

Spot number	MALDI well number	Match Quality	Top Ranked Protein Name (Sh)	Accession No.	Protein MW	Protein pI	Pept.Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I.%	Comments / Other Possible H
1	E1		Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic OS=Vigna radiata var. radiata G	RCA_VIGRR	47,871	7.6	7	62	98	41	99	dimer? Or modified?
3	E2		Chaperone protein CtpC, chloroplastic OS=Pisum sativum PE=2 SV=1	CLPC_PEA	102,647	6.6	25	312	100	162	100	
6	E3		PREDCTED: ATP-dependent zinc metalloprotease FTSH, chloroplastic [Vitis vinifera]	g 225459844	75,584	6.4	16	127	100	38	0	other hits could be contaminated protein
8	E4		Ribulose biphosphate carboxylase large chain OS=Viscum album GN=rbcL PE=3 SV=1	RBL_VISAL	52,357	6.4	17	199	100	96	100	dimer? Or modified?
10	E5		Stromal 70 kDa heat shock-related protein, chloroplastic OS=Pisum sativum GN=HSP70 PE=2 SV=1	HSP7S_PEA	75,469	5.2	14	604	100	546	100	
13	E6		Ribulose biphosphate carboxylase large chain (Fragment) OS=Tasmania insipida GN=rbcL PE=3 SV=2	RBL_TASIN	51,844	6.0	15	111	100	26	58	dimer? Or modified?
14	E7		Ribulose biphosphate carboxylase large chain (Fragment) OS=Humiria balsamifera GN=rbcL PE=3 SV=1	RBL_HUMBA	51,530	6.2	21	421	100	266	100	dimer? Or modified?
16	E8		Ribulose biphosphate carboxylase large chain (Fragment) OS=Pachira aquatica GN=rbcL PE=3 SV=1	RBL_PACAA	52,040	6.2	15	151	100	62	100	dimer? Or modified?
18	E9		ATP synthase subunit alpha, chloroplastic OS=Manihot esculenta GN=atpA PE=3 SV=1	ATPA_MANES	55,564	5.2	14	637	100	559	100	
20	E10		ATP synthase subunit beta, chloroplastic OS=Monus indica GN=atpB PE=3 SV=1	ATPB_MORIN	53,758	5.5	30	1,010	100	716	100	
21	E11		Ribulose biphosphate carboxylase large chain (Fragment) OS=Aesculus pavia GN=rbcL PE=3 SV=2	RBL_AESPA	51,619	6.2	24	799	100	611	100	
23	E12		Enolase 2 OS=Hevea brasiliensis GN=ENO2 PE=1 SV=1	ENO2_HEVBR	47,884	5.9	9	167	100	130	100	
24	E13		Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GOAT1 PE=1 SV=1	GST1_ARATH	53,267	6.5	11	240	100	189	100	
25	E14		Ribulose biphosphate carboxylase/oxygenase activase A, chloroplastic OS=Hordeum vulgare GN=RCAA R	RCAA_HORVU	51,041	8.0	10	512	100	481	100	hit10 isoform has correct pI and MW
34	E15		Phosphoglycerate kinase, chloroplastic OS=Nicotiana tabacum PE=2 SV=1	PGKH_TOBAC	50,146	8.5	12	505	100	446	100	
41	E16		mucunain [Mucuna pruriens]	gi 82375363	46,649	0	7	255	100	233	100	could also contain hit#2: cysteine proteinase RD21a
43	E17		Sedheptulose-1,7-biphosphatase, chloroplastic OS=Spinacia oleracea PE=2 SV=1	S17P_SPIOL	42,054	5.9	10	146	100	96	100	
46	E18		Fructose biphosphate aldolase 1, chloroplastic (Fragment) OS=Pisum sativum PE=1 SV=1	ALFC1_PEA	38,633	5.8	8	185	100	148	100	
47	E19		glutamine synthase [Gossypium hirsutum]	gi 211906462	39,189	0	5	138	100	123	100	
49	E20		glutamine synthase isoform GSel [Triticum aestivum]	gi 40317420	39,459	0	1	79	99	79	100	
50	E21		Fructose biphosphate aldolase 1, chloroplastic (Fragment) OS=Pisum sativum PE=1 SV=1	ALFC1_PEA	38,633	5.8	7	272	100	243	100	
52	E22		ATP synthase gamma chain 1, chloroplastic OS=Arabidopsis thaliana GN=ATPC1 PE=1 SV=1	ATPG1_ARATH	40,886	8.1	6	195	100	172	100	hit#4: correct pI and MW (ATP synthase gamma chain)
55	E23		Isolavone reductase, putative [Ricinus communis]	gi 255543713	31,307	6.5	5	180	100	162	100	
63	E24		lyase [Streptomyces viveus ATCC 29083]	gi 297199592	14,211	5.9	7	65	0			
64	F1		Ferredoxin--NADP reductase, leaf isozyme, chloroplastic OS=Pisum sativum GN=PETH PE=1 SV=1	FENR1_PEA	40,169	8.6	10	335	100	291	100	
65	F2		Isolavone reductase homologue OS=Solanum tuberosum PE=3 SV=1	FRNH_SOLTU	33,831	6.2	5	161	100	142	100	
66	F3		Ribulose biphosphate carboxylase large chain (Fragment) OS=Sinapis alba GN=rbcL PE=3 SV=1	RBL_SINAL	52,405	6.2	13	144	100	75	100	fragment
69	F4		Ribulose biphosphate carboxylase small chain, chloroplastic OS=Glycine tabacina GN=RBCS PE=3 SV=1	RBS_GLYTA	20,005	8.9	6	101	100	49	100	
70	F5		Oxygen-evolving enhancer protein 1, chloroplastic OS=Spinacia oleracea GN=PSBO PE=1 SV=1	PSBO_SPIOL	35,149	5.6	9	349	100	301	100	
72	F6		Coproporphyrinogen-III oxidase, chloroplastic OS=Oryza sativa subsp. japonica GN=CPX PE=2 SV=2	HEMB_ORYSJ	43,844	6.2	9	40	0			
74	F7		Ribulose biphosphate carboxylase large chain (Fragment) OS=Sinapis alba GN=rbcL PE=3 SV=1	RBL_SINAL	52,405	6.2	14	76	100	7	0	
77	F8		BTB/POZ domain-containing protein At5g48130 OS=Arabidopsis thaliana GN=At5g48130 PE=2 SV=1	Y5813_ARATH	71,317	8.0	11	38	0			
81	F9		Ribulose biphosphate carboxylase large chain OS=Carica papaya GN=rbcL PE=3 SV=2	RBL_CARPA	52,457	6.2	18	569	100	449	100	fragment
82	F10		Endochitinase A2 OS=Pisum sativum GN=CH2 PE=1 SV=2	CH2_PEA	34,655	7.3	3	207	100	198	100	
83	F11		Oxygen-evolving enhancer protein 1-2, chloroplastic OS=Arabidopsis thaliana GN=PSBO2 PE=1 SV=1	PSBO2_ARATH	34,998	5.9	10	52	77			
87	F12		caffeoyl-CoA-O-methyltransferase [Leucaena leuccephala]	gi 105671415	27,561	0	8	103	100	59	99	NCBI 1
89	F13		Triosephosphate isomerase, cytosolic OS=Zea mays PE=3 SV=3	TPIS_MAIZE	27,008	5.5	5	104	100	82	100	
90	F15		Triosephosphate isomerase, chloroplastic OS=Spinacia oleracea GN=TPIP1 PE=1 SV=1	TPIC_SPIOL	34,388	6.5	5	191	100	172	100	
92	F16		Carbonic anhydrase OS=Flaveria bidentis PE=2 SV=2	CAHX_FLABR	35,523	5.9	4	294	100	260	100	
96	F17		2-Cys peroxiredoxin BAS1-like, chloroplastic OS=Arabidopsis thaliana GN=At5g06290 PE=2 SV=3	BAS1B_ARATH	29,761	5.6	5	163	100	141	100	
97	F18		Oxygen-evolving enhancer protein 2, chloroplastic OS=Solanum tuberosum GN=PSBP PE=2 SV=1	PSBP_SOLTU	27,987	8.3	6	111	100	83	100	
98	F19		20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN21 PE=1 SV=2	CH10C_ARATH	26,786	8.9	5	110	100	89	100	could also contain hit#4: ATP synthase subunit alpha
99	F20		Oxygen-evolving enhancer protein 2, chloroplastic OS=Solanum tuberosum GN=PSBP PE=2 SV=1	PSBP_SOLTU	27,987	8.3	6	113	100	85	100	
103	F21		Carbonic anhydrase OS=Flaveria brownii PE=2 SV=1	CAHX_FLABR	35,525	5.7	4	144	100	131	100	
104	F22		ATP synthase delta chain, chloroplastic OS=Spinacia oleracea GN=ATPD PE=1 SV=2	ATPD_SPIOL	27,664	5.8	3	142	100	132	100	
105	F23		(3S,6E)-nerolidol synthase 1 OS=Fragaria ananassa PE=1 SV=1	NES1_FRAAN	59,747	5.8	12	53	84			
109	F24		Gemin-like protein (Pisum sativum)	gi 13277342	22,005	7.8	1	212	100	212	100	other hits could be contaminated protein
110	G1		Putative protein phosphatase 2C 22 OS=Oryza sativa subsp. japonica GN=Os02g0607500 PE=3 SV=2	P2C22_ORYSJ	63,261	4.9	9	37				
119	G6		Probable protein arginine N-methyltransferase 6.1 OS=Oryza sativa subsp. indica GN=PRMT6.1 PE=2 SV=4	ANM61_ORYSI	42,193	5.4	9	44				
124	G7		Ribulose biphosphate carboxylase large chain (Fragment) OS=Humiria balsamifera GN=rbcL PE=3 SV=1	RBL_HUMBA	51,530	6.2	13	239	100	176	100	C-terminus
126	G8		Histone H3-like 5 OS=Arabidopsis thaliana GN=At5g08350 PE=2 SV=3	H3L5_ARATH	15,582	11.3	4	63	98	50	100	
127	G9		Histone H2B.3 OS=Arabidopsis thaliana GN=At2g28720 PE=1 SV=3	H2B3_ARATH	16,519	10.0	6	156	100	113	100	
128	G10		Peptidyl-prolyl cis-trans isomerase OS=Catharanthus roseus GN=PKR1 PE=2 SV=1	CYPH_CATRO	18,273	8.4	7	147	100	100	100	
129	G11		Photosystem I reaction center subunit II, chloroplastic OS=Solanum lycopersicum GN=psaD PE=2 SV=1	PSAD_SOLLIC	22,904	9.7	6	254	100	220	100	
132	G12		Rae-related protein RAB11b OS=Arabidopsis thaliana GN=RAB11B PE=2 SV=1	RAB1B_ARATH	23,161	6.5	7	43				
133	G13		Ribulose biphosphate carboxylase small chain 3, chloroplastic OS=Solanum tuberosum GN=RBCS-3 PE=1	RBS3_SOLTU	20,424	8.3	7	126	100	83	100	
135	G14		putative cold-inducible protein-like protein [Heliothis orientalis]	gi 317454922	15,598	0	2	114	100	106	100	could also be hit#2: putative early light induced protein 2
10-B	G15		Stromal 70 kDa heat shock-related protein, chloroplastic OS=Pisum sativum GN=HSP70 PE=2 SV=1	HSP7S_PEA	75,469	5.2	19	685	100	573	100	
1 fmol	G18		Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2	BGAL_ECOLI	116,409	5.3	20	181	100	96	100	
1 fmol	G19		Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2	BGAL_ECOLI	116,409	5.3	24	244	100	123	100	
1 fmol	G20		Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2	BGAL_ECOLI	116,409	5.3	21	163	100	70	100	
1 fmol	G21		Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2	BGAL_ECOLI	116,409	5.3	20	146	100	62	100	

high confidence
low confidence
no confidence