

Supplementary Information :

Table 1 : List of the identified proteins in *H.rhamnoides* Leaf Protein fractions, identified using QExactive Orbitrap High resolution mass spectrometer

Accession	Description	Function	Coverage	# Protein	# Unique Peptide	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
75264335	Cell division protein	Cell division	8.03	7	1	2	2	473	50.3	5.96
332645529	cell division control protein 48-D [Arabidopsis thaliana]	Cell division	6.01	10	2	3	3	815	90.3	5.16
984678	lipoamide dehydrogenase [Pisum sativum]	Energy metabolism	8.98	1	1	3	3	501	53.3	7.17
3334404	V-type proton ATPase catalytic subunit A	Energy metabolism	9.47	5	3	4	5	623	68.8	5.24
9558599	vacuolar ATP synthase subunit B [Arabidopsis thaliana]	Energy metabolism	13.61	8	2	4	4	485	54.2	5.24
34539247	F1-ATPase alpha subunit [Ceratophyllum demersum]	Energy metabolism	15.7	90	1	5	7	414	44.4	7.03
34539467	F1-ATPase alpha subunit [Trithrinax acanthocoma]	Energy metabolism	19.44	140	2	5	8	391	41.8	6.95
68164810	ATP synthase CF1 beta subunit [Cucumis sativus]	Energy metabolism	20.88	22	2	5	15	498	53.9	5.26
68164859	NADH dehydrogenase subunit I [Cucumis sativus]	Energy metabolism	5.57	2	1	1	1	359	40	4.81
75264759	Dihydrolipoyl dehydrogenase 1	Energy metabolism	9.07	1	1	3	5	507	54	7.4
114804250	ATP synthase CF1 alpha subunit [Morus indica]	Energy metabolism	20.12	39	3	8	27	507	55.4	5.21
114804251	ATP synthase CF0 subunit I [Morus indica]	Energy metabolism	11.96	1	1	2	3	184	21	7.34
125634056	vacuolar ATPase subunit c [Cucumis sativus]	Energy metabolism	16.98	15	1	1	1	106	10.5	8.91
159227488	ATP synthase beta subunit [Physalis sp. P078]	Energy metabolism	55.65	34	1	13	33	336	35.9	5.29
159232196	ATP synthase beta subunit [Salpiglossis sinuata]	Energy metabolism	66.87	116	0	15	38	335	35.8	5.3
159232284	ATP synthase beta subunit [Jaltomata dentata]	Energy metabolism	68.29	92	0	15	39	328	35.1	5.73
164597823	ATP synthase CF1 alpha subunit [Oenothera elata subsp. hookeri]	Energy metabolism	11.88	19	2	5	12	505	55.2	5.35
164597823	ATP synthase CF1 alpha subunit [Oenothera elata subsp. hookeri]	Energy metabolism	11.88	18	2	5	10	505	55.2	5.35
213495617	AtpB [Acacia schweinfurthii]	Energy metabolism	56.54	76	0	16	44	428	46.2	5.26
225544131	atpB [Jatropha curcas]	Energy metabolism	15.56	5	1	4	10	495	53.2	5.2
323149068	ATP synthase CF0 subunit I [Anthriscus cerefolium]	Energy metabolism	10.5	5	1	2	4	181	20.5	9.64

332644946	Clp ATPase [Arabidopsis thaliana]	Energy metabolism	7.27	12	3	5	6	921	102.2	6.21
334702331	ATP synthase CF1 beta subunit [Jacobaea vulgaris]	Energy metabolism	15.86	9	1	4	17	498	53.7	5.31
342316381	ATP synthase CF1 beta subunit (chloroplast) [Wolffia australiana]	Energy metabolism	36.95	15	0	12	29	498	53.6	5.02
350996610	ATP synthase CF1 beta subunit (chloroplast) [Ginkgo biloba]	Energy metabolism	14.78	10	1	3	6	487	52.4	5.22
355331896	ATP synthase F0 complex c subunit [Asclepias coulteri]	Energy metabolism	7.58	13	1	1	1	132	14.5	6.55
355477374	ATP synthase subunit alpha [Medicago truncatula]	Energy metabolism	4.84	28	1	4	6	1116	122.7	8.81
355481024	ATP synthase subunit d [Medicago truncatula]	Energy metabolism	9.72	2	1	1	1	144	16.8	5.73
391348916	ATP synthase F1 subunit 1 (mitochondrion) [Mimulus guttatus]	Energy metabolism	11.44	16	1	4	6	507	55	6.92
449326886	ATP synthase CF1 beta subunit [Xiphidium caeruleum]	Energy metabolism	19.28	21	1	5	20	498	53.7	5.4
452848863	ATP synthase CF1 beta subunit (chloroplast) [Magnolia grandiflora]	Energy metabolism	20.48	10	1	6	17	498	53.7	5.33
452848996	ATP synthase CF1 alpha subunit (chloroplast) [Cycas revoluta]	Energy metabolism	9.47	22	1	4	8	507	55.3	5.49
473798701	ATP synthase subunit beta, mitochondrial [Triticum urartu]	Energy metabolism	13.48	10	3	5	8	534	57.6	5.41
474222243	V-type proton ATPase subunit B 2 [Triticum urartu]	Energy metabolism	17.72	5	1	1	1	79	8.7	6.54
473764712	Histone H4 [Triticum urartu]	Others	14.29	19	1	1	1	140	15.5	11.55
115392303	putative polyphenol oxidase [Vauquelinia californica]	Others	4.42	1	1	1	2	453	50.6	6.35
226887787	Chain B, Ketol-Acid Reductoisomerase (Kari) In Complex With Mg2+	Others	3.62	5	1	1	1	525	57.3	5.67
297326580	hypothetical protein ARALYDRAFT_481465 [Arabidopsis lyrata subsp. lyrata]	Others	7.29	28	1	5	8	1043	113.7	6.79
297338518	hypothetical protein ARALYDRAFT_471361 [Arabidopsis lyrata subsp. lyrata]	Others	2.23	1	1	1	3	494	55.9	6.1
300153650	hypothetical protein SELMODRAFT_449459 [Selaginella moellendorffii]	Others	5.3	2	1	1	1	283	30.9	5.06
300168456	hypothetical protein SELMODRAFT_29306 [Selaginella moellendorffii]	Others	11.54	7	1	1	1	78	7.9	9.38
300169947	hypothetical protein SELMODRAFT_438313 [Selaginella moellendorffii]	Others	7.23	3	1	3	8	484	55.5	7.91
300171323	hypothetical protein SELMODRAFT_139726 [Selaginella moellendorffii]	Others	6.37	1	1	2	2	628	67.1	5.25
300171687	hypothetical protein SELMODRAFT_229825 [Selaginella moellendorffii]	Others	18.18	82	1	3	3	253	28.5	4.81
300171855	hypothetical protein SELMODRAFT_73428 [Selaginella moellendorffii]	Others	2.69	2	1	1	1	372	40.9	7.88

332005110	anthranilate phosphoribosyltransferase [Arabidopsis thaliana]	Others	3.15	1	1	1	1	444	46.5	7.27
332189503	prohibitin 2 [Arabidopsis thaliana]	Others	6.79	7	1	1	1	221	24.9	9.11
332189615	3-ketoacyl-CoA thiolase 1 [Arabidopsis thaliana]	Others	9.03	3	2	2	3	443	46.6	8.29
355490293	Anthranilate phosphoribosyltransferase [Medicago truncatula]	Others	3.05	1	1	1	2	394	41.8	7.77
355515793	Allene oxide cyclase [Medicago truncatula]	Others	5.56	1	1	1	1	252	28	9.23
428622063	PsbA, partial (chloroplast) [Encephalartos lanatus]	Others	15.53	58	3	3	10	264	29.1	5.44
132009	Ribulose biphosphate carboxylase large chain;	Photosynthesis	9.89	60	1	4	30	475	52.7	7.02
134101	RuBisCO large subunit-binding protein subunit alpha; AltName: Full=60 kDa chaperonin subunit alpha; AltName: Full=CPN-60 alpha	Photosynthesis	8.28	5	1	3	3	495	52.3	4.87
11134146	Oxygen-evolving enhancer protein	Photosynthesis	14.5	2	1	4	8	331	35	6.16
11465988	cytochrome b6 [Nicotiana tabacum]	Photosynthesis	15.81	18	1	2	5	215	24.1	8.76
17865467	ATP-dependent zinc metalloprotease	Photosynthesis	3.27	3	1	2	2	704	75.2	5.49
28558077	Chlorophyll a-b binding protein	Photosynthesis	17.5	1	1	3	4	280	30.1	6.37
37959640	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Neomaria northiana]	Photosynthesis	28.27	149	2	9	79	382	42.7	6.76
75313128	Chloroplast stem-loop binding protein of 41 kDa b	Photosynthesis	4.5	1	1	1	2	378	42.6	8.16
84468288	putative rubisco subunit binding-protein alpha subunit [Trifolium pratense]	Photosynthesis	10.9	11	3	4	4	578	61.2	5.29
108802638	photosystem II protein D2 [Eucalyptus globulus subsp. globulus]	Photosynthesis	24.36	53	5	6	17	353	39.5	5.55
108802671	cytochrome b6 [Eucalyptus globulus subsp. globulus]	Photosynthesis	15.81	38	1	2	8	215	24.2	8.76
114804264	photosystem I P700 apoprotein A2 [Morus indica]	Photosynthesis	10.49	60	1	6	9	734	82.3	7.4
114804276	cytochrome f [Morus indica]	Photosynthesis	19.06	24	1	5	11	320	35.3	8.56
114804294	cytochrome b6 [Morus indica]	Photosynthesis	19.53	38	1	3	11	215	24.2	8.76
149242538	Chain L, The Structure Of A Plant Photosystem I Supercomplex At 3.4 Angstrom Resolution	Photosynthesis	10.98	2	1	1	1	164	17.5	8.41
149242543	Chain 4, The Structure Of A Plant Photosystem I Supercomplex At 3.4 Angstrom Resolution	Photosynthesis	13.94	6	2	2	3	165	18.5	6.15
157325538	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Ipomoea purpurea]	Photosynthesis	26.25	219	0	9	91	480	53.4	6.87
157325543	cytochrome f [Ipomoea purpurea]	Photosynthesis	18.44	12	0	5	11	320	35.1	9.19
157812662	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Ehretia rigida]	Photosynthesis	6.05	1	1	1	3	215	24	7.75
193783447	major chlorophyll a/b binding protein LHCb1.3 [Spinacia oleracea]	Photosynthesis	13.86	1	1	1	5	267	28.4	5.44

223931047	photosystem II phosphoprotein (chloroplast) [Syntrophia ruralis]	Photosynthesis	22.97	1	1	1	3	74	7.9	6.58
268612196	Chain 3, Improved Model Of Plant Photosystem I	Photosynthesis	16.67	1	1	2	2	276	29.8	8.66
268612196	Chain 3, Improved Model Of Plant Photosystem I	Photosynthesis	22.83	1	2	3	6	276	29.8	8.66
295060640	photosystem II CP43 chlorophyll apoprotein [Carthamus oxyacanthus]	Photosynthesis	25.99	56	5	8	16	431	47.1	6.89
303324967	Chain D, Improved Model Of Plant Photosystem I	Photosynthesis	31.16	10	2	3	4	138	15.5	9.44
303324978	Chain 1, Improved Model Of Plant Photosystem I	Photosynthesis	8.24	5	1	2	2	170	18.6	5.83
303324980	Chain 3, Improved Model Of Plant Photosystem I	Photosynthesis	13.37	1	1	2	4	172	18.7	7.24
319976422	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [unidentified plant]	Photosynthesis	32.26	19	1	3	41	186	20.7	5.14
332002974	chlorophyll a-b binding protein CP29.1 [Arabidopsis thaliana]	Photosynthesis	8.62	4	1	2	6	290	31.1	6.14
332197675	Plastocyanin minor isoform [Arabidopsis thaliana]	Photosynthesis	14.04	1	1	1	7	171	17.6	5.95
355332330	photosystem II protein H, partial [Asclepias macrotis]	Photosynthesis	25.76	2	1	1	1	66	7	9.42
355485538	Chlorophyll a/b-binding protein [Medicago truncatula]	Photosynthesis	3.79	3	1	1	1	264	28.5	5.64
355486134	Cytochrome b6-f complex iron-sulfur subunit [Medicago truncatula]	Photosynthesis	5.24	1	1	1	1	229	23.9	7.62
355493298	Carbonic anhydrase [Medicago truncatula]	Photosynthesis	9.19	6	1	1	1	185	20.1	7.06
355494182	Chlorophyll a-b binding protein 3C-like protein [Medicago truncatula]	Photosynthesis	10.04	1	2	3	7	229	24.8	5.82
355496541	Photosystem II CP43 chlorophyll apoprotein [Medicago truncatula]	Photosynthesis	13.11	1	1	1	1	122	12.8	8.82
355500984	CP12 [Medicago truncatula]	Photosynthesis	25.78	1	1	1	1	128	13.8	4.91
355505708	Chlorophyll a-b binding protein [Medicago truncatula]	Photosynthesis	11.24	4	2	3	4	347	38	8.13
355506654	Apocytochrome f [Medicago truncatula]	Photosynthesis	11.79	20	2	5	8	543	61.8	7.43
355507110	Photosystem II CP47 chlorophyll apoprotein [Medicago truncatula]	Photosynthesis	13.64	58	1	11	28	968	107.3	7.49
355517785	Ribulose-1 5-bisphosphate carboxylase/oxygenase activase [Medicago truncatula]	Photosynthesis	28.57	10	1	7	32	476	52.3	6.46
355519283	Chlorophyll a/b binding protein [Medicago truncatula]	Photosynthesis	20.75	41	1	3	6	265	28.7	5.44
372862615	PSII 47 kDa protein (chloroplast) [Magnolia officinalis subsp. biloba]	Photosynthesis	22.24	64	1	9	23	508	56	6.7
409181063	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Myriophyllum heterophyllum]	Photosynthesis	20.65	1	1	1	3	184	20.4	7.24
440233676	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Vicia	Photosynthesis	4.56	1	1	1	2	329	36.8	7.3

	megalotropis]									
449326635	photosystem II cytochrome b559 alpha subunit [Calectasia narragara]	Photosynthesis	26.51	27	2	2	4	83	9.4	4.94
449326791	photosystem I P700 apoprotein A2 [Alpinia zerumbet]	Photosynthesis	10.49	52	1	6	8	734	82.4	7.24
459014473	photosystem II protein D1 (chloroplast) [Salvia miltiorrhiza]	Photosynthesis	13.92	57	2	4	9	352	38.8	5.25
470127432	PREDICTED: thylakoid lumenal 29 kDa protein, chloroplastic-like [Fragaria vesca subsp. vesca]	Photosynthesis	5.19	1	1	1	1	347	38	6
473808783	Chlorophyll a-b binding protein of LHCII type III, chloroplastic [Triticum urartu]	Photosynthesis	6.46	1	1	1	3	263	28.2	5.15
474153435	Ribulose biphosphate carboxylase/oxygenase activase A, chloroplastic [Triticum urartu]	Photosynthesis	15.95	2	2	4	20	464	50.9	7.3
474352688	Oxygen-evolving enhancer protein 1, chloroplastic [Triticum urartu]	Photosynthesis	11.59	3	1	3	5	328	34.4	5.9
474357515	RuBisCO large subunit-binding protein subunit beta, chloroplastic [Triticum urartu]	Photosynthesis	14.44	5	1	5	5	561	59.8	5.35
474413348	Chlorophyll a-b binding protein, chloroplastic [Triticum urartu]	Photosynthesis	13.16	2	1	1	1	266	28.3	5.44
474425491	Sedoheptulose-1,7-bisphosphatase, chloroplastic [Triticum urartu]	Photosynthesis	6.78	4	1	2	3	369	39.7	6.01
354618591	ribulose-1,5-bisphosphate carboxylase oxygenase, partial (chloroplast) [Aglaia sp. PA3E0160]	Photosynthesis	8	1	1	1	1	125	13.9	4.75
125606	Pyruvate kinase, cytosolic isozyme;	Primary metabolism	6.27	3	1	2	2	510	55.1	7.02
166710	glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]	Primary metabolism	9.76	9	2	2	3	338	37	6.81
231970	Cysteine synthase	Primary metabolism	5.23	2	1	1	2	325	34.2	5.62
336390	Ubiquitin	Primary metabolism	18.91	2	1	7	10	402	42.8	5.91
426476	glucose-1-phosphate adenylyltransferase [Solanum tuberosum]	Primary metabolism	6	3	1	2	2	483	53.6	8.79
437995	glycine hydroxymethyltransferase [Flaveria pringlei]	Primary metabolism	17.6	5	2	6	9	517	57	8.68
438247	glycine hydroxymethyltransferase [Solanum tuberosum]	Primary metabolism	12.36	9	1	4	7	518	57.1	8.38
556622	ADP-glucose pyrophosphorylase [Beta vulgaris subsp. vulgaris]	Primary metabolism	14.31	13	4	4	4	489	53.8	5.83
972511	phosphoenolpyruvate carboxylase [Solanum tuberosum]	Primary metabolism	2.9	10	1	2	2	965	110.3	5.77
1658322	transketolase precursor [Solanum tuberosum]	Primary metabolism	9.45	3	1	6	8	741	79.9	6.35
6899947	O-acetylserine (thiol) lyase [Arabidopsis thaliana]	Primary metabolism	3.36	4	1	1	1	387	41.2	7.18
12644209	Cysteine synthase, chloroplastic/chromoplastic;	Primary metabolism	3.13	6	1	1	1	383	40.6	7.18

29293057	putative NADH-dependent hydroxypyruvate reductase [Glycine max]	Primary metabolism	23.58	5	3	6	9	386	42.2	7.43
32527831	UDP-glucose pyrophosphorylase [Populus tremula x Populus tremuloides]	Primary metabolism	4.47	3	1	2	2	470	51.8	5.96
34597330	Enolase [Brassica rapa subsp. oleifera]	Primary metabolism	8.78	1	1	2	4	444	47.3	5.66
39841613	sucrose-phosphate synthase [Medicago sativa]	Primary metabolism	2.08	1	1	1	1	1058	117.8	6.52
45477193	Pyridoxal biosynthesis protein	Primary metabolism	12.62	4	2	3	3	309	33.2	6.11
51701455	Full=Serine hydroxymethyltransferase, mitochondrial	Primary metabolism	11.61	11	1	4	8	517	57.4	8.13
56542167	vacuolar pyrophosphatase [Vitis vinifera]	Primary metabolism	5.1	21	3	3	3	764	80	5.48
73919692	GDP-mannose 3,5-epimerase	Primary metabolism	3.71	1	1	1	1	377	42.7	6.21
75172658	Plastidal glycolate/glycerate translocator 1, chloroplastic; AltName: Bacterial membrane protein LrgB-like protein	Primary metabolism	3.71	1	1	1	1	512	54	9.57
75266240	Cytosolic isocitrate dehydrogenase [NADP]	Primary metabolism	6.83	3	1	2	2	410	45.7	6.57
75295508	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic	Primary metabolism	7.72	5	1	2	3	337	36.7	6.81
75313899	Aldehyde dehydrogenase family 2 member B4, mitochondrial	Primary metabolism	7.25	4	1	3	3	538	58.6	7.46
158277965	MPBQ/MSBQ methyltransferase [Chlamydomonas reinhardtii]	Primary metabolism	4.45	1	1	1	1	337	37.4	8.9
241915985	hypothetical protein SORBIDRAFT_10g002220 [Sorghum bicolor]	Primary metabolism	9.48	1	2	3	4	633	68.7	5.64
241916611	hypothetical protein SORBIDRAFT_10g015890 [Sorghum bicolor]	Primary metabolism	11.66	1	1	1	1	163	17.4	8.48
241917020	hypothetical protein SORBIDRAFT_10g026440 [Sorghum bicolor]	Primary metabolism	5.15	5	2	2	2	621	68.4	5.45
241918275	hypothetical protein SORBIDRAFT_01g017860 [Sorghum bicolor]	Primary metabolism	3.75	1	1	1	1	534	58.2	8.69
241918276	hypothetical protein SORBIDRAFT_01g017890 [Sorghum bicolor]	Primary metabolism	5.88	1	1	1	1	221	23.3	6.6
241919227	hypothetical protein SORBIDRAFT_01g037430 [Sorghum bicolor]	Primary metabolism	4.95	3	1	1	1	283	30.5	8.57
241919322	hypothetical protein SORBIDRAFT_01g039390 [Sorghum bicolor]	Primary metabolism	18.1	28	2	9	10	652	71.4	5.3
241919607	hypothetical protein SORBIDRAFT_01g045210 [Sorghum bicolor]	Primary metabolism	6.1	2	1	1	1	246	27.4	6.55
241920484	hypothetical protein SORBIDRAFT_01g011310 [Sorghum bicolor]	Primary metabolism	17.66	3	1	6	7	487	52.5	5.64
241920933	hypothetical protein SORBIDRAFT_01g019280 [Sorghum bicolor]	Primary metabolism	23.19	3	1	4	7	332	35.4	6.09
241921399	hypothetical protein SORBIDRAFT_01g030010	Primary	22.73	1	1	2	2	88	10.3	10.73

	[Sorghum bicolor]	metabolism								
241922445	hypothetical protein SORBIDRAFT_01g048660 [Sorghum bicolor]	Primary metabolism	8.95	13	2	3	3	380	41.3	9.79
241923602	hypothetical protein SORBIDRAFT_02g024880 [Sorghum bicolor]	Primary metabolism	25.49	60	2	3	11	153	17.1	6.06
241923956	hypothetical protein SORBIDRAFT_02g031180 [Sorghum bicolor]	Primary metabolism	10.04	3	1	2	2	249	27.2	7.84
241923999	hypothetical protein SORBIDRAFT_02g032040 [Sorghum bicolor]	Primary metabolism	17.94	1	1	2	6	262	27.8	5.26
241924014	hypothetical protein SORBIDRAFT_02g032250 [Sorghum bicolor]	Primary metabolism	5.63	5	1	2	2	462	50.5	5.52
241924197	hypothetical protein SORBIDRAFT_02g035610 [Sorghum bicolor]	Primary metabolism	5.05	4	1	1	1	218	23	9.8
241924236	hypothetical protein SORBIDRAFT_02g036420 [Sorghum bicolor]	Primary metabolism	14.32	17	2	4	4	447	49.2	9.07
241925145	hypothetical protein SORBIDRAFT_02g007760 [Sorghum bicolor]	Primary metabolism	4.43	1	1	1	3	361	38.8	5.47
241925951	hypothetical protein SORBIDRAFT_02g028460 [Sorghum bicolor]	Primary metabolism	2.95	1	1	1	2	610	64.4	9.79
241926695	hypothetical protein SORBIDRAFT_02g041740 [Sorghum bicolor]	Primary metabolism	4.07	3	1	4	6	1500	163.5	6.29
241927175	hypothetical protein SORBIDRAFT_03g006130 [Sorghum bicolor]	Primary metabolism	5.53	1	1	1	1	253	26.9	5.47
241927404	hypothetical protein SORBIDRAFT_03g010660 [Sorghum bicolor]	Primary metabolism	10.81	1	1	1	1	148	16.7	6.35
241928026	hypothetical protein SORBIDRAFT_03g029570 [Sorghum bicolor]	Primary metabolism	12.35	7	1	3	6	340	35.6	7.81
241928486	hypothetical protein SORBIDRAFT_03g037630 [Sorghum bicolor]	Primary metabolism	17.93	1	1	2	2	184	20.5	4.74
241928679	hypothetical protein SORBIDRAFT_03g041100 [Sorghum bicolor]	Primary metabolism	15.67	6	2	3	8	268	28	9.09
241930884	hypothetical protein SORBIDRAFT_03g042460 [Sorghum bicolor]	Primary metabolism	4.64	5	1	1	1	323	34.7	5
241931104	hypothetical protein SORBIDRAFT_03g046340 [Sorghum bicolor]	Primary metabolism	10.33	6	1	3	4	368	41	6.92
241932140	hypothetical protein SORBIDRAFT_04g023430 [Sorghum bicolor]	Primary metabolism	2.64	1	1	1	1	455	49.6	8.6
241932302	hypothetical protein SORBIDRAFT_04g026360 [Sorghum bicolor]	Primary metabolism	4.27	2	1	1	1	422	45.1	6.32
241932314	hypothetical protein SORBIDRAFT_04g026650 [Sorghum bicolor]	Primary metabolism	4.84	1	1	1	1	289	30.4	7.01
241934099	hypothetical protein SORBIDRAFT_04g027770 [Sorghum bicolor]	Primary metabolism	7.22	1	1	1	1	277	30	5.39
241936406	hypothetical protein SORBIDRAFT_05g007070 [Sorghum bicolor]	Primary metabolism	10.64	2	1	2	4	282	30.1	5.49
241937572	hypothetical protein SORBIDRAFT_06g015130 [Sorghum bicolor]	Primary metabolism	4.58	1	1	1	1	306	32.5	7.81

241938345	hypothetical protein SORBIDRAFT_06g029630 [Sorghum bicolor]	Primary metabolism	4.69	1	1	1	1	320	34.2	5.68
241938544	hypothetical protein SORBIDRAFT_06g033640 [Sorghum bicolor]	Primary metabolism	3.9	7	1	1	1	461	48.4	6.93
241939278	hypothetical protein SORBIDRAFT_06g021010 [Sorghum bicolor]	Primary metabolism	6.46	1	1	2	2	356	38.5	5.63
241939421	hypothetical protein SORBIDRAFT_06g023840 [Sorghum bicolor]	Primary metabolism	2.58	3	1	1	1	775	85.1	5.6
241939820	hypothetical protein SORBIDRAFT_06g030600 [Sorghum bicolor]	Primary metabolism	3.63	1	1	1	3	523	56.5	5.92
241940446	hypothetical protein SORBIDRAFT_07g007610 [Sorghum bicolor]	Primary metabolism	2.73	11	1	2	2	953	104.1	6.81
241940504	hypothetical protein SORBIDRAFT_07g009956 [Sorghum bicolor]	Primary metabolism	16.03	1	1	1	1	131	14.8	8.15
241940621	hypothetical protein SORBIDRAFT_07g019320 [Sorghum bicolor]	Primary metabolism	3.52	1	1	1	1	426	46.4	4.93
241942122	hypothetical protein SORBIDRAFT_07g025540 [Sorghum bicolor]	Primary metabolism	8.17	1	1	1	2	306	34.4	8.75
241942143	hypothetical protein SORBIDRAFT_07g025840 [Sorghum bicolor]	Primary metabolism	4.77	2	1	2	3	692	76.7	6.4
241942772	hypothetical protein SORBIDRAFT_08g009580 [Sorghum bicolor]	Primary metabolism	7.98	2	1	4	8	702	74.4	5.26
241945522	hypothetical protein SORBIDRAFT_09g028260 [Sorghum bicolor]	Primary metabolism	29.93	2	1	2	2	147	15.3	10.05
241946598	hypothetical protein SORBIDRAFT_09g024340 [Sorghum bicolor]	Primary metabolism	20.29	3	2	6	14	483	50	6.23
241947011	hypothetical protein SORBIDRAFT_0011s005440 [Sorghum bicolor]	Primary metabolism	1.24	1	1	1	8	1292	144.2	8
241947172	hypothetical protein SORBIDRAFT_1599s002010 [Sorghum bicolor]	Primary metabolism	40.71	23	1	3	4	113	12.9	4.32
300678122	plastid glutamine synthetase [Vigna radiata]	Primary metabolism	15.15	15	2	4	7	429	47.2	7.24
330252038	triosephosphate isomerase [Arabidopsis thaliana]	Primary metabolism	4.58	2	1	1	1	306	32.3	7.49
330252259	malate dehydrogenase [Arabidopsis thaliana]	Primary metabolism	11.58	1	1	2	6	354	37.4	7.96
332004040	malate dehydrogenase [Arabidopsis thaliana]	Primary metabolism	4.2	4	1	1	2	333	35	7.66
332005103	5methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [Arabidopsis thaliana]	Primary metabolism	3.4	5	1	2	2	765	84.3	6.51
332005533	methionine synthase 3 [Arabidopsis thaliana]	Primary metabolism	4.56	5	1	2	2	812	90.5	8.05
332009653	lactate/malate dehydrogenase family protein [Arabidopsis thaliana]	Primary metabolism	4.79	3	1	1	1	334	36.4	5.07
332010081	D-ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]	Primary metabolism	6.76	1	1	1	3	281	30	8.07
332190370	2,3-bisphosphoglycerate-independent	Primary	5.03	3	1	1	1	557	60.5	5.53

	phosphoglycerate mutase 1 [Arabidopsis thaliana]	metabolism								
332190826	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]	Primary metabolism	21.43	9	4	7	17	350	37.6	7.77
332191393	uridylyltransferase-related protein [Arabidopsis thaliana]	Primary metabolism	5.63	2	1	1	1	213	22.7	5.41
332193864	fructose-1,6-bisphosphatase, cytosolic [Arabidopsis thaliana]	Primary metabolism	17.6	3	2	4	4	341	37.3	5.47
332195236	phosphoglycerate kinase [Arabidopsis thaliana]	Primary metabolism	26.17	7	2	7	15	405	42.6	5.54
332198142	phosphoglycerate kinase [Arabidopsis thaliana]	Primary metabolism	12.47	3	1	3	6	401	42.1	5.68
332640615	ribose 5-phosphate isomerase A [Arabidopsis thaliana]	Primary metabolism	6.88	1	1	1	1	276	29.3	6.02
332645491	fructose-bisphosphate aldolase 8 [Arabidopsis thaliana]	Primary metabolism	7.54	13	2	2	4	358	38.5	6.46
332646583	Transketolase [Arabidopsis thaliana]	Primary metabolism	3.38	4	1	2	3	740	79.8	6.43
332646583	Transketolase [Arabidopsis thaliana]	Primary metabolism	5.81	4	1	4	5	740	79.8	6.43
332657948	adenosylhomocysteinase 1 [Arabidopsis thaliana]	Primary metabolism	12.92	6	1	2	2	325	35.5	5.16
343466219	UDP-glucosyltransferase [Siraitia grosvenorii]	Primary metabolism	4.57	2	1	1	2	481	53.5	6.37
355479073	Malate dehydrogenase [Medicago truncatula]	Primary metabolism	13.55	2	2	4	5	332	35.5	6.54
355479444	Pyruvate kinase [Medicago truncatula]	Primary metabolism	6.82	8	1	2	4	513	56	6.9
355483140	Glutamine synthetase [Medicago truncatula]	Primary metabolism	6.22	15	2	5	11	1639	182.4	7.36
355483260	Fumarylacetoacetase [Medicago truncatula]	Primary metabolism	4.89	4	1	1	1	327	36.1	6.01
355485139	Phosphoglycerate kinase [Medicago truncatula]	Primary metabolism	19.21	4	3	6	13	479	50	7.14
355486173	Phosphoenolpyruvate carboxylase [Medicago truncatula]	Primary metabolism	2.37	17	1	1	1	506	57.4	7.24
355489207	Alanine glyoxylate aminotransferase [Medicago truncatula]	Primary metabolism	12.97	6	1	4	6	401	43.9	7.11
355490876	Glyceraldehyde 3-phosphate dehydrogenase [Medicago truncatula]	Primary metabolism	11.47	1	1	2	4	340	37	7.47
355492899	Glyceraldehyde-3-phosphate dehydrogenase [Medicago truncatula]	Primary metabolism	18.18	2	1	9	10	451	47.9	7.2
355493107	Glutamate-1-semialdehyde 2,1-aminomutase [Medicago truncatula]	Primary metabolism	6.84	4	2	2	2	468	49.7	6.57
355494658	Enolase [Medicago truncatula]	Primary metabolism	13.59	4	2	3	4	434	46.7	6.23
355506196	Transketolase [Medicago truncatula]	Primary metabolism	4.65	2	1	2	3	581	63	6.21

355508120	Fructose-bisphosphate aldolase [Medicago truncatula]	Primary metabolism	16	11	3	4	11	400	43.2	7.3
355510033	Mitochondrial aldehyde dehydrogenase [Medicago truncatula]	Primary metabolism	5.7	8	2	2	2	544	59.1	8.09
355511407	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Medicago truncatula]	Primary metabolism	7.74	4	1	3	3	478	51.3	7.11
355511512	Aminomethyltransferase [Medicago truncatula]	Primary metabolism	19.05	3	1	5	6	357	38.5	7.8
355512843	Malate dehydrogenase, glyoxysomal [Medicago truncatula]	Primary metabolism	12.57	5	1	3	7	358	38	8.06
355513928	Acyl-CoA-binding protein [Medicago truncatula]	Primary metabolism	13.33	1	1	1	2	90	10	5.48
355514290	Serine hydroxymethyltransferase [Medicago truncatula]	Primary metabolism	16.61	7	1	4	9	319	35.1	8.82
355516131	Transketolase [Medicago truncatula]	Primary metabolism	4.49	1	1	2	6	735	79.7	6.43
355521470	Alanine aminotransferase [Medicago truncatula]	Primary metabolism	2.67	1	1	1	1	524	58	6.54
355524524	Glutamyl-tRNA(Gln) amidotransferase subunit A [Medicago truncatula]	Primary metabolism	2.71	1	1	1	1	517	56.2	9.13
355524907	Phosphoglucomutase [Medicago truncatula]	Primary metabolism	2.23	10	1	1	1	582	63.2	5.68
378405156	Citrate synthase 5, mitochondrial	Primary metabolism	3.02	4	1	1	1	464	51.7	6.67
449450349	glycine dehydrogenase [decarboxylating], mitochondrial-like [Cucumis sativus]	Primary metabolism	8.13	31	1	4	6	1046	113.3	7.08
464895711	UDP-D-glucose pyrophosphorylase, partial [Prunus persica]	Primary metabolism	5	3	1	2	2	440	48.3	6.57
473802892	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial [Triticum urartu]	Primary metabolism	2.37	6	1	1	1	591	65.2	6.43
473912215	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic [Triticum urartu]	Primary metabolism	14.19	4	1	6	7	444	46.9	6.47
474041936	Glutamine synthetase leaf isozyme, chloroplastic [Triticum urartu]	Primary metabolism	11.03	13	2	4	6	535	58.7	7.06
474093626	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Triticum urartu]	Primary metabolism	3.89	1	1	1	2	386	42.5	9.11
474195824	Alanine aminotransferase 2 [Triticum urartu]	Primary metabolism	3.77	1	1	1	2	478	53	6.7
474293105	Cysteine synthase, chloroplastic/chromoplastic [Triticum urartu]	Primary metabolism	1.25	1	1	1	1	883	97.4	5.15
474378278	NADP-dependent D-sorbitol-6-phosphate dehydrogenase [Triticum urartu]	Primary metabolism	5.04	3	1	1	1	258	28.6	6.54
474427784	Aldehyde dehydrogenase family 3 member H1 [Triticum urartu]	Primary metabolism	10.78	2	1	2	2	334	36.3	8.73
474432364	Malate dehydrogenase, chloroplastic [Triticum urartu]	Primary metabolism	8.88	10	1	3	5	394	41.1	8.1
474443197	Lysosomal alpha-mannosidase [Triticum urartu]	Primary metabolism	2.03	7	1	1	1	739	83.2	7.96

3152562	Similar to proteasome component, micropain (multi-catalytic endopeptidase complex) subunit Y7, gb X56731 from <i>S. cerevisiae</i> . EST gb Z25719 comes from this gene [<i>Arabidopsis thaliana</i>]	Protein degradation	9.33	7	1	1	1	225	24.8	5.96
5822249	Chain B, Crystal Structure Of Prophytepsin, A Zymogen Of A Barley Vacuolar Aspartic Proteinase.	Protein degradation	3.35	2	1	1	1	478	51.2	5.44
75318709	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	Protein degradation	12.95	4	4	6	7	695	74.1	6.35
84468286	putative zinc dependent protease [<i>Trifolium pratense</i>]	Protein degradation	5.06	1	2	2	4	692	74.6	6.13
85700452	Leucine aminopeptidase 3	Protein degradation	2.74	1	1	1	1	583	61.3	7.08
108802666	ATP-dependent Clp protease proteolytic subunit [<i>Eucalyptus globulus</i> subsp. <i>globulus</i>]	Protein degradation	7.65	4	1	1	2	196	22	4.78
473890577	U-box domain-containing protein 7 [<i>Triticum urartu</i>]	Protein degradation	1.16	1	1	1	3	1123	123.4	5.96
473912635	Protease Do-like 1, chloroplastic [<i>Triticum urartu</i>]	Protein degradation	7.47	3	1	1	1	308	32.3	5.54
474138685	Presequence protease 1, chloroplastic/mitochondrial [<i>Triticum urartu</i>]	Protein degradation	1.85	5	1	1	1	974	109.8	5.11
26985221	non-cell-autonomous heat shock cognate protein 70 [<i>Cucurbita maxima</i>]	Protein folding	24.39	40	2	11	17	652	71.4	5.21
27735252	Chaperonin 60 subunit beta 1, chloroplastic	Protein folding	11.17	5	1	5	7	600	63.8	6.51
75170759	Chaperone protein ClpC1, chloroplastic; AltName: Full=Casein lytic proteinase C1; AltName: Protein DE-REGULATED CAO ACCUMULATION 1; AltName: Protein IRON-RESCUED MUTANT 1; Flags: Precursor	Protein folding	11.95	11	5	8	9	929	103.4	6.77
330253668	protein disulfide-isomerase like 2-3 [<i>Arabidopsis thaliana</i>]	Protein folding	3.86	1	1	1	5	440	47.7	5.85
332661452	mitochondrial heat shock protein 70-1 [<i>Arabidopsis thaliana</i>]	Protein folding	7.18	9	3	3	3	682	73	5.62
355480691	Chaperonin CPN60-like protein [<i>Medicago truncatula</i>]	Protein folding	2.61	5	1	1	1	574	61.1	6.09
355481961	Heat shock protein [<i>Medicago truncatula</i>]	Protein folding	15.84	2	1	8	13	707	75.7	5.34
355489198	Small heat shock protein [<i>Medicago truncatula</i>]	Protein folding	4.68	1	1	1	1	235	26.9	9.66
355496884	Heat shock protein [<i>Medicago truncatula</i>]	Protein folding	22.69	38	1	11	16	648	70.9	5.19
355521119	Chaperonin CPN60-like protein [<i>Medicago truncatula</i>]	Protein folding	3.47	6	1	1	1	576	61.6	7.39
365222886	Hop-interacting protein THI032 [<i>Solanum lycopersicum</i>]	Protein folding	12.97	4	1	4	7	401	44	8.05
473956238	Endoplasmic [<i>Triticum urartu</i>]	Protein folding	3.59	9	2	2	2	725	82.9	4.94
473983421	Heat shock cognate 70 kDa protein 1 [<i>Triticum urartu</i>]	Protein folding	17.39	57	2	11	16	759	82.5	5.24

474265113	DnaJ protein-like protein [Triticum urartu]	Protein folding	6.73	12	1	2	2	446	49.6	6.15
496684329	small heat shock protein 16.6CI [Boea hygrometrica]	Protein folding	9.52	8	1	1	1	147	16.5	5.71
496684331	small heat shock protein 17.4BCII [Boea hygrometrica]	Protein folding	9.49	2	1	1	1	158	17.5	6.8
119194	Elongation factor Tu, chloroplastic; AltName: Ras-related protein RAB8D; AltName: Ras-related protein Rab8D	Protein synthesis	3.36	1	1	1	2	476	51.6	6.19
1169476	Elongation factor 1-alpha; AltName: Vitronectin-like adhesion protein 1	Protein synthesis	16.11	16	1	5	8	447	49.3	9.13
4574240	ribosomal protein S14 [Syntrichia ruralis]	Protein synthesis	9.7	4	1	1	1	134	14.4	11.08
75313795	RecName: Full=40S ribosomal protein S28-1	Protein synthesis	18.75	4	1	1	1	64	7.4	10.83
313103630	Chain B, Localization Of The Small Subunit Ribosomal Proteins Into A 5.5 A Cryo-Em Map Of Triticum Aestivum Translating 80s Ribosome	Protein synthesis	5.73	9	1	1	1	227	25.4	9.6
315113251	Chain E, Localization Of The Large Subunit Ribosomal Proteins Into A 5.5 A Cryo-Em Map Of Triticum Aestivum Translating 80s Ribosome	Protein synthesis	7.78	4	1	1	1	180	20.7	9.96
330250326	60S ribosomal protein L7-2 [Arabidopsis thaliana]	Protein synthesis	6.2	1	1	1	1	242	28.2	9.94
330253794	30S ribosomal protein S5 [Arabidopsis thaliana]	Protein synthesis	4.62	1	1	1	1	303	32.6	8.97
332006494	small subunit ribosomal protein S1 [Arabidopsis thaliana]	Protein synthesis	3.61	1	1	1	1	416	45.1	5.25
332195217	elongation factor EF-2 [Arabidopsis thaliana]	Protein synthesis	5.81	6	1	2	2	843	93.8	6.25
332195268	heat shock protein ERD2 [Arabidopsis thaliana]	Protein synthesis	17.5	24	1	8	13	617	68.3	5.35
332643851	50S ribosomal protein L12-3 [Arabidopsis thaliana]	Protein synthesis	16.58	4	2	3	5	187	19.7	5.64
355490208	Elongation factor Tu [Medicago truncatula]	Protein synthesis	3.27	1	1	1	1	489	53.2	6.65
355516830	60S ribosomal protein I9 [Medicago truncatula]	Protein synthesis	8.85	1	1	1	1	192	21.8	9.41
355524949	40S ribosomal protein S15-like protein [Medicago truncatula]	Protein synthesis	11.04	1	1	1	1	154	17.2	10.4
388540218	translation elongation factor 2 [Prunus persica]	Protein synthesis	9.02	14	2	3	3	843	94	6.11
474247447	60S ribosomal protein L12 [Triticum urartu]	Protein synthesis	14.55	10	1	2	2	165	17.6	8.91
8778996	Contains similarity to ferredoxin-NADP+ reductase from Arabidopsis thaliana gb AJ243705 and contains an oxidoreductase FAD/NAD-binding [Arabidopsis thaliana]	Redox regulation	5.46	4	1	1	3	348	38.8	8.47
56481265	ascorbate peroxidase [Pseudotsuga menziesii var. menziesii]	Redox regulation	18.68	14	1	1	1	91	10.2	4.7
114804319	NADH-plastoquinone oxidoreductase subunit 7 [Morus indica]	Redox regulation	8.65	20	2	2	2	393	45.5	5.53
332003320	ferredoxin-dependent glutamate synthase 1 [Arabidopsis thaliana]	Redox regulation	3.95	8	1	4	4	1622	176.6	6.32

332010792	ferredoxin--NADP reductase, leaf isozyme 1 [Arabidopsis thaliana]	Redox regulation	18.7	7	1	3	7	262	29.7	6.15
332640734	Methionine sulfoxide reductase (MSS4-like) protein [Arabidopsis thaliana]	Redox regulation	12.5	4	1	1	2	168	19.3	4.59
332642000	putative peroxisomal (S)-2-hydroxy-acid oxidase 2 [Arabidopsis thaliana]	Redox regulation	8.33	6	1	2	5	348	38.1	9.2
332659277	PGR5-like protein 1A [Arabidopsis thaliana]	Redox regulation	6.85	3	1	1	1	321	35.4	5.29
332661063	catalase 2 [Arabidopsis thaliana]	Redox regulation	13.71	16	5	5	8	474	55	6.83
341865450	ascorbate peroxidase [Nicotiana benthamiana]	Redox regulation	16.15	19	2	3	5	192	21.1	5.02
355489123	Peptide methionine sulfoxide reductase [Medicago truncatula]	Redox regulation	5.45	4	1	1	1	202	23.1	7.99
355496700	Aldo-keto reductase yakc [Medicago truncatula]	Redox regulation	5.68	3	1	1	1	229	25.7	7.78
355500022	Ferredoxin-dependent glutamate synthase [Medicago truncatula]	Redox regulation	4.77	6	2	5	5	1676	183	7.09
355511016	Peroxioredoxin Q [Medicago truncatula]	Redox regulation	5.66	2	1	1	1	212	23.3	9.54
355513520	Ferredoxin-NADP reductase [Medicago truncatula]	Redox regulation	12.19	5	1	3	4	361	40.3	8.21
355518696	NAD(P)H-quinone oxidoreductase subunit [Medicago truncatula]	Redox regulation	8.02	1	1	1	2	187	21.2	8.94
355524779	Lactoylglutathione lyase [Medicago truncatula]	Redox regulation	7.78	8	1	2	3	347	38.8	7.02
473907056	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 [Triticum urartu]	Redox regulation	9.35	1	1	2	6	353	39.4	6.93
474192996	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5 [Triticum urartu]	Redox regulation	7.02	1	1	2	2	342	37.2	8.47
334302882	Callose synthase 7; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 7	Secondary metabolism	2.25	1	1	2	2	1958	227.9	8.32
340707718	Chain A, Crystal Structure Of Shikimate Kinase From Arabidopsis Thaliana (Atsk2)	Secondary metabolism	4.8	6	1	1	2	250	27.6	6.44
730129	Nucleoside diphosphate kinase 1	Signalling	10.74	2	1	1	1	149	16.5	6.79
1552396	14-3-3-like protein [Vicia faba]	Signalling	10.5	11	1	1	1	181	20.4	5.31
3023217	14-3-3-like protein GF14 nu; AltName: General regulatory factor 7	Signalling	11.7	42	2	2	3	265	29.8	4.82
4056456	Strong similarity to gb U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family [Arabidopsis thaliana]	Signalling	3.56	2	1	1	1	309	32.8	5.85
75219197	CBS domain-containing protein CBSX1, chloroplastic; AltName: Protein LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2;	Signalling	5.08	1	1	1	1	236	25.8	8.56

178847272	Chain A, Solution Structure Of Calcium Bound Soybean Calmodulin Isoform 1 C-Terminal Domain	Signalling	47.83	26	2	2	3	69	8	4.32
219870184	SUMO1a protein [Zea mays]	Signalling	10.1	5	1	1	1	99	10.9	5.1
332005731	calcium sensing receptor [Arabidopsis thaliana]	Signalling	3.1	1	1	1	1	387	41.3	9.39
355480401	ADP ribosylation factor [Medicago truncatula]	Signalling	12.8	24	1	1	2	164	18.7	5.86
355486673	Somatic embryogenesis receptor kinase [Medicago truncatula]	Signalling	2.45	1	1	1	1	695	76.7	6.77
355499334	Ras-like protein [Medicago truncatula]	Signalling	14.85	56	2	2	2	202	22.5	5.16
355499816	Calmodulin [Medicago truncatula]	Signalling	30.87	4	1	3	3	149	16.8	4.27
474381232	Ras-related protein Rab-2-B [Triticum urartu]	Signalling	6.43	5	1	1	1	171	19	5.21
461903	Peptidyl-prolyl cis-trans isomerase; AltName: Cyclophilin of 18 kDa 3; AltName: Cyclosporin A-binding protein; AltName: Rotamase cyclophilin-1	Stress/Defense related	26.74	2	1	2	3	172	18.4	7.81
62900642	Probable plastid-lipid-associated protein 2, chloroplastic; AltName: Fibrillin-2	Stress/Defense related	4.84	2	1	1	1	310	33.6	5.83
75311568	Heat shock 70 kDa protein 7, chloroplastic; AltName: Chloroplast heat shock protein 70-2; AltName: Heat shock protein 70-7;	Stress/Defense related	15.32	3	0	6	8	718	76.9	5.3
332009391	TCP-1/cpn60 chaperonin family protein [Arabidopsis thaliana]	Stress/Defense related	15.91	7	3	6	8	597	63.3	5.87
332198285	VQ motif-containing protein [Arabidopsis thaliana]	Stress/Defense related	5.08	1	1	1	1	177	19.9	9.28
355492471	Lipoxygenase [Medicago truncatula]	Stress/Defense related	6.9	1	1	1	3	174	20.5	5.96
460389014	PREDICTED: GDSL esterase/lipase At2g04570-like [Solanum lycopersicum]	Stress/Defense related	7.06	1	1	1	1	354	40.1	6.86
474036632	Disease resistance RPP8-like protein 3 [Triticum urartu]	Stress/Defense related	3.3	1	1	1	1	940	105.5	7.36
474219338	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic [Triticum urartu]	Stress/Defense related	4.07	1	1	1	1	418	45.9	4.93
1216389	myrosinase-associated protein [Brassica napus]	Structure	3.23	1	1	1	1	371	41.8	8.24
4512327	actin [Glycyrrhiza echinata]	Structure	38.71	13	1	3	6	155	17.1	6.19
332003395	ACT domain-containing protein [Arabidopsis thaliana]	Structure	4.5	2	1	1	2	200	22	6.35
355491594	Actin [Medicago truncatula]	Structure	24.17	29	2	5	11	360	40	5.99
471271028	actin 1 [Dionaea muscipula]	Structure	37.14	33	5	8	14	377	41.7	5.49
84453194	putative ADP ATP carrier protein [Trifolium pratense]	Transport	6.47	13	2	2	2	371	39.9	9.83
332004440	dicarboxylate transporter 1 [Arabidopsis thaliana]	Transport	3.6	4	1	2	2	556	59	9.73
332007956	Glucose-6-phosphate/phosphate translocator-like protein [Arabidopsis thaliana]	Transport	7.74	8	1	2	2	297	32.7	9.45

332192250	glutamate:glyoxylate aminotransferase [Arabidopsis thaliana]	Transport	6.58	3	1	2	2	441	48.5	8.31
332197185	alanine aminotransferase 2 [Arabidopsis thaliana]	Transport	2.78	3	1	1	1	431	47.7	6.8
332659663	ABC transporter B family member 28 [Arabidopsis thaliana]	Transport	3.67	2	1	1	2	545	59.2	8.72
332660627	F-type H+-transporting ATPase subunit b [Arabidopsis thaliana]	Transport	11.42	1	2	3	6	219	23.9	5.86
355492580	Plasma membrane H+ ATPase [Medicago truncatula]	Transport	5.89	24	2	4	5	951	104.6	6.83
355514169	Plastoglobulin-1 [Medicago truncatula]	Transport	2.82	2	1	1	1	355	37.7	4.7
438005	T protein [Flaveria pringlei]	Unknown	13.76	11	2	4	7	407	44.3	8.72
438217	T-protein [Pisum sativum]	Unknown	23.53	10	1	7	10	408	44.3	8.57
683488	Glp1 [Sinapis alba]	Unknown	10.9	1	1	1	3	211	22	6.77
1469219	unknown [Brassica oleracea var. gemmifera]	Unknown	6.18	8	1	1	2	259	28.9	4.98
24797022	At4g33010/F26P21_130 [Arabidopsis thaliana]	Unknown	8.58	37	1	6	10	1037	112.9	7.02
95113973	chloroplast At1g16080 protein [Coffea canephora]	Unknown	20.29	3	1	1	1	69	7.3	6.57
112806819	PsbC [Ostreococcus tauri]	Unknown	3.17	1	1	1	3	473	52.1	6.9
113631907	Os09g0516700 [Oryza sativa Japonica Group]	Unknown	8.86	3	1	2	3	463	49.5	9.94
113644534	Os11g0163100 [Oryza sativa Japonica Group]	Unknown	18.04	21	1	4	8	377	41.6	5.49
113644815	Os11g0242800 [Oryza sativa Japonica Group]	Unknown	14.13	2	1	3	7	283	30.3	5.71
113644981	Os11g0312400 [Oryza sativa Japonica Group]	Unknown	6.17	1	1	1	1	243	26.7	7.8
113645432	Os11g0595200 [Oryza sativa Japonica Group]	Unknown	8.15	3	2	2	2	270	28.4	8.79
217071972	unknown [Medicago truncatula]	Unknown	7.19	2	1	1	1	167	18.9	8.05
217072016	unknown [Medicago truncatula]	Unknown	11.57	15	1	1	1	121	13.1	4.41
217072964	unknown [Medicago truncatula]	Unknown	14.89	3	1	1	1	94	10.4	4.22
227202864	AT1G07890 [Arabidopsis thaliana]	Unknown	10.53	3	1	1	1	190	20.9	5.19
255638071	unknown [Glycine max]	Unknown	4.86	1	1	1	1	370	40.4	8.18
255680378	Os11g0687900 [Oryza sativa Japonica Group]	Unknown	2.12	1	1	1	1	471	53.1	8.9
255680411	Os11g0707000 [Oryza sativa Japonica Group]	Unknown	26.86	4	1	5	17	350	38.9	7.71
307106152	hypothetical protein CHLNCDRAFT_31785 [Chlorella variabilis]	Unknown	4.65	3	1	1	1	258	29.4	5.02
332005181	uncharacterized protein AT5G18440 [Arabidopsis thaliana]	Unknown	3.19	1	1	2	5	470	53.6	9.54
332659963	uncharacterized protein AT4G27595 [Arabidopsis thaliana]	Unknown	2.7	1	1	2	4	1221	138.9	5.07

355483828	hypothetical protein MTR_2g034550 [Medicago truncatula]	Unknown	12.64	1	1	1	2	182	19.2	7.5
355484261	hypothetical protein MTR_2g039760 [Medicago truncatula]	Unknown	20.55	1	1	1	2	73	8.4	9.79
355501163	Limkain-b1 [Medicago truncatula]	Unknown	3.29	1	1	1	3	638	69.1	9.17
355508641	177 protein [Medicago truncatula]	Unknown	11.93	1	1	1	2	176	19.7	9.38
355511362	Complex interacting protein [Medicago truncatula]	Unknown	5.76	1	1	1	2	191	20.4	7.91
355512214	hypothetical protein MTR_5g008050 [Medicago truncatula]	Unknown	14.91	2	1	2	2	275	28.8	9.74
355516499	hypothetical protein MTR_5g064610 [Medicago truncatula]	Unknown	8.6	2	1	1	2	221	24.7	8.46
355516939	hypothetical protein MTR_5g069990 [Medicago truncatula]	Unknown	12.26	1	1	1	1	106	11.1	9.88
460371793	PREDICTED: uncharacterized protein LOC101267175 [Solanum lycopersicum]	Unknown	1.62	1	1	1	4	1171	134.1	5.53
462423997	hypothetical protein PRUPE_ppa000675mg [Prunus persica]	Unknown	7.99	30	2	6	8	1039	112.7	6.84
473721135	hypothetical protein TRIUR3_11555 [Triticum urartu]	Unknown	17.33	1	1	1	1	150	16.5	9.92
473904336	hypothetical protein TRIUR3_32478 [Triticum urartu]	Unknown	1.42	1	1	1	1	1762	198.8	4.81
474149852	hypothetical protein TRIUR3_22737 [Triticum urartu]	Unknown	11.22	5	2	2	2	303	33.7	5.85
474262273	hypothetical protein TRIUR3_11994 [Triticum urartu]	Unknown	16.48	1	1	1	1	91	10.1	10.1
474326910	hypothetical protein TRIUR3_21375 [Triticum urartu]	Unknown	8.02	1	1	1	1	212	23.6	9.82
474353635	hypothetical protein TRIUR3_17311 [Triticum urartu]	Unknown	3.86	1	1	1	2	570	63.1	8.05
474353901	hypothetical protein TRIUR3_16800 [Triticum urartu]	Unknown	8.77	1	1	1	1	171	18.4	8.07
474448545	hypothetical protein TRIUR3_14005 [Triticum urartu]	Unknown	6.35	1	1	1	2	189	19.5	6.38
				3959						

Table 2 : List of the identified proteins in *H.rhamnoides* Berry Protein fractions, identified using QExactive Orbitrap High resolution mass spectrometer

Accession	Description	Function	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
319976488	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [unidentified plant]	Photosynthesis	28.14	115	2	2	5	167	18.5	6.00
355523560	Ubiquitin [Medicago truncatula]	Protein degradation	30.77	59	1	1	5	52	5.8	5.19
241946598	hypothetical protein SORBIDRAFT_09g024340 [Sorghum bicolor]	Primary metabolism	8.70	3	1	2	3	483	50.0	6.23
159232284	ATP synthase beta subunit [Jaltomata dentata]	Energy metabolism	19.51	165	3	3	4	328	35.1	5.73
332190824	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]	Primary metabolism	9.78	9	2	2	2	317	34.3	6.64
330251134	serine--glyoxylate aminotransferase [Arabidopsis thaliana]	Primary metabolism	3.74	7	1	1	2	401	44.2	7.83
355507110	Photosystem II CP47 chlorophyll apoprotein [Medicago truncatula]	Photosynthesis	1.76	1	1	1	1	968	107.3	7.49
241929847	hypothetical protein SORBIDRAFT_03g017600 [Sorghum bicolor]	Primary metabolism	4.34	14	1	1	1	484	53.3	6.29
29293057	putative NADH-dependent hydroxypyruvate reductase [Glycine max]	Primary metabolism	7.51	1	1	1	1	386	42.2	7.43
376339354	hypothetical protein CL304Contig1_01, partial [Abies alba]	unknown	19.54	3	1	1	1	87	9.8	5.19
355506196	Transketolase [Medicago truncatula]	Primary metabolism	2.24	2	1	1	1	581	63.0	6.21
332640615	ribose 5-phosphate isomerase A [Arabidopsis thaliana]	Primary metabolism	6.88	1	1	1	1	276	29.3	6.02
222873579	predicted protein [Populus trichocarpa]	Primary metabolism	3.16	2	1	1	1	412	47.0	6.79
158939577	glyceraldehyde 3-phosphate dehydrogenase, partial [Ficus caulocarpa]	Primary metabolism	14.74	40	1	1	1	95	10.0	9.70
75313128	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic; AltName: Heteroglycan-interacting protein 1.3; AltName: Protein CHLOROPLAST RNA BINDING; AltName: Full=Protein Gb5f	Photosynthesis	4.50	1	1	1	1	378	42.6	8.16
474350516	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic [Triticum urartu]	Protein degradation	3.04	2	1	1	1	494	54.4	5.82
241940213	hypothetical protein SORBIDRAFT_07g003490 [Sorghum bicolor]	Primary metabolism	1.23	1	1	1	1	972	111.4	6.74
355492684	hypothetical protein MTR_3g109860 [Medicago truncatula]	Unknown	8.84	1	1	1	1	147	16.9	5.48
114804250	ATP synthase CF1 alpha subunit [Morus indica]	Energy metabolism	3.16	1	1	1	1	507	55.4	5.21
300169100	hypothetical protein SELMODRAFT_79425 [Selaginella moellendorffii]	Others	3.77	5	1	1	1	451	50.0	5.15