

**Supplemental Table 1.** Proteins identified from 2-dimensional CN-PAGE+SDS-PAGE gel with purified stroma from wt and *clpr2-1*. Proteins were identified by nanoLC-ESI-MS/MS

gel spot #	native mass in kDa <sup>(a)</sup>	Accession number <sup>(b)</sup>	ambiguity <sup>(c)</sup>	Mowse Score <sup>(d)</sup>	# matching peptides <sup>(e)</sup>	highest peptide score <sup>(f)</sup>	lab annotation <sup>(g)</sup>	comment on ambiguity
1	325	At1g09130		367	10 (1)	80	ClpR3	
		At1g49970		140	3	65	ClpR1	
		At1g66670		58	1	58	ClpP3	
2	325	At1g09130		426	9	77	ClpR3	
		At1g49970		361	7 (1)	97	ClpR1	
		At1g66670		124	2	70	ClpP3	
3	325	At5g45390		565	10 (2)	118	ClpP4	
		At3g01500		307	6 (1)	84	carbonic anhydrase-1 (CA1)	
4	325	At3g01500		762	18 (5)	81	carbonic anhydrase-1 (CA1)	
		At1g12410		198	4 (1)	83	ClpR2	
		At4g17040		195	4	58	ClpR4	
		At1g09130		49	2	34	ClpR3	
		At5g45390		40	1	40	ClpP4	
5	325	At1g12410		448	8 (1)	101	ClpR2	
		At3g01500		340	10 (2)	74	carbonic anhydrase-1 (CA1)	
		At4g17040		222	5	79	ClpR4	
6	325	At1g06680		349	7	65	psbP OEC23	
		At1g02560		184	5 (1)	68	ClpP5	
		At4g25370		116	2	71	ClpS1	
7	325	At4g25370		382	8 (2)	78	ClpS1	
		At4g12060		368	9 (2)	83	ClpS2	
		At3g11630		340	9 (1)	67	2-Cys Peroxiredoxin A	
		At5g06290	At3g11630	231	5 (1)	61	2-Cys Peroxiredoxin B	no unique peptides
		At1g02560		218	6 (2)	72	ClpP5	
8	325	At1g11750		88	1	88	ClpP6	
		At4g12060		295	9 (3)	70	ClpS2	
		At1g02560		231	6 (2)	62	ClpP5	
		At4g25370		196	5 (1)	68	ClpS1	
		At1g11750		135	2	70	ClpP6	
		At3g11630	At5g06290	115	2	60	2-Cys Peroxiredoxin A	
9	325	At5g06290	At3g11630	94	1	55	2-Cys Peroxiredoxin B	no unique peptides
		At1g11750		220	4	82	ClpP6	
		At4g12060		139	3	58	ClpS2	
10	720	At1g02560		123	4 (1)	57	ClpP5	
		At4g25370		111	2	56	ClpS1	
		AtCg00670		35	1	35	ClpP1	
		At1g16880		94	3	42	uridylyltransferase-related	
11	750	At1g12900	At3g26650	311	7 (1)	62	glyceraldehyde-3-phosphate dehydrogenase A-1 (GAPA-1)	
		At3g26650	At1g12900	291	6 (1)	62	glyceraldehyde 3-phosphate dehydrogenase A-2 (GAPA-2)	no unique peptides
12	800	At3g13470		1145	24 (5)	107	Cpn60-beta-1	
		At1g55490		1088	21 (4)	107	Cpn60-beta-2	2 unique peptides
		At2g28000		886	14 (1)	110	Cpn60-alpha-1	
13	770	At5g04140		1016	22	ferredoxin-dependent glutamate synthase/glu1/Fd-GOGAT 1		
14r	200	At5g50920		1297	25 (3)	103	ClpC1	
		At3g48870	At5g50920	820	19 (4)	99	ClpC2	no unique peptides
		At5g51070		40	1	39	ClpD (Erd1)	
14w	200	At5g50920		1303	28 (3)	115	ClpC1	
		At3g48870	At5g50920	801	21 (3)	109	ClpC2	no unique peptides

15	120	At3g19170	1173	23 (1)	89	Zn-MP - Zn-metalloprotease (AtPreP1)	
		At1g49630	304	5	89	Metallo peptidase (M16) (AtPreP2)	unique peptide score 57
16	100	At3g45140	PPDB	PPDB	PPDB	lipoxygenase AtLOX2	
17	120	At2g04030	968	20 (1)	104	cpHsp90	
		At1g62750	874	18 (1)	90	elongation factor Tu-G (EF-G)	
		At5g03650	248	7	55	starch branching enzyme class II (SBEII)	
18	120	At5g49910	PPDB	PPDB	PPDB	cpHSP70-1 (DnaK homologue)	
		At4g24280	PPDB	PPDB	PPDB	cpHSP70-2 (DnaK homologue)	
19	150	At3g60750	PPDB	PPDB	PPDB	transketolase-1 (TKL-1)	
20	100	At5g51820	PPDB	PPDB	PPDB	plastid phosphoglucomutase (PGM1) (starch free mutant 1)	
21	180	At2g21330	PPDB	PPDB	PPDB	fructose-bisphosphate aldolase-1 (SFBA-1)	
		At4g38970	PPDB	PPDB	PPDB	fructose-bisphosphate aldolase-2 (SFBA-2)	
22	145	At3g54050	PPDB	PPDB	PPDB	fructose-bisphosphatase (FBPA)	
23	110	At1g63940	PPDB	PPDB	PPDB	monodehydroascorbate reductase (MDHAR)	
24	130	At1g56190	292	7	69	phosphoglycerate kinase-1 (PGK-2)	
25	60	At1g56190	PPDB	PPDB	PPDB	phosphoglycerate kinase-1 (PGK-2)	
		At3g12780	PPDB	PPDB	PPDB	phosphoglycerate kinase-1 (PGK-1)	
26	60	At1g35720	60	1	56	Annexin - AnnAt1	
27	100	At3g55800	PPDB	PPDB	PPDB	sedoheptulose-bisphosphatase (SBPase)	
28	155	At5g17710	121	2	68	GrpE-1	
29	200	At5g54770	830	11	122	THI1 -involved in thiamine synthesis (vitamine B) (ARA6)	
30	50	At2g37660	57	2	30	3-beta-hydroxy-delta5-steroid dehydrogenase	
31	105	At2g21170	PPDB	PPDB	PPDB	triosephosphate isomerase-1 (TPI-1)	
32	170	At5g20720	503	10 (1)	76	Cpn21 (also Cpn20)	
		At3g01500	314	4	91	carbonic anhydrase-1 (CA1)	
33	105	At3g62030	PPDB	PPDB	PPDB	peptidylprolyl isomerase ROC4	

- a Apparent molecular weight of protein complex (native mass) in kDa  
b Accession number from TAIR ([www.arabidopsis.org](http://www.arabidopsis.org))  
c Ambiguous identifications with the reported accession numbers  
d Mowse score of identification (from Mascot)  
e Number of relevant matching peptides (Number of peptides with different charge state or oxidated Methionine matching to the same sequence). Peptides have score  $\geq 20$  and rank 1.  
f Maximum recorded peptide score (from Mascot)  
g Annotation curated by the van Wijk laboratory, based on primary literature, TAIR, and functional domain predictors  
PPDB Protein identities projected based on identifications from <http://ppdb.tc.cornell.edu/list.aspx>