Supplemental Table S1

Arabidopsis proteins whose *de novo* synthesis occurss during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	pI Th	% Cov.
1[b]	dnaK-type molecular chaperone BiP	At5g42020	79.36	5.08	71.17	5.08	21%
3[b]	Enolase	At1g74030	55.87	5.29	51.44	5.79	26%
4[b]	Tubulin beta 2 beta 3 chain	At5g62700	57.35	4.89	50.70	4.70	35%
5[b]	Tubulin-alpha-3.5	At5g19770	57.86	5.11	49.62	4.95	23%
6[b]	Tubulin-alpha-2.4	At1g04820	54.71	5.06	49.51	4.93	52%
7[b]	60S acidic ribosomal protein P0-B	At3g09200	37.55	5.09	34.13	4.99	24%
8[b]	HSP 17.4	At3g46230	17.93	4.99	17.45	5.20	25%
9[b]	HSP 17.7	At5g12030	17.94	5.50	17.83	5.22	14%
10[b]	Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	57.36	5.77	53.47	6.25	17%
11[b]	Em-like protein GEA1 (EM1)	At3g51810	19.61	5.75	16.61	5.75	26%
13[b]	MLO-like-protein	At1g61560	72.97	6.3	67.21	10.06	15%
17[b]	Phosphoenol pyruvate carboxykinase	At4g37870	73.40	6.58	73.40	6.61	17%
23[b]	Catalase 2	At4g35090	56.48	6.64	56.91	6.63	16%
24[b]	Actin 7	At5g09810	42.94	5.06	41.96	5.26	23%
25[b]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At4g28520	23.32	6.89	21.20	6.19	27%
26[b]	Aconitate hydratase cytoplasmic	At2g05710	96.38	5.75	98.15	5.79	34%
34[b]	Major latex protein	At1g14950	13.19	5.90	18.06	6.88	58%
36[b]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	40.42	6.44	36.99	6.34	34%
37[b]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	40.29	6.49	36.99	6.34	17%
38[b]	Aminopeptidase	At2g24200	59.99	5.61	54.49	5.72	27%
39[b]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	38.52	6.23	36.99	6.34	26%
40[b]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	38.55	6.26	36.99	6.34	27%
42[b]	Cell division cycle protein (CDC48)	At3g09840 or At5g03340	96.32	5.21	89.34	5.13	35%
43[b]	Heat shock cognate 70 kDa protein 3	At3g09440	78.90	5.06	71.13	4.69	15%
44[b]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At1g03880	16.14	7.42	20.80	7.03	7%
45[b]	HSP 70	At1g16030	76.38	5.24	70.91	5.3	24%
46[b]	Jasmonate inducible protein-like	At3g16460	77.81	5.29	72.46	5.17	10%
48[b]	Cupin family protein	At2g28490	72.99	4.99	55.69	6.08	25%
49[b]	S-adenosylmethionine synthétase	At3g17390	42.67	5.51	42.79	5.51	19%
50[b]	Translation elongation factor Tu (chloroplast) (without transit peptide)	At4g20360	42.94	5.43	51.62	5.84	27%
56[b]	Late embryogenesis abundant (LEA)	At3g22500	34.02	5.36	26.82	5.46	31%
58[b]	Jasmonate inducible protein-like	At3g16420	36.28	5.49	32.16	5.46	41%
59[b]	Succinate dehydrogenase [ubiquinone] flavoprotein subunit. mitochondrial	At5g66760	66.68	5.39	69.64	6.24	16%
61[b]	Late embryogenesis abundant (LEA)	At2g42560	66.68	5.78	67.19	5.78	43%
62[b]	S-adenosylmethionine synthetase 2	At4g01850	43.25	5.67	43.24	5.94	30%
64[b]	Elongation factor 1-beta-gamma	At1g09640	41.75	5.66	46.64	5.13	17%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	pI Th	% Cov.
66[b]	Jasmonate inducible protein-like	At1g52110	62.82	6.33	62.00	6.00	12%
67[b]	Glycosyl hydrolase family 1 protein	At3g09260	63.25	6.47	60.26	6.91	46%
68[b]	Glycosyl hydrolase family 1 protein	At3g09260	63.47	6.56	60.26	6.45	27%
69[b]	12S seed storage protein [Precursor]	At1g03880	43.67	6.29	48.03	6.56	18%
70[b]	12S seed storage protein [Precursor]	At5g44120	49.43	7.19	52.59	7.68	22%
71[b]	12S seed storage protein [Precursor]	At5g44120	50.44	7.67	52.59	7.68	34%
78[b]	12S seed storage protein [Precursor]	At5g44120	27.26	6.61	52.59	7.68	13%
80[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At4g28520	32.64	5.85	34.68	6.42	33%
83[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At4g28520	34.35	6.42	34.68	6.42	33%
84[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	30.46	6.61	31.75	6.49	42%
85[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At1g03880	27.20	6.50	27.24	6.34	32%
87[b]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At1g03880	18.43	6.36	20.80	7.03	33%
88[b]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At4g28520	22.82	8.68	21.20	6.19	44%
91[b]	Late embryogenesis abundant (LEA)	At3g53040	61.88	5.06	52.08	5.29	17%
92[b]	Jasmonate inducible protein-like	At2g33070	53.10	5.59	51.61	5.58	22%
93[b]	Actin 7	At5g09810	42.55	5.27	41.96	5.26	19%
97[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	28.89	7.90	31.75	6.49	40%
99[b]	Major latex protein	At1g14950	13.32	6.28	18.06	6.88	27%
101[b]	Hydrolase. alpha/beta fold family protein	At3g54240	41.07	5.16	39.46	9.27	19%
102[b]	Late embryogenesis abundant (LEA)	At2g36640	60.51	5.22	48.49	5.43	16%
103[b]	Enolase	At2g36530	57.95	5.58	47.72	5.54	16%
104[b]	ATP synthase beta-chain (mitochondrial)	At5g08670	58.87	5.48	54.13	5.13	24%
105[b]	Elongation factor 1-gamma 2	At1g57720	48.63	5.61	46.40	5.55	41%
106[b]	Alcohol dehydrogenase	At1g77120	41.64	5.77	41.84	6.11	22%
107[b]	Glutamine synthase	At3g17820	40.94	5.79	38.59	5.72	21%
110[b]	12S seed storage protein [Precursor]	At4g28520	57.97	6.40	55.86	6.36	19%
112[b]	Short-chain dehydrogenase/reductase (SDR) family protein	At5g50600 or At5g50700	40.31	5.88	39.07	6.15	21%
113[b]	Fructose bisphosphate aldolase-like protein	At3g52930	40.36	5.90	38.52	6.41	31%
114[b]	Malate dehydrogenase cytoplasmic 1	At1g04410	39.56	5.87	35.57	6.11	21%
116[b]	Expressed protein	At5g45690	31.06	5.60	28.78	5.92	40%
121[b]	Phosphoglycerate kinase cytosolic	At1g79550	40.92	5.45	42.19	5.43	10%
127[b]	Elongation factor EF-2	At1g56070	93.92	5.89	94.25	5.89	24%
128[b]	Elongation factor 1-beta-gamma	At1g09640	47.45	5.45	46.64	5.13	26%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	PI Th	% Cov.
129[b]	Eukaryotic initiation factor 4A-1	At3g13920 or At1g72730	47.22	5.50	46.70	5.47	28%
131[b]	Aldose reductase	At5g01670	38.48	6.22	36.38	6.23	24%
136[b]	Heat shock cognate 70 kDa protein 1	At5g02500	77.87	4.87	71.37	5.03	21%
137[b]	HSP 70	At3g12580	76.06	5.07	71.37	5.03	19%
138[b]	HSP 70	At5g09590	71.33	5.21	72.99	5.63	17%
144[b]	Peptidyl-prolyl cis-trans isomerase	At4g38740	15.87	6.82	18.60	7.83	47%
146[b]	Mercaptopyruvate sulfurtransferase	At1g79230	37.85	5.04	41.88	6.35	35%
148[b]	Mitochondrial chaperonin	At2g33210	65.31	5.37	61.96	6.59	33%
149[b]	Mitochondrial chaperonin	At3g23990	64.96	5.18	61.26	5.41	25%
154[b]	Cupin family protein Alpha subunit	At4g36700	26.35	4.79	30.21	7.53	5%
155[b]	Cupin family protein Alpha subunit	At4g36700	26.35	4.79	59.07	5.21	17%
159[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At4g28520	23.54	5.33	27.24	6.34	15%
164[b]	Aspartic proteinase (Precursor)	At1g62290	35.03	5.60	35.22	5.90	8%
167[b]	Malate synthase	At5g03860	62.96	8,00	63.87	8.04	29%
168[b]	Malate synthase	At5g03860	62.91	7.08	63.87	8.04	13%
171[b]	Transketolase	At3g60750	80.53	5.37	79.95	6.32	12%
173[b]	Phosphoglycerate kinase	At3g12780	42.52	5.05	50.09	6.11	7%
174[b]	O-acetylserine-thiol-lyase	At4g14880	38.71	5.73	33.79	5.95	9%
176[b]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	39.27	6.33	36.99	6.34	13%
181[b]	Jasmonate inducible protein-like	At2g33070	54.36	5.52	51.61	5.58	27%
182[b]	DEAD box RNA helicase RH15	At5g11200	49.11	5.53	48.32	5.37	32%
184[b]	Replication factor A	At5g08020	55.12	5.37	67.27	6.41	26%
185[b]	Glutamine synthase	At3g17820	41.02	5.59	38.59	5.72	54%
186[b]	DNA topoisomerase I	At5g55300	96.47	5.78	102.78	10.05	8%
187[b]	DNA topoisomerase I	At5g55300	96.47	5.81	102.78	10.05	8%
188[b]	Aconitate hydratase cytoplasmic	At4g35830	96.69	5.83	98.13	6.36	10%
190[b]	Heat shock protein 101	At1g74310	101.62	5.82	101.27	5.99	16%
191[b]	Mitochondrial processing peptidase (MBP)	At3g02090	72.99	5.79	59.14	6.76	16%
192[b]	ATP synthase alpha-chain (mitochondrial)	AtMg01190	60.54	5.92	55.05	6.54	19%
196[b]	Aspartate aminotransferase (cytoplasmic isozyme 1)	At5g19550	41.46	6.57	44.31	6.80	28%
197[b]	Fructose-bisphosphate Aldolase	At2g36460	40.91	6.77	38.37	7.46	23%
198[b]	Fructose-bisphosphate Aldolase	At2g36460	40.72	6.89	38.37	7.46	41%
200[b]	Thioredoxin family protein	At2g47470	40.38	5.73	39.48	5.85	20%
201[b]	Vacuolar ATP synthase catalytic subunit A	At1g78900	68.75	5.20	68.79	4.86	26%
202[b]	MutT/nudix family protein	At1g79690	82.15	5.20	86.84	5.09	18%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	PI Th	% Cov.
206[b]	5-methyl-tetra-hydropteroyl-tri-glutamate-homocysteine methyltransferase	At5g17920	82.05	6.09	84.34	6.47	17%
209[b]	Glycosyl hydrolase family 35 protein	At4g36360	65.24	6.02	95.18	7.23	8%
210[b]	Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	88.93	4.93	65.95	4.81	20%
212[c]	Actin 2	At3g18780	42.57	5.18	41.21	5.43	33%
215[c]	RuBisCO subunit binding-protein alpha subunit. chloroplast [Precursor]	At2g28000	64.96	4.90	62.05	4.81	19%
235[b]	Ubiquitin protein ligase	At5g02240	32.51	5.81	41.60	6.05	38%
241[b]	Alpha-cruciferin 12S (Seed storage protein fragment)	At4g28520	34.11	5.87	34.68	6.42	32%
242[c]	Dormancy related protein	At1g54870	32.62	5.76	31.37	6.11	43%
245[b]	12S seed storage protein [Precursor]	At1g03880	27.22	6.64	50.61	6.77	25%
246[b]	Storage proteins 7S	At3g22640	29.45	6.70	55.04	7.14	28%
247[b]	Storage proteins 7S	At3g22640	34.02	6.77	55.04	7.14	18%
253[c]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	40.29	5.84	36.99	6.34	18%
254[b]	Dehydrin	At5g66400	17.96	5.20	18.44	7.95	6%
255[b]	Dehydrin	At5g66400	17.96	5.37	18.44	7.95	6%
259[b]	Expressed protein	At1g05510	27.01	6.10	27.28	6.70	21%
260[c]	1-Cys peroxiredoxin	At1g48130	27.22	6.22	24.06	6.60	39%
265[b]	Superoxide dismutase (Mn)	At3g56350	24.37	6.10	26.87	6.76	54%
269[c]	40S ribosomal protein SA (RPSaA)	At1g72370	38.55	5.02	32.28	5.13	25%
271[c]	12S seed storage protein [Precursor]	At4g28520	59.96	6.52	55.86	6.36	9%
281[c]	Ferritin 3. chloroplast [Precursor]	At3g11050	26.37	5.21	28.36	5.61	15%
284[c]	GSH-dependent DEHYDROASCORBATE reductase	At1g19570	25.34	5.43	23.62	5.79	57%
285[c]	Glutathione S-transferase	At1g78370	25.34	5.60	25.65	5.80	24%
287[c]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At5g44120	23.44	5.58	20.84	9.06	22%
290[b]	Aconitate hydratase cytoplasmic	At4g35830	96.69	5.88	98.13	6.36	7%
291[c]	Subtilase family protein	At4g20850	151.97	5.30	152.35	5.93	9%
293[c]	Peptidase M1 family protein.	At1g63770	96.69	5.61	103.40	6.09	4%
294[c]	Peptidase M1 family protein.	At1g63770	96.65	5.54	103.40	6.09	9%
295[b]	Peptidase M1 family protein.	At1g63770	96.42	5.43	103.40	6.09	5%
296[b]	Pyruvate.orthophosphate dikinase	At4g15530	96.35	5.37	98.22	5.53	9%
297[b]	Cell division cycle protein (CDC48)	At3g09840	97.41	5.20	89.38	4.88	35%
298[c]	Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	92.73	4.96	65.95	4.81	18%
299[c]	Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	93.01	4.94	65.95	4.81	16%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	pI Th	% Cov.
302[c]	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At1g13440	40.34	6.03	36.90	7.21	30%
305[c]	Phosphoglucomutase. cytoplasmic 2	At1g70730	68.25	5.70	63.46	5.57	34%
314[c]	60S acidic ribosomal protein P0-C	At3g11250	37.54	5.22	34.37	4.78	7%
320[b]	Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	57.36	5.82	53.47	6.25	24%
321[b]	Ribulose bisphosphate carboxylase large chain [Precursor] or rubisco	AtCg00490	57.36	5.84	53.47	6.25	28%
323[c]	protein disulfide isomerase	At1g77510	64.95	4.81	56.35	4.64	47%
328[c]	Hydroxymethyltransferase	At4g13930	56.99	6.47	51.70	7.26	19%
335[c]	Quinone oxidoreductase	At5g61510	39.25	6.51	44.00	8.56	16%
336[c]	Cinnamyl-alcohol dehydrogenase	At1g72680	39.27	6.57	38.65	6.67	26%
358[c]	Pyruvate decarboxylase	At5g54960	60.53	5.77	65.78	5.63	5%
359[c]	S-adenosyl-L-homocysteine hydrolase	At4g13940	56.90	5.57	53.36	5.83	13%
360[c]	Glycosyl hydrolase family 3 protein	At5g64570	64.96	5.75	84.29	7.71	14%
361[b]	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein	At3g14990	47.75	5.22	41.84	5.08	6%
364[c]	T-complex protein 1. theta subunit (TCP-1-Theta)	At3g03960	65.22	5.56	58.92	5.01	2%
365[b]	Isocitrate lyase	At3g21720	62.77	6.30	50.42	6.29	16%
370[c]	Glutamate dehydrogenase	At5g18170 or At3g03910	41.66	6.50	44.51	6.02	13%
371[c]	Aspartate aminotransferase. chloroplast	At4g31990	42.92	6.42	49.81	8.39	34%
374[c]	Glycyl-tRNA synthetase / glycine--tRNA ligase	At1g29880	80.51	5.91	81.93	6.59	19%
376[c]	Tubulin beta-8 chain	At5g23860	57.35	4.92	50.59	4.46	9%
378[c]	Subtilisin-like serine proteinase. putative. 3' partial	At3g14067	80.28	5.77	81.80	6.76	19%
380[c]	Nucleoside diphosphate kinase II. chloroplast	At5g63310	26.31	5.89	25.53	9.30	12%
392[c]	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	13.31	5.89	31.75	6.49	14%
393[c]	Major latex protein	At1g14950	11.85	5.89	18.06	6.37	44%
421[c]	Late embryogenesis abundant (LEA)	At3g17520	34.93	5.07	29.55	5.21	55%
422[c]	Thioredoxin family protein	At3g16110	61.85	4.89	59.55	4.66	8%
425[c]	Eukaryotic translation initiation factor 3	At5g25780 or At5g27640	92.72	5.16	82.16	4.87	6%
426[c]	NAD-dependent epimerase/dehydratase family protein	At5g28840	43.25	5.77	42.74	6.15	54%
427[c]	10-formyltetrahydrofolate synthetase	At1g50480	76.41	6.22	67.78	6.70	19%
438[b]	20S proteasome alpha subunit B (PAB1) (PRC3)	At1g16470	27.21	5.49	25.68	5.39	8%
445[b]	Protein phosphatase 2C	At3g15260	31.89	5.36	31.61	5.61	23%
450[b]	Monodehydroascorbate reductase	At1g63940	52.13	5.77	52.48	7.53	26%
455[b]	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein	At3g14990	42.53	5.26	41.84	5.08	11%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	pI Th	% Cov.
458[c]	Xylose isomerase	At5g57655	55.89	5.58	32.39	7.89	12%
459[c]	Strictosidine synthase-related	At3g57020	41.41	6.57	41.43	6.57	7%
508[c]	Elongation factor 1B alpha-subunit 2	At5g19510	34.04	3.99	24.18	4.17	29%
509[b]	Nascent Polypeptide-associated Complex (NAC) domain-containing protein	At5g13850	34.11	4.01	17.87	4.85	24%
510[b]	20S proteasome alpha subunit E2 (PAE2)	At3g14290 or At1g53850	25.98	4,00	25.96	4.41	9%
525[c]	Actin	At5g59370 or At5g09810 or At3g53750 or At3g46520	34.08	4.81	41.78	5.29	8%
543[c]	D-fructose-1.6-bisphosphate 1-phosphohydrolase	At1g43670	40.92	5.29	37.26	5.28	25%
544[c]	Methyl-CpG-binding domain-containing protein	At1g15340	65.27	3.50	42.34	4.34	8%
546[c]	Stress-inducible protein	At1g62740 or At1g12270 or At4g12400	71.33	6.00	64.50	6.05	16%
548[c]	Phosphoglycerate kinase	At1g79550	40.94	5.56	42.13	5.34	64%
551[c]	HSP 90	At2g04030	91.66	4.00	88.65	4.65	5%
552[c]	Shepherd protein (SHD)	At4g24190	96.35	4.58	94.19	4.66	17%
554[c]	Heat shock protein 17.6A	At5g12030	17.93	5.51	17.68	5.59	22%
556[c]	Acetyl-CoA C-acyltransferase	At2g33150	44.48	8.60	48.56	8.47	38%
557[c]	26S proteasome regulatory subunit S5A (RPN10). identical to multiubiquitin chain binding protein (MBP1)	At4g38630	56.46	4,00	40.74	4.22	7%
561[c]	Succinyl-CoA ligase (GDP-forming) alpha-chain. mitochondrial	At5g08300	39.27	6.59	36.15	8.39	9%
562[c]	Translation elongation factor EF-Tu precursor. mitochondrial	At4g02930	42.94	5.85	49.41	6.68	45%
564[c]	Cucumisin-like serine protease (ARA12)	At5g67360	87.84	6.40	79.28	5.91	14%
570[c]	AMP-dependent synthetase or ligase family or GMP synthase	At3g48990 or At1g63660	60.53	5.96	55.60 or 59.20	6.08 or 6.01	17% or 6%
571[c]	Peroxiredoxin type 2	At1g65980	16.14	5.18	17.42	5.17	38%
575[c]	20 kDa chaperonin. chloroplast (CPN21)	At5g20720	25.42	5.19	26.78	9.44	41%
576[c]	Glutathione S-transferase (2.4-D-inducible)	At1g78370	24.01	5.18	24.99	5.48	16%
579[c]	glycine-rich protein similar to P23 co-chaperone.	At4g02450	36.05	3.98	25.47	4.17	24%
580[c]	Elongation factor 1B alpha-subunit 2 (eEF1Balpha2)	At5g19510	35.06	4.02	24.20	4.17	31%

Supplemental Table S1 (continued)

Arabidopsis proteins whose *de novo* synthesis occurs during germination *sensu stricto* (1-d post-imbibition) of non-deteriorated control seeds (0d). % Cov, coverage; Exp, experimental; MW, molecular weight; Th, theoretical; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	MW Exp (kDa)	pI Exp	MW Th (kDa)	pI Th	% Cov.
584[c]	Nucleosome assembly protein (NAP) family protein	At1g74560 or At1g18800	38.32	3.19	29.46	4.18	11%
585[c]	14-3-3 protein GF14 psi (GRF3) (RCI1)	At5g38480	32.64	4.80	28.59	4.75	23%
586[c]	Elongation factor 1-alpha	At5g60390	54.96	9.00	49.48	9.64	23%
587[c]	Expressed protein	At5g02240	32.62	5.81	27.09	6.19	31%
588[c]	Glucose and ribitol dehydrogenases	At3g05260	34.08	5.79	31.43	6.09	62%
590[c]	Cinnamoyl-CoA reductase	At5g58490	38.71	5.59	35.74	5.80	30%
592[c]	Ketol-acid reductoisomerase. chloroplast precursor	At3g58610	61.88	5.61	63.80	6.36	13%
593[c]	T-complex protein 1. beta subunit (TCP-1-beta)	At5g20890	61.90	5.72	57.25	5.59	22%
614[c]	Aspartyl-tRNA synthetase	At4g31180	68.68	5.83	62.90	6.12	26%
705[c]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At1g03880	11.75	8.9	21.20	6.19	44%
728[c]	Phosphoenolpyruvate carboxykinase (ATP)	At4g37870	72.97	6.44	73.36	6.61	11%
729[c]	S-adenosyl-L-homocysteine hydrolase	At4g13940	59.97	5.71	53.34	5.66	18%
731[c]	Cell division cycle protein (CDC48)	At3g09840 or At5g03340 or At3g53230	96.47	5.09	89.33	5.13	6%
732[c]	Heat shock protein	At1g79930	101.44	5.04	91.56	5.10	4%
739[c]	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	31.04	5.81	31.75	6.49	47%
741[c]	Succinate-semialdehyde dehydrogenase (SSADH1)	At1g79440	59.99	5.66	56.52	6.10	8%
775[c]	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	At3g25530	31.94	5.63	30.69	5.88	23%
810[c]	ATP-dependent Clp protease ATP-binding subunit / ClpC	At5g50920	94.01	5.59	103.45	6.36	23%
1137[c]	TATA box-binding protein-interacting protein	At5g22330	59.96	5.71	50.29	5.67	17%
1138[c]	Expressed protein	At5g45690	28.06	5.80	28.76	5.92	16%
1151[c]	Glutathione S-transferase	At2g30870	25.32	5.60	24.23	5.49	18%
1153[c]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At4g28520	11.51	9.02	21.20	6.19	39%
1154[c]	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	11.78	9.05	31.75	6.49	5%
1155[c]	Alpha/beta-cruciferin 12S (Seed storage protein fragment)	At5g44120	10.43	9.02	31.64	9.80	17%
1156[c]	Beta-cruciferin 12S (seed storage protein precursor fragment)	At5g44120	10.68	9.05	20.84	9.06	41%

[a] Protein numbering following Arabidopsis seed protein reference maps available on this web site: http://www.seed-proteome.com ; [b] Listed proteins correspond to previously identified proteins (Gallardo et al., 2001, 2002a; Rajjou et al., 2004, 2006a; Job et al., 2005); [c] Listed proteins correspond to proteins identified during this work; the peptide sequences determined are available in Supplemental Table S2.

Supplemental Table S2

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
212	Actin 2	At3g18780	33%	R.AVFPSVVGRPR.H K.IWHHTFYNELR.I R.IAPEEHPVLLTEAPLNPK.A R.TTGIVLDSGDGVSHTVPIYEGFSLPHAILR.L K.TSSSIEKNYELPDGQVITIGAER.F K.NYELPDGQVITIGAER.F K.DLYGNIVLSGGTTMFSGIADR.M Oxidation (M) K.AEYDEAGPGIVHR.K
215	RuBisCO subunit binding-protein alpha subunit. chloroplast [Precursor]	At2g28000	19%	K.LADCVGLTLGPR.G R.NVVLDEFGSPK.V R.AIELPNAMENAGAALIR.E K.HGLLSVTSGANPVSLKR.G R.GYISPQFVTNPEK.L K.LLAEFENAR.V K.DSTTLIADAASKDELQAR.I K.ELFETDSVYDSEK.L K.ELFETDSVYDSEKLAER.I
242	Dormancy related protein	At1g54870	43%	K.QHAQPGKEHVMESSPQFSSSDYQPSNK.L Oxidation (M) R.GKVALITGGDSGIGR.A K.VALITGGDSGIGR.A K.TSDSKEPIAIPTDLGFDENCKR.V Carbamidomethyl (C) R.VVDEVVNAFGR.I R.IDVLINNAAEQYESSTIEEIDEPR.L R.IDVLINNAAEQYESSTIEEIDEPRLER.V R.TNIFSYFFLTR.H K.IKNFGSEVPMKR.A Oxidation (M)
253	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At3g04120	18%	K.YDSVHGQWK.H K.TLLFGEKPVTVFGIR.N K.KVVISAPSK.D R.AASFNIIPSSTGAAK.A K.VLPALNGK.L K.AGIALSDK.F
260	1-Cys peroxiredoxin	At1g48130	39%	K.LLGLSCDDVQSHKDWIK.D K.VNYPIIADPNKEIIPQLNMIDPIENGPSR.A K.EIIPQLNMIDPIENGPSR.A K.IKLSFLYPSTTGR.N K.LSFLYPSTTGR.N K.IATPVNWKPDQPVVISPAVSDEEAK.K K.IATPVNWKPDQPVVISPAVSDEEAKK.M
269	40S ribosomal protein SA (RPSaA)	At1g72370	25%	R.NDGIYIFNLGK.T K.FAQYTGANAIAGR.H R.LLILTDPR.T K.EGALGNIPIIAFCDTDSPMR.F R.FVDIGIPANNK.G R.FVDIGIPANNKGK.H
271	12S seed storage protein [Precursor]	At4g28520	9%	K.ISYVVQGTGISGR.V R.VKGPFQVVRPPLR.Q K.GPFQVVRPPLR.Q R.QPYESEEWRHPR.S K.IKFNTLETTLTR.A

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
281	Ferritin 3. chloroplast [Precursor]	At3g11050	15%	K.FFNDSSLEER.G R.GHAEMFMEYQNKR.G R.GHAEMFMEYQNKR.G Oxidation (M) K.ISEYVAQLR.R K.ISEYVAQLRR.I
284	GSH-dependent DEHYDROASCORBATE reductase	At1g19570	57%	K.AAVGAPDHLGDCPFSQR.A K.AAVGAPDHLGDCPFSQR.A Carbamidomethyl (C) K.IDDKWVTDSDVIVGILEEK.Y K.DSNDGSEHALLVELEALENHLK.S K.SHDGPFIAGER.V K.LYHLQVALGHFK.S K.SWSVPESFPHVHNYMK.T Oxidation (M) K.TLFSLDSFEK.T K.TLFSLDSFEKTKTEEK.Y K.TEEKYVISGWAPK.V K.YVISGWAPK.V
285	Glutathione S-transferase	At1g78370	24%	K.DFIEILK.T R.FWADFIDK.K R.FWADFIDKK.L K.NPILPSDPYLR.A K.FANFSIESEVPK.L K.SPLLLQMNPIHK.K K.SPLLLQMNPIHK.K K.SPLLLQMNPIHK.K + Oxidation (M) K.SPLLLQMNPIHK.K + Oxidation (M) K.SPLLLQMNPIHKK.I + Oxidation (M) R.NKSPLLLQMNPIHK.K + Oxidation (M)
287	Beta-cruciferin 12S (seed storage protein precursor fragment)	At5g44120	22%	K.VIPGCAETFQDSSEFQPR.F Carbamidomethyl (C) R.FEGQGQSQR.F R.FRDMHQK.V Oxidation (M) K.NIFNGFGPEVIAQALK.I K.IDLQTAQQLQNQDDNR.G R.VQGPFGVIRPPLR.G R.GQRPQEEEEEEGR.H R.ADVYKPQLGYISTLNSYDLPILR.F
291	Subtilase family protein	At4g20850	9%	YGTLTVLR SSVLMPGVK + Oxidation (M) LVPIAVLNK SVDVDELAR FVDLVTEAVNK LGSMETGTGLTR + Oxidation (M) SVSERLEQEVR FVDLVTEAVNKR QSTEWTIQVDPK IRVPYQPIDAQLK LVYQLFTDDLTSR VYAMGDVYPESSKLPK + Oxidation (M)
293	Peptidase M1 family protein.	At1g63770	4%	K.VYSLIGGFCGSPVNFHAK.D + Carbamidomethyl (C) K.AITLPGEGEIMDMMAVADPDAVHAVR.K + 3 Oxidation (M)
294	Peptidase M1 family protein.	At1g63770	9%	K.SLNIFNSK.L K.TLLGTQGFR.K K.GIDLYFER.H K.VVSSYNADAR.T R.KGIDLYFER.H K.IWTPAEDLPK.T K.KLLDHPAFDLR.N K.GSSAALVLDGHDLK.L K.LLKEGDYQLDSR.H

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
298	Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	18%	K.SLSHAGETNVPASEEIVPPGTK.V R.EAPTHYPLGVSEFSDR.G R.EAPTHYPLGVSEFSDRGESR.E R.EAHQEPLNTPVSLLSATEDVTR.T R.TFAPGGEDDYLGGQR.K K.GGEAGVPEIAESLGR.M R.DLPTGTHDQFSPELSRPK.E
299	Low-temperature-induced 65 kDa protein or Desiccation-responsive protein 29B	At5g52300	16%	R.EAPTHYPLGVSEFSDR.G R.EAPTHYPLGVSEFSDRGESR.E R.EAHQEPLNTPVSLLSATEDVTR.T R.TFAPGGEDDYLGGQR.K R.TFAPGGEDDYLGGQRK.V K.RLEEDPAAPGGGSDYLSGVSNYQSK.V K.VTDPTHKGGEAGVPEIAESLGR.M K.GGEAGVPEIAESLGR.M
302	Glyceraldehyde-3-phosphate dehydrogenase. cytosolic	At1g13440	30%	K.VKDDKTLLFGEKPVTVFGIR.N K.TLLFGEKPVTVFGIR.N K.DAPMFVVGVNEHEYK.S Oxidation (M) R.FGIVEGLMTTVHSITATQK.T Oxidation (M) R.VPTVDVSVVDLTVR.L K.GILGYTEDDVVSTDFVGDNR.S K.LVSWYDNEWGYSSR.V
305	Phosphoglucomutase. cytoplasmic 2	At1g70730	34%	K.VSLVSTSPIDGQKPGTSGLR.K R.YYSEQAIQIIVK.M R.VWVGQNSLLSTPAVSAIIR.E R.VDISTIGITSFEGPEGK.F K.FDVEVFDSADDYVK.L K.FTFCYDALHGVAGAYAHR.I Carbamidomethyl (C) K.EDFGGGHPDPNLTYAK.E K.TDDAGGEPPEFGAAADGDADR.N K.FFEVPTGWK.F K.LVTVEDIVR.Q R.QHWATYGR.H R.HYYTR.Y R.YLFEDGSR.L R.LYIEQYEK.D R.DSQDALGPLVDVALK.L
314	60S acidic ribosomal protein P0-C	At3g11250	7%	~.MVKATKAEK.K K.ATKAEKK.I K.GTVEIITPVELIK.Q

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
323	protein disulfide isomerase	At1g77510	47%	IQGFPTLK FFESPATK GESVEGPAVR DFNGEALEK NVVAVGVFPK SVQDYNGPR SADSATEVVGEK KTEETAAKDEL EAEGIVTYLKK ADYDFAHTLDAK SQPIPAENNEPVK VVVAESLDDIVFK FLPRGESVEGPAVR LFKPFDELFVDSK LRADYDFAHTLDAK LSGDEFDSFMALAEK + Oxidation (M) LDATANDIPSDTFDVK IDASEEANKEFANEYK ESSIPLVTVFDSDPNNHPYVAK LFKPFDELFVDSKDFNGEALEK LFKPFDELFVDSKDFNGEALEK SASGNVVVYEGDRTKEDFINFVEK SQPIPAENNEPVKVVVAESLDDIVFK KSQPIPAENNEPVKVVVAESLDDIVFK
328	Hydroxymethyltransferase	At4g13930	19%	YSEGIPGNR LLICGGSAYPR LCDLCSITLNK DFEQIGEFLSR NAVFGDSSALAPGGVR ISATSIYFESLPYK GLVEKDFEQIGEFLSR VNFTTGYIDYDKLEEK YYGGNEFIDEIENLCR
335	Quinone oxidoreductase	At5g61510	16%	GMTAQFLLR VNHKYPLSR VADAHADLENR VYEHGGPEVLK AIGLNFIDVYFR GVNVVYDSVGKDTFK
336	Cinnamyl-alcohol dehydrogenase	At1g72680	26%	R.DPSGLLSPHTITR.R R.NQHGDSKYPLVPGHEIAGIVTK.V R.ECEYCNEGQEVNCAK.G K.GVFTFNGIDHDGSVTK.G K.GGYSSHIVVHER.Y K.IAGTYVLVGFPSEIK.I K.ISPANLNLGMR.M K.ISPANLNLGMR.M Oxidation (M) K.IYPNIEVIPIQK.I
358	Pyruvate decarboxylase	At5g54960	5%	VSAANSRPPNPQ AADAFVELADASGYGLAVMPSAK AADAFVELADASGYGLAVMPSAK + Oxidation (M)
359	S-adenosyl-L-homocysteine hydrolase	At4g13940	13%	R.TEFGPSQPFKGAR.I K.GETLQEYWWCTER.A Carbamidomethyl (C) K.SKFDNLYGCR.H Carbamidomethyl (C) R.ATDVMIAGKVAVICGYGDVGK.G K.AGIIVLAEGR.L

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
360	Glycosyl hydrolase family 3 protein	At5g64570	14%	R.WGRGQETPGEDPLLASK.Y K.HYTAYDVDNWKGVER.Y R.LGFFDGNPK.N R.LGFFDGNPKNQIYGGLGPTDVCTSANQELAADAAR.Q K.NQIYGGLGPTDVCTSANQELAADAAR.Q K.LAATADVSVLVIGADQSIEAESR.D R.DRVDLHLPGQQQELVIQVAK.A R.VDLHLPGQQQELVIQVAKAAK.G
364	T-complex protein 1. theta subunit (TCP-1-Theta)	At3g03960	2%	K.AQQEEIGDGANLTISFAGELLQNAEELIR.M K.AVEILEQLVETGSETMDVR.N Oxidation (M) K.NPTNFNVDNVR.V K.LLGGGLHNSCIVR.G Carbamidomethyl (C) K.VIVSGGSIGEMALHFCER.Y Carbamidomethyl (C); Oxidation (M) R.GSTDSILDDLERAVDDGVNTYK.A R.IVPGAAATEIELAQR.L
370	Glutamate dehydrogenase 1 or 3	At5g18170 ou At3g03910	13%	K.VECTIPKDDGTLASFVGFR.V Carbamidomethyl (C) K.GGIGCDPSKLSISELER.L Carbamidomethyl (C) K.FIIEAANHPTDPDADEILSK.K K.FIIEAANHPTDPDADEILSKK.G
371	Aspartate aminotransferase. chloroplast	At4g31990	34%	K.DKLKLGTSASNPFLK.A K.LNLGVGAYR.T R.TEELQPYVLNVVK.K K.EYLPIEGLAAFNK.A K.ATAELLFGAGHPVIK.E R.VATIQGLSGTGSLR.L K.VVISSPTWGNHK.N K.VPWSEYR.Y K.VPWSEYRYYDPK.T K.NHIPFFDVAYQGFASGSLDEDAASVR.L K.NLGLYAER.I R.IARPMYSNPPVHGAR.I Oxidation (M)
374	Glycyl-tRNA synthetase / glycine--tRNA ligase	At1g29880	19%	K.SSSVEAQGNAVR.A R.KAVVNTLER.R K.AVVNTLER.R R.LFYIPSFK.I K.SNVLSFWR.Q R.EYGITAPDTK.N K.LPFAAAQIGQAFR.N K.GTVNNETLGYFIGR.V K.LVITPVKK.E K.ELGLAFKGNQK.N R.VFTPSVIEPSFGIGR.I K.AGDEQLNLFR.F K.EAASVVSSVSEGK.M
376	Tubulin beta-8 chain	At5g23860	9%	K.LAVNLIPFPR.L K.EVDEQMINVQNK.N Oxidation (M) R.VSEQFTAMFR.R R.VSEQFTAMFR.R Oxidation (M)

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
378	Subtilisin-like serine proteinase. putative. 3' partial	At3g14067	19%	R.AFYRGYLTQR.N R.LCYPGKLNSSLVEGK.I Carbamidomethyl (C) K.AGDQIRDYIK.T K.AGDQIRDYIKTSDSPTAK.I R.KAHPDWSPAAIK.S K.AHPDWSPAAIK.S K.SALVTTAYDVENSGEPIEDLATGK.S K.NVGSNVDAVYEVGVK.S K.SVLEYEVTFK.S K.SVVLGGGVGSVPGHEFGSIEWTDGEHVVK.S
380	Nucleoside diphosphate kinase II. chloroplast	At5g63310	12%	TALAAFRPQFR.L K.EGELCKWDSALATWLRE.~
392	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	14%	R.IEVWDHHAPQLR.C R.CSGVSFAR.Y Carbamidomethyl (C) K.GLYLPSFFNTAK.L K.VIPGCAETFQDSSEFQPR.F Carbamidomethyl (C) R.FEGQGQSQR.F
393	Major latex protein	At1g14950	44%	K.SWNYTCDGK.Q Carbamidomethyl (C) K.MAVTFR.G R.GLDGHVMEQLK.V R.GLDGHVMEQLK.V Oxidation (M) K.VYDVIFQFVPK.S K.VTMFWEK.R K.RYEDSPEPIK.Y K.FVTSLAADMDDHILK.N K.FVTSLAADMDDHILK.N Oxidation (M)
421	Late embryogenesis abundant (LEA)	At3g17520	55%	IGLKHEDNIQPTHTTTTVQDDAWR HEDNIQPTHTTTTVQDDAWR KAEEAVGAAK AGSAYETAK DKASQSYDSAGQVKDDVSHK DKASQSYDSAGQVKDDVSHK ASQSYDSAGQVK QVKDSLSGDENDESWTGWAK IGIKNEDINSPNLGETVSEK NEDINSPNLGETVSEK EKLAETVETAKEK EKLAETVETAKEK LAETVETAK LAETVETAKEK ESYETAKSK SKADETLESAK SKADETLESAKDK SKADETLESAKDKASQSYDSAAR ADETLESAKDK ADETLESAKDKASQSYDSAAR ADETLESAKDKASQSYDSAAR ASQSYDSAAR VKESLTDDDAEL
422	Thioredoxin family protein	At3g16110	8%	LTESNTVR GFENLVFAR TVVAAFDNNLNSK YTSYDGPCQAEK + Carbamidomethyl (C)

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
425	Eukaryotic translation initiation factor 3	At5g25780 or At5g27640	6%	LVDFSPGEK IIAFAWEPK STYSGFELFR YLVTYHSQEPSNPR
426	NAD-dependent epimerase/dehydratase family protein	At5g28840	54%	LATEELCK + Carbamidomethyl (C) ITYFWIK EKAPAAFCR + Carbamidomethyl (C) GSDVSLYGSSK QLETTNVSLK NSDNNLIKEK EQYWPSENLK VVGTQAPVQLGSLR HYNKDFGIECR + Carbamidomethyl (C) FHNIYGPFGTWK KLPIHHIPGPEGVR ISITGAGGFIASHIAR FFYASSACIYPEFK + Carbamidomethyl (C) RFFYASSACIYPEFK + Carbamidomethyl (C) ESDAWPAEPQDAYGLEK KAQTSTDRFEMWGDGLQTR + Oxidation (M)
427	10-formyltetrahydrofolate synthetase	At1g50480	19%	VMDVNDR + Oxidation (M) ITIGQGPEEK GAVDLGIAVEK RSFSDIMFR IFHETSQSDK KITIGQGPEEK ACQNITQPLR + Carbamidomethyl (C) TQYSFSHDASK TSPEELTPEEIKK SYGASGVEYSDQAEK MHGGGPDVVAGRPLDR + Oxidation (M) IFHETSQSDKALFNR
458	Xylose isomerase	At5g57655	12%	FFEAAVAYK GTGGDPFGAATK NGGIAPGGFNFDAK EGYQTLLNTDMGR + Oxidation (M) GTLLIEPKPQEPTK
459	Strictosidine synthase-related	At3g57020	7%	R.DVFFVAVSGER.S K.VPGYPDNIR.L K.YVSEAYER.D
508	Elongation factor 1B alpha-subunit 2	At5g19510	29%	TYISGDQLSVDDVK VYAAVPVKPSDAFPNASK WYESVASQLAK GVEMPGLFWGASK Oxidation (M) GVEMPGLFWGASKLVPVGYGIK LVPVGYGIKK
525	Actin	At5g59370 or At5g09810 or At3g53750 or At3g46520	8%	AGFAGDDAPR GYSFTTTAER AVFPSIVGRPR

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
543	D-fructose-1.6-bisphosphate 1-phosphohydrolase	At1g43670	25%	R.FVLNEQSK.Y R.GDFTILLSHIVLGCK.F R.GDFTILLSHIVLGCK.F Carbamidomethyl (C) K.FVCSAVNK.A K.FVCSAVNK.A Carbamidomethyl (C) K.LIGLAGETNIQGEEQK.K K.LIGLAGETNIQGEEQK.K R.YVGSMVADVHR.T R.YVGSMVADVHR.T R.YVGSMVADVHR.T Oxidation (M) R.YVGSMVADVHR.T Oxidation (M) R.TLLYGGIFLYPADK.K R.SPIFLGSYDDVEEIK.A
544	Methyl-CpG-binding domain-containing protein	At1g15340	8%	EAQEVVTEADVEK SLEANQVQQQQGAAASVSC + Carbamidomethyl ©
546	stress-inducible protein	At1g62740 or At1g12270 or At4g12400	16%	LGAMPEGLKDAEK + Oxidation (M) DYEPVIQTYQK NPSNLNLYLQDQR QVLSDLQENPAAAQK VSKDYEPVIQTYQK ELEQQEYYDPNIGDEEREK DFETAIQHYSTAMEIDDEDISYITNR + Oxidation (M)
548	Phosphoglycerate kinase	At1g79550	64%	R.SVGTLKEADLK.G R.VDLNVPLDDNSNITDDTR.I R.AAVPTIK.Y R.VVLCSHLGRPK.G R.VVLCSHLGRPK.G Carbamidomethyl (C) K.YSLKPLVPR.L K.LVAGLPEGGVLLLENVR.F R.FYAEEEKNDPEFAK.K K.LAALADVYVNDAFGTAHR.A K.FLKPSVAGFLMQK.E K.FLKPSVAGFLMQK.E Oxidation (M) K.ELDYLVGAVANPK.K K.KPFAAIVGGSK.V K.GVSLLLPTDVVIADK.F K.GVSLLLPTDVVIADKFAPDANSK.I K.TFSEALDTTK.T
551	HSP 90	At2g04030	5%	LSSSPCVLVSGK + Carbamidomethyl (C) GVVDSDDLPLNVSR AQALGDTSSLEFMR + Oxidation (M)
552	Shepherd protein (SHD)	At4g24190	17%	SPFLER VLEINPR GNLASENVDDVK LADTPCVVVTSK + Carbamidomethyl (C) IMQSQTLSDANK + Oxidation (M) GLVDSDTLPLNVSR VFISDEFDELLPK RVFISDEFDELLPK FLALTDKDVLGEGDTAK EVTEEEYTKFYHSLSK LHLRDEAGEYLEESKLK LMDIIINSLYSNKDIFLR + Oxidation (M)

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
554	Heat shock protein 17.6A	At5g12030	22%	R.KFQLPDNADLEK.I R.KFQLPDNADLEKISAACNDGVLK.V R.KFQLPDNADLEKISAACNDGVLK.V Carbamidomethyl (C) K.FQLPDNADLEK.I K.ISAACNDGVLK.V K.ISAACNDGVLK.V Carbamidomethyl (C) K.VTIPKLPPPEPK.K
556	Acetyl-CoA C-acyltransferase	At2g33150	38%	DTYPDDLLAPVLR MAAFYAGFPETVAVR + Oxidation (M) FGVSRQEQDQAAVDSHR GNFKDTYPDDLLAPVLR FGVSRQEQDQAAVDSHRK FGVSRQEQDQAAVDSHRK RGNFKDTYPDDLLAPVLR DGTTTAGNSSQVSDGAGAVLLMKR + Oxidation (M) TFAAVGVDPAIMGIGPAVAIPAAVK + Oxidation (M) KFAQAQNCLLPMGVTSENVAQR + Carbamidomethyl (C); Oxidation (M) ALIEKTNLNPSEVGDIVVGTVLAPGSQR
557	26S proteasome regulatory subunit S5A (RPN10). identical to multiubiquitin chain binding protein (MBP1)	At4g38630	7%	TQSNPENTVGILTMAGK Oxidation (M) VLTTPTSDLGK
561	Succinyl-CoA ligase (GDP-forming) alpha-chain. mitochondrial	At5g08300	9%	K.KGGTEHLGLPVFNSVAEAK.A K.IGIMPGYIHKPGK.I K.IGIMPGYIHKPGK.I Oxidation (M)
562	Translation elongation factor EF-Tu precursor. mitochondrial	At4g02930	45%	K.TTLTAAITK.V K.AIAFDEIDKAPEEK.K K.AIAFDEIDKAPEEKK.R R.GITIATAHVEYETAK.R R.HYAHVDCPGHADYVK.N R.HYAHVDCPGHADYVK.N Carbamidomethyl (C) K.EHILLAR.Q R.GSALSALQGTNDEIGR.Q K.LMDAVDEYIPDPVR.V K.LMDAVDEYIPDPVR.V Oxidation (M) R.VLDKPFLMPIEDVFSIQGR.G R.VLDKPFLMPIEDVFSIQGR.G Oxidation (M) R.IEQGVIK.V R.EGGVPLKSTVTGVEMFK.K R.EGGVPLKSTVTGVEMFK.K Oxidation (M) K.STVTGVEMFK.K K.STVTGVEMFK.K Oxidation (M) K.STVTGVEMFKK.I K.STVTGVEMFKK.I Oxidation (M) K.ILDNGQAGDNVGLLLR.G R.GMVIAKPGSCK.T R.GMVIAKPGSCK.T Oxidation (M) R.GMVIAKPGSCK.T Carbamidomethyl (C) K.KFEAEIYVLTKDEGGR.H R.HTAFFSNYRPQFYLR.T R.TADITGKVELPENVK.M K.VELPENVK.M

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
564	Cucumisin-like serine protease (ARA12)	At5g67360	14%	TVTSVGGAGTYSVK VEFNIISGTSMSCPHVSGLAALLK + Carbamidomethyl (C); Oxidation (M) RVEFNIISGTSMSCPHVSGLAALLK + Carbamidomethyl (C); Oxidation (M) AAGGVGMILANTAANGEELVADAHLLPATTVGEK + Oxidation (M) HYVTTDPNPTASISILGTVVGVKPSPVVAAFSSR AAGGVGMILANTAANGEELVADAHLLPATTVGEKAGDIIR + Oxidation (M)
570	AMP-dependent synthetase or ligase family and GMP synthase	At3g48990 or At1g63660	17% or 6%	EGTTVTEEDIK SCSASLAPVILSR + Carbamidomethyl (C) GVPLTQLNLASSVK ATAAPLNAAYTAEEFEFYLSDSDSK ISPIEVDAVLLTHPDVSQGVAFGVPDEK or ILNVPVGFLK QVDEIFIQSIR SLNVFSLVISGTSSLK K.TVASDEHVICALSGGVDSTVAATLVHK.A + Carbamidomethyl (C)
571	Peroxiredoxin type 2	At1g65980	38%	FALLLDDLK VILFGVPGAFTPTCSMK + Carbamidomethyl (C); Oxidation (M) KVILFGVPGAFTPTCSMK + Carbamidomethyl (C); Oxidation (M) APIAVGDVVPDGTISFFDENDQLQTASVHSLAAGK
575	20 kDa chaperonin. chloroplast (CPN21)	At5g20720	41%	DGSNYIALR YTSIKPLGDR TAGGLLLTETTK YAGTEVEFNDVK ITPLPVSTGSTVLYSK EKPSIGTVIAVGPGSLDEEGK TLGGILLPSTAQSKPQGGEVVAVGEGR
576	Glutathione S-transferase (2.4-D-inducible)	At1g78370	16%	K.EFIEAVK.I K.FGNFSIESESPK.L K.SLPDSEKIVAYAAEYR.K K.IVAYAAEYR.K
579	glycine-rich protein similar to P23 co-chaperone.	At4g02450	24%	K.IFLTVVLADTK.D K.IFLTVVLADTKDTK.V K.VNLDPEGVFDFSAK.V K.VGPENHVYELK.L K.LELADKVNVEESK.I R.SIFCIIEK.A R.SIFCIIEK.A Carbamidomethyl
580	Elongation factor 1B alpha-subunit 2 (eEF1Balpha2)	At5g19510	31%	M.AVTFSDLHTEEGVK.S K.TYISGDQLSVDDVK.V K.VYAAVPVKPSDAFPNASK.W R.GVEMPGLFWGASK.L R.GVEMPGLFWGASK.L Oxidation (M) K.LVPVGYGIK.K
584	Nucleosome assembly protein (NAP) family protein	At1g74560 or At1g18800	11%	R.KPVYDK.R K.TFTFLEEGTTK.I K.ITATPIKWK.E

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
585	14-3-3 protein GF14 psi (GRF3) (RCI1)	At5g38480	23%	R.YLAEFK.A R.GKIESELSK.I K.TVDVEELSVEER.N K.SASDIATAELAPTHPIR.L K.SASDIATAELAPTHPIR.L K.LAEQAERYEEMVEFMEK.V + 2 Oxidation (M)
586	Elongation factor 1-alpha	At5g60390	23%	QTVAVGVIK LPLQDVYK IGGIGTVPVGR STTTGHLIYK EHALLAFTLGVK YYCTVIDAPGHR + Carbamidomethyl (C) MTPTKPMVVETFSEYPPLGR + Oxidation (M) MTPTKPMVVETFSEYPPLGR + 2 Oxidation (M) VETGMIKPGMVVTFAPTGLTTEVK + 2 Oxidation (M)
587	Expressed protein	At5g02240	31%	K.HIVVVGSMGGTNPDHPLNK.L K.HIVVVGSMGGTNPDHPLNK.L Oxidation (M) R.KAEQYLADSGTPYTIIR.A R.ELLVGKDDELLQTDTK.T K.AFDLGSKPEGTSTPTK.D K.AFDLGSKPEGTSTPTKDFK.A K.ALFSQVTSR.F
588	Glucose and ribitol dehydrogenases	At3g05260	62%	K.QETQPGIQHVMEPTPEFSSSNYKPSNK.L K.QETQPGIQHVMEPTPEFSSSNYKPSNK.L Oxidation (M) K.VALVTGGDSGIGK.A K.AVCHCYALEGASVAFTYVK.G K.AVCHCYALEGASVAFTYVK.G 2 Carbamidomethyl (C) K.GREDKDAEETLR.L R.EAKEPIMIATDLGFEENCK.R R.EAKEPIMIATDLGFEENCK.R Oxidation (M) R.EAKEPIMIATDLGFEENCK.R Carbamidomethyl (C) R.VVEEVVNSFGR.I R.IDVLVNCAAEQHEVSIEDIDEAR.L R.IDVLVNCAAEQHEVSIEDIDEAR.L Carbamidomethyl (C) R.IDVLVNCAAEQHEVSIEDIDEARLER.V R.IDVLVNCAAEQHEVSIEDIDEARLER.V Carbamidomethyl (C) R.TNIFSQFFLVK.Y K.EGSSIINTTSVVAYAGNSSLLEYTATK.G K.GAIVSFTR.G R.GLALQLAPK.G
590	Cinnamoyl-CoA reductase	At5g58490	30%	R.GYSVHATVK.N K.QLLDPAVK.G K.GTINVLTAAK.E K.AAWEFAEEK.G R.HLCVEAISHYGDFVAK.V R.HLCVEAISHYGDFVAK.V Carbamidomethyl (C) K.VAELYPNYNVPK.L K.VAELYPNYNVPKLPR.E R.ETQPGLLR.D K.LIDLGLK.F K.FISMEEIIKEGVESLK.S K.FISMEEIIKEGVESLK.S Oxidation (M)

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
592	Ketol-acid reductoisomerase. chloroplast precursor	At3g58610	13%	HLPDAFK NISVVAVCPK + Carbamidomethyl (C) NTVECITGTISR + Carbamidomethyl (C) GVSFMVDNCSTTAR + Carbamidomethyl (C) GVSFMVDNCSTTAR + Carbamidomethyl (C); Oxidation (M) EGLPAFPMGNIDQTR + Oxidation (M) QIGVIGWGSQGPAQAQNLR
593	T-complex protein 1. beta subunit (TCP-1-beta)	At5g20890	22%	SHAIEAFSR SLHIDNPAAK VDEIITCAPR + Carbamidomethyl (C) GSTNLEAIQIIK MASFVGAMAISDLVK + 2 Oxidation (M) SLHDALCVLSQTVNDTR + Carbamidomethyl (C) RIENANILVANTAMDTDKVK + Oxidation (M) ALVAIPTTIADNAGLDSAELVAQLR
614	Aspartyl-tRNA synthetase	At4g31180	26%	KVYCINK + Carbamidomethyl (C) AGECGIDVK + Carbamidomethyl (C) LPLSVEDAAR TISTYIDSFR VHIPEVLEQR LTFEEGVQMLK LTFEEGVQMLK + Oxidation (M) LMAGSSEGGSAVFR + Oxidation (M) VVMLFCALNNIR + Carbamidomethyl (C) VVMLFCALNNIR + Carbamidomethyl (C); Oxidation (M) SLAKLPLSVEDAAR ESFVDVIGVVTLPK ESGSTVQCVVSQSEK + Carbamidomethyl (C) EPLTGTTQQVEIQVR SEADIEASLQTPSPAAR ESGSTVQCVVSQSEKTK + Carbamidomethyl (C)
705	Beta-cruciferin 12S (seed storage protein precursor fragment)	At1g03880	44%	K.FEWISFK.T R.GVLQGNAMVLPK.Y + Oxidation (M) K.TNENAMISTLAGR.T K.IKFNTLETTLTR.A R.IQVVNDNGQNVLDQQVQK.G R.ALPLEVISNGFQISPEEAR.K K.GQLVVIPQGFAYVVQSHGNK.F
728	Phosphoenolpyruvate carboxykinase (ATP)	At4g37870	11%	R.IKLAYTR.K K.YAAMLAEK.M K.IIDAIHSGSLLK.A K.IIDAIHSGSLLK.A R.AAYPIEFIPNAK.I R.EKEPDIWNAIK.F R.KIIDAIHSGSLLK.A R.DATTEDELWWGK.G R.EVDYSDKSVTENTR.A

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
729	S-adenosyl-L-homocysteine hydrolase	At4g13940	18%	R.TEFGPSQPFK.G K.AEEIFEK.T R.LVGVSEETTTGVK.R R.LVGVSEETTTGVKR.L K.SKFDNLYGCR.H K.SKFDNLYGCR.H Carbamidomethyl (C) K.FDNLYGCR.H K.FDNLYGCR.H Carbamidomethyl (C) R.HSLPDGLMR.A R.ATDVMIAGK.V K.VAVICGYGDVGK.G K.VAVICGYGDVGK.G Carbamidomethyl (C) K.VAVICGYGDVGKGCAAAMK.T K.VAVICGYGDVGKGCAAAMK.T 2 Carbamidomethyl (C) K.AGIIVLAEGR.L
731	Cell division cycle protein (CDC48)	At3g09840 or At5g03340 or At3g53230	6%	K.DFSTAILERK.K R.VRLGDVISVHQCPDVK.Y Carbamidomethyl (C) R.LGDVISVHQCPDVK.Y Carbamidomethyl (C) K.GILLYGPPGSGK.T K.LAEDVDLER.I K.GVLFYGPPGCGK.T Carbamidomethyl (C)
732	Heat shock protein	At1g79930	4%	K.ILSHAFDR.S R.GCALQCAILSPTFK.V 2 Carbamidomethyl (C) K.NAVESYVYDMR.N Oxidation (M) K.VGDPVEVR.Y
739	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	47%	~.MGKVIPGCAETFQDSSEFQPR.F Oxidation (M) R.FRDMHQKVEHIR.S R.FRDMHQKVEHIR.S Oxidation (M) R.DMHQKVEHIR.S K.IDLQTAQQLQNQDDNR.G R.VQGPFGVIRPPLR.G
741	Succinate-semialdehyde dehydrogenase (SSADH1)	At1g79440	8%	K.ITFTGSTAVGKK.L R.HSLGMTFYEPTVIR.D Oxidation (M) K.EEIFGPVAPLIR.F R.FKTEEDAIR.I
775	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	At3g25530	23%	K.INEAITGK.G R.FVEGPVSGSK.K K.SSYPPAFPLK.H K.GGVLEQICEGK.G + Carbamidomethyl (C) R.SFYLGQVGNGAK.M K.KPAEDGQLIILAAGDK.A

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
810	ATP-dependent Clp protease ATP-binding subunit / ClpC	At5g50920	23%	K.EIADILLK.E R.ELEKELR.Q R.DREIELR.A R.IIGQDEAVK.A R.LDEMIVFR.Q K.TAIAEGLAQR.I R.LDEMIVFR.Q + Oxidation (M) R.LLEDSMAEK.M + Oxidation (M) K.YRGEFEER.L K.RIIGQDEAVK.A R.LDMSEFMER.H R.VLELSLEEAR.Q K.AIDLIDEAGSR.V K.VIMLAQEEAR.R R.LDMSEFMER.H + Oxidation (M) K.VIMLAQEEAR.R + Oxidation (M) K.HIEKDPALER.R R.LRHAQVPEEAR.E R.IASGDVPETIEGK.K K.NNPCLIGEPGVGK.T + Carbamidomethyl (C) K.HIEKDPALERR.F K.QYFRPEFLNR.L K.LAEEGKLDPVVGR.Q R.VLENLGADPSNIR.T K.MPTLEEYGTNLTK.L + Oxidation (M) R.HAQVPEEARELEK.E R.TKNNPCLIGEPGVGK.T + Carbamidomethyl (C) R.VVDEGYNPSYGARPLR.R
1137	TATA box-binding protein-interacting protein	At5g22330	17%	K.GLGLEPTGIPIK.L K.LAAGFVGQLEAR.E R.EAAGLVVDMIKQKK.M R.EAAGLVVDMIKQKK.M Oxidation (M) K.ALLLAGPPGTGKTALALGISQELGSKVPFCPMVGSEVYSSEVK.K
1138	Expressed protein	At5g45690	16%	K.GLAVDIIETEMQK.L + Oxidation (M) K.RDDEYGISTESLK.T K.KRDDEYGISTESLK.T R.VPELVAKTELENIAK.T
1151	Glutathione S-transferase	At2g30870	18%	R.SQGPDLLGK.T M.VLTIYAPLFASSK.R M.VLTIYAPLFASSKR.A K.GVSFETVNVDLMKGEQR.Q + Oxidation (M)
1153	Beta-cruciferin 12S (seed storage protein precursor fragment)	At4g28520	39%	K.AHIQMVNDNGER.V K.TNENAQVNTLAGR.T K.AHIQMVNDNGER.V + Oxidation (M) K.HAIGEQFEWIEFK.T R.GLPLEVITNGYQISPEEAK.R
1154	Alpha-cruciferin 12S (Seed storage protein fragment)	At5g44120	5%	K.NIFNGFGPEVIAQALK.I R.VQGPFGVIRPPLR.G R.LSALRGSIR.Q
1155	Alpha/beta-cruciferin 12S (Seed storage protein fragment) plus de Alpha	At5g44120	17%	K.IDLQTAQQLQNQDDNR.G R.VQGPFGVIRPPLR.G R.CTDNLDDPSR.A

Supplemental Table S2 (continued)

Peptide sequences identified by MS-MS sequencing and corresponding to novel proteins in Arabidopsis seeds identified in this work. % Cov, coverage; AGI, Arabidopsis Genome Initiative.

No.[a]	Arabidopsis Protein Name.	AGI No.	% Cov.	Identified peptides by mass spectrometry
1156	Beta-cruciferin 12S (seed storage protein precursor fragment)	At5g44120	41%	R.VFDGQVSQGQLIAVPQGFSVVKR.A R.ATSNRFQWVEFK.T R.FQWVEFK.T K.TNANAQINTLAGR.T R.GLPLEVITNGFQISPEEAR.R K.FNTLETTLTHSSGPASYGRPR.V

[a] Protein numbering following Arabidopsis seed protein reference maps available on this web site: http://www.seed-proteome.com