

## Supplementary Materials

**Table S1.** Protein identification information for 7 cm tube gel section >100 kDa. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Histone H4	jgi Thaps3 3184 fgenes1_pg.C_chr_3000118	P35057	DNIQGITKPAIR VFLENVIR VLRDNIQGITKPAIR	<i>Thalassiosira pseudonana</i>	0.9998	11383.6	N	22.3
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gij 118411104 ref YP_874498.1	YP_874498	MSGVDHIHAGTVVVGK VALEAM[147]VLAR FLNCLEGINR	<i>Thalassiosira pseudonana</i>	0.9992	54324.7	C	7.1
Fucoxanthin chlorophyll a/c binding protein 2	jgi Thaps3 38667 e_gw1.22.164.1	Q42395	IAQLAFLGNIITR	<i>Thalassiosira pseudonana</i>	0.9841	21807.2	C	6.8
ATP synthase CF1 beta chain	gij 118411134 ref YP_874528.1	YP_874528	FTQAGSEVSALLGR	<i>Thalassiosira pseudonana</i>	0.9733	51143.1	C	3.0
DNA-directed RNA polymerase subunit gamma	gij 33862040 ref NP_893601.1	Q7V5P2	FATSDLNDLYR	<i>Prochlorococcus marinus</i>	0.9422	72277.0	S	1.7
ATP-dependent protease ATP-binding subunit	gij 33862213 ref NP_893774.1	Q7V9L5	DVSGEGVQQALLK	<i>Prochlorococcus marinus</i>	0.9350	49496.0	S	3.1
Putative cysteine synthase, localized to the mitochondrial outer membrane; Ygr012wp	jgi Thaps3 38294 e_gw1.19a.45.1	NP_011526	MENLNPGGTGKDRAAR	<i>Thalassiosira pseudonana</i>	0.9200	37867.3	M	4.6

**Table S2.** Protein identification information for 7 cm tube gel section 50–100 kDa. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gi 118411104 ref YP_874498.1	YP_874498	DTDVLALFR MSGVDHIIHAGTVVGK YESGVIPYAK M[147]GYWDAAYTVK	<i>Thalassiosira pseudonana</i>	1.0000	54324.7	C	9.2
Histone H4	jgi Thaps3 3184 fgenes1_pg.C_chr_3000118	P35057	ISGLIYEETR DNIQGITKPAIR	<i>Thalassiosira pseudonana</i>	1.0000	11383.6	N	21.4
ATP synthase CF1 beta chain	gi 118411134 ref YP_874528.1	YP_874528	FTQAGSEVSALLGR	<i>Thalassiosira pseudonana</i>	0.9656	51143.1	C	3.0
Fucoxanthin chlorophyll a/c binding protein 2	jgi Thaps3 38667 e_gw1.22.164.1	Q42395	IAQLAFLGNIIR	<i>Thalassiosira pseudonana</i>	0.9428	21807.2	C	6.8

**Table S3.** Protein identification information for 7 cm tube gel section 25–50 kDa. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Histone H4	jgi Thaps3 3184 fgenes1_pg.C_chr_3000118	P35057	ISGLIYEETR VFLENVIR	<i>Thalassiosira pseudonana</i>	0.9999	11383.6	N	17.5
Photosystem II chlorophyll A core antenna apoprotein	gi 118411113 ref YP_874507.1	YP_874507	YQWDSGYFQQEIER TSLESDGVFR	<i>Thalassiosira pseudonana</i>	0.9988	56408.1	C	4.7
ATP synthase CF1 beta chain	gi 118411134 ref YP_874528.1	YP_874528	FTQAGSEVSALLGR	<i>Thalassiosira pseudonana</i>	0.9606	51143.1	C	3.0
Fucoxanthin chlorophyll a/c binding protein 2	jgi Thaps3 38667 e_gw1.22.164.1	Q42395	IAQLAFLGNIITR	<i>Thalassiosira pseudonana</i>	0.9606	21807.2	C	6.8
Photosystem II 10 kDa phosphoprotein	gi 118411116 ref YP_874510.1	YP_874510	LGEILRPLNAEY GK	<i>Thalassiosira pseudonana</i>	0.9276	7388.0	C	21.2

**Table S4.** Protein identification information for 7 cm tube gel section 10–25 kDa. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Photosystem II 10 kDa phosphoprotein	gi 118411116 ref YP_874510.1	YP_874510	LGEILRPLNAEYGK	<i>Thalassiosira pseudonana</i>	1.0000	7388.0	C	21.2
Histone H4	jgi Thaps3 3184 fgenes1_pg.C_c_hr_3000118	P35057	ISGLIYEETR VFLENVIR DNIQGITKPAIR	<i>Thalassiosira pseudonana</i>	1.0000	11383.6	N	29.1
ATP synthase CF1 beta chain	gi 118411134 ref YP_874528.1	YP_874528	IGLFGGAGVGK FTQAGSEVSALLGR	<i>Thalassiosira pseudonana</i>	0.9996	51143.1	C	5.3
Fucoanthin chlorophyll a/c binding protein 2	jgi Thaps3 38667 e_gw1.22.164.1	Q42395	IAQLAFLGNIITR	<i>Thalassiosira pseudonana</i>	0.9698	21807.2	C	6.8
Fucoanthin chlorophyll a/c binding protein 1	jgi Thaps3 268127 estExt_thaps1_ua_kg.C_chr_10394	CAA04401	IAQLAFLGQVVTR	<i>Thalassiosira pseudonana</i>	0.9554	22628.0	C	6.2
Fucoanthin chlorophyll a/c binding protein 3	jgi Thaps3 38494 e_gw1.20.149.1	CAA04226	ISQLAFLGQIVTR	<i>Thalassiosira pseudonana</i>	0.9224	20354.4	C	6.8

**Table S5.** Protein identification information for 2 cm tube gel. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Fucoanthin chlorophyll a/c binding protein 2	jgi Thaps3 38667 e_gw1.22.164.1	Q42395	DIEGTGNEFVGDFR	<i>Thalassiosira pseudonana</i>	0.9042	21807.2	C	7.3
Photosystem II reaction center protein D2	gi 118411148 ref YP_874542.1	YP_874542	AAEDPEFETFYTK	<i>Thalassiosira pseudonana</i>	0.9093	39064.0	C	3.7
Histone-like DNA-binding protein	gi 33861877 ref NP_893438.1	A2BSP2	TDVSLVVDAAIETIV DSVVEGK	<i>Prochlorococcus marinus</i>	0.9413	9768.0	S	24.2

**Table S6.** Protein identification information for 2 cm 1D gel. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Histone-like DNA-binding protein	gi 33861877 ref NP_893438.1	A2BSP2	TDVSLVVDAAIETIVDS VVEGK	<i>Prochlorococcus marinus</i>	0.9413	9768.0	S	24.2

**Table S7.** Protein identification information for direct digest. Information includes: protein, annotation name, accession number, peptide sequence, species, database matching score, molecular weight (MW), cellular location and percent sequence coverage. For cellular location: C = chloroplast; M = mitochondria; N = nucleus; S = secretory.

Protein	Annotation Name	Accession Number	Peptide Sequence	Species	Database Matching Score	MW	Location	Sequence Coverage (%)
Histone-like DNA-binding protein	gi 33861877 ref NP_893438.1	A2BSP2	TDVSLVVDAAIETIVDSVVEG K	<i>Prochlorococcus marinus</i>	0.9413	9768.0	S	24.2