ***	3,4542E-05 5/5	1,81801198	1,827202547 ***
5,3900458 3/3	0,9582433	0,953723	0,3565928 3/3	0,9769748	0,918661218 NS
15,176181 4/4	0,9625874	0,9576486	0,1179708 4/4	0,9810154	0,927431328 NS
36,119548 4/4	1,32292697	1,32758079 ***	7,6606E-06 4/4	1,70550189	2,016525757 *
14,483651 2/2	1,44477909	1,44477909 *	0,03529949 2/2	0,4695593	0,469559326 NS
6,1299847 3/3	0,76160856	0,72434804 **	0,00147392 3/3	0,47135399	0,457060707 ***
2,7407586 5/5	1,12835687	1,12235639 ***	0,00052524 5/5	0,5472484	0,537552682 ***
29,50206 4/4	1,0716331	1,0721457	0,3227792 4/4	2,09614071	2,47048466 **
24,440979 3/3	0,9119931	0,8947106	0,2760263 3/3	4,00768862	4,662361175 ***
72,204772 3/3	1,33040856	1,37093483 *	0,01507826 3/3	3,48859308	6,156132022 *
9,3897002 3/3	0,81504649	0,74098771 *	0,04875113 3/3	0,57418092	0,648202607 **
28,619472 2/2	0,7289165	0,7289165	0,2886995 2/2	0,2914048	0,291404754 NS
18,150477 3/3	0,8089799	0,8279841	0,0547144 3/3	0,7172801	0,593271665 NS
4,9661208 3/3	1,27231848	1,21200628 *	0,01042264 3/3	0,48761931	0,518323116 ***
12,63381 4/4	1,08580838	1,08309773 ***	0,00083981 4/4	0,9404624	0,956424328 NS
4,9819783 5/5	0,85238169	0,84529312 *	0,03698256 5/5	0,88266974	0,882630996 **
20,576537 3/3	1,70300221	1,60186246 ***	0,00074533 3/3	5,93002001	6,15723039 ***
35,026863 5/5	0,9808651	0,8401891	0,8283128 5/5	1,974747	2,511841749 **
26,590507 7/7	1,77132183	1,84900551 ***	2,9217E-10 7/7	3,64573018	3,377063628 ***
7,5360601 3/3	1,0279363	1,0512036	0,7873642 3/3	0,54448875	0,534558561 **
15,566458 3/3	1,2027521	1,3299644	0,4944911 3/3	4,74878984	4,349709038 ***
45,930374 4/4	0,76458985	0,78290098 ***	0,00020158 4/4	1,1835438	1,19089501 NS
19,284781 7/7	0,9645053	0,9505439	0,4069858 7/7	0,64811351	0,563071433 **
13,76837 5/5	0,8641318	0,7979769	0,0507935 5/5	0,9445447	0,841604553 NS
26,137508 2/2	0,8793508	0,8793508	0,0702237 2/2	0,4647787	0,464778745 NS
21,209283 3/3	0,9265609	0,8083726	0,5426544 3/3	1,1706608	1,376017619 NS
16,911739 4/4	0,80023031	0,80872601 *	0,04174073 4/4	2,3629247	2,350512802 ***
28,382018 4/4	1,173731	1,2471907	0,1659304 4/4	1,0719375	0,970636036 NS
3,2330298 3/3	1,0059889	1,085847	0,9223085 3/3	0,50290303	0,508174307 ***
25,186636 4/4	1,0310583	0,9665851	0,6859255 4/4	1,056812	0,909109062 NS
28,086022 3/3	1,8481214	1,75984693 ***	0,00085062 3/3	1,0162163	1,377392541 NS
64,014224 4/4	0,92469219	0,92764463 **	0,00512557 4/4	2,61089722	3,996610143 *
55,488455 5/5	1,0144112	0,8529871	0,8935015 5/5	1,1002262	0,589065298 NS
14,922205 3/3	0,8311848	0,7687735	0,0999681 3/3	0,6489149	0,668982488 *
1,8819955 2/2	1,38506875	1,38506875 **	0,00837252 2/2	0,9468253	0,946825265 NS
15,654139 3/3	1,5613746	1,47470059 ***	0,000579 3/3	4,31786013	4,179877409 ***
7,552516 3/3	1,1691888	1,1913694	0,0518857 3/3	0,81606785	0,795671547 *
9,8152238 3/3	0,8656145	0,8071161	0,1463094 3/3	0,8150929	0,761891597 NS
23,517013 3/3	0,64203087	0,70951639 **	0,00373909 3/3	0,8624008	0,662249053 NS
9,8382008 3/3	0,9631835	1,0175721	0,7013106 3/3	0,8982112	0,934469586 NS
37,582387 3/3	1,1261658	1,1885544	0,1015374 3/3	0,9487064	0,790185055 NS
26,90145 3/3	0,53446636	0,54278701 **	0,00612869 3/3	1,88168674	1,50506129 *
16,180426 3/3	1,42675403	1,43316133 *	0,01850449 3/3	0,6335817	0,769071892 NS

14,362312 3/3	0,79386477	0,79516078 *	0,01070969 3/3	0,66152279	0,719561931 *
31,932986 6/6	1,3320949	1,5228526	0,1065798 6/6	2,92218114	3,038412116 ***
5,4129765 2/2	1,0897669	1,0897669	0,7513778 2/2	0,49316958	0,493169578 *
7,9058633 3/3	1,0446269	1,1694809	0,765356 3/3	0,51069352	0,534438464 **
21,777006 4/4	0,73860596	0,73992546 *	0,02686515 4/4	2,23491846	2,281156698 ***
16,821574 3/3	1,0588537	1,1058886	0,2374051 3/3	0,9063628	0,857044585 NS
20,048121 3/3	1,44770406	1,54644624 **	0,00171998 3/3	1,165574	1,365025932 NS
6,1314229 2/2	1,6140662	1,6140662	0,0716498 2/2	0,45843949	0,458439485 *
9,7522197 6/6	1,40642442	1,36565631 ***	3,286E-06 6/6	0,80985126	0,752750842 **
38,602952 3/3	0,9445748	1,0456129	0,582566 3/3	1,0630159	1,196260086 NS
22,1462 2/2	0,67848141	0,67848141 *	0,04137485 2/2	1,3469473	1,346947312 NS
13,024186 4/4	1,19352502	1,19124527 **	0,00361255 4/4	3,88968436	3,814122968 ***
13,41818 4/4	0,60007172	0,580638 ***	7,6351E-05 4/4	0,995862	1,069627666 NS
17,122909 2/2	0,9683194	0,9683194	0,7801311 2/2	2,42520739	2,425207395 *
21,217916 3/3	1,72481799	1,67169594 ***	4,7815E-05 3/3	1,67051612	1,666313002 *
34,432912 2/2	0,53119803	0,53119803 **	0,0054258 2/2	0,5825077	0,58250767 NS
77,775763 2/2	0,92888329	0,92888329 *	0,0170132 2/2	1,6130761	1,613076107 NS
27,17439 3/3	0,76051686	0,74442899 ***	0,00042993 3/3	1,162761	1,479574928 NS
45,470939 4/4	1,47150866	1,48128064 ***	0,00070947 4/4	1,3254055	1,116180466 NS
37,315556 2/2	2,52228231	2,52228231 *	0,02795936 2/2	0,9726385	0,972638462 NS
4,9195749 4/4	1,27838416	1,29456516 ***	0,00067213 4/4	0,60720751	0,591375986 ***
9,1321043 3/3	2,03716382	2,05216037 ***	1,7774E-06 3/3	0,49834267	0,544407109 **
66,435953 2/2	1,0710884	1,0710884	0,7593542 2/2	1,2200367	1,220036654 NS
23,527787 3/3	1,27633539	1,24362988 *	0,01974495 3/3	1,1722577	1,246111037 NS
37,207657 5/5	0,9707453	0,9776117	0,5542967 5/5	2,44479937	3,041493857 ***
13,89531 8/8	1,0568874	1,0063609	0,1326367 8/8	0,72554445	0,671179578 **
12,40176 2/2	0,9726599	0,9726599	0,1071962 2/2	0,6432033	0,643203332 NS
1,0761894 3/3	0,71992643	0,70182903 ***	0,00059295 3/3	0,6693471	0,675051231 ***
3,3114036 3/3	1,1321295	1,2828161	0,2683901 3/3	0,55526708	0,576226527 ***
45,065992 2/2	0,8734862	0,8734862	0,7457198 2/2	0,7463203	0,746320253 NS
0,9776204 3/3	1,179431	1,15126569 *	0,0404713 3/3	1,15604536	1,16138186 ***
3,0180173 2/2	1,4051522	1,4051522	0,0650429 2/2	0,34331172	0,343311725 **
1,1094937 2/2	0,9646424	0,9646424	0,3573362 2/2	0,62195751	0,621957511 ***
17,147774 3/3	0,8383556	0,8487549	0,0970763 3/3	2,13494341	1,888161859 **
32,690534 2/2	0,5153911	0,5153911	0,4006513 2/2	1,2144592	1,214459192 NS
8,8331458 2/2	1,004627	1,004627	0,9678366 2/2	1,39765425	1,397654252 *
16,380356 3/3	1,0191273	1,2050344	0,8984178 3/3	2,474885	2,679318486 ***
14,847904 2/2	0,8569092	0,8569092	0,4893343 2/2	0,5294207	0,52942065 NS
10,642725 3/3	1,95785219	2,23489545 **	0,00263701 3/3	3,65137451	3,869111046 ***
10,85429 2/2	0,79937436	0,79937436 *	0,01921437 2/2	0,37646619	0,376466188 *
24,744571 3/3	0,9235419	0,8980337	0,3852665 3/3	0,7244348	0,730732648 NS
23,000387 2/2	0,9681151	0,9681151	0,6388146 2/2	0,5706749	0,570674873 NS
15,239098 3/3	0,87763574	0,87030339 *	0,01611235 3/3	0,8765708	0,756704692 NS
13,124905 3/3	1,1040852	1,0741765	0,0968995 3/3	0,59865675	0,615469943 *
26,864098 2/2	0,70041918	0,70041918 *	0,03172767 2/2	2,1222531	2,122253073 NS
43,588121 2/2	1,13322461	1,13322461 **	0,00804854 2/2	1,0871051	1,087105118 NS
1,1598087 3/3	1,21396005	1,28313948 *	0,04564257 3/3	0,69630165	0,693350449 ***
0,4523064 3/3	0,42862755	0,45823185 ***	0,00047725 3/3	0,85838234	0,86163592 ***
14,301654 3/3	1,10781972	1,11055459 **	0,00489003 3/3	0,6945895	0,651314932 NS
18,391053 4/4	0,9859582	1,0687467	0,858507 4/4	0,825219	0,709345458 NS
8,8279669 3/3	0,9424516	0,8560154	0,4778266 3/3	2,32964617	2,172661954 ***
27,106087 4/4	0,78310972	0,79768613 **	0,00157787 4/4	2,11496927	2,090262948 **

1,378253 2/2	1,2155839	1,2155839	0,0503103 2/2	0,59239253	0,592392534 **
10,764955 3/3	1,41856764	1,34310481 *	0,01014818 3/3	0,7701443	0,670340004 NS
13,326733 2/2	0,6796628	0,6796628	0,0998259 2/2	0,5752793	0,575279309 NS
6,888451 2/2	0,7260544	0,7260544	0,3017471 2/2	0,64970263	0,649702634 *
22,667022 2/2	1,45662684	1,45662684 **	0,00918254 2/2	2,34002855	2,34002855 *
17,455875 3/3	0,62775876	0,6140119 **	0,00955932 3/3	0,5235093	0,452365642 *
34,864932 2/2	0,8964703	0,8964703	0,1665922 2/2	1,5312311	1,531231115 NS
7,8770343 2/2	0,761482	0,761482	0,1941233 2/2	4,33743773	4,337437728 ***
13,175033 2/2	0,9280266	0,9280266	0,3101193 2/2	0,6521431	0,6521431 NS
5,6337712 2/2	1,01016	1,01016	0,8952944 2/2	0,8887334	0,888733372 NS
3,3664705 4/4	2,0310006	2,03615787 ***	9,6107E-07 4/4	0,72027921	0,726852633 ***
14,705958 2/2	0,9500161	0,9500161	0,7111262 2/2	0,8952662	0,895266236 NS
35,919882 3/3	0,71892297	0,71934999 ***	3,4069E-07 3/3	0,8899877	0,775882596 NS
2,360969 2/2	1,0304393	1,0304393	0,6486224 2/2	0,49846325	0,498463248 **
7,7341069 3/3	0,77389872	0,78317922 **	0,0049577 3/3	0,74956689	0,772776094 *
31,503775 3/3	0,79398255	0,8332549 *	0,01373387 3/3	1,1657448	1,499573489 NS
18,564776 2/2	1,9351164	1,9351164	0,2126544 2/2	0,6638792	0,663879161 NS
6,307304 2/2	0,4796503	0,4796503	0,113269 2/2	1,0001127	1,000112684 NS
7,3152697 4/4	0,61327064	0,57608101 ***	0,00011737 4/4	0,52654397	0,537687471 ***
37,789982 2/2	1,004925	1,004925	0,910493 2/2	2,9094581	2,909458102 *
20,904194 2/2	1,1279805	1,1279805	0,4887825 2/2	2,00305389	2,003053887 *
19,993951 3/3	0,9427962	0,8609353	0,6865862 3/3	1,0676486	1,164678468 NS
1,9040876 2/2	1,1093228	1,1093228	0,4178768 2/2	0,57128017	0,571280173 **
29,294964 3/3	1,47817234	1,42699776 ***	0,00040817 3/3	1,2343319	1,274294745 NS
12,434895 2/2	1,3150871	1,3150871	0,2546437 2/2	0,45416456	0,45416456 *
14,228392 3/3	0,8745716	0,9635232	0,1274861 3/3	0,42609434	0,469403137 **
17,627292 2/2	0,7620705	0,7620705	0,2796965 2/2	0,9861	0,986100034 NS
1,1225011 3/3	0,844358	0,8942098	0,0559394 3/3	0,88587805	0,893892618 ***
1,6055466 2/2	1,3989594	1,3989594	0,0603549 2/2	1,0641325	1,064132499 NS
0,3310066 2/2	0,8400098	0,8400098	0,2513708 2/2	0,65122003	0,651220034 ***
17,481741 3/3	0,78681614	0,710719 *	0,03336195 3/3	2,54333431	2,300239524 ***
9,0141424 2/2	0,68258223	0,68258223 ***	0,00012772 2/2	2,95001986	2,950019856 **
2,6182664 3/3	1,2316839	1,3627202	0,0708792 3/3	1,0042345	1,010190984 NS
6,5684547 2/2	0,63778263	0,63778263 **	0,00149788 2/2	4,7609389	4,760938902 ***
40,614894 5/5	1,1295439	1,0553748	0,2543252 5/5	0,9862189	0,562077059 NS
18,345167 2/2	0,9922506	0,9922506	0,9510565 2/2	1,2702725	1,270272481 NS
19,996737 3/3	0,9467534	0,886666	0,4965589 3/3	0,9940514	0,802481508 NS
8,9601411 3/3	0,79617183	0,80697698 **	0,00140808 3/3	1,40287052	1,480480304 **
11,847895 4/4	0,8957608	0,8124223	0,2108294 4/4	0,8214754	0,744116551 NS
15,919302 4/4	1,62368278	1,53257487 **	0,0046044 4/4	2,5512663	2,386161215 ***
9,614203 2/2	1,0325532	1,0325532	0,7173082 2/2	1,3890798	1,389079818 NS
13,036599 2/2	2,68837853	2,68837853 *	0,0125956 2/2	5,41540982	5,415409817 ***
4,7557228 3/3	1,6696229	1,4732792	0,0536025 3/3	0,67676029	0,673632855 **
0,8495951 2/2	1,712153	1,712153 **	0,00139008 2/2	0,92049948	0,920499478 *
17,09266 3/3	0,73571091	0,72985822 ***	0,00012534 3/3	3,04734126	3,293079389 ***
19,355471 4/4	1,27223917	1,09581144	0,0860003 4/4	0,994736	0,896230953 NS
2,7070998 2/2	0,8957574	0,8957574	0,5760444 2/2	1,41545985	1,41545985 **
11,945462 2/2	0,9393401	0,9393401	0,715108 2/2	0,768033	0,768033001 NS
46,338986 2/2	0,8035829	0,8035829	0,2620934 2/2	1,3412249	1,34122495 NS
33,415199 2/2	1,362434	1,362434	0,1029878 2/2	1,4206591	1,420659112 NS
8,7589851 3/3	0,74789475	0,72739612 **	0,00761639 3/3	1,59575736	1,59915359 **
23,696607 2/2	0,9932444	0,9932444	0,946735 2/2	1,7403936	1,740393628 NS

6,8793011 5/5	1,0267578	0,9888907	0,6439164 5/5	0,52705883	0,464842475 ***
13,916257 2/2	1,1718533	1,1718533	0,1627615 2/2	1,0187593	1,018759273 NS
22,178729 3/3	0,974452	0,9716758	0,2757935 3/3	0,6739319	0,889798853 NS
27,517488 2/2	0,8250902	0,8250902	0,3784934 2/2	1,5148764	1,514876441 NS
25,353997 2/2	1,27760617	1,27760617 *	0,04066741 2/2	1,1636018	1,163601756 NS
62,095666 2/2	1,54416324	1,54416324 *	0,03282206 2/2	2,6283762	2,628376203 NS
10,477121 2/2	1,0028888	1,0028888	0,9882186 2/2	0,54295619	0,542956189 *
4,6365437 2/2	1,25856504	1,25856504 ***	0,00037783 2/2	0,72458732	0,724587321 *
18,522905 3/3	1,0197559	1,0280833	0,0707186 3/3	0,9081285	0,875346182 NS
12,242966 5/5	0,79344469	0,80402719 **	0,00365041 5/5	0,6138562	0,610109654 **
25,970516 2/2	1,0095566	1,0095566	0,9239606 2/2	0,8988834	0,898883435 NS
9,1319585 2/2	0,7139986	0,7139986	0,0615045 2/2	0,8950964	0,895096383 NS
0,9893852 2/2	0,7912854	0,7912854	0,0849682 2/2	1,56723436	1,567234362 ***
9,1082524 4/4	0,8947068	0,8436849	0,3532815 4/4	0,72295885	0,767734738 **
11,396579 2/2	0,8424422	0,8424422	0,3210349 2/2	0,6353017	0,635301713 NS
0,9415392 2/2	2,04585441	2,04585441 ***	7,1015E-05 2/2	0,52160914	0,521609138 ***
27,023944 2/2	0,63752026	0,63752026 *	0,02642506 2/2	0,6538445	0,653844533 NS
14,301532 3/3	1,26376484	1,26554325 *	0,04529009 3/3	1,44030409	1,546045373 *
28,768422 2/2	1,4194545	1,4194545	0,1911175 2/2	2,81885572	2,818855716 *
6,2300345 3/3	4,11712349	5,16409856 ***	0,00085817 3/3	0,4897576	0,438222165 ***
8,2624355 3/3	1,0295494	1,0306317	0,6887921 3/3	1,74302692	1,621537829 ***
6,3483065 2/2	0,8477864	0,8477864	0,0818098 2/2	0,69228159	0,692281589 *
27,578981 2/2	1,11493661	1,11493661 *	0,03100497 2/2	0,9455156	0,945515646 NS
11,985517 2/2	0,8367808	0,8367808	0,4592592 2/2	0,7781677	0,778167739 NS
3,2015297 3/3	0,81049444	0,83382354 **	0,00550833 3/3	0,65751382	0,62920182 ***
9,7501169 4/4	1,12529126	1,05389379	0,0831289 4/4	1,34645775	1,28023262 **
48,281015 4/4	1,26496699	1,14904888 *	0,01738859 4/4	0,7872104	0,474603675 NS
20,799192 4/4	0,53177319	0,55717102 ***	2,2111E-06 4/4	1,79380283	1,607141138 **
15,821018 4/4	0,9189815	0,9475869	0,4352993 4/4	1,97819496	1,922854712 ***
20,120623 5/5	1,22903276	1,37388637 *	0,01053559 5/5	0,8583792	0,667865574 NS
1,3154331 4/4	0,9699703	0,9863481	0,3606801 4/4	0,72433531	0,73131583 ***
8,4358526 4/4	0,9082717	0,9789226	0,1717481 4/4	1,76999387	1,825250878 ***
3,8583269 2/2	1,19288617	1,19288617 **	0,00372743 2/2	0,54635965	0,546359648 **
9,16783 3/3	1,40865422	1,42829467 **	0,00209739 3/3	0,844325	0,88935751 NS
18,963001 4/4	1,2967896	1,3533902	0,1241234 4/4	3,71244018	3,687067825 ***
10,187823 2/2	1,6146971	1,6146971 *	0,01503137 2/2	0,36553575	0,365535747 *
17,535989 4/4	0,9819682	0,9577199	0,6417227 4/4	0,9659981	0,973176707 NS
21,213123 3/3	1,0333474	0,8886418	0,8297193 3/3	1,294758	1,584439713 NS
3,9701115 2/2	1,37387365	1,37387365 *	0,04949077 2/2	0,76082198	0,760821977 *
4,6445685 2/2	0,9700323	0,9700323	0,6848054 2/2	0,62689435	0,626894349 *
9,4934118 4/4	0,66126392	0,62763989 ***	9,0038E-05 4/4	1,0773508	1,134774326 NS
17,822249 2/2	0,59415624	0,59415624 **	0,0062376 2/2	0,4979083	0,497908288 NS
0,9148138 2/2	1,0931741	1,0931741	0,8110845 2/2	2,18166501	2,181665013 ***
30,00714 3/3	0,925613	0,8924605	0,3794986 3/3	1,6502124	2,09124215 NS
3,727785 2/2	0,979569	0,979569	0,6733005 2/2	0,63719667	0,637196667 *
16,035577 2/2	0,7840105	0,7840105	0,1252525 2/2	0,7173061	0,717306088 NS
13,957925 2/2	0,7374441	0,7374441	0,101547 2/2	0,754834	0,754834044 NS
2,9879983 2/2	0,668853	0,668853	0,073361 2/2	0,77340496	0,773404958 *
9,590981 2/2	1,322663	1,322663	0,1779901 2/2	0,50586461	0,505864613 *
9,8700317 2/2	0,9578176	0,9578176	0,8373667 2/2	0,57001305	0,570013052 *
4,9793058 2/2	0,9540545	0,9540545	0,6750264 2/2	0,8993298	0,899329821 NS
21,67075 6/6	1,3857205	1,36328633 *	0,02141571 6/6	1,0929198	1,062718937 NS

0,9554251 2/2	1,2035545	1,2035545	0,1262688 2/2	0,42074852	0,420748518 ***
18,897756 2/2	0,67517807	0,67517807 *	0,04990318 2/2	0,9638223	0,963822338 NS
5,2704815 3/3	1,009925	0,9474416	0,8448751 3/3	0,50274478	0,514069153 ***
12,158337 2/2	1,9419007	1,9419007	0,0511135 2/2	2,97307941	2,973079413 **
20,596709 2/2	1,166173	1,166173	0,1015639 2/2	0,5417069	0,541706878 NS
10,276003 3/3	1,40864184	1,33026264 **	0,00255405 3/3	0,71534263	0,658190473 *
14,598579 2/2	1,1331225	1,1331225	0,2270087 2/2	0,5825714	0,582571425 NS
27,392748 3/3	0,9323377	1,0242939	0,3634843 3/3	1,1430381	0,852670339 NS
47,065221 2/2	0,95344542	0,95344542 ***	0,00047451 2/2	4,04272632	4,042726322 *
8,103857 4/4	0,75379109	0,7428514 ***	0,00087378 4/4	1,0905487	1,085958817 NS
28,15269 2/2	0,7445442	0,7445442	0,2040811 2/2	0,663961	0,663961015 NS
6,1809273 2/2	1,3138013	1,3138013	0,2426598 2/2	1,112347	1,112347032 NS
11,489527 3/3	0,60672738	0,6384263 **	0,00115053 3/3	0,7656728	0,66197123 NS
4,2893553 2/2	1,1546134	1,1546134	0,5379625 2/2	0,50197044	0,501970444 **
16,381139 3/3	0,9273041	0,9557867	0,0791744 3/3	0,9338122	0,919633639 NS
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