

Table S1. Proteins identified and quantified in *E.coli* extract samples.

#	Access ID	Unique Peptide Sequence	Labeling Site(s)	MW (kDa)	Abundance Ratio				
					Mea*	Ave	Exp'd	%SD	%Err
1	P02990	TYGGAAR	1	43.924	0.33	0.34	0.33	10.6	2.9
		LLDEGR	1		0.39				
		HTPFFK	2		0.35				
		GYRPQFY	1		0.32				
		REEIER	1		0.34				
		EHILLGR	1		0.37				
		LLPIEDVF	1		0.35				
		AGENVGVLLR	1		0.32				
		VGEEVEIVGIK	2		0.39				
		DFPGDDTPIVR	1		0.35				
		IHPIAMDDGLR	1		0.39				
		TTLTAAITTVLAK	2		0.31				
		AIDKPFLLPIEDVF	2		0.28				
		GQVLAKPGTIKPHTK	4		0.39				
		GITINTSHVEYDTPTR	1		0.32				
		TKPHVNVTGTTIGHVDHGK	3		0.35				
		ILELAGFLDSYIPEPER	1		0.32				
		ELLSQYDFPGDDTPIVR	1		0.26				
		AIDKPFLLPIEDVFSISGR	2		0.37				
2	P09373	LHTYR	1	86.805	0.33	0.34	0.33	9.0	1.8
		IFTEYR	1		0.37				
		ALIPFGGIK	2		0.35				
		QMQFFGAR	1		0.34				
		LATAWEGFTK	2		0.39				
		GDWQNEVNVR	1		0.32				
		VDDLAVDLVER	1		0.33				
		LREEIAEQHR	1		0.32				
		SGVLTGLPDAYGR	1		0.30				
		TSTFLDVYIER	1		0.33				
		IVGLQTEAPLKR	2		0.36				
		AGAPFGPGANPMHGR	1		0.30				
		KSGVLTGLPDAYGR	2		0.32				
		RAGAPFGPGANPMHGR	1		0.38				
		ITEQEAQEMVDHLVMK	2		0.30				
		EMLLDAMENPEKYPQLTIR	2		0.39				
3	P80063	LLTDFR	1	53.352	0.39	0.33	0.33	0.0	6.6
		YLSDHPK	2		0.27				
		YWDVELR	1		0.33				
		RFPLHEMR	1		0.36				

EIPMRPGQLF	1	0.33					
LQGIAQQNSFK	2	0.38					
QIINDELYLDGNAR	1	0.29					
EIPMRPGQLFMDPK	2	0.37					
GFEMDFAELLLEDYK	2	0.32					
NWIDKEEYPQSAAIDLRL	2	0.35					
GWQVPAFTLGGEATDIVVMR	1	0.31					
DDVAFQIINDELYLDGNAR	1	0.28					
4P05313 ADQIQW	1	48.196	0.30	0.33	0.33	10.5	0.5
INNTFR	1	0.34					
EWTQPR	1	0.33					
TSEGFFR	1	0.42					
SAGIEPGDPR	1	0.35					
RFAQAIHAK	2	0.32					
VQQPEFAAAK	2	0.36					
THAGIEQAISR	1	0.33					
VLVPTQEAIQK	2	0.35					
RADQIQWSAGIEPGDPR	1	0.33					
FLPIVADAEAGFGGVLNDF	1	0.28					
DGYTFVSHQQEVGTGYFDK	2	0.31					
5P02934 SLGVSYR	1	37.818	0.42	0.34	0.33	11.0	1.6
LGGMVWR	1	0.31					
AITPEIATR	1	0.36					
DNTWYTGAK	2	0.34					
EMGYDWLGR	1	0.37					
DGSVVVLGYTDR	1	0.32					
IGSDAYNQGLSER	1	0.35					
VGFEMGYDWLGR	1	0.35					
NHDTGVSPVFAGGVVEY	1	0.29					
ATLKPEGQAALDQLY	2	0.30					
FGQGEAAPVAVAPAPAPAPEVQTK	2	0.32					
6P27430 ATVELLNR	1	18.917	0.34	0.33	0.33	10.7	0.5
QAHWNMR	1	0.37					
DLDKFLW	2	0.32					
YAIIVANDVR	1	0.35					
IAVHEMLDGFR	1	0.40					
TALIDHLDTMAER	1	0.34					
QVIQFIDLSSLITK+Pyro-glu(N-term Q)	1	0.29					
QVIQFIDLSSLITK	2	0.30					
GANFIAVHEMLDGFR	1	0.35					
SYPLDIHNVQDHDK	2	0.31					
AVQLGGVALGTTQVINSK	2	0.28					

7	P08997	FSQGR	1	61.1	0.36	0.34	0.33	7.9	2.3
		VIDGQINLR	1		0.39				
		KNQLEVMR	2		0.33				
		VIASELGEER	1		0.33				
		TRPYGEQEK	2		0.35				
		RVEITGPVER	1		0.36				
		AFTRPYGEQEK	2		0.33				
		LTELVTHFTPQR	1		0.36				
		VFMADFEDSLAPDWNK	2		0.29				
		TEQATTTDELA	2		0.34				
		TRPYGEQEK	1		0.31				
8	P14825	SWGLGR	1	58.332	0.29	0.34	0.33	10.7	2.6
		VFEINR	1		0.40				
		LVVGGFER	1		0.35				
		WDLGDIIGAR	1		0.39				
		ASFVTLQDVGGR	1		0.32				
		DVILFPAMRPQK	2		0.34				
		GANEAIDFNDEL R	1		0.38				
		ADYHDLIELTESLFR	1		0.33				
		ALRPLPDKFHGLQDQEVR	2		0.34				
		MAYADYHDLIELTESLFR	1		0.30				
9	P37192	AQNISR	1	31.209	0.33	0.33	0.33	7.6	1.5
		TNPAQAR	1		0.33				
		DYLQSAK	2		0.37				
		NAFSQALK	2		0.29				
		ASAPALDFSR	1		0.30				
		NYLTEHPEATDPR	1		0.34				
		THAGTENLLALVSAMAK	2		0.32				
		QYHHPLAIHLDHHTK+Pyro-glu(N-term Q)	1		0.34				
		QYHHPLAIHLDHHTK	2		0.35				
		EFAEATGIDS LAVAIGTAHGMY	1		0.31				
10	P33633	LGDIEYR	1	14.532	0.37	0.35	0.33	9.6	5.8
		LLDSEKG EAR	2		0.36				
		FNSLTPEQQR	1		0.38				
		AANDDLLNSFW	1		0.36				
		EVPVEVKPEVR	2		0.34				
		AGYADEV VAVSK	2		0.27				
		HPEKYPQLTIR	2		0.34				
		VEGGQHLNVNVLR	1		0.39				
		ETLEDAVKHPEKYPQLTIR	3		0.36				

11	P03815	TIQVLQR	1	96.967	0.35	0.33	0.33	5.3	0.3
		WTGIPVSR	1		0.34				
		TAIVEGLAQR	1		0.32				
		MEQELHHR	1		0.35				
		YRGEFEER	1		0.36				
		NILLQVLDDGR	1		0.32				
		GGESVNDQGAEDQR	1		0.32				
		VFVAEAPSVEDTIALR	1		0.33				
		LVGAPPGYVGYEEGGYLTEAVR	1		0.30				
12	P06958	AFLEGR	1	100.848	0.35	0.33	0.33	11.5	0.9
		LFAEQVR	1		0.32				
		LVPIIADEAR	1		0.32				
		LTQEQLDNFR	1		0.27				
		FNIDADKVNP'R	2		0.39				
		DWLQAIESVIR	1		0.30				
		AQYlidQLLAEAR	1		0.33				
		LEPLSLQDFGALLEEQSK	2		0.36				
13	P02354	MGFGATR	1	23.996	0.33	0.31	0.33	7.4	5.5
		LDNVVYR	1		0.33				
		AALELAEQR	1		0.30				
		IEQAPGQHGAR	1		0.34				
		EKPTWLEVDAGK	3		0.28				
		GNTGENLLALLEGR	1		0.33				
		LKGNTGENLLALLEGR	2		0.29				
14	P31217	YGDEQVK	2	29.144	0.38	0.33	0.33	8.2	1.4
		WNETILPR	1		0.32				
		DDERYPGHDPR	1		0.35				
		HGESQWNKENR	2		0.34				
		FTGWYDVLSEK	2		0.30				
		VIPYWNETILPR	1		0.31				
		NVLDELDQAWLPVEK	2		0.30				
15	P11665	EFPNFR	1	41.987	0.39	0.34	0.33	7.6	3.2
		VMDAFTAH'R	1		0.33				
		ALKEPARPMVAIVGGSK	3		0.33				
		SIAGGGDTLAAIDLFGIADK	2		0.32				
		VMVTSHLGRPTEGEYNEEF	1		0.36				
		ADEQILDIGDASAQELAEILK	2		0.33				
16	P06977	YDSTHGR	1	36.276	0.35	0.36	0.33	10.8	8.6
		VTAERDPANLK	2		0.40				
		TVDGPSHKDWR	2		0.34				

	VPTPNVSVDLTVR	1	0.39						
	RVPTPNVSVDLTVR	1	0.30						
	LVSWYDNETGYSNK	2	0.39						
17 P06139	APGFGDR	1	58.475	0.33	0.35	0.33	8.1	6.5	
	AMEAPLR	1	0.35						
	QQIEEATSDYDREK+Pyro-glu(N-term Q)	1	0.40						
	QQIEEATSDYDR	1	0.38						
	FINKPETGAVELESPF	2	0.33						
	DTTTIIDGVGEEAAIQGR	1	0.35						
18 P02390	RPEPYK	2	19.238	0.37	0.34	0.33	13.1	2.0	
	YADEVVR	1	0.34						
	KLQLVGVGYR	2	0.32						
	HADNTLTFGPR	1	0.27						
	DGYADGWAQAGTAR	1	0.35						
	ALLNSMVGIVTEGFTK	2	0.40						
19 P13030	SWGLGR	1	58.237	0.29	0.32	0.33	14.3	3.2	
	VFEINR	1	0.39						
	LVVGGFER	1	0.35						
	ASFVTLQDVGGR	1	0.32						
	DLIELTESLFR	1	0.27						
20 P02349	AISLSVR	1	62.53	0.35	0.33	0.33	9.4	2.0	
	AFLPGSLVDVRPVR	1	0.33						
	TESFAQLFEESLK	2	0.29						
	MTESFAQLFEESLK	2	0.36						
	VVNVDVVEVMVLIDIEER	1	0.30						
21 Q8XB34	HLPEPFR	1	53.717	0.34	0.35	0.33	3.3	6.5	
	GDEAYSGSR	1	0.35						
	AYREEAIK	2	0.36						
	GNFDLEGLER	1	0.37						
	DWTIEQITR	1	0.36						
22 P02389	DFPFR	1	20.702	0.39	0.35	0.33	11.5	3.7	
	LITIAVPR	1	0.32						
	NYNSVMQVPR	1	0.39						
	ALLAAFDFPFRK	2	0.32						
	EQIIFPEIDYDKVDR	2	0.32						
23 P60438	GLWEFR	1	22.87	0.32	0.31	0.33	5.7	7.4	
	DLANDGYR	1	0.33						
	VTVQSLDVVR	1	0.30						

	IFTEDGVSIPVTVIEVEANR	1	0.29					
24 P26427	EDEGLADR	1	21.098	0.30	0.32	0.33	11.2	3.1
	YAMIGDPTGALTR	1		0.38				
	VVDPQGIIQAIETVAEGIGR	1		0.30				
	ATFVVDPQGIIQAIETVAEGIGR	1		0.31				
25 P11056	LNIGEDVEEMLR	1	18.804	0.39	0.36	0.33	9.4	6.7
	MGLQNYLQAQIR	1		0.31				
	EAIGYADSVHDYVSR	1		0.37				
	ILFLEGLPNLQDLGK	2		0.36				
26 P37194	GNNQPDIQK	2	21.239	0.33	0.33	0.33	9.7	0.2
	QSGFLDPVNRYR	1		0.38				
	SFVAVHNQPGLY	1		0.32				
	AKPDIEANYQGR	2		0.30				
27 P02363	SLEQYFGR	1	15.068	0.40	0.36	0.33	8.9	6.6
	GGGISGQAGAIR	1		0.34				
	AENQYYGTGR	1		0.32				
	ALMEYDESLR	1		0.36				
28 P02384	KSDQNVN	2	25.352	0.40	0.34	0.33	11.5	2.3
	VVGQLGQVLGPR	1		0.35				
	ENLEALLVALK	2		0.31				
	QYDINEAIALLK+Pyro-glu(N-term Q)	1		0.32				
29 P02372	MVTIR+Oxidation(M)	1	9.377	0.35	0.33	0.33	9.2	0.4
	VGFFNPIASEK	2		0.36				
	IAHWVGQGATISDR	1		0.29				
	VGFFNPIASEKEEGTR	2		0.32				
30 P37191	YYWPHSR	1	47.559	0.37	0.33	0.33	8.2	0.6
	AQWIENTR	1		0.32				
	TGFNDSLLDIR	1		0.33				
	MVYEAHSTDYQTR	1		0.31				
31 P30849	FGNMSGQMR	1	20.958	0.35	0.30	0.33	11.2	8.6
	AAQELFDVSQVR	1		0.29				
	GGTPYGATTIAGGDGSR	1		0.27				
	RVPETMPPQLFEK	2		0.31				
32 P02413	FGFTSR	1	15.364	0.29	0.33	0.33	14.2	2.1
	GFEFGQMPLYR	1		0.37				
	RGFEGGQMPLYR	1		0.29				

	VILAGEVTTPVTVR	1	0.36					
33 P02996	AGPLAGYPVWDMGIR	1	78.843	0.34	0.35	0.33	5.3	5.8
	IATDPFVGNLTFFR	1		0.34				
	EFNVEANVGKPQVAYR	2		0.37				
34 P21364	LGGAAQQHDSVR	1	23.17	0.33	0.36	0.33	8.6	6.7
	MATDNIGVELLAATPFR	1		0.35				
	TYMATDNIGVELLAATPFR	1		0.39				
35 P11096	IAGVGTGGTLTGCSR	1	35.106	0.32	0.34	0.33	5.3	2.8
	IGANMIWDAEKR	2		0.34				
	IFEDNSLTIGHTPLVR	1		0.36				
36 P39811	SPAIEEWLR	1	24.943	0.31	0.32	0.33	5.1	2.6
	SAFDEFSTPAAR	1		0.34				
	EASAGNFADLLAHSDGLIK	2		0.33				
37 P25553	AQPEWEALPAIER	1	52.845	0.37	0.34	0.33	12.0	2.0
	GYYYPPTLLLDR	1		0.39				
	GDAWIDVVNPATEAVISR	1		0.31				
38 P02356	VGFGYGK	2	17.878	0.33	0.35	0.33	14.2	4.6
	AYGSTNPINVVR	1		0.31				
	VFMQPASEGTGIIAGGAMR	1		0.41				
39 P02359	AFAHYR	1	20.356	0.35	0.37	0.33	5.5	11.5
	SALETLAQR	1		0.37				
	SELEAFEVALENVRPTVEVK	2		0.39				
40 P02420	LQAFEGVVIAIR	1	13.379	0.38	0.35	0.33	11.7	4.0
	QDVPSFRPGDTVEVK	2		0.36				
	QDVPSFRPGDTVEVK+Pyro-glu(N-term Q)	1		0.30				
41 P07016	GLVTPVLR	1	44.686	0.37	0.36	0.33	6.9	9.0
	KQYGEAFEKR	3		0.39				
	ESAPAAAAPAAQPALAAR	1		0.34				
42 P02428	FVTLR	1	9.126	0.35	0.36	0.33	7.0	9.3
	FWVESEKR	2		0.35				
	FLPNLHSHR	1		0.39				
43 P02352	LGIVKPW	2	26.605	0.29	0.31	0.33	7.8	8.2
	VTIHTARPGIVIGK	2		0.30				
	KVVADIAGVPAQINIAEV	2		0.33				

44 P11604	ANEAYLQGQLGNPK	2	39.824	0.39	0.37	0.33	10.1
	IFDFVKPGVITGDDVQK	3		0.35			
45 P08324	DAGYTAVISHR	1	46.713	0.37	0.35	0.33	5.4
	AFTSEEFTHFLEELTK	2		0.33			
46 P08936	REEESAAAAEVEER	1	15.815	0.29	0.31	0.33	7.4
	EMLIADGIDPNELLNSLAALK	2		0.33			
47 P42617	ADEYVR	1	11.333	0.38	0.33	0.33	0.2
	SKEHTTEHLR	2		0.29			
48 P03948	FADYDEAR	1	30.322	0.37	0.37	0.33	10.7
	MQQLQNIIETAFER	1		0.36			
49 P02341	ALDAIIASVTESLK	2	9.54	0.36	0.35	0.33	5.1
	TGRNPQTGK	2		0.34			
50 P09372	VANLEAQLAEAQTR	1	22.233	0.42	0.37	0.33	11.7
	FINELLPVIDSLDR	1		0.33			
51 P04475	FQDEEVQR	1	70.575	0.37	0.37	0.33	11.7
	AKLESLVEDLVNR	2		0.38			
52 P32691	EVVDWETR	1	8.672	0.33	0.35	0.33	3.6
	MNKDEAGGNWK	3		0.36			
53 P02388	SILSELVR	1		0.34	0.36	0.33	7.5
	AARPQDHSQLK	2		0.37			
54 P08837	IAEEGQR	1	18.685	0.31	0.32	0.33	5.0
	LSGSVTVGETPVIR	1		0.32			
55 P39330	IEIEAIAVR	1	13.76	0.38	0.36	0.33	8.3
	TGEVPADVAAQAR	1		0.35			
56 P02408	LATLPTYEEAIAR	1	17.986	0.38	0.37	0.33	10.5
	AAAFEGELIPASQIDR	1		0.36			
57 P23887	YVSEQHEEEK	2	19.732	0.30	0.32	0.33	3.5
	LFDYLTDTGNLPR	1		0.34			
58 P39169	IYPGQVLR	1	16.499	0.33	0.33	0.33	1.8
	LWDAVTGQHDKDDQAK	3		0.32			

59 P02342	TGRNPQTGK	2	9.866	0.34	0.36	0.33	9.0
	AALESTLAAITESLK	2		0.36			
60 P09743	THEQTTAAER	1	26.282	0.32	0.30	0.33	11.4
	YIAETFLEDAR	1		0.27			
61 P17547	LLAWLETLK	2	98.05	0.35	0.35	0.33	5.3
	SIYFR	1		0.35			
62 P07460	DQSQEDPR	1	42.167	0.40	0.35	0.33	4.7
	AVLVNIFGGIVR	1		0.30			
63 P00824	GQMNEPPGNR	1	50.835	0.37	0.35	0.33	5.3
	DVLLFVDNIYR	1		0.33			
64 P37190	HQDEVR	1	37.911	0.28	0.29	0.33	12.2
	SSPWPGQEWEETASR	1		0.31			
65 P06994	FGLSLVR	1	33.022	0.35	0.31	0.33	8.0
	LFGVTTLIDIIR	1		0.27			
66 P02392	TEFDVILK	2	12.605	0.42	0.37	0.33	11.4
	FGVSAAAVALAAGPVEAAEEK	2		0.32			
67 P02379	AGVLAEV	1	8.684	0.31	0.32	0.33	4.4
	EFYEKPTTER	2		0.32			
68 P76402	SNSPQEER	1	12.369	0.36	0.36	0.33	9.3
	AGWFELSK	2		0.37			
69 P02435	AVQQNKPTR	2	6.536	0.34	0.32	0.33	4.1
	HHITADGYYR	1		0.30			
70 P36546	NQYYGITAGPAYR	1	18.879	0.39	0.37	0.33	9.8
	YRYEEDNSPLGVIGSF	1		0.34			
71 P22986	GYQAGIAGR	1	6.631	0.38	0.36	0.33	6.8
	SQWLGGWR	1		0.33			
72 P19928	HNQQPTETEHQPGNEDK	2	41.167	0.33	0.36	0.33	9.3
	RHNQQPTETEHQPGNEDK	2		0.40			
73 P09157	SLEEIIR	1	21.474	0.41	0.36	0.33	8.4
	NARPGYLEHFW	1		0.32			

74 P78258	NIYDYYK	2	36.373	0.33	0.31	0.33
	LIPPSQTFPRPAPMSEAEFR	1		0.29		
75 P06959	VPDIGADEVEITEILVK	2	67.653	0.34	0.35	0.33
	QEAAAPAAAPAPAAGVK+Pyro-glu(N-term Q)	1		0.29		
76 P02373	SWTLVR	1	9.92	0.26	0.30	0.33
	SIVVAIER	1		0.34		
77 P02418	LFGSIGTR	1	16.144	0.36	0.37	0.33
	NIEFFEAR	1		0.39		
78 P39177	RFEHLQHEAQER	1	16.053	0.35	0.36	0.33
	HANLPVLVVR	1		0.38		
79 P02421	GYYGAR	1	13.838	0.32	0.35	0.33
	QLWIAR	1		0.38		
80 P31658	VMPFFEQQHK	2	31.648	0.32	0.32	0.33
	TSPVSDLDGVDPKPYR	2		0.31		
81 P52084	IDDDLTLLSETLEEVLR	1	11.555	0.34		0.33
					0.33	0.9
82 P00574	AATILAEQLEAFVDLR	1	37.034	0.29		0.33
					0.33	13.2
83 P14178	LNFSHGDYAEHGQR	1	51.818	0.41		0.33
					0.33	23.1
84 P37797	ESIEEA VSEVVNALK	2	63.426	0.32		0.33
					0.33	3.9
85 P21599	GLPADVVP GDILLDDGR	1	52.091	0.35		0.33
					0.33	4.5
86 P23933	AQVAQIAGKPSSEVSMIHAR	2	12.301	0.28		0.33
					0.33	17.4
87 P05055	LHILGVMEQAINAPR	1	78.174	0.39		0.33
					0.33	17.7
88 P02414	VLYEMDGVP EELAR	1	15.816	0.34		0.33
					0.33	1.2
89 P25516	VLMQDFTGVPAVVDLAAMR	1	98.864	0.36		0.33
					0.33	7.8
90 P00509	MFENITAAPADPILGLADLFR	1	44.155	0.28		0.33
					0.33	16.5
91 P76504	ITPTFTEESDGVR	1	10.317	0.39		0.33
					0.33	18.3
92 P02371	TAQINHLQGHFAEHK	2	10.356	0.35		0.33
					0.33	5.7

Sequence and Structural Data					
Index	Sequence	Start	End	Length	Score
93	P00831 LNALPDVLEQFIHLR	1	19.608	0.36	0.33
7.5					
94	P02429 SVEELNTELLNLLR	1	7.493	0.34	0.33
1.8					
95	P08330 TLTLSGMLAEAIR	1	34.354	0.31	0.33
8.4					
96	P04790 SATPAQAQAVHK	2	27.499	0.36	0.33
8.1					
97	P07459 GGTTHLGLPVFNTVR	1	30.364	0.29	0.33
11.7					
98	P23843 AQGNMPAYGYTPPYTDGAK	2	62.206	0.31	0.33
8.1					
99	P08200 STQVYGQDVWLPAETLDLIR	1	46.752	0.32	0.33
4.8					
100	P23842 AALSVL	1	84.303	0.38	0.33
12.9					
101	P15034 EIYDIVLESLETSLR	1	50.102	0.30	0.33
11.4					
102	P10408 ALVDEVDSILIDEAR	1	103.625	0.32	0.33
3.6					
103	P08839 IMFFPMIISVEEVR	1	64.675	0.29	0.33
14.1					
104	P06981 LNIPMLSAAMDTVTEAR	1	52.791	0.39	0.33
16.8					
105	P21179 GPTLLEDIFLR	1	85.328	0.34	0.33
0.9					
106	P45473 VEIPIDAPGIDALLR	1	18.618	0.35	0.33
6.0					
107	P24247 IGIIGAMEEEVTLLR	1	24.723	0.30	0.33
11.4					
108	P11026 YHFEQSSTTQPAR	1	58.872	0.40	0.33
18.6					
109	P46131 TDKDSLFWGEQTIER	2	8.775	0.38	0.33
14.4					
110	P75691 ADQINEAYER	1	38.498	0.39	0.33
16.2					
111	P07651 AAGLELFDR	1	45.079	0.27	0.33
19.2					
112	P02411 MIQEQTMLNVADNSGAR	1	13.917	0.33	0.33
0.3					
113	P11668 TQPDYDYQDGK	2	27.195	0.28	0.33
16.2					
114	P00391 YDAVLVAIGR	1	51.807	0.37	0.33
11.4					

115 P00859	AEAEQER	1	17.766	0.37	0.33	11.7
116 P36950	IAEQEGIAEDGYR	1	13.361	0.38	0.33	13.2
117 P02369	FVVEGDLR	1	13.345	0.40	0.33	21.3
118 P02410	DWYVVVDATGK	2	16.489	0.29	0.33	13.2
119 P11457	AQAFEQDR	1	18.254	0.37	0.33	10.2
120 P27302	HNPQNPSWADRDR	1	73.309	0.28	0.33	14.7
121 P71295	AINYGYTDDR	1	38.467	0.36	0.33	9.0
122 P17963	FLFDEYVR	1	35.48	0.38	0.33	12.6
123 P17169	DVAEILLEGLR	1	67.394	0.36	0.33	6.6
124 P02423	LVADLIR	1	12.667	0.32	0.33	3.0
125 P33398	VPLFVQIGEVIK	2	20.896	0.35	0.33	4.8
126 P37010	FAYVDILQNPDIR	1	13.127	0.30	0.33	8.7
127 P02409	GLPIPVVITVY	1	15.247	0.26	0.33	21.6
128 P02375	LGEFAPTR	1	10.741	0.30	0.33	9.9
129 P02366	ALNAAGFR	1	14.026	0.36	0.33	9.3
130 P02351	AGVHFGHQTR	1	27.236	0.35	0.33	4.8
131 P02378	AFNEMQPIVDR	1	10.028	0.41	0.33	22.8
132 P46129	ESLWQELADITDK	2	19.042	0.33	0.33	0.0
133 P12283	TGWLDTVAVR	1	47.921	0.38	0.33	15.3
134 P39100	FRPDTPEEYKPTVR	2	23.334	0.29	0.33	14.1
135 P02997	AQFEEER	1	31.202	0.30	0.33	8.7
136 P02937	VDQLSNDVNAMR	1	8.575	0.32	0.33	4.5
137 P52083	DDTWVTLR	1	14.322	0.36	0.33	8.1

138	P28242	AVSMARPY	1	16.213	0.39
0.33					16.5
139	P02416	LFNELGPR	1	14.644	0.37
					0.33
					12.0
140	P05380	MNIRPLHDR	1	10.669	0.38
					0.33
					14.4
141	P00891	LMGFGHR	1	48.753	0.34
					0.33
					2.7
142	P02925	ERGEQFQQAVAAHK	2	31.796	0.35
					0.33
					5.1
143	P37187	GVVHDTWPQALIAR	1	17.153	0.39
					0.33
					16.5
144	P02419	SGFQYHGR	1	13.082	0.40
					0.33
					19.5
145	P23929	KGQAHWEGDIK	3	15.364	0.39
					0.33
					18.0
146	P26604	QANFKDK	3	12.331	0.38
					0.33
					12.9
147	Q47413	GEAEAAR	1	12.472	0.41
					0.33
					21.9
148	P11537	EVVEQEYR	1	62.528	0.36
					0.33
					7.5
149	P37903	TILVPIDISDSELTQR	1	16.327	0.26
					0.33
					21.3
150	P60624	HQKPVPALNQPGGIVEK	3	11.723	0.34
					0.33
					0.6
151	P00448	EFWNVVNWDEAAAR	1	23.528	0.36
					0.33
					9.0
152	P22257	ANDIDVPAALIDSEIDVLR	1	49.316	0.29
					0.33
					14.1
153	P37095	LMIIDWVR	1	46.824	0.29
					0.33
					12.3
154	P31057	IEGGEWLVETVQMLTER	1	28.604	0.29
					0.33
					14.1
155	P17288	VEGWENAEAAK	2	20.105	0.35
					0.33
					3.6
156	P60422	GTAMNPVDHPHGGGEGR	1	30.544	0.31
					0.33
					5.7
157	P32168	NNWGQTEQQQEPSAAR	1	50.556	0.39
					0.33
					16.5
158	P52697	EGFQPTETQPR	1	36.573	0.39
					0.33
					16.8
159	P02358	LEDWGR	1	15.918	0.36
					0.33
					8.7

160P00353 NVGFIGWR	1	40.441	0.34	0.33	3.0
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* The average ratio of all measured pairs is 0.34 and relative standard deviation is 10.3%