

Accession	Description	Score	Coverage	#Peptides	MW[kDa]	calc. pI
P27481	Linoleate 9S-lipoxygenase (Fragment) OS=Phaseolus vulgaris	1314.45	44.40 %	26	84.1	6.58
P27322	Heat shock cognate 70 kDa protein 2 OS=Solanum lycopersicum	1696.19	47.98 %	24	70.7	5.19
P22953	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana	1613.36	34.41 %	20	71.3	5.12
P29357	Chloroplast envelope membrane 70 kDa heat shock-related protein OS=Spinacia oleracea	1363.43	37.83 %	17	71.7	5.48
P24629	Heat shock cognate 70 kDa protein 1 OS=Solanum lycopersicum	1081.55	35.69 %	16	71.2	5.26
Q01390	Sucrose synthase OS=Vigna radiata var. radiata	499.37	20.37 %	16	92.0	6.51
P13708	Sucrose synthase OS=Glycine max	423.90	19.38 %	15	92.2	6.48
O23755	Elongation factor 2 OS=Beta vulgaris	670.75	19.81 %	14	93.7	6.30
Q02028	Stromal 70 kDa heat shock-related protein, chloroplastic OS=Pisum sativum	655.61	21.95 %	14	75.5	5.35
Q9FGX1	ATP-citrate synthase beta chain protein 2 OS=Arabidopsis thaliana	776.97	25.99 %	13	65.8	7.64
P38417	Linoleate 9S-lipoxygenase-4 OS=Glycine max	551.09	20.16 %	13	96.5	6.04
A4GG89	Ribulose biphosphate carboxylase large chain OS=Phaseolus vulgaris	518.25	26.68 %	12	52.8	6.39
Q9LTX9	Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana	530.00	17.69 %	11	76.9	5.30
Q93VT8	ATP-citrate synthase beta chain protein 1 OS=Oryza sativa subsp. japonica	617.85	20.89 %	11	66.0	7.68
P27480	Linoleate 9S-lipoxygenase 1 OS=Phaseolus vulgaris	225.20	10.67 %	9	97.1	6.96
Q43155	Ferredoxin-dependent glutamate synthase, chloroplastic OS=Spinacia oleracea	267.04	6.99 %	9	165.3	6.19
Q01899	Heat shock 70 kDa protein, mitochondrial OS=Phaseolus vulgaris	218.68	13.93 %	8	72.5	6.20
Q9AWB2	Sulfite reductase [ferredoxin], chloroplastic (Fragment) OS=Glycine max	213.93	15.53 %	8	63.8	9.06
Q05045	Chaperonin CPN60-1, mitochondrial OS=Cucurbita maxima	270.49	14.26 %	8	61.0	5.77
O49169	Elongation factor 1-alpha OS=Manihot esculenta	290.87	16.93 %	7	49.3	9.13
P07219	Phaseolin, alpha-type OS=Phaseolus vulgaris	200.89	19.27 %	7	49.2	5.38
Q69RJ0	Ferredoxin-dependent glutamate synthase, chloroplastic OS=Oryza sativa subsp. japonica	201.98	4.77 %	7	174.9	6.84
P35007	Adenosylhomocysteinase OS=Catharanthus roseus	208.35	15.26 %	7	53.2	5.88
P50249	Adenosylhomocysteinase OS=Phalaenopsis sp.	191.61	14.64 %	7	53.1	6.14
P32112	Adenosylhomocysteinase OS=Triticum aestivum	216.26	14.23 %	7	53.4	5.92
P29185	Chaperonin CPN60-1, mitochondrial OS=Zea mays	228.85	14.04 %	7	61.2	5.85
Q8L7B5	Chaperonin CPN60-like 1, mitochondrial OS=Arabidopsis thaliana	222.55	12.48 %	7	61.9	6.68
P25698	Elongation factor 1-alpha OS=Glycine max	293.54	13.65 %	6	49.3	9.06
Q9S9N1	Heat shock 70 kDa protein 5 OS=Arabidopsis thaliana	301.75	15.63 %	6	70.9	5.41
Q40079	V-type proton ATPase subunit B 2 OS=Hordeum vulgare	158.21	12.84 %	6	53.7	5.24
P24095	Seed linoleate 9S-lipoxygenase OS=Glycine max	249.59	6.25 %	6	96.8	6.15
P02853	Phaseolin, beta-type OS=Phaseolus vulgaris	219.46	17.10 %	6	47.5	5.44
P80607	Alpha-1,4-glucan-protein synthase [UDP-forming] OS=Zea mays	136.41	17.03 %	6	41.2	6.13
O49485	D-3-phosphoglycerate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana	215.56	10.61 %	6	63.3	6.58
Q39857	Xyloglucan endotransglucosylase/hydrolase 1 OS=Glycine max	223.60	21.96 %	6	34.4	8.19
Q42962	Phosphoglycerate kinase, cytosolic OS=Nicotiana tabacum	166.53	16.96 %	5	42.3	5.97
P29409	Phosphoglycerate kinase, chloroplastic (Fragment) OS=Spinacia oleracea	238.68	14.32 %	5	45.5	6.16
Q03684	Luminal-binding protein 4 OS=Nicotiana tabacum	191.28	7.20 %	5	73.5	5.19
P46257	Fructose-bisphosphate aldolase, cytoplasmic isozyme 2 OS=Pisum sativum	381.72	17.55 %	5	38.5	7.25
P0CG84	Polyubiquitin (Fragment) OS=Nicotiana sylvestris	198.63	62.33 %	5	42.2	7.58
Q9FLW9	Plastidial pyruvate kinase 2 OS=Arabidopsis thaliana	174.31	8.64 %	5	63.5	7.03
P09439	Seed linoleate 9S-lipoxygenase-2 OS=Glycine max	272.50	5.90 %	5	97.1	6.74
P43210	Delta-aminolevulinic acid dehydratase, chloroplastic OS=Glycine max	122.47	14.81 %	5	45.0	7.09
Q9SF16	T-complex protein 1 subunit eta OS=Arabidopsis thaliana	145.80	10.59 %	5	59.7	6.39
Q940P8	T-complex protein 1 subunit beta OS=Arabidopsis thaliana	133.87	11.95 %	5	57.2	5.87
Q8LNZ5	Probable xyloglucan endotransglucosylase/hydrolase protein B OS=Phaseolus angularis	134.01	14.68 %	5	34.1	8.76
P49034	Sucrose synthase OS=Alnus glutinosa	172.19	5.73 %	5	91.6	6.81
Q5QMN3	DEAD-box ATP-dependent RNA helicase 20 OS=Oryza sativa subsp. japonica	151.31	11.13 %	5	54.6	8.27
P05088	Erythroagglutinating phytohemagglutinin OS=Phaseolus vulgaris	159.17	25.45 %	5	29.7	5.38
O80377	40S ribosomal protein SA OS=Daucus carota	190.84	10.44 %	4	32.4	5.02
P54765	GTP-binding nuclear protein Ran1A (Fragment) OS=Lotus japonicus	115.66	17.70 %	4	23.8	7.12
P46523	ATP-dependent Clp protease ATP-binding subunit clpA homolog, chloroplastic (Fragment) OS=Arabidopsis thaliana	124.69	5.95 %	4	97.3	6.18
Q9SMQ6	Ras-related protein RABA4b OS=Arabidopsis thaliana	126.96	17.86 %	4	24.4	6.09
Q42560	Aconitate hydratase 1 OS=Arabidopsis thaliana	67.14	4.45 %	4	98.1	6.40
Q6Y2X6	Putative aconitate hydratase, cytoplasmic OS=Oryza sativa subsp. japonica	86.75	4.34 %	4	98.0	6.01
Q04865	Phospholipase D alpha 1 OS=Vigna unguiculata	116.59	4.94 %	4	91.5	5.85
Q96558	UDP-glucose 6-dehydrogenase 1 OS=Glycine max	120.78	10.00 %	4	52.9	6.04
Q9LF33	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana	130.05	10.63 %	4	53.1	6.04
Q43468	Hsp70-Hsp90 organizing protein 1 OS=Glycine max	196.28	7.87 %	4	64.1	5.69
P93254	S-adenosylmethionine synthase OS=Mesembryanthemum crystallinum	98.36	15.82 %	4	42.9	5.71
Q9SRT9	UDP-arabinopyranose mutase 1 OS=Arabidopsis thaliana	95.78	11.48 %	4	40.6	5.92
P85413	Alpha-1,4-glucan-protein synthase [UDP-forming] (Fragments) OS=Phoenix dactylifera	102.83	66.67 %	4	6.8	8.16
Q9SN95	UDP-glucuronic acid decarboxylase 5 OS=Arabidopsis thaliana	114.31	18.48 %	4	38.4	7.52
Q84WU2	Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana	81.75	4.57 %	4	130.6	5.58
P52780	Glutamine--tRNA ligase OS=Lupinus luteus	146.10	4.66 %	4	90.4	6.76
Q41141	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta OS=Ricinus communis	140.46	8.33 %	4	60.1	6.64
P49039	Sucrose synthase OS=Solanum tuberosum	142.34	5.09 %	4	92.5	6.40
P24007	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Pyrus pyrifolia	122.73	15.85 %	3	20.5	8.87
O81221	Actin OS=Gossypium hirsutum	76.47	8.22 %	3	41.6	5.49
Q9SGE0	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana	90.66	8.23 %	3	43.8	5.87
O82802	Sulfite reductase 1 [ferredoxin], chloroplastic OS=Nicotiana tabacum	101.82	4.18 %	3	77.9	9.04
O80988	Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana	116.54	3.07 %	3	113.7	6.65
O49939	Peptidyl-prolyl cis-trans isomerase, chloroplastic OS=Spinacia oleracea	105.99	7.35 %	3	49.8	5.41
P93400	Phospholipase D alpha 1 OS=Nicotiana tabacum	78.15	3.34 %	3	91.9	5.63
P09559	Phosphoribulokinase, chloroplastic OS=Spinacia oleracea	133.47	7.46 %	3	45.0	6.21

P42896	Enolase OS=Ricinus communis	45.54	10.34 %	3	47.9	5.78
P31300	Cysteine synthase, chloroplastic/chromoplastic OS=Capsicum annuum	93.43	12.30 %	3	40.0	5.27
P08927	RuBisCO large subunit-binding protein subunit beta, chloroplastic OS=Pisum sativum	160.00	4.03 %	3	62.9	6.04
O82392	Phosphomethylpyrimidine synthase, chloroplastic OS=Arabidopsis thaliana	56.46	5.75 %	3	71.9	6.44
P27774	Phosphoribulokinase, chloroplastic OS=Mesembryanthemum crystallinum	71.56	7.81 %	3	44.1	6.46
Q8W250	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica	120.68	8.03 %	3	51.4	6.18
Q9XI91	Eukaryotic translation initiation factor 5A-1 OS=Arabidopsis thaliana	76.81	18.35 %	3	17.3	5.76
Q84WV1	T-complex protein 1 subunit gamma OS=Arabidopsis thaliana	87.99	5.23 %	3	60.3	5.77
Q9AXJ4	Eukaryotic translation initiation factor 5A OS=Manihot esculenta	74.49	18.13 %	3	17.6	6.20
P53780	Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana	103.47	6.03 %	3	50.4	7.36
Q9XF59	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Arabidopsis thaliana	136.59	6.29 %	3	51.9	7.05
Q9SYM5	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-glucose 4-epimerase OS=Arabidopsis thaliana	86.14	5.38 %	3	75.3	7.28
Q8W4M5	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana	127.23	9.19 %	3	61.4	6.10
O23735	Cysteine synthase OS=Brassica juncea	144.93	9.88 %	3	34.1	5.59
Q42806	Pyruvate kinase, cytosolic isozyme OS=Glycine max	97.48	5.68 %	3	55.3	7.56
O22718	ATP-citrate synthase alpha chain protein 2 OS=Arabidopsis thaliana	136.10	6.38 %	3	46.7	5.27
P51061	Phosphoenolpyruvate carboxylase OS=Glycine max	79.37	5.48 %	3	110.7	6.47
O49835	Phenylalanine ammonia-lyase 1 OS=Lithospermum erythrorhizon	51.43	5.35 %	3	77.5	6.00
B9DGT7	Tubulin alpha-2 chain OS=Arabidopsis thaliana	88.64	7.33 %	3	49.5	5.06
Q42662	5-methyltetrahydropteroyltryglutamate-homocysteine methyltransferase OS=Plectranthus scaber	100.35	2.49 %	2	84.5	6.51
P09044	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic (Fragment) OS=Nicotiana tabacum	56.92	4.57 %	2	47.4	8.57
Q01525	14-3-3-like protein GF14 omega OS=Arabidopsis thaliana	65.77	6.18 %	2	29.1	4.79
P46266	14-3-3-like protein OS=Pisum sativum	71.91	7.31 %	2	29.3	4.79
P00865	Ribulose biphosphate carboxylase small chain 1, chloroplastic OS=Glycine max	87.95	14.04 %	2	20.1	8.66
A6MML4	ATP synthase subunit beta, chloroplastic OS=Dioscorea elephantipes	59.23	4.64 %	2	53.4	5.39
P36181	Heat shock cognate protein 80 OS=Solanum lycopersicum	49.88	2.86 %	2	80.1	5.03
P37829	Fructokinase OS=Solanum tuberosum	60.25	7.52 %	2	33.7	5.71
Q40466	Eukaryotic initiation factor 4A-13 (Fragment) OS=Nicotiana tabacum	55.17	5.35 %	2	40.2	5.33
P02873	Alpha-amylase inhibitor 1 OS=Phaseolus vulgaris	61.92	10.98 %	2	27.2	5.24
Q6ESI7	Tripeptidyl-peptidase 2 OS=Oryza sativa subsp. japonica	31.07	1.32 %	2	148.5	6.58
P10933	Ferredoxin--NADP reductase, leaf isozyme, chloroplastic OS=Pisum sativum	46.50	6.39 %	2	40.2	8.40
O04977	Ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic OS=Nicotiana tabacum	42.57	4.70 %	2	40.4	8.21
O04130	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana	97.68	3.21 %	2	66.4	6.13
Q01289	Protochlorophyllide reductase, chloroplastic OS=Pisum sativum	96.67	7.27 %	2	42.9	9.04
Q96372	Cell division cycle protein 48 homolog OS=Capsicum annuum	83.31	2.24 %	2	89.3	5.20
Q94A28	Aconitate hydratase 3, mitochondrial OS=Arabidopsis thaliana	48.24	2.41 %	2	108.4	7.15
Q00834	Cysteine synthase OS=Spinacia oleracea	131.74	7.69 %	2	34.2	5.62
Q01517	Fructose-bisphosphate aldolase 2, chloroplastic OS=Pisum sativum	86.96	4.87 %	2	37.8	5.59
Q40255	Probable aldehyde dehydrogenase OS=Linum usitatissimum	51.29	3.45 %	2	61.0	7.28
O24457	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic OS=Arabidopsis thaliana	71.92	5.37 %	2	47.1	7.49
O20252	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Spinacia oleracea	61.97	5.94 %	2	42.1	6.20
P29356	Fructose-bisphosphate aldolase, cytoplasmic isozyme OS=Spinacia oleracea	75.78	4.20 %	2	38.4	6.28
P46283	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Arabidopsis thaliana	53.32	7.63 %	2	42.4	6.57
Q42669	Aconitate hydratase (Fragment) OS=Cucumis melo var. conomon	89.39	2.62 %	2	83.2	6.80
Q95TH1	Hsp70-Hsp90 organizing protein 3 OS=Arabidopsis thaliana	117.02	3.23 %	2	63.7	6.32
P31239	1-aminocyclopropane-1-carboxylate oxidase OS=Pisum sativum	72.50	8.52 %	2	36.0	5.19
Q9SIU0	NAD-dependent malic enzyme 1, mitochondrial OS=Arabidopsis thaliana	32.02	4.65 %	2	69.6	5.45
P56821	Eukaryotic translation initiation factor 3 subunit B OS=Nicotiana tabacum	64.20	2.36 %	2	82.5	5.02
Q9SU63	Aldehyde dehydrogenase family 2 member B4, mitochondrial OS=Arabidopsis thaliana	115.49	3.53 %	2	58.6	7.46
O48593	Asparagine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana	79.46	2.82 %	2	63.7	6.05
P08824	RuBisCO large subunit-binding protein subunit alpha (Fragment) OS=Ricinus communis	73.85	4.24 %	2	52.3	4.87
Q9ZPI1	Lysine--tRNA ligase OS=Arabidopsis thaliana	45.57	2.40 %	2	70.8	6.24
P37221	NAD-dependent malic enzyme 62 kDa isoform, mitochondrial OS=Solanum tuberosum	37.53	4.31 %	2	69.9	5.94
Q5Z5B2	Protein argonaute 1D OS=Oryza sativa subsp. japonica	38.85	1.73 %	2	115.9	9.03
Q9LIR4	Dihydroxy-acid dehydratase, chloroplastic OS=Arabidopsis thaliana	71.79	2.63 %	2	64.9	6.23
F4JVN6	Tripeptidyl-peptidase 2 OS=Arabidopsis thaliana	63.70	2.03 %	2	152.3	6.07
O81154	Cysteine synthase OS=Solanum tuberosum	133.99	7.38 %	2	34.3	6.62
P29038	L-lactate dehydrogenase OS=Zea mays	89.02	7.63 %	2	38.5	8.87
P85984	Profilin (Fragments) OS=Beta vulgaris	71.98	100.00 %	2	2.5	4.23
O23627	Glycine--tRNA ligase 1, mitochondrial OS=Arabidopsis thaliana	41.62	3.16 %	2	81.9	7.01
Q5Z7L0	Beta-galactosidase 9 OS=Oryza sativa subsp. japonica	95.24	2.66 %	2	78.2	7.65
Q957C0	Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana	44.76	3.13 %	2	91.7	5.25
P55964	Pyruvate kinase isozyme G, chloroplastic (Fragment) OS=Ricinus communis	99.93	4.55 %	2	46.0	6.58
Q2QKB3	Splicing factor U2af large subunit A OS=Triticum aestivum	76.20	2.88 %	2	67.9	8.29
Q9FG38	Sorting nexin 1 OS=Arabidopsis thaliana	117.00	4.23 %	2	46.5	7.24
Q42800	4-hydroxy-tetrahydrodipicolinate synthase, chloroplastic OS=Glycine max	54.41	4.82 %	2	36.4	6.32
P51074	Annexin-like protein RJ4 OS=Fragaria ananassa	191.70	6.37 %	2	35.6	7.23
Q9XEA8	Cysteine synthase OS=Oryza sativa subsp. japonica	89.72	7.08 %	2	34.3	5.41
Q93Z53	Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana	74.30	4.73 %	2	62.6	7.81
O82013	17.3 kDa class II heat shock protein OS=Solanum peruvianum	47.57	16.77 %	2	17.3	6.80
Q07176	Mitogen-activated protein kinase homolog MMK1 OS=Medicago sativa	69.08	6.46 %	2	44.4	5.85
Q43621	Glutathione reductase, cytosolic OS=Pisum sativum	50.22	5.82 %	2	53.9	7.01
P21342	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit alpha OS=Solanum tuberosum	32.57	5.03 %	2	67.3	7.43
Q94K05	T-complex protein 1 subunit theta OS=Arabidopsis thaliana	72.54	4.74 %	2	58.9	5.35
O04905	UMP-CMP kinase 3 OS=Arabidopsis thaliana	92.95	8.42 %	2	22.5	6.01
P93394	Uracil phosphoribosyltransferase OS=Nicotiana tabacum	55.22	11.16 %	2	24.2	7.03
O48659	Spermidine synthase 2 OS=Hyoscyamus niger	52.57	8.44 %	2	33.9	5.11

Q9LV21	T-complex protein 1 subunit delta OS=Arabidopsis thaliana	35.63	4.66 %	2	57.7	7.68
P06525	Alcohol dehydrogenase class-P OS=Arabidopsis thaliana	32.46	8.71 %	2	41.2	6.24
O04450	T-complex protein 1 subunit epsilon OS=Arabidopsis thaliana	40.64	3.74 %	2	59.3	5.66
P17817	Pyrroline-5-carboxylate reductase OS=Glycine max	90.53	7.30 %	2	28.6	8.32
Q9C9K3	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana	62.81	3.40 %	2	67.5	7.23
P19588	Lectin DB58 OS=Vigna unguiculata subsp. cylindrica	99.48	6.55 %	2	29.4	5.00
Q8SKU2	Protein TIC 62, chloroplastic OS=Pisum sativum	55.54	4.12 %	2	56.9	8.72
Q41607	Sucrose synthase 2 OS=Tulipa gesneriana	97.99	2.93 %	2	93.0	6.38
P85952	Unknown protein 25 (Fragments) OS=Pseudotsuga menziesii	50.44	59.46 %	2	4.2	7.25
P49231	Profilin-1 OS=Phaseolus vulgaris	95.99	17.56 %	2	14.2	5.00
Q03878	Glycine-rich RNA-binding protein OS=Daucus carota	139.57	15.29 %	2	15.7	5.38
O80574	4-hydroxy-tetrahydronicotinate reductase 1, chloroplastic OS=Arabidopsis thaliana	138.00	7.20 %	2	37.5	6.46