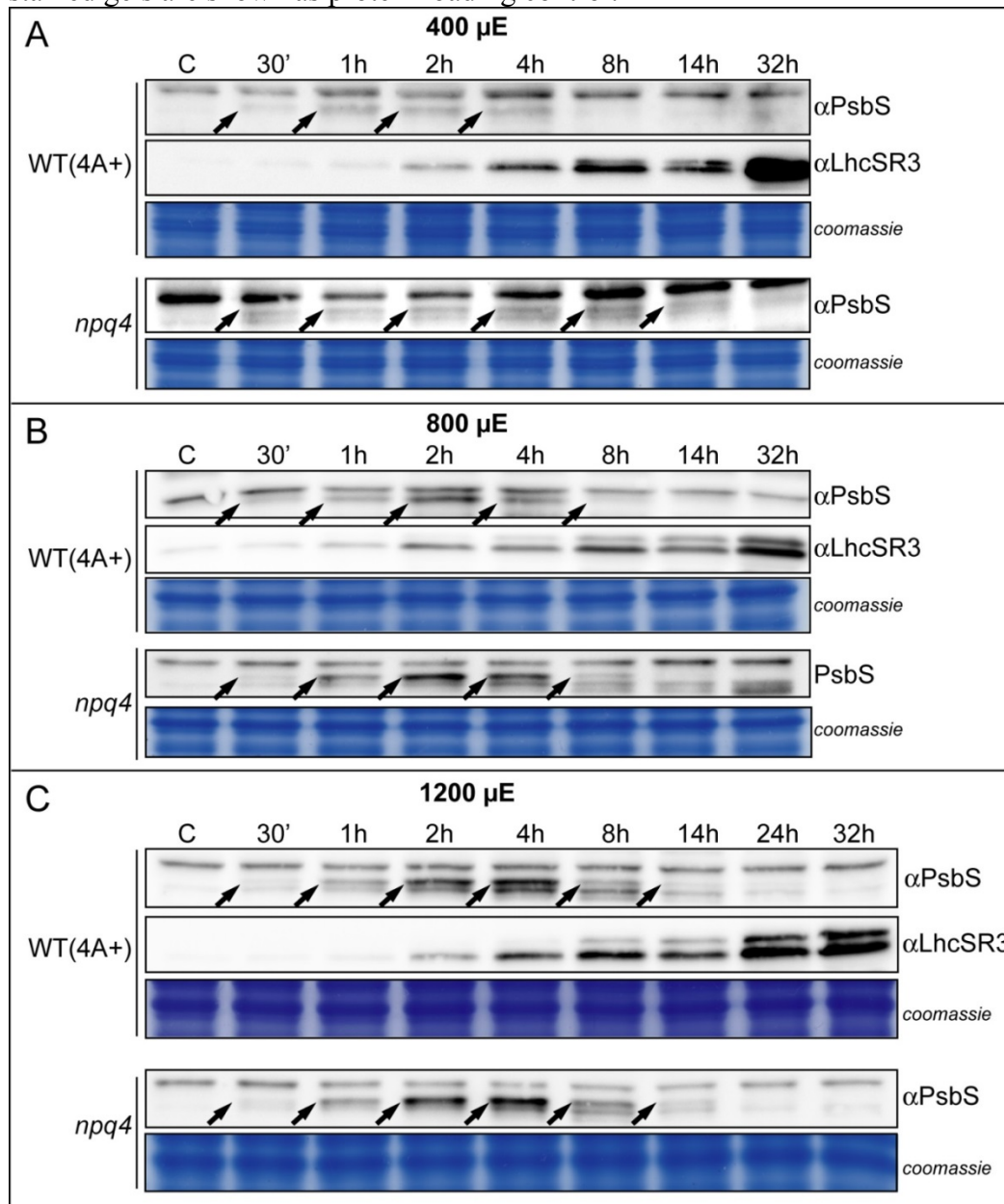


## SUPPLEMENTAL INFORMATION

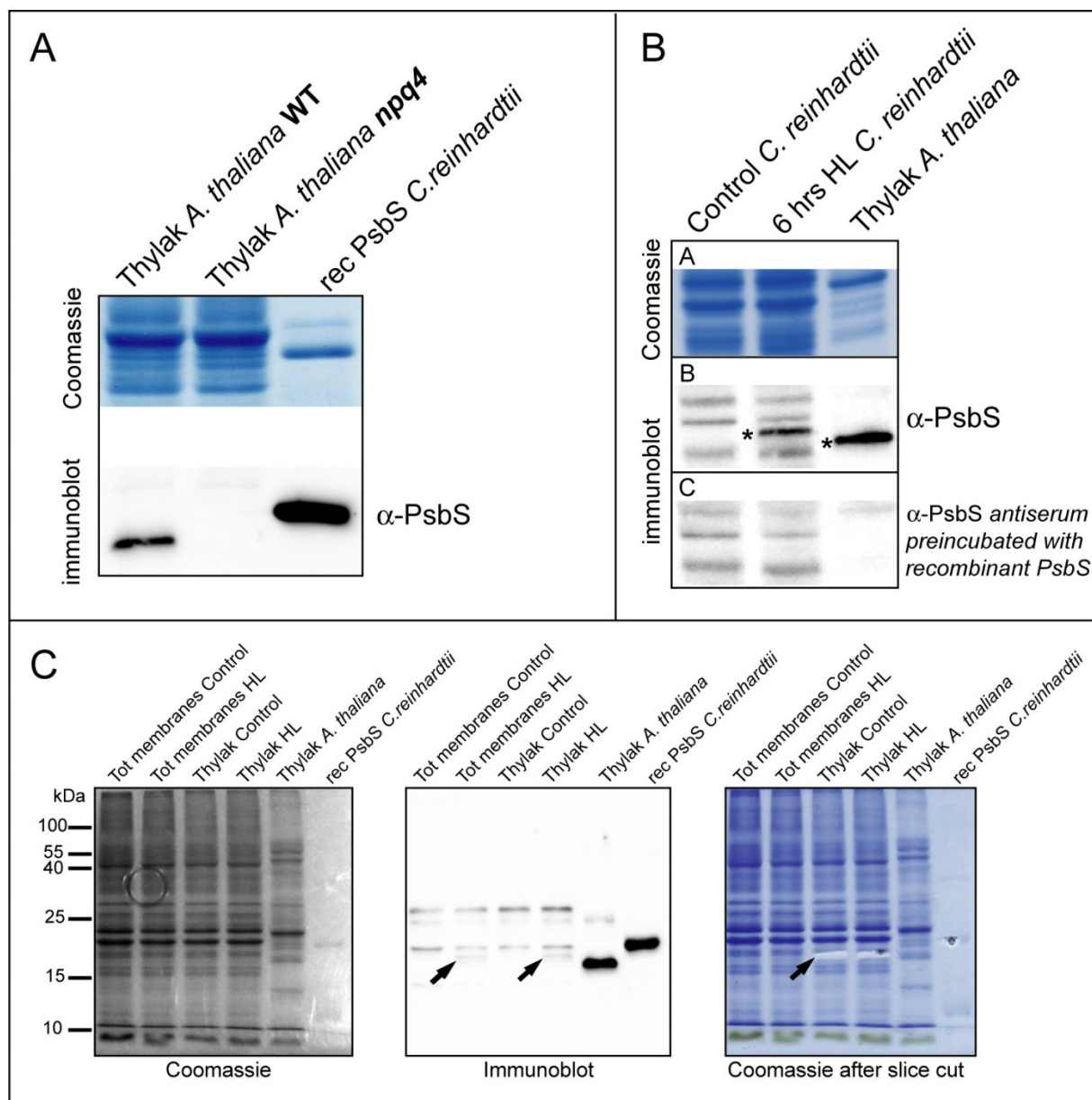
### *Chlamydomonas reinhardtii* PsbS is functional and accumulates rapidly and transiently under high light.

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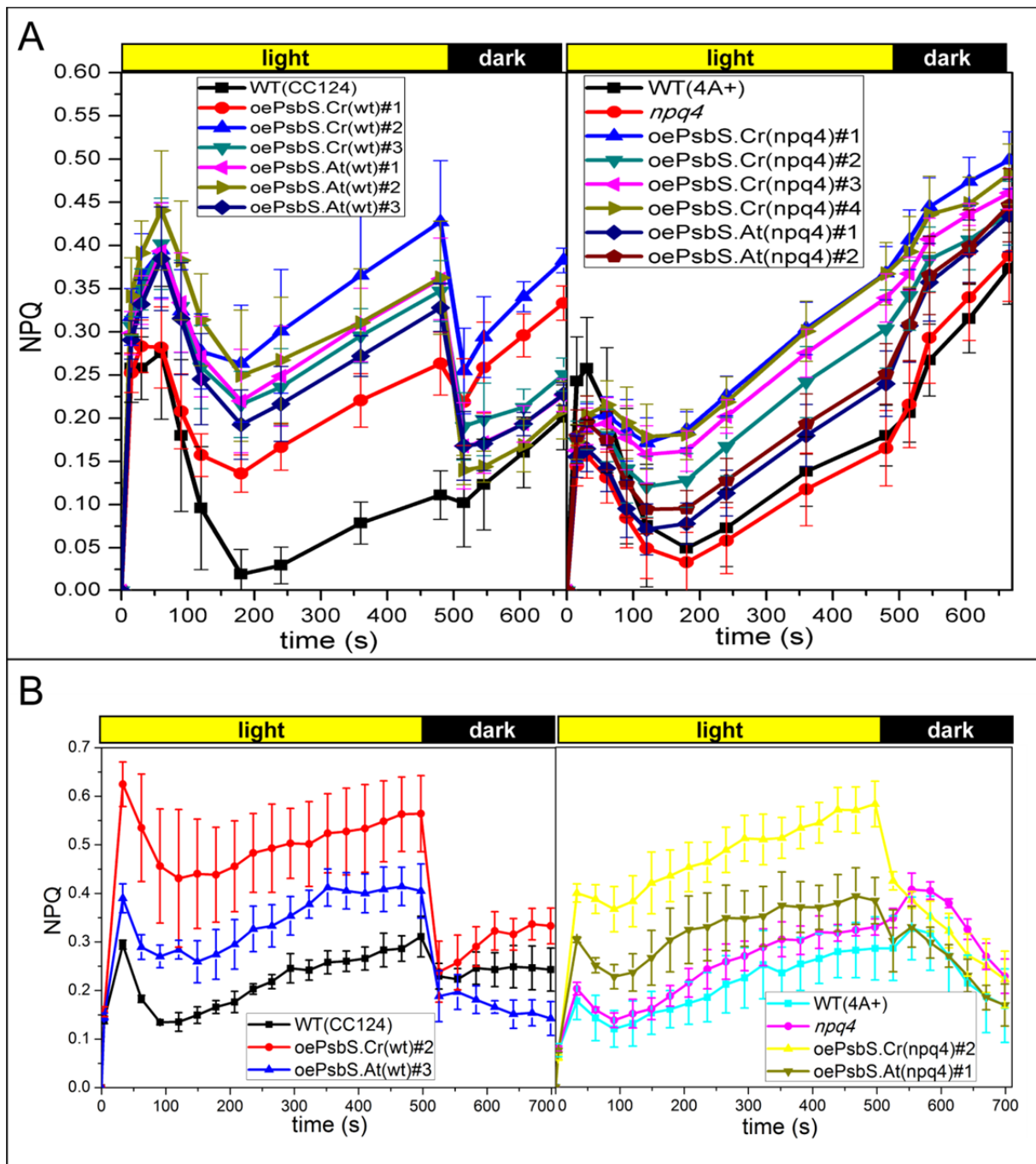
**Supplemental Figure S1. Kinetics of PsbS accumulation in *Chlamydomonas* WT(4A+) and *npq4* cells during a high light treatment at three different light intensities** Cells grown in minimal medium were exposed to 400 (A), 800 (B) and 1200 (C)  $\mu\text{mol photons m}^{-2} \text{s}^{-1}$  for 32 hr and aliquots were harvested at different times as indicated. 2  $\mu\text{g}$  (in Chls) of total membranes were analysed by SDS-PAGE and by immunoblot assays using antiPsbS and antiLhcSR3 antibodies. PsbS showed a transient accumulation at all light intensities, while LhcSR3 showed a slightly delayed induction and a strong accumulation till the end of the treatment. The PsbS amount seems somehow proportional to the light intensities (see the unspecific cross-reactions, which are rather constant in all our experiments). The Coomassie stained gels are shown as protein loading control.



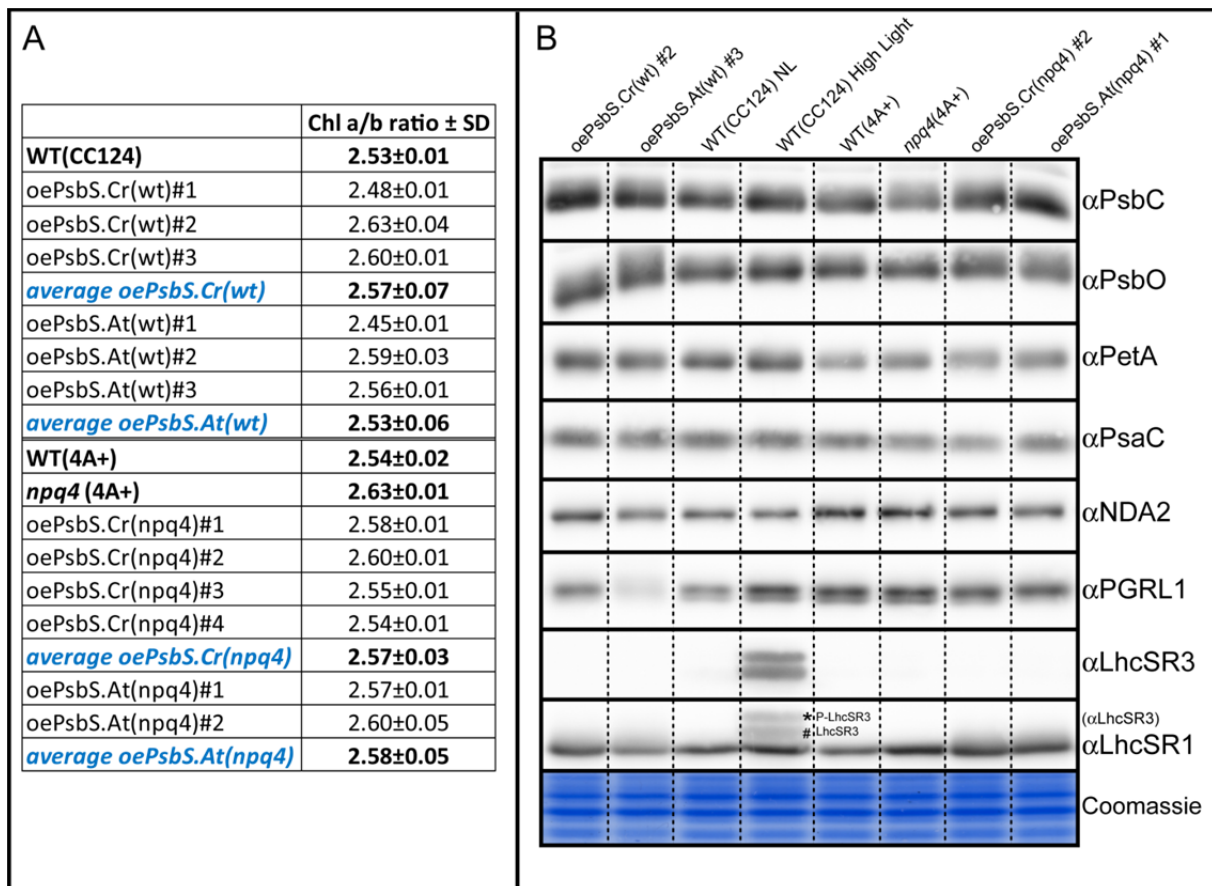
**Supplemental Figure S2. Test of the antibody against PsbS.** A) Thylakoids membranes from Arabidopsis WT and *npq4* mutant plants (lacking PsbS) were analysed by immunoblot analysis together with the recombinant *Chlamydomonas* PsbS protein. The *npq4* sample lacks a cross-reactive band, indicating that plant PsbS is correctly detected, as well the recombinant *Chlamydomonas* PsbS. B) The antibody against PsbS showed various cross-reactions on proteins extracted from *Chlamydomonas* cells, but one specific band appears in high light treated cell at the MW of PsbS (around 20-25 kDa). This high light-band, as well as the band specific to PsbS in Arabidopsis, disappeared (and it was the only one disappearing) when the PsbS antibody was preincubated with an excess of recombinant *Chlamydomonas* PsbS before decorating the membranes, indicating the correct recognition and assignment of the PsbS band. C) Slices of a SDS-PAGE at the PsbS position were cut and analysed by mass spectrometry (see [Supplemental Material MM1](#)). Seven specific PsbS peptides ([Supplemental Material MM1](#)) were detected only in the high light treated sample.



**Supplemental Figure S3. NPQ of individual oePsbS strains and on liquid cultures.** A) The NPQ kinetics of the single independent strains averaged in [Figure 4](#) (3 oePsbS.Cr(wt); 3 oePsbS.At(wt); 4 oePsbS.Cr(npq4); 2 oePsbS.At(npq4)) are shown. Data are the average $\pm$ SD of the averaged values of the 3 spots for each strain per 5 replicate plates. B) NPQ of oePsbS cells (one strain per construction/genotype) and control cells grown in liquid minimal medium and CO<sub>2</sub>-enriched environment have been measured with a PAM fluorimeter. Results were similar to those obtained on solid medium. Note the much important NPQ reversibility at the end of the light phase in oePsbS strains as compared to the controls, a mark for PsbS activation by the low luminal pH. Reversibility in WT(4A+) and *npq4*(4A+) cells is even absent, despite some accumulation of LhcSR1, which was similar in all strains ([Supplemental Figure S4](#)). Data are the average $\pm$ SD of 3 measurements.



**Supplemental Figure S4. Biochemical characterization of oePsbS and control strains.** A) Chls *a/b* ratio of cells grown on minimal medium was measured by fitting the absorption spectrum of the pigments extracted in acetone 80% (Croce et al., 2002). All strains showed a very similar Chl *a/b* ratio. Values are the average±SD of three measurements per strain. The average of the Chl *a/b* ratio of strains with the same construction is also shown in blue. B) Immunoblots against proteins representatives of different photosynthetic complexes (CP43 and PsbO for PSII, PetA for Cyt b6f and PsaC for PSI), for proteins involved in cyclic electron transport (PGRL1 and NDA2) and for LhcSR3 and LhcSR1. No significant differences were detected between oePsbS strains and their control, expect for a lower amount of PGRL1 in oePsbS.At(wt). Immunoblots were performed on thylakoids purified from cells used for PAM measurements shown in Supplemental Figure S3B. Results on thylakoids from WT(CC124) treated under high light are also shown. The Coomassie stained gel is an example of protein loading. Note that the immunoblot against LhcSR1 was previously decorated with αLhcSR3, showing that LhcSR1 migrates in a distinct and lower band with respect to LhcSR3 and phosphorylated LhcSR3 (P-LhcSR3).



**Reference:** Croce R, Canino g, Ros F, Bassi R (2002) Chromophore organization in the higher-plant photosystem II antenna protein CP26. *Biochemistry* 41: 7334-7343

## Supplemental Materials and Methods MM1.

### *Mass spectrometry analysis.*

Trypsin digestion of gel band containing proteins was manually performed as previously described (Abdelkafi et al., 2009). LC-MS/MS analyses were performed on an ESI-Q-Exactive plus mass spectrometer (ThermoFisher) coupled to a nano liquid chromatography (Ultimate 3000, Dionex). Peptides were loaded onto a nano trap (Acclaim PepMap100, 100µm x 2cm, 5µm, 100Å, Dionex) mounted in a 6-port valve before elution onto a C18 column (Acclaim PepMap RSLC, 75µm x 150 mm, 2µm, 100Å, Dionex). A linear gradient from 4% to 55% of mobile phase B (20% water, 80% acetonitrile/0.1% formic acid) in A (0.1% formic acid in water) for 30 min and then to 95% mobile phase B in 5 min. The peptides were detected into the mass spectrometer in a positive ion mode, alternating a scan event full MS in the Orbitrap analyzer at 70 000 resolution in a 350-1900 m/z range (Auto Gain Control set at  $3 \times 10^6$ ) and scan events of fragmentation of the 10 top ion parents, in the Higher Energy Collisional Dissociation cell (HCD). MS/MS fragments were analyzed in the Orbitrap at 17 500 resolution in a 200-2000 m/z range (Auto Gain Control set at  $1 \times 10^5$ ).

For protein identification, spectra were processed by the Proteome Discoverer software (ThermoFisherScientific, version: 1.4.0.288) using the pipeline tree (0) Spectrum Files, (1) Spectrum Selector, (2) Sequest HT algorithm and (3) Percolator. The following parameters were set at : *Chlamydomonas reinhardtii* extracted from nr NCBI; enzyme: Trypsin; dynamic modification: oxidation / +15.995 Da (Met), static modification: carbamidomethyl / +57.021 Da (Cys); mass values : monoisotopic; precursor mass tolerance:  $\pm 10$  ppm; fragment mass tolerance:  $\pm 0.02$  Da; missed cleavages : 2. Proteins were considered as identified by 2 unique “rank 1” peptides passing the high confidence filter, with validation on q-Value (Strict Target FDR : 0.01) and maximum Delta Cn: 0.05.

The mass spectrometry results are given in [Supplemental Table S2](#). For PsbS identification, the following peptides were detected:

GALAQFDIETGLSLR; FFGVQGFQFTK; TNELFVGR; ENELFVGR;  
QATGLPAPAIN GK; AAQLGFAFSLIGEAVTGK; ITLLEPK

**Reference:** S. Abdelkafi, H. Ogata, N. Barouh, B. Fouquet, R. Lebrun, M. Pina, F. Scherlinckx, P. Villeneuve et F. Carrière. Identification and biochemical characterization of a GDSL-motif carboxylester hydrolase from *Carica papaya* latex. *BBA: Molecular and Cell Biology of Lipids*, 2009;1791(11):1048-5.

**Supplemental Table S1. Primers used for the quantitative Real Time PCR experiments.**

<b>Target gene</b>	<b>Primer name</b>	<b>Sequence 5'-3'</b>
<i>CBLP</i>	Cblp fw	CTTCTCGCCCATGACCAC
<i>CBLP</i>	Cblp rev	CCCACCAGGTTGTTCTTCAG
<i>IDA5</i>	Ida5 fw	GCCAGGTCTCTGCTCTGGTG
<i>IDA5</i>	Ida5 rev	TACTCGGACTTGCGGATCCA
<i>LHCSR3.2</i>	LhcSR3.2 fw	TGTGAGGCACTCTGGTGAAG
<i>LHCSR3.2</i>	LhcSR3.2 rev	CGCCTGTTGTCACCATCTTA
<i>LHCSR3.1</i>	LhcSR3.1 fw	CACAACACCTTGATGCGAGATG
<i>LHCSR3.1</i>	LhcSR3.1 rev	CCGTGTCTTGTGTCAGTCCCTG
<i>LHCSR1</i>	LhcSR1 fw	GAGTCTGAGATCACCCACGG
<i>LHCSR1</i>	LhcSR1 rev	CCGATCTGCTGGAAGTGGTA
<i>PSBS2</i>	PsbS2 fw	GGTTACGCACGTTATCACTTGT
<i>PSBS2</i>	PsbS2 rev	CTCTCTGCACGCGTTGTACG
<i>PSBS1</i>	PsbS1 fw	TAAACCGTGTATTGGA ACTCCG
<i>PSBS1</i>	PsbS1 rev	CTCTGCACGCGGCGTGTT

**Supplemental Table S2. Full gene of proteins identified by mass spectrometry.** The full lists of proteins identified on SDS-PAGE slices shown in [Supplemental Figure S2](#) is given. A) List from control sample. B) List from high light sample. PsbS is highlighted in yellow. For PsbS, 7 different peptides have been detected (see [Supplemental Materials and Methods MM1](#)).

A)

Accession	Description	Score	Coverage	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
131389	RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; Flags: Precursor	203.75	60.82	15	15	78	245	25.9	9.11
158282427	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	139.33	69.55	10	10	34	243	25.9	9.00
158279717	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	97.16	47.15	10	10	28	246	26.9	8.65
158273869	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	74.71	73.93	11	11	19	257	27.8	8.97
2493039	RecName: Full=ATP-synthase delta chain, chloroplastic; AltName: Full=F-ATPase delta chain; Flags: Precursor	70.00	53.42	12	12	20	219	24.0	8.72
40714511	light-harvesting chlorophyll-a/b binding protein of photosystem I (Type II) [Chlamydomonas reinhardtii]	58.41	44.57	6	6	13	267	28.9	8.32
60391855	RecName: Full=Chlorophyll a-b binding protein CP29; AltName: Full=Lhcbm4	46.56	33.93	8	8	14	280	29.9	6.60
158272804	ser-type small GTPase [Chlamydomonas reinhardtii]	44.34	65.63	10	10	13	192	21.9	7.42
158275545	mitochondrial ATP synthase subunit 5, OSCP subunit [Chlamydomonas reinhardtii]	41.61	49.36	10	10	13	233	25.9	7.37
2500073	RecName: Full=GTP-binding protein YPTC1	37.87	52.71	9	9	12	203	22.6	6.21
158272172	ribosomal protein L9 [Chlamydomonas reinhardtii]	37.82	50.26	9	9	11	191	21.5	9.89
158276449	small rab-related GTPase [Chlamydomonas reinhardtii]	36.71	61.50	9	9	11	213	23.6	7.46
158280301	predicted protein [Chlamydomonas reinhardtii]	35.49	33.91	8	8	11	233	24.2	9.89
158275957	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii]	35.20	45.95	7	7	11	222	23.6	9.16
158272872	low molecular mass early light-induced protein [Chlamydomonas reinhardtii]	34.86	53.01	9	9	13	249	27.5	6.15
158269914	histone H4 [Chlamydomonas reinhardtii]	29.20	37.23	4	4	9	94	10.5	11.50
158271158	rhodase-like Ca-sensing receptor [Chlamydomonas reinhardtii]	27.19	25.13	6	6	7	378	38.9	9.19
284073116	40S ribosomal protein S9 [Chlamydomonas reinhardtii]	26.70	38.76	9	9	10	178	21.0	10.89
158280752	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	21.87	29.57	6	6	7	257	28.2	8.76
158281602	2-cys peroxiredoxin [Chlamydomonas reinhardtii]	21.22	44.44	7	7	8	198	21.6	5.66
158270548	light-harvesting complex II chlorophyll a-b binding protein M3 [Chlamydomonas reinhardtii]	21.12	40.08	3	5	5	257	27.4	5.96
158278261	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	21.00	37.09	4	4	5	213	22.8	9.00
117814	RecName: Full=Cytochrome b6	20.38	25.12	4	4	7	215	24.1	8.60
158276041	predicted protein [Chlamydomonas reinhardtii]	20.03	38.40	7	7	7	237	25.3	9.89
266851	RecName: Full=Photosystem I iron-sulfur center; AltName: Full=PSI-C; AltName: Full=PSI-C	19.57	74.07	5	5	7	81	8.9	5.95
158272508	predicted protein [Chlamydomonas reinhardtii]	18.26	30.04	5	5	5	273	29.2	7.11
1717956	RecName: Full=Cytochrome b6-f complex iron-sulfur subunit, chloroplastic; AltName: Full=Plastohydroquinone-plastoquinone	18.20	32.52	5	5	6	206	21.5	8.57
158282386	peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	17.91	29.49	6	6	6	234	24.9	9.10
18201978	RecName: Full=30S ribosomal protein S9, chloroplastic	17.76	61.26	6	6	6	191	21.0	9.74
158282956	NADH:ubiquinone oxidoreductase 18 kDa subunit [Chlamydomonas reinhardtii]	17.63	31.52	4	4	5	165	17.9	5.29
158277154	light-harvesting protein of photosystem II [Chlamydomonas reinhardtii]	17.46	35.34	3	4	4	249	26.6	5.62
158275836	chlorophyll a-b binding protein of LHCII Type I, chloroplast precursor [Chlamydomonas reinhardtii]	17.05	33.20	2	4	4	253	26.9	6.35
135394	RecName: Full=Tubulin alpha-1 chain	15.75	7.76	3	3	5	451	49.6	5.14
158276249	flagellar associated protein [Chlamydomonas reinhardtii]	15.71	31.63	4	4	5	196	21.7	9.55
158282291	flagellar flavodoxin [Chlamydomonas reinhardtii]	15.66	33.33	5	5	5	201	21.4	7.06
1323549	carbonic anhydrase precursor [Chlamydomonas reinhardtii]	15.60	25.47	5	5	5	267	27.6	8.62
27542569	light-harvesting complex I protein [Chlamydomonas reinhardtii]	13.85	19.92	3	3	3	241	26.2	8.10
158282259	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	13.68	19.85	3	3	4	262	28.4	8.94
2499965	RecName: Full=Photosystem I reaction center subunit II, chloroplastic; AltName: Full=Photosystem I 20 kDa subunit; S	13.28	13.78	3	3	4	196	21.3	10.30
158271939	predicted protein [Chlamydomonas reinhardtii]	13.24	13.79	3	3	4	232	24.2	9.45
158277493	eukaryotic initiation factor [Chlamydomonas reinhardtii]	13.14	25.74	4	4	4	202	23.1	5.35
158282209	predicted protein [Chlamydomonas reinhardtii]	12.33	15.12	3	3	4	258	28.3	9.58
18125	light harvesting complex protein I-20 [Chlamydomonas reinhardtii]	12.09	27.23	3	3	4	224	23.5	8.38
158283136	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii]	12.02	19.64	4	4	5	280	29.1	9.79
158282957	ribosomal protein L17 [Chlamydomonas reinhardtii]	11.46	18.82	3	3	4	186	21.1	10.33
158269830	histone H2B [Chlamydomonas reinhardtii]	11.35	45.21	3	3	4	73	8.2	9.70
125987860	RecName: Full=50S ribosomal protein L5, chloroplastic	10.96	29.61	5	5	5	179	20.2	9.73
1245907	Rieske protein (cytochrome b6 f complex) [Chlamydomonas reinhardtii, Peptide Partial, 27 aa, segment 1 of 2]	10.55	48.15	2	2	3	27	2.8	6.37

1703151	RecName: Full=Actin	10.38	9.55	3	3	4	377	41.8	5.48
27542565	light-harvesting complex II protein [Chlamydomonas reinhardtii]	9.63	23.05	3	3	3	256	27.5	6.35
158278368	cytochrome c oxidase subunit III [Chlamydomonas reinhardtii]	9.34	12.30	3	3	4	382	41.4	8.53
158274577	membrane AAA-metalloprotease [Chlamydomonas reinhardtii]	9.32	8.13	2	3	3	689	74.3	6.62
158275877	predicted protein [Chlamydomonas reinhardtii]	8.90	14.46	4	4	4	242	25.6	9.94
158274405	chlorophyll a-b binding protein of LHCl1 [Chlamydomonas reinhardtii]	8.68	15.30	1	2	2	268	28.7	8.07
158270530	plastidic ADP/ATP translocase [Chlamydomonas reinhardtii]	8.32	4.85	2	2	3	577	62.3	9.35
158279924	ribosomal protein S13 [Chlamydomonas reinhardtii]	8.32	29.14	3	3	3	151	17.1	10.51
158283731	ribosomal protein L18a [Chlamydomonas reinhardtii]	7.97	23.63	4	4	4	182	21.4	10.40
1311183	RecName: Full=Photosystem I reaction center subunit III, chloroplastic; AltName: Full=Light-harvesting complex I 17 k	7.83	13.66	3	3	3	227	24.0	9.48
1311382	RecName: Full=Oxygen-evolving enhancer protein 1, chloroplastic; Short=OEE1; Flags: Precursor	7.81	16.15	3	3	3	291	30.5	8.16
158279720	OEE2-like protein of thylakoid lumen [Chlamydomonas reinhardtii]	7.41	13.76	2	2	2	218	23.6	9.41
158270952	predicted protein [Chlamydomonas reinhardtii]	6.83	12.88	3	3	3	233	25.2	9.31
158271809	heat shock protein 70A [Chlamydomonas reinhardtii]	6.45	5.53	3	3	3	651	71.2	5.38
158283480	F1F0 ATP synthase subunit 6 [Chlamydomonas reinhardtii]	6.29	7.94	2	2	2	340	35.5	9.58
15011441	LC15 [Chlamydomonas reinhardtii]	6.17	19.00	2	2	3	321	32.7	12.13
158277341	plastid ribosomal protein L9 [Chlamydomonas reinhardtii]	5.94	11.27	2	2	2	204	22.5	9.80
135478	RecName: Full=Tubulin beta-1/beta-2 chain; AltName: Full=Beta-tubulin	5.92	8.13	3	3	3	443	49.6	4.92
158275614	predicted protein [Chlamydomonas reinhardtii]	5.65	14.35	2	2	2	223	24.8	9.99
158279575	membrane AAA-metalloprotease [Chlamydomonas reinhardtii]	5.48	3.99	1	2	2	727	77.5	5.90
17432909	RecName: Full=ATP synthase subunit a, chloroplastic; AltName: Full=ATP synthase FO sector subunit a; AltName: Full=	5.24	11.76	2	2	3	238	26.2	4.70
158278438	ARF-like GTPase [Chlamydomonas reinhardtii]	5.21	16.22	2	2	2	185	20.6	5.72
1702984	RecName: Full=14-3-3-like protein	5.17	6.95	2	2	2	259	29.5	5.00
158283935	hypothetical protein CHL1REDRAFT_183568 [Chlamydomonas reinhardtii]	5.13	11.42	2	2	2	219	23.8	8.63
158279650	E3 ubiquitin ligase [Chlamydomonas reinhardtii]	5.11	21.66	3	3	3	157	17.9	4.70
158275273	luminal PspB-like protein [Chlamydomonas reinhardtii]	4.98	7.78	2	2	2	257	28.4	9.01
113465	RecName: Full=ADP-ATP carrier protein; AltName: Full=ADP/ATP translocase; AltName: Full=Adenine nucleotide transk	4.85	7.14	2	2	2	308	33.5	9.74
158281739	ribosomal protein S3 [Chlamydomonas reinhardtii]	4.73	8.70	2	2	2	230	25.8	9.64
158282786	plastid ribosomal protein L13 [Chlamydomonas reinhardtii]	4.60	10.22	2	2	2	225	24.5	10.20
158269913	histone H2A [Chlamydomonas reinhardtii]	4.49	13.33	2	2	2	120	12.7	10.04
75338601	RecName: Full=Dynein light chain 1, axonemal; AltName: Full=Flagellar outer arm dynein light chain 1	3.87	10.10	2	2	2	198	22.1	5.74
158272892	small arf-related GTPase ARFRP1 [Chlamydomonas reinhardtii]	3.72	11.94	2	2	2	201	22.7	9.17
158269042	histone H3 [Chlamydomonas reinhardtii]	3.72	27.38	3	3	3	84	9.6	11.74
158275158	plastid ribosomal protein L6 [Chlamydomonas reinhardtii]	2.37	7.73	2	2	2	207	22.2	10.35
224593221	translation elongation factor-like protein [Chlamydomonas reinhardtii]	2.27	5.00	2	2	2	320	35.3	7.87
125090	Keratin, type I microfibrillar 48 kDa, component 8C-1 OS=Ovis aries PE=1 SV=2	919.47	78.64	11	40	386	412	46.6	4.81
125091	Keratin, type I microfibrillar, 47.6 kDa OS=Ovis aries PE=3 SV=2	675.43	69.55	6	36	304	404	46.0	4.93
125117	Keratin, type II microfibrillar, component 5 OS=Ovis aries PE=1 SV=1	653.65	79.88	24	56	258	502	55.2	6.46
125116	Keratin, type II microfibrillar, component 7C OS=Ovis aries PE=1 SV=1	638.98	75.15	21	49	286	491	53.6	5.57
48474780	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	474.21	50.69	2	36	208	507	55.8	6.55
311033435	Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 PE=1 SV=3	391.98	48.91	5	32	199	505	54.9	5.47
223590075	Keratin, type I cuticular Ha3-1 OS=Homo sapiens GN=KRT33A PE=2 SV=2	298.32	36.14	3	21	158	404	45.9	4.82
148887391	Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3	233.30	16.76	3	12	89	513	56.6	6.74
6486299	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT33B PE=2 SV=3	226.84	32.43	3	15	138	404	46.2	4.84
125115	Keratin, type II microfibrillar (Fragment) OS=Ovis aries PE=1 SV=1	221.00	95.41	11	17	73	109	12.7	4.59
296439499	Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=5	216.18	30.77	7	21	81	455	50.3	4.91
6485565	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1	144.08	25.27	4	13	80	467	52.2	4.94
311033432	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=3	114.13	17.63	2	11	69	448	50.3	4.84
249849769	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	68.60	45.03	16	18	23	584	58.8	5.21
238054406	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT11 PE=1 SV=6	52.34	32.45	14	16	18	644	66.0	8.12
136429	Trypsin OS=Sus scrofa PE=1 SV=1	45.55	25.11	4	4	17	231	24.4	7.18
239938886	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	29.05	21.67	8	9	10	623	62.0	5.24
239938850	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	25.03	20.19	9	11	11	639	65.4	8.00
547810	Keratin-associated protein 6-1 OS=Ovis aries GN=KRTAP6-1 PE=1 SV=2	16.60	56.63	3	3	6	83	8.4	8.22
125644	Keratin, high-sulfur matrix protein, IIIA3 OS=Ovis aries PE=1 SV=1	16.33	24.43	1	2	5	131	14.2	8.12
125633	Keratin, high-sulfur matrix protein, IIIA3A OS=Ovis aries PE=1 SV=1	9.39	26.92	1	2	4	130	13.9	8.06



## B)

Accession	Description	Score	Coverage	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pl
131389	RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; Flags: Precursor	236.50	65.31	19	19	143	245	25.9	9.11
158282427	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	144.33	69.55	10	10	67	243	25.9	9.00
158273869	light-harvesting protein I [Chlamydomonas reinhardtii]	77.16	65.81	10	10	27	257	27.8	8.97
60391855	RecName: Full=Chlorophyll a-b binding protein CP29; AltName: Full=Lhcbm4	61.82	34.29	9	9	31	280	29.9	6.60
1323549	carbonic anhydrase precursor [Chlamydomonas reinhardtii]	51.06	44.57	9	9	22	267	27.6	8.62
158272804	sar-type small GTPase [Chlamydomonas reinhardtii]	50.16	69.27	12	12	23	192	21.9	7.42
158275545	mitochondrial ATP synthase subunit 5, OSCP subunit [Chlamydomonas reinhardtii]	47.28	56.22	15	15	29	233	25.9	7.37
2493039	RecName: Full=ATP synthase delta chain, chloroplastic; AltName: Full=F-ATPase delta chain; Flags: Precursor	47.17	38.36	13	13	18	219	24.0	8.72
158279717	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	46.50	33.74	9	9	34	246	26.9	8.65
158271158	rhodanese-like Ca-sensing receptor [Chlamydomonas reinhardtii]	41.76	39.15	12	12	20	378	38.9	9.19
158272872	low molecular mass early light-induced protein [Chlamydomonas reinhardtii]	40.56	37.75	9	9	23	249	27.5	6.15
158280301	predicted protein [Chlamydomonas reinhardtii]	39.46	36.91	9	9	16	233	24.2	9.89
158275957	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii]	38.84	51.35	11	11	20	222	23.6	9.16
158277154	light-harvesting protein of photosystem II [Chlamydomonas reinhardtii]	34.92	39.36	3	6	13	249	26.6	5.62
2500073	RecName: Full=GTP-binding protein YPTC1	34.83	52.22	8	9	15	203	22.6	6.21
158281602	2-cys peroxiredoxin [Chlamydomonas reinhardtii]	34.10	60.61	9	9	17	198	21.6	5.66
158272172	ribosomal protein L9 [Chlamydomonas reinhardtii]	33.21	54.45	10	10	16	191	21.5	9.89
158270548	light-harvesting complex II chlorophyll a-b binding protein M3 [Chlamydomonas reinhardtii]	32.30	43.97	3	7	17	257	27.4	5.96
40714511	light-harvesting chlorophyll a/b protein of photosystem I (Type II) [Chlamydomonas reinhardtii]	31.87	35.58	5	5	14	267	28.9	8.32
158275836	chlorophyll a-b binding protein of LHClI type I, chloroplast precursor [Chlamydomonas reinhardtii]	31.29	41.50	3	7	14	253	26.9	6.35
158274405	chlorophyll a-b binding protein of LHClI [Chlamydomonas reinhardtii]	28.85	35.82	4	7	12	268	28.7	8.07
158270530	plastidic ADP/ATP translocase [Chlamydomonas reinhardtii]	27.54	19.41	9	9	13	577	62.3	9.35
158280752	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	27.06	45.53	9	9	16	257	28.2	8.76
284073116	40S ribosomal protein S9 [Chlamydomonas reinhardtii]	26.14	53.37	11	11	18	178	21.0	10.89
117814	RecName: Full=Cytochrome b6	24.41	28.84	5	5	11	215	24.1	8.60
158282956	NADH:ubiquinone oxidoreductase 18 kDa subunit [Chlamydomonas reinhardtii]	24.15	61.21	7	7	12	165	17.9	5.29
27542565	light-harvesting complex II protein [Chlamydomonas reinhardtii]	21.72	17.58	2	4	8	256	27.5	6.35
266851	RecName: Full=Photosystem I iron-sulfur center; AltName: Full=PSI-C; AltName: Full=	19.94	64.20	5	5	11	81	8.9	5.95
158280416	GR008 protein [Chlamydomonas reinhardtii]	19.82	35.00	10	10	11	300	32.8	7.12
2499965	RecName: Full=Photosystem I reaction center subunit II, chloroplastic; AltName: Full=Photosystem I 20 kDa subunit; Sh	19.26	33.67	9	9	12	196	21.3	10.30
27542569	light-harvesting complex I protein [Chlamydomonas reinhardtii]	18.66	39.83	7	7	12	241	26.2	8.10
158273974	CP1D51 protein required for cyt b6 assembly [Chlamydomonas reinhardtii]	16.59	27.14	7	7	11	269	29.6	9.06
158276449	small rab-related GTPase [Chlamydomonas reinhardtii]	16.23	57.28	11	11	14	213	23.6	7.46
131382	RecName: Full=Oxygen-evolving enhancer protein 1, chloroplastic; Short=OEE1; Flags: Precursor	15.48	45.36	10	10	10	291	30.5	8.16
158282291	flagellar flavodoxin [Chlamydomonas reinhardtii]	14.86	45.77	3	8	10	201	21.4	7.06
158274577	membrane AAA-metalloprotease [Chlamydomonas reinhardtii]	14.31	11.18	6	6	6	689	74.3	6.62
158276041	predicted protein [Chlamydomonas reinhardtii]	14.14	61.60	10	10	12	237	25.3	9.89
131183	RecName: Full=Photosystem I reaction center subunit III, chloroplastic; AltName: Full=Light-harvesting complex I 17 kD	13.86	30.84	6	6	7	227	24.0	9.48
<b>158283346</b>	<b>chloroplast photosystem II-associated 22 kDa protein [Chlamydomonas reinhardtii]</b>	<b>13.82</b>	<b>32.65</b>	<b>7</b>	<b>7</b>	<b>8</b>	<b>245</b>	<b>26.1</b>	<b>6.87</b>
158279720	OEE2-like protein of thylakoid lumen [Chlamydomonas reinhardtii]	13.15	43.12	7	7	8	218	23.6	9.41
158282386	peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	13.03	28.63	6	6	8	234	24.9	9.10
158273823	ribosomal protein L21 [Chlamydomonas reinhardtii]	12.64	38.65	7	7	9	163	18.3	10.78
158275309	stress-related chlorophyll a/b binding protein 3 [Chlamydomonas reinhardtii]	12.57	37.45	5	6	8	259	28.2	4.98
131290	RecName: Full=Photosystem II D2 protein; Short=PSII D2 protein; AltName: Full=Photosystem Q(A) protein	12.34	14.77	4	4	5	352	39.4	5.73
125987860	RecName: Full=50S ribosomal protein L5, chloroplastic	12.30	52.51	9	9	9	179	20.2	9.73
158283731	ribosomal protein L18a [Chlamydomonas reinhardtii]	12.12	48.90	9	9	10	182	21.4	10.40
158277111	ribosomal protein L13a [Chlamydomonas reinhardtii]	11.89	32.43	6	6	7	185	20.7	11.30

158278474	low-CO2-inducible chloroplast envelope protein [Chlamydomonas reinhardtii]	11.43	24.23	1	7	8	355	38.0	8.68
158278383	low-CO2-inducible chloroplast envelope protein [Chlamydomonas reinhardtii]	11.40	29.61	3	9	10	358	38.3	8.85
158275883	ribosomal protein S5 [Chlamydomonas reinhardtii]	11.31	29.02	5	5	5	193	21.7	9.79
158271777	zeta-cop. subunit of COP-1 complex [Chlamydomonas reinhardtii]	11.28	25.00	4	4	6	184	20.5	4.91
158278402	R-SNARE protein, VAMP72-family [Chlamydomonas reinhardtii]	11.23	39.27	9	9	10	219	25.2	8.21
158277493	eukaryotic initiation factor [Chlamydomonas reinhardtii]	11.23	39.11	7	7	7	202	23.1	5.35
158279739	predicted protein [Chlamydomonas reinhardtii]	11.03	50.43	6	6	7	232	24.2	9.45
1717956	RecName: Full=Cytochrome b6-F complex iron-sulfur subunit, chloroplastic; AltName: Full=Plastohydroquinone:plastocya	11.02	35.44	5	5	8	206	21.5	8.57
158276249	flagellar associated protein [Chlamydomonas reinhardtii]	10.99	57.65	8	8	9	196	21.7	9.55
158283935	hypothetical protein CHLREDRAFT_183568 [Chlamydomonas reinhardtii]	10.98	37.90	6	6	7	219	23.8	8.63
158282292	flagellar flavodoxin [Chlamydomonas reinhardtii]	10.92	29.85	1	6	7	201	21.4	6.70
75058787	Keratin, type I cytoskeletal 15 OS=Ovis aries GN=KRT15 PE=2 SV=1	10.89	10.38	1	6	12	453	48.7	4.79
15827573	luminal PsbP-like protein [Chlamydomonas reinhardtii]	10.55	22.96	6	6	6	257	28.4	9.01
158272508	predicted protein [Chlamydomonas reinhardtii]	10.44	25.64	5	5	6	273	29.2	7.11
40714509	light-harvesting chlorophyll-a/b protein of photosystem I [Chlamydomonas reinhardtii]	10.43	30.30	5	5	6	264	28.7	9.13
124484361	transcription regulator Pbt-2 [Chlamydomonas reinhardtii]	10.43	30.25	5	5	5	238	24.9	9.60
158279575	membrane AAA-metalloprotease [Chlamydomonas reinhardtii]	10.38	13.76	7	7	8	727	77.5	5.90
158275158	plastid ribosomal protein L6 [Chlamydomonas reinhardtii]	10.15	31.88	6	6	7	207	22.2	10.35
158280089	predicted protein [Chlamydomonas reinhardtii]	10.09	33.18	5	5	5	223	24.2	10.62
132167	RecName: Full=Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic; Short=RA; Short=Rubisco activase	9.96	12.99	4	4	7	408	45.0	8.54
158270661	peptidyl-Ima hydrolase [Chlamydomonas reinhardtii]	9.91	49.14	4	4	4	116	12.2	8.48
158275654	predicted protein [Chlamydomonas reinhardtii]	9.89	29.32	4	4	4	191	21.1	7.62
158278261	light-harvesting protein of photosystem I [Chlamydomonas reinhardtii]	9.87	32.86	4	4	8	213	22.8	9.00
158282793	eukaryotic translation elongation factor 1 alpha 1 [Chlamydomonas reinhardtii]	9.80	21.81	10	10	10	463	50.8	8.54
158275368	mitochondrial substrate carrier protein [Chlamydomonas reinhardtii]	9.09	18.39	4	4	5	299	31.6	9.76
158282957	ribosomal protein L17 [Chlamydomonas reinhardtii]	9.09	23.66	4	4	5	186	21.1	10.33
18201978	RecName: Full=30S ribosomal protein S9, chloroplastic	9.05	21.47	4	4	4	191	21.0	9.74
131242	RecName: Full=Photosystem C(B) protein; AltName: Full=32 kDa thylakoid membrane protein; AltName: Full=Photosyst	8.78	16.48	5	5	5	352	39.0	5.50
158281401	magnesium chelatase subunit D [Chlamydomonas reinhardtii]	8.50	12.26	7	7	7	767	82.6	5.80
158270952	predicted protein [Chlamydomonas reinhardtii]	8.39	40.34	8	8	8	233	25.2	9.31
158275877	predicted protein [Chlamydomonas reinhardtii]	8.27	35.12	7	7	7	242	25.6	9.94
158275614	predicted protein [Chlamydomonas reinhardtii]	8.02	34.08	5	5	5	223	24.8	9.99
158278804	predicted protein [Chlamydomonas reinhardtii]	7.98	25.20	5	5	6	246	26.6	9.85
158279571	ribosomal protein L18 [Chlamydomonas reinhardtii]	7.62	26.20	4	4	4	187	20.9	11.17
158273394	flagellar associated protein [Chlamydomonas reinhardtii]	7.62	15.23	4	4	5	302	32.6	6.52
158275296	stress-related chlorophyll a/b binding protein 1 [Chlamydomonas reinhardtii]	7.27	30.43	3	4	4	253	27.5	5.05
158275934	ribosomal protein L23a [Chlamydomonas reinhardtii]	7.26	31.29	4	4	4	147	16.4	10.14
158276000	ribosomal protein L32 [Chlamydomonas reinhardtii]	6.99	45.86	6	6	6	133	15.5	11.18
158278368	cytochrome c oxidase subunit III [Chlamydomonas reinhardtii]	6.91	12.30	3	3	5	382	41.4	8.53
158278750	fibrillin [Chlamydomonas reinhardtii]	6.82	25.63	4	4	4	199	22.0	8.43
158283136	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii]	6.77	27.14	6	6	8	280	29.1	9.79
6685565	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT136 PE=1 SV=1	6.67	6.00	1	3	4	467	52.2	4.94
158277204	R-SNARE protein, Sec22-family [Chlamydomonas reinhardtii]	6.65	21.46	4	4	4	219	25.1	9.47
158282209	predicted protein [Chlamydomonas reinhardtii]	6.62	32.17	7	7	8	258	28.3	9.58
158272892	small arf-related GTPase ARF-RP1 [Chlamydomonas reinhardtii]	6.53	27.36	4	4	4	201	22.7	9.17
158280354	hypothetical protein CHLREDRAFT_188153 [Chlamydomonas reinhardtii]	6.45	12.24	5	5	5	392	41.3	9.04
158281106	peroxiredoxin type II [Chlamydomonas reinhardtii]	6.44	33.19	7	7	7	226	24.4	8.76
1350947	RecName: Full=40S ribosomal protein S18	6.39	32.03	5	5	5	153	17.4	10.48
158271807	TatB-like sec-independent protein translocon subunit [Chlamydomonas reinhardtii]	6.36	20.54	4	4	4	224	22.7	10.26
158282264	110 kDa translocon of chloroplast envelope inner membrane [Chlamydomonas reinhardtii]	6.35	7.68	4	4	4	703	78.9	6.93

158273732	mitochondrial transcription termination factor [Chlamydomonas reinhardtii]	6.29	34.62	6	6	6	234	25.7	9.41
128635	RecName: Full=NADH-ubiquinone oxidoreductase chain 1; AltName: Full=NADH dehydrogenase subunit 1	6.27	5.48	3	3	4	292	31.6	7.02
158276683	glycine-rich RNA-binding protein [Chlamydomonas reinhardtii]	6.08	21.82	3	3	3	165	15.8	8.41
158283480	F1F0 ATP synthase subunit 6 [Chlamydomonas reinhardtii]	6.03	7.94	2	2	4	340	35.5	9.58
113465	RecName: Full=ADP,ATP carrier protein; AltName: Full=Adenine nucleotide transloc; RecName: Full=ATPase, ras GTPase-like protein [Chlamydomonas reinhardtii]	5.97	16.23	5	5	5	308	33.5	9.74
158283657	flagellar ATPase, ras GTPase-like protein [Chlamydomonas reinhardtii]	5.87	24.48	4	4	4	192	21.3	5.60
217315585	ATP synthase CF1 alpha subunit [Chlamydomonas reinhardtii]	5.68	13.24	3	3	3	272	29.1	5.25
1173201	RecName: Full=40S ribosomal protein S14	5.62	22.22	3	3	3	153	16.3	10.32
158277797	translocase of outer mitochondrial membrane [Chlamydomonas reinhardtii]	5.57	28.86	4	4	4	201	21.7	5.00
131395	RecName: Full=Oxygen-evolving enhancer protein 3, chloroplastic; Short=OEE3; Flags: Precursor	5.55	17.09	3	3	3	199	21.8	9.58
1245907	Rieske protein (cytochrome b6 f complex) [Chlamydomonas reinhardtii]; Peptide Partial, 27 aa, segment 1 of 2	5.54	48.15	2	2	3	207	22.2	6.37
158275019	mitochondrial F1F0 ATP synthase associated 19.5 kDa protein [Chlamydomonas reinhardtii]	5.44	18.84	3	3	3	27	22.2	9.55
158272413	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii]	5.27	22.67	3	3	3	172	18.4	7.78
158271626	predicted protein [Chlamydomonas reinhardtii]	5.27	20.65	4	4	4	276	29.6	8.84
158284019	predicted protein [Chlamydomonas reinhardtii]	5.23	13.51	2	2	2	148	16.2	9.74
158270522	predicted protein [Chlamydomonas reinhardtii]	5.02	27.61	3	3	3	134	14.4	10.05
25090906	RecName: Full=Cytochrome b6-f complex subunit v; AltName: Full=Cytochrome b6-f complex subunit v	4.99	38.89	5	5	5	198	20.2	9.92
158283348	glutathione S-transferase, mitochondrial [Chlamydomonas reinhardtii]	4.96	10.33	2	2	2	242	26.4	9.36
158284016	predicted protein [Chlamydomonas reinhardtii]	4.95	18.18	3	3	3	264	26.5	8.70
158279001	predicted protein [Chlamydomonas reinhardtii]	4.92	9.77	3	3	3	348	36.2	9.66
158274884	ribosomal protein L12 [Chlamydomonas reinhardtii]	4.83	34.94	4	4	4	166	17.6	9.06
158278749	plastid lipid associated protein [Chlamydomonas reinhardtii]	4.76	10.95	3	3	3	347	36.4	11.05
158274972	acidic ribosomal protein P0 [Chlamydomonas reinhardtii]	4.71	7.19	2	2	2	320	34.6	6.42
158283478	predicted protein [Chlamydomonas reinhardtii]	4.54	3.46	3	3	3	1328	135.7	7.23
1418674	ubiquinol-cytochrome c oxidoreductase [Chlamydomonas reinhardtii]	4.53	13.41	3	3	3	261	28.4	8.09
158274929	signal peptidase, 25 kDa subunit [Chlamydomonas reinhardtii]	4.51	12.63	2	2	2	198	21.6	6.58
158281981	aspartate aminotransferase [Chlamydomonas reinhardtii]	4.48	7.71	3	3	3	428	47.0	8.92
158283202	mitochondrial cytochrome c oxidase subunit 4, 13 kD [Chlamydomonas reinhardtii]	4.46	17.71	2	2	2	175	19.0	5.27
158271676	ribosomal protein L28 [Chlamydomonas reinhardtii]	4.46	23.73	4	4	4	177	19.5	10.83
158273022	predicted protein [Chlamydomonas reinhardtii]	4.46	20.27	3	3	3	222	24.4	10.23
262527093	large subunit of ribulose-1, 5-bisphosphate carboxylase/oxygenase [Chlamydomonas reinhardtii]	4.45	10.64	4	4	4	376	41.9	7.30
158282786	plastid ribosomal protein L13 [Chlamydomonas reinhardtii]	4.41	19.56	4	4	4	225	24.5	10.20
158281596	ribosomal protein L27a [Chlamydomonas reinhardtii]	4.41	26.53	4	4	4	147	16.4	10.43
158275974	predicted protein [Chlamydomonas reinhardtii]	4.39	7.91	2	2	2	316	32.9	9.72
158269914	histone H4 [Chlamydomonas reinhardtii]	4.35	34.04	3	3	3	94	10.5	11.50
158280397	predicted protein [Chlamydomonas reinhardtii]	4.29	7.45	2	2	2	322	33.1	9.69
18125	light harvesting complex protein L20 [Chlamydomonas reinhardtii]	4.29	16.96	2	2	3	224	23.5	8.38
131278	RecName: Full=Photosystem II CP43 chlorophyll apoprotein; AltName: Full=PS II 43 kDa protein; AltName: Full=Photosys	4.26	9.11	3	3	3	461	50.6	6.34
158277987	predicted protein [Chlamydomonas reinhardtii]	4.26	21.90	3	3	3	137	15.5	8.51
158275121	rieske [2Fe-2S] protein [Chlamydomonas reinhardtii]	4.25	8.82	2	2	2	306	33.2	8.09
158275715	component of TRAPP complex [Chlamydomonas reinhardtii]	4.20	21.36	4	4	5	206	23.5	9.04
158270827	small rab-related GTPase [Chlamydomonas reinhardtii]	4.19	10.09	1	2	4	218	24.2	8.15
158274126	predicted protein [Chlamydomonas reinhardtii]	3.99	12.68	2	2	2	213	23.2	6.87
158282108	ribosomal protein S24 [Chlamydomonas reinhardtii]	3.97	32.06	4	4	4	131	15.1	10.62
1730149	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic; AltName: Full=NADP-dependent glyceralde	3.95	23.80	7	7	7	374	40.3	9.09
158278893	ARF-related small GTPase [Chlamydomonas reinhardtii]	3.92	25.93	4	4	5	189	21.3	9.07
158275843	mitochondrial substrate carrier protein [Chlamydomonas reinhardtii]	3.90	10.60	4	4	4	368	38.4	9.79
158271600	Emp24/gp25L/p24 family protein [Chlamydomonas reinhardtii]	3.89	9.22	2	2	2	206	24.3	9.41
158277341	plastid ribosomal protein L9 [Chlamydomonas reinhardtii]	3.88	28.43	4	4	4	204	22.5	9.80
158277646	thylakoid lumen protein [Chlamydomonas reinhardtii]	3.88	6.05	2	2	3	248	26.6	8.91

158270361	peroxiredoxin [Chlamydomonas reinhardtii]	3.86	20.00	3	3	3	3	185	20.4	5.86
158278637	non-catalytic subunit of chloroplast ClpP complex [Chlamydomonas reinhardtii]	3.84	9.93	3	3	3	3	282	31.6	9.60
158279650	E3 ubiquitin ligase [Chlamydomonas reinhardtii]	3.79	45.86	5	5	7	157	17.9	42.9	4.70
158275172	predicted protein [Chlamydomonas reinhardtii]	3.79	5.71	2	2	2	420	42.9	8.24	8.24
11995220	peroxiredoxin [Chlamydomonas reinhardtii]	3.78	24.12	3	3	4	199	22.2	5.68	5.68
158273807	R-SNARE protein, VAMP71-family [Chlamydomonas reinhardtii]	3.75	21.56	5	5	5	218	24.9	8.84	8.84
158274869	small rab-related GTPase [Chlamydomonas reinhardtii]	3.70	10.89	2	2	2	2	175	20.1	9.48
32699336	RecName: Full=ATP synthase subunit b, chloroplastic; AltName: Full=ATP synthase F(0) sector subunit b; AltName: Full=	3.69	23.43	4	4	4	4	175	20.1	9.48
158283494	succinate dehydrogenase subunit b560 [Chlamydomonas reinhardtii]	3.69	10.93	2	2	2	183	19.5	9.45	9.45
158271558	predicted protein [Chlamydomonas reinhardtii]	3.68	35.44	4	4	5	158	16.5	5.10	5.10
560221404	ATP synthase beta-subunit, partial (chloroplast) [Chlamydomonas reinhardtii]	3.66	33.03	6	6	6	218	23.5	6.60	6.60
158275612	NADH:ubiquinone oxidoreductase 18 kDa subunit [Chlamydomonas reinhardtii]	3.60	27.27	4	4	4	187	20.6	9.70	9.70
158278946	ribosomal protein L14 [Chlamydomonas reinhardtii]	3.57	16.06	2	2	2	137	15.3	10.33	10.33
158279924	ribosomal protein S13 [Chlamydomonas reinhardtii]	3.44	37.75	6	6	6	151	17.1	10.51	10.51
158283821	plastid lipid associated protein [Chlamydomonas reinhardtii]	3.32	11.45	3	3	3	227	23.7	9.29	9.29
158274660	predicted protein [Chlamydomonas reinhardtii]	3.27	4.18	3	3	3	837	91.5	7.25	7.25
257071857	chloroplast Fe superoxide dismutase 1 precursor [Chlamydomonas reinhardtii]	3.09	11.54	2	2	2	234	25.9	9.35	9.35
158274005	cyclopropyl isomerase-like protein [Chlamydomonas reinhardtii]	3.07	8.00	2	2	2	275	31.9	9.26	9.26
158272001	high intensity light-inducible lhc-like gene [Chlamydomonas reinhardtii]	2.83	12.98	2	2	2	285	30.1	8.88	8.88
158274025	hypothetical protein CHLEDRAFT_193064 [Chlamydomonas reinhardtii]	2.78	11.89	2	2	2	227	24.9	8.88	8.88
158271862	predicted protein [Chlamydomonas reinhardtii]	2.76	10.18	2	2	2	275	30.2	9.92	9.92
158278229	predicted protein [Chlamydomonas reinhardtii]	2.66	21.83	2	2	2	197	21.4	9.31	9.31
158276432	predicted protein [Chlamydomonas reinhardtii]	2.60	10.18	2	2	2	226	24.6	8.56	8.56
158276330	ribosomal protein L24 [Chlamydomonas reinhardtii]	2.60	13.42	2	2	2	149	17.0	11.00	11.00
158277796	peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	2.47	13.10	4	4	4	252	27.5	9.06	9.06
158284180	predicted protein [Chlamydomonas reinhardtii]	2.41	8.84	2	2	2	215	22.9	8.15	8.15
158284294	signal peptidase, 22 kDa subunit [Chlamydomonas reinhardtii]	2.38	11.31	2	2	2	168	19.3	9.54	9.54
158272747	predicted protein [Chlamydomonas reinhardtii]	2.38	4.65	2	2	2	387	40.3	11.90	11.90
29429167	RecName: Full=Photosystem I P700 chlorophyll a apoprotein A2; AltName: Full=PSI-B; AltName: Full=Psab	2.38	2.99	2	2	2	735	82.1	7.03	7.03
158282998	ribosomal protein S16 [Chlamydomonas reinhardtii]	2.33	17.61	2	2	2	142	16.0	10.46	10.46
158275510	predicted protein [Chlamydomonas reinhardtii]	2.31	11.84	2	2	2	245	26.7	8.82	8.82
247309	histone H2B [Chlamydomonas reinhardtii, CW-15, Peptide Partial, 92 aa]	2.31	38.04	3	3	3	92	10.2	9.82	9.82
158278644	methionine synthase reductase [Chlamydomonas reinhardtii]	2.28	3.50	2	2	3	628	68.2	7.96	7.96
158274981	predicted protein [Chlamydomonas reinhardtii]	2.23	11.63	2	2	2	258	27.4	9.63	9.63
158277738	vacuolar ATP synthase subunit E [Chlamydomonas reinhardtii]	2.22	18.10	4	4	4	232	26.2	7.11	7.11
158283663	ribosomal protein L26 [Chlamydomonas reinhardtii]	2.22	19.31	3	3	3	145	16.5	10.58	10.58
158281371	predicted protein [Chlamydomonas reinhardtii]	2.16	13.23	2	2	2	189	21.0	9.44	9.44
75338601	RecName: Full=Dynein light chain 1, axonemal; AltName: Full=Flagellar outer arm dynein light chain 1	2.14	11.11	2	2	2	198	22.1	5.74	5.74
158279168	predicted protein [Chlamydomonas reinhardtii]	2.12	8.36	2	2	2	299	31.0	4.63	4.63
158275741	S-isoprenylcysteine O-methyltransferase [Chlamydomonas reinhardtii]	2.12	18.39	3	3	3	223	24.0	8.69	8.69
158279933	Sigma4-Adaptin [Chlamydomonas reinhardtii]	2.11	12.50	2	2	2	144	17.0	5.08	5.08
158279185	anion transporter [Chlamydomonas reinhardtii]	2.10	11.90	3	3	4	336	34.7	9.29	9.29
158283366	cytochrome b5 protein [Chlamydomonas reinhardtii]	2.08	16.67	2	2	2	138	15.4	5.74	5.74
158281659	predicted protein [Chlamydomonas reinhardtii]	2.01	9.66	2	2	2	176	19.7	8.76	8.76
158279424	eukaryotic initiation factor 4A-like protein [Chlamydomonas reinhardtii]	2.00	13.08	5	5	5	413	47.0	5.72	5.72
158271135	predicted protein [Chlamydomonas reinhardtii]	1.96	16.25	3	3	3	240	25.9	9.38	9.38
158284195	predicted protein [Chlamydomonas reinhardtii]	1.89	6.32	2	2	2	538	58.5	7.47	7.47
158275255	ribosomal protein S15 [Chlamydomonas reinhardtii]	1.86	15.86	2	2	2	145	16.6	10.56	10.56
158274279	mitochondrial inner membrane translocase [Chlamydomonas reinhardtii]	1.86	10.00	3	3	3	250	27.2	9.20	9.20
3025293	RecName: Full=Ras-related protein YPTC6	1.83	16.67	3	3	3	216	24.2	5.91	5.91

158277391	predicted protein [Chlamydomonas reinhardtii]	1.83	22.11	4	4	4	4	190	21.4	8.94
158271074	predicted protein [Chlamydomonas reinhardtii]	1.82	12.95	2	2	2	2	139	16.2	7.74
17432909	RecName: Full=ATP synthase subunit a, chloroplastic; AltName: Full=ATP synthase FO sector subunit a; AltName: Full=F	1.82	11.76	2	2	3	3	238	26.2	4.70
158281688	ribosomal protein S19 [Chlamydomonas reinhardtii]	1.81	20.67	3	3	3	3	150	17.0	9.96
158275624	component of TRAPP complex [Chlamydomonas reinhardtii]	1.81	14.05	2	2	2	2	185	21.2	4.70
158276480	clathrin assembly factor-like protein [Chlamydomonas reinhardtii]	1.81	5.78	3	3	3	3	571	60.6	6.87
109692744	putative sphingomyelinase [Chlamydomonas reinhardtii]	1.80	6.42	2	2	3	3	530	55.4	7.23
158272501	acetolactate synthase, small subunit [Chlamydomonas reinhardtii]	1.80	8.59	3	3	3	3	489	52.4	8.69
158277499	predicted protein [Chlamydomonas reinhardtii]	1.79	8.02	2	2	2	2	262	28.8	8.88
158278226	predicted protein [Chlamydomonas reinhardtii]	1.78	6.61	2	2	2	2	333	36.0	7.85
158278438	ARF-like GTPase [Chlamydomonas reinhardtii]	1.76	22.70	2	2	3	4	185	20.6	5.72
158277688	ARF-like small GTPase [Chlamydomonas reinhardtii]	1.76	18.23	1	2	2	2	181	20.5	5.43
14917039	RecName: Full=30S ribosomal protein S7, chloroplastic	1.73	15.48	2	2	2	2	168	19.1	10.43
158281517	glutathione S-transferase-related protein, partial [Chlamydomonas reinhardtii]	1.72	20.00	2	2	2	2	150	16.5	10.07
213517417	ribosomal protein S2 [Chlamydomonas reinhardtii]	1.70	2.20	2	2	2	2	910	102.5	10.71
32699675	RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymeras	1.70	8.73	4	4	5	5	550	62.3	9.44
158272203	plastid ribosomal protein S13 [Chlamydomonas reinhardtii]	1.69	12.80	2	2	2	2	164	18.5	10.73
158269913	histone H2A [Chlamydomonas reinhardtii]	1.69	13.33	2	2	2	2	120	12.7	10.04
158278553	metacaspase type II [Chlamydomonas reinhardtii]	1.69	10.51	2	2	2	2	409	42.4	5.31
158276757	pre-apolferitin [Chlamydomonas reinhardtii]	1.69	8.84	2	2	2	2	249	27.3	5.48
158279994	predicted protein [Chlamydomonas reinhardtii]	1.67	11.58	3	3	3	3	259	27.9	9.32
1710480	RecName: Full=60S ribosomal protein L11	1.66	16.47	3	3	3	3	170	19.5	9.95
158272225	NADH:ubiquinone oxidoreductase subunit 10 [Chlamydomonas reinhardtii]	1.66	13.41	2	2	2	2	164	18.1	9.31
158271298	L-ascorbate peroxidase [Chlamydomonas reinhardtii]	1.65	11.24	3	3	3	3	347	36.5	9.20
158281258	tetrapyrrole-binding protein [Chlamydomonas reinhardtii]	1.63	13.85	3	3	3	3	260	29.0	9.64
158276831	phytol kinase-related protein [Chlamydomonas reinhardtii]	1.61	10.86	2	2	2	2	304	31.3	8.90
158272162	predicted protein [Chlamydomonas reinhardtii]	1.61	9.36	2	2	2	2	235	25.2	9.04
158272302	predicted protein [Chlamydomonas reinhardtii]	1.60	5.14	2	2	2	2	370	40.5	7.81
10720232	RecName: Full=Protochlorophyllide reductase, chloroplastic; Short=PCR; AltName: Full=NADPH-protochlorophyllide oxid	0.00	7.05	2	2	2	2	397	41.8	9.42
158283853	predicted protein [Chlamydomonas reinhardtii]	0.00	17.11	2	2	2	2	187	20.4	5.27
158282771	plastid ribosomal protein L28 [Chlamydomonas reinhardtii]	0.00	10.77	2	2	2	2	195	21.9	9.91
158282316	aspartate kinase [Chlamydomonas reinhardtii]	0.00	2.57	2	2	2	2	545	58.4	7.88
158282283	PIC1 permease [Chlamydomonas reinhardtii]	0.00	19.20	2	2	2	2	125	13.3	10.10
158281827	predicted protein [Chlamydomonas reinhardtii]	0.00	7.45	2	2	2	2	282	30.4	8.07
158280982	delta-cop [Chlamydomonas reinhardtii]	0.00	5.28	2	2	2	2	511	55.9	5.52
158280495	predicted protein [Chlamydomonas reinhardtii]	0.00	14.57	2	2	2	2	151	16.1	9.36
158280394	mitochondrial phosphate carrier 1, minor isoform [Chlamydomonas reinhardtii]	0.00	6.60	2	2	2	2	318	34.1	8.98
158279807	predicted protein [Chlamydomonas reinhardtii]	0.00	14.98	2	2	2	2	207	23.3	9.82
158278628	ribosomal protein S26 [Chlamydomonas reinhardtii]	0.00	23.76	2	2	2	2	101	11.8	11.37
158278601	predicted protein [Chlamydomonas reinhardtii]	0.00	13.18	2	2	2	2	220	22.7	9.45
158277870	omega-6-FAD, chloroplast isoform [Chlamydomonas reinhardtii]	0.00	5.66	3	3	3	3	424	48.3	8.53
158277731	peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	0.00	13.94	2	2	2	2	208	21.8	9.11
158276417	predicted protein [Chlamydomonas reinhardtii]	0.00	14.48	3	3	3	3	221	23.0	10.21
158276108	dihydropyrimidine acetyltransferase [Chlamydomonas reinhardtii]	0.00	3.82	2	2	2	2	628	64.2	7.56
158274601	predicted protein [Chlamydomonas reinhardtii]	0.00	11.62	2	2	2	2	198	21.1	9.51
158274346	pyrroline-5-carboxylate reductase [Chlamydomonas reinhardtii]	0.00	11.23	2	2	2	2	276	28.4	6.80
158274278	hypothetical protein CHLEDRAFT_192823 [Chlamydomonas reinhardtii]	0.00	10.45	2	2	2	2	268	28.0	8.85
158274006	VID72-domain protein [Chlamydomonas reinhardtii]	0.00	3.67	2	2	2	2	600	65.8	5.59
158273712	predicted protein [Chlamydomonas reinhardtii]	0.00	12.69	2	2	2	2	197	21.6	10.39
158270887	ribosomal protein S11 [Chlamydomonas reinhardtii]	0.00	14.10	2	2	2	2	156	17.8	10.46

158270659	dual function alcohol dehydrogenase / acetaldehyde dehydrogenase [Chlamydomonas reinhardtii]	0.00	2.41	2	2	2	2	2	954	102.2	7.52
2887383	rps18 [Chlamydomonas reinhardtii]	0.00	16.00	2	2	2	2	2	125	14.9	11.82
393463	unnamed protein product [Chlamydomonas reinhardtii]	0.00	7.38	2	2	2	2	2	271	31.3	11.02
15011441	LCI5 [Chlamydomonas reinhardtii]	0.00	11.84	2	2	2	2	2	321	32.7	12.13
18241	thioredoxin Ch2 [Chlamydomonas reinhardtii]	0.00	28.30	2	2	2	2	2	106	11.5	5.19
238054406	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	65.15	45.81	24	28	41	644	66.0	8.12		
269849769	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	48.64	53.42	20	25	29	584	58.8	5.21		
125116	Keratin, type II microfilillar, component 7C OS=Ovis aries PE=1 SV=1	45.02	22.61	5	10	45	491	53.6	5.57		
48474780	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	44.13	12.82	2	6	40	507	55.8	6.55		
125117	Keratin, type II microfilillar, component 5 OS=Ovis aries PE=1 SV=1	42.93	19.72	3	8	42	502	55.2	6.46		
239938650	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	37.25	45.54	18	23	25	639	65.4	8.00		
311033397	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2	35.71	5.67	1	4	28	600	64.8	7.56		
239938886	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	34.39	47.35	20	21	28	623	62.0	5.24		
125090	Keratin, type I microfilillar 48 kDa, component 8C-1 OS=Ovis aries PE=1 SV=2	32.53	35.92	2	13	40	412	46.6	4.81		
125091	Keratin, type I microfilillar, 47.6 kDa OS=Ovis aries PE=3 SV=2	27.85	36.39	3	12	32	404	46.0	4.93		
209572740	Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 PE=2 SV=3	19.95	20.91	1	8	26	416	47.2	4.88		
125115	Keratin, type II microfilillar (fragment) OS=Ovis aries PE=1 SV=1	13.58	32.11	3	3	5	109	12.7	4.59		
136429	Trypsin OS=Sus scrofa PE=1 SV=1	33.03	25.11	4	4	22	231	24.4	7.18		