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Identifying and tracking proteins through the marine water column: insights into the inputs and preservation mechanisms of protein in sediments

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Abstract

Proteins generated during primary production represent an important fraction of marine organic nitrogen and carbon, and have the potential to provide organism-specific information in the environment. The Bering Sea is a highly productive system dominated by seasonal blooms and was used as a model system for algal proteins to be tracked through the water column and incorporated into detrital sedimentary material. Samples of suspended and sinking particles were collected at multiple depths along with surface sediments on the continental shelf and deeper basin of the Bering Sea. Modified standard proteomic preparations were used in conjunction with high pressure liquid chromatography-tandem mass spectrometry to identify the suite of proteins present and monitor changes in their distribution. In surface waters 207 proteins were identified, decreasing through the water column to 52 proteins identified in post-bloom shelf surface sediments and 24 proteins in deeper (3490 m) basin sediments. The vast majority of identified proteins in all samples were diatom in origin, reflecting their dominant contribution of biomass during the spring bloom. Identified proteins were predominantly from metabolic, binding/structural, and transport-related protein groups. Significant linear correlations were observed between the number of proteins identified and the concentration of total hydrolysable amino acids normalized to carbon and nitrogen. Organelle-bound, transmembrane, photosynthetic, and other proteins involved in light harvesting were preferentially retained during recycling. These findings suggest that organelle and membrane protection represent important mechanisms that enhance the preservation of protein during transport and incorporation into sediments.

Keywords

proteomics; amino acids; mass spectrometry; marine sediments; organic nitrogen; peptides; sediment traps; Bering Sea; diatom; organelles; gel-electrophoresis

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INTRODUCTION

As the building blocks of proteins, amino acids represent the largest portion of characterized biochemicals in most marine environments, and are important contributors to both carbon and nitrogen pools (Burdige and Martens, 1988; Hedges, 1991; Benner et al., 1992; Lee et al., 2000). Estimates suggest that amino acids make up 2–30% of organic carbon and 15–42% of organic nitrogen in coastal and deep ocean sediments (Wakeham et al., 1997; Keil, 1999). Evidence from solid state N-15 NMR spectroscopy shows that the majority of organic nitrogen present in dissolved and particulate marine organic matter contains amide bonds, like those that occur in proteins (McCarthy et al., 1997; Knicker, 2000; Zang et al., 2001). In several cases, protein products as well as intact proteins have been observed in deep ocean waters (Tanoue, 1992; Suzuki et al., 1997; Dong et al., 2010).

Traditional approaches of measuring hydrolysable amino acids (THAAs) in environmental samples as a proxy for total protein material destroy the amide bond, and thus the inherent source information encoded in the protein's amino acid sequence is lost. Our aim is to link the observed THAA distributions to the defined amino acid sequences of identifiable proteins. This will enhance the information obtained between the biosynthetic building blocks of macromolecular organic nitrogen and the geochemical fate of their protein products. The recent characterization of the marine diatom *Thalassiosira pseudonana* genome (Armbrust et al., 2004; Oudot-Le Secq et al., 2007) and now the proteome (Nunn et al., 2009) provided insight into the biochemical pathways utilized by marine diatoms. In addition, it presents the opportunity to track the distribution of proteins from this major algal contributor in natural settings.

With primary production rates up to $570 \text{ g C m}^{-2} \text{ y}^{-1}$, the Bering Sea is perhaps the most productive region in the world (Sambrotto et al., 1986; McRoy et al., 1987; Walsh et al., 1989). As in many high latitude systems, diatoms dominate spring production (Banahan and Goering, 1986; Springer et al., 1996), leading to a carbon export flux in the range of $10 \text{ mmol C m}^{-2} \text{ day}^{-1}$ (Chen et al., 2003). This combination of high productivity of known algal communities and rapid transport to sediments make the Bering Sea an ideal system to study the early diagenetic fate of algal proteins in marine systems.

Here we link proteomic approaches with geochemical cycling to examine the environmental fate of proteins in a system where diatoms provide the bulk of new organic matter. We have merged traditional protein buffer extraction and gel electrophoresis purification techniques with mass spectrometry-based proteomics in order to identify individual proteins in these complex environmental samples. The goal of this study was to track proteins derived from the spring diatom bloom in the Bering Sea through the water column to eventual incorporation into the sedimentary organic nitrogen pool. In doing so, we have the opportunity to identify potential mechanism(s) which regulate the distributions observed during the initial stages of diagenesis.

METHODS

Bering Sea sample collection

All suspended particles from filtration, particle trap, and sediment samples were collected on the Bering Sea outer shelf and basin during the Bering Sea Ecosystem Study (BEST) cruises in the spring and summer of 2009 (Fig. 1). Particulate and trap samples were collected at multiple depths during the spring diatom bloom as ice retreated; samples included both suspended and sinking material inclusive of chlorophyll maximum to bottom waters (Table 1). Suspended particles, collected by Niskin bottles, were filtered onto 47 mm combusted glass fiber filters (GF/Fs) at three depths: chlorophyll max (4 m), 50 m, and 100 m. Sinking

particles were collected from 12 hour trap deployments (40 m, 60 m, and 100 m) at the same location as suspended particles. No preservatives were used with particle trap cups prefilled with brine solution prior to deployment. After collection, 100 mL aliquots of the particle trap samples were filtered onto combusted 25 mm GF/Fs. Undisturbed sediments were collected using a multicore on both the outer shelf and in the deeper basin (3490 m) before the spring phytoplankton bloom and two months after the bloom to allow sampling of recently arrived material at the sediment-water interface (Table 1). Visible phytodetritus was present post-bloom on the surface of both shelf and basin sediments. Surface material (0–1 cm) was removed and samples were frozen and stored at -70°C until analysis.

Amino acid analysis

To provide a metric for comparison of protein content and more traditional measures, total hydrolysable amino acids (THAAs) were quantified and analyzed in parallel with protein identification. Individual amino acids were identified and quantified by gas chromatography (GC) and GC mass spectrometry (GC/MS) using the EZFaast method (Phenomex) which uses derivatization of AAs with propyl chloroformate and propanol for sensitive detection (see Waldhier et al., 2010 for a comparison of methods). Briefly, suspended particles, particle traps, and sediment samples were hydrolyzed for 4 hours at 110°C (Cheng et al., 1975; Cowie and Hedges, 1992) with 6 M analytical-grade HCl and L- γ -Methylleucine as the recovery standard. Following hydrolysis and derivatization, amino acids were quantified using an Agilent 6890 capillary GC with samples injected at 250°C and separated via a DB-5MS (0.25 mm ID, 30 m) column with H_2 as the carrier gas. The oven was ramped from an initial temperature of 110°C to 280°C at 10°C per minute followed by a 5 minute hold. For amino acid identification, the GC was coupled to an Agilent 5973N mass spectrometer run under the same conditions with helium as the carrier gas and acquisition of spectra over the 50–600 Da range. Bovine serum albumin (BSA) was analyzed in parallel to correct for responses among individual amino acids and calculation of molar ratios. Amino acids were normalized to percent carbon or nitrogen using bulk samples analyzed by standard combustion methods.

Protein extraction

To extract proteins from suspended particle and particle trap samples, filters were sliced into sections, fully submerged in 3 mL of extraction buffer, (7 M urea, 2 M thiourea, 0.01 M Tris-HCl, 1 mM EDTA, 10% v/v glycerol, 2% w/v CHAPS, 0.2% w/v ampholytes, 2 mM Tributyl phosphine, see Kan et al., 2005) and pulse sonicated on ice with a Branson 250 Sonifier sonication probe at 20 kHz for 1 minute. The sonication probe was in full contact with filters and particulate material to enhance extraction. The extraction process of sonication in concentrated urea denaturing solution was very similar to past studies on marine particulate proteins identified from multiple cell types by proteomic mass spectrometry (Dong et al. 2010). Extracted material was then centrifuged for 5 min ($5,000 \times g$) to remove particles. For suspended and sinking particles, protein extraction efficiencies were estimated by comparing Bradford Assay protein concentrations of protein extracts to total hydrolysable amino acids (THAAs) of whole samples as a proxy for total protein. The extraction efficiencies for chlorophyll max, 50 m, and 100 m suspended particulate samples (Bradford Assay Protein Concentration/THAA concentration) were 105%, 81%, and 90% respectively.

For sediment protein extraction, known weights of sediment were treated with 500 μL of extraction buffer in 1.5 mL Eppendorf tubes and pulse sonicated for one minute on ice. The entire sediment+extract buffer mixture was then loaded onto gel-prep cell tubes for isolation and molecular weight class separation of proteins. Amounts of protein material loaded onto gels were determined by measuring the concentration of THAAs in filter extracts and

sediment buffer mixtures as a proxy for total protein. The extraction efficiencies (THAA concentration of extract/THAA concentration of sediment) were consistent, ranging from 11–12% for shelf and basin sediments. The extraction protocol and efficiency is described in greater detail in Moore et al. (2012, in press).

To purify extracts and separate proteins based on molecular weight (MW), 1 mL of extract from each sample was loaded onto individual preparatory electrophoresis tubes (prep-gel: 17% Acrylamide/Bis, 0.125 Tris-HCl) for one dimensional separation. Gels were covered with running buffer (0.25 M Tris, 0.192 M glycine, 0.1% SDS, pH 8.3; 180 V) and run until the ion front traveled 7 cm from the top of the gel. After electrophoresis, gels were washed and cut into five molecular weight ranges (<10, 10–25, 25–50, 50–100, and >100 kDa) based on prior separations of MW standards (Kaleidoscope) using identical gels.

In-gel protein digestion

Before enzymatic digestion, gel MW sections were cut into 2 × 2 mm slices to increase surface area for enzyme and chemical access. Pieces were covered with 100 mM ammonium bicarbonate and rinsed for 15 min to hydrate gel sections, and then rinsed for 15 minutes in acetonitrile to dehydrate gel sections and remove detergents and other chemical interferences. The rinse cycle was repeated five times and gel sections then were dried by speed-vac for 45 min. Subsequent reduction, alkylation, and digestion followed standard procedure by Shevchenko et al. (1996). Digests were dried and volumes were adjusted to give a final protein concentration of 1 µg protein/10 µL based upon THAA concentrations and measured recoveries.

Mass spectrometry and database searching

Proteins were identified via shotgun proteomics with samples introduced into the ion trap (LTQ Velos) mass spectrometer (Thermo Fisher) via NanoAcquity high performance liquid chromatography (HPLC, Waters) (Nunn et al., 2010). New analytical and trapping columns were packed in-house prior to batch analyses of Bering Sea samples in order to ensure no proteins were carried over from previous cell lysate proteomic experiments. Analytical columns were made using 11 cm long, 75 µm i.d. fused silica capillaries packed with C18 particles (Magic C18AQ, 100 Å, 5 µm; Michrom, Bioresources) preceded by a 2 cm long, 100 µm i.d. trapping-column (Magic C18AQ, 200 Å, 5 µm; Michrom). Samples were loaded onto the trapping column with a flow rate of 4 µl min⁻¹ (7 min), and then entered the analytical column at a flow rate of 250 nL min⁻¹ (total run time 100 min). Peptides were eluted using an acidified (formic acid, 0.1% v/v) water-acetonitrile linear gradient (5 to 35% acetonitrile in 60 min), and ionized in atmospheric pressure before entering the mass spectrometer. Following a survey of the ions that entered the ion trap (MS¹), the fourteen most intense ions from scans having either +2, +3, +4, or +5 charge states were selected for collision induced dissociation (CID) and tandem mass spectral (MS²) detection (for review see Nunn and Timperman, 2007). Sample digests were analyzed using full scan (*m/z* 350–2000), followed by gas phase fractionation with repeat analyses over multiple narrow, but overlapping mass to charge ranges (e.g. *m/z* 350–444, 444–583, 583–825, 825–1600) (Yi et al., 2002; Nunn et al., 2006; Scherl et al. 2008).

Mass spectra were interpreted and searched using an in-house copy of SEQUEST on a Beowolf-style computer cluster with 800 dedicated processing cores and 22 terabytes of storage (Eng et al., 1994; Eng et al., 2008). All data searches were performed with no assumption of proteolytic enzyme (e.g. trypsin) specificity to allow for identification of the maximal number of protein degradation products. Fixed modifications were set for 57 Da on cysteine (resulting from IAM alkylation step) and 16 Da on methionine via oxidation. Each tandem mass spectrum was then searched against a protein sequence database to correlate

predicted peptide fragmentation patterns with observed sample ions. To objectively validate peptide and protein identifications, two statistical evaluations using PeptideProphet and ProteinProphet were used to provide probability based scores (Keller et al., 2002; Nesvizhskii et al., 2003). Probability thresholds for positive identifications of proteins and peptides were strictly set at 90% confidence on ProteinProphet and PeptideProphet for SEQUEST search results. Mass spectra from all samples were searched against a database (referred to as “Thaps database”) containing the proteomes of *Thalassiosira pseudonana* (marine diatom), *Prochlorococcus marinus* (marine cyanobacterium), and *Pelagibacter ubique* (marine bacterium belonging to the SAR11 clade). The proteomes of *P. marinus* and *P. ubique* were included to account for potential input of bacterial proteins through the water column. The Thaps database was chosen after extensive comparison revealed that larger databases, including the NCBI non-redundant database containing over 11.9 million protein sequences, did not enhance the number of protein identifications, added limited species diversity to identified proteins, and had 95% functional agreement between Thaps and larger database identified peptides from Bering Sea sediment (Moore et al., 2012 in press). False discovery rate was calculated to be 0.5% for Thaps database searches.

A second separate database search was conducted to investigate correlations with a highly diverse assemblage of microbial peptides. This database included the proteome of *T. pseudonana*, plus the Global Ocean Survey (GOS) Combined Assembly Protein database (Rusch et al., 2007; Yooseph et al., 2007; Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis, CAMERA, downloaded on 29 September 2008). Although the GOS database has over 6,000,000 marine microbial proteins sequenced from genomic data, limited functional data are available. In this combined database inclusive of Thaps and GOS sequences, proteins from *T. pseudonana* account for approximately 0.1% of the total protein sequences, suggesting that randomly identified false spectra correlation to a *T. pseudonana* peptide was highly unlikely. Searches using the GOS/Thaps database were only completed on the post bloom surface sediments where microbial products were expected to be most prevalent. The GOS/Thaps-searches were also limited because they were computationally intensive, consuming over 720 hours of search time (~1 month), even on the large computer cluster used. The intent of this search was to seek identifiable bacterial proteins in sediments which were expected to have high levels of microbial recycling.

RESULTS

Protein distribution

Using a mass-spectrometry based approach, 207 proteins were identified in suspended particles from the chl-max of the Bering Sea (Table 2, Fig. 2A). Substantially fewer proteins were identified in suspended particles at 50 m (11 proteins) and 100 m (22 proteins). The number of identified proteins in the particle traps decreased from 136 at 40 m to 53 at 60 m, and 82 at 100 m. In post-bloom shelf sediment 52 proteins were identified, with slightly less than half the number of identifications in post-bloom basin and over-wintered shelf sediment. The majority of identified proteins at depth were also identified in the chlorophyll max, representing transport down the water column (Fig. 3). Sequence coverage, defined as the percentage of a specific protein sequence observed using tandem mass spectrometry, was highest on average in the chl-max and lowest in 50m POC.

The vast majority of peptides observed in all samples correlated to diatom proteins (Table 2). In the two samples with the highest number of protein identifications, chl-max particles and the 40 m particle trap, there were 200 and 129 diatom proteins, respectively, plus seven bacterial identifications in each sample. Overall, the number of observed bacterial proteins accounts for 5% of the total identifications, with the remaining 95% of identifications

correlating to a diatom origin. Post-bloom shelf sediment mass spectra searched against the larger combined Thaps/GOS database yielded no unique bacterial protein identifications with confidence. The majority of identified bacterial protein amino acid sequences overlapped with the amino acid sequences of *T. pseudonana* proteins as well.

As the number of identified proteins declined with increasing depth, the functional distribution of observed proteins changed. Protein categorization by gene ontology (Ashburner et al., 2000) revealed that metabolic proteins made up the largest functional group in chl-max particles at 63%, followed by structure/binding proteins at 18%, and transport proteins at 13% (Table 3). A more even distribution of proteins among the metabolic, structure/binding, and transport groups was observed in 50 m and 100 m suspended particles. In all particle trap and sediment samples, metabolic proteins make up the largest group. Within the metabolic category, translation proteins were the largest subgroup in the chl-max at 17% followed by photosynthesis/carbon fixation proteins at 15% (Table 3). Deeper in the water column, photosynthesis/carbon fixation proteins accounted for 7% to 25% of identified proteins in suspended particles and particle traps; this fraction increased slightly in post-bloom shelf sediment to 26%, then considerably increased to 46% in post-bloom basin sediment and 52% in over-wintered shelf sediment. Conversely, the proportion of transport proteins decreased from water column suspended particles and traps to post-bloom basin and over-wintered shelf sediment. The percentage of proteins classified as structural or binding proteins did not change to the same degree as photosynthesis or transport proteins.

The comparison of protein abundance with more traditional measures found that THAAs decreased from the chl-max (520 $\mu\text{g/L}$) to 50 m suspended particles (14.2 $\mu\text{g/L}$), with a much smaller reduction from 50 m to 100 m (9.0 $\mu\text{g/L}$) (Table 1, Figure 2). Sediment trap THAAs decreased more steadily with depth than seen in suspended particles, not unlike identified proteins. Post-bloom shelf sediment had greater THAA concentrations than post-bloom basin sediment and over-wintered shelf sediment. Hydrophobic amino acids (Leu, Gly, Ala, Phe, Ile, Val) were the most represented amino acids in all samples, making up 56% of the average amino acid distribution in THAAs and 47% of the amino acid distribution of identified protein amino acid sequences (Fig. 4, Appendix 2).

Molecular weight distribution of surviving proteins

To compare the potential for selective loss of individual proteins based on molecular weight, identified proteins were grouped into five molecular weight ranges (<10, 10–25, 25–50, 50–100, >100 kDa) based on two categories. The first category was the predicted molecular weight of intact proteins as identified using mass spectrometry. The second was the molecular weight range in which each protein was observed following gel purification. Proteins identified in their anticipated gel molecular weight range can be categorized as “expected” since molecular weights were in agreement. In contrast, proteins observed by gel electrophoresis to be outside their predicted molecular weight range were categorized as “observed” in order to denote the disparity between gel mobility and expected molecular weight (Fig. 5). Of the proteins grouped by “expected” molecular weight, the vast majority of proteins identified in particles, traps, and sediments were in the intermediate size ranges (10–25, 25–50, 50–100 kDa) expected for many cellular proteins (Fig. 5A). The group with the most identifications comprises those proteins in particles and traps from 25–50 kDa. This changed as the proportion of 25–50 kDa proteins decreased in sediments compared to water particles and traps. The majority of “observed” proteins in suspended particles and particle traps were found to have greater than expected molecular weights (“observed larger”) based on gel migratory behavior (Fig. 5B). The proportion of proteins with lower than expected molecular weights (“observed smaller”) increased in sediments, especially post-bloom basin and over-wintered shelf sediments.

DISCUSSION

Through the identification of unique peptide sequences, we are able to demonstrate that proteins derived from primary production are able to survive the degradation processes during initial transit to the sediment water interface. Over 70% of all proteins identified in suspended particles at depth, and over 80% of proteins identified in particle traps were also detected in the diatom dominated chlorophyll maximum. The importance of proteins derived from primary producers extended to both shelf sediment samples, representing >80% of identified proteins, and basin sediments where 67% of identified proteins were identical to those observed in the chl-max. Diatoms may contribute organic matter to sediments because they are encapsulated in high-density silica frustules that can rapidly transport OM to depth (Dunne et al., 2005; Ragueneau, et al., 2006; Miki et al., 2009). Multiple fucoxanthin chlorophyll a/c binding proteins (FCPs), important light harvesting complex proteins in diatoms and other marine algae (Grossman et al., 1995; Lang and Kroth, 2001; Nunn et al., 2009), were observed in all sediment samples. The presence of these proteins is not completely unexpected; FCPs are central in the light harvesting complex, representing the most abundant protein class discovered in mid-exponential growth *T. pseudonana* (Nunn et al., 2009) and later observed to remain after extensive microbial attack in a controlled month-long degradation experiment (Nunn et al., 2010). Since diatoms dominate spring bloom production in the Bering Sea, and their density and aggregation result in sinking after bloom termination (Smetacek et al., 1985), it is very likely that diatoms are the source of algal-derived light harvesting proteins to Bering Sea sediments.

The discovery of diatom and algal specific proteins in ocean basin sediments reveals that, despite the intensive recycling processes active in oceanic waters, highly organized macromolecules such as proteins can be transported intact from their biosynthetic origins in surface waters to sediments. While fewer proteins were identified in this study than Dong et al. (2010), greater statistical rigor was applied by way of PeptideProphet and ProteinProphet to identify peptides and proteins in the system with greater confidence. In addition, the diatom/algal proteins identified were not only observed over the shallow productive continental shelf, but also in the deeper ocean surface sediments, suggesting that seasonal primary production in the Bering Sea is also an important contributor to deeper environments. Given that diatom sinking rates can range from 40 m per day to over 100 m per day (Smetacek, 1985 and references therein), the sinking time for bloom material to the shelf sediment-water interface (101–136 m) would be on the order of days, while sinking time over the basin (3490 m) would be on the order of weeks. Recent laboratory studies by Nunn et al., (2010) found that a subset of diatom proteins can be retained over a 23 day degradation period, which could encompass the potential sinking time of bloom material to sediments and initial sedimentary recycling. Many more proteins were identified in sinking sediment trap material than in suspended particle samples (Table 2), reinforcing previous observations that sinking material has a distinct composition compared to suspended particles (Sheridan et al., 2002; Abramson et al., 2010). To our knowledge, this is the first demonstration that intracellular, cytosolic and soluble proteins can be transported to depth from sources in the upper water column. These factors suggest that in the Bering Sea and other diatom-dominated systems, the large size and density of diatoms is central to transport, burial, and eventual preservation of sedimentary proteins from a range cellular compartments.

It has long been observed that as marine organic matter becomes more degraded, there is a decrease in the ratios of total hydrolysable amino acids to organic carbon (THAA/OC), and THAA-nitrogen to particulate nitrogen (THAA-N/PN) (e.g. Cowie and Hedges, 1994 and references therein). Here, these two ratios were used to normalize amino acid amounts across multiple sample types, and compare amino acid concentrations with the number of

identifiable proteins in each sample. Plotting the number of identified proteins against the ratios of THAA/OC and THAA-N/PN, strong correlations are observed for both carbon and nitrogen (Fig. 6A, B). The correlation between protein identifications and THAA-N/PN is particularly strong, displaying the importance of protein to marine organic nitrogen (Brown, 1991; Lourenco et al., 1998). These relationships also show that over a wide range of concentrations, THAAs present in particles and even surface sediments likely include a portion of intact proteins, with the number of identified proteins reflecting the extent to which proteins have been degraded during diagenesis. In the case of this study where diatoms are the primary source material, the relationship likely reflects the freshness of produced organic matter and retention of diatom proteins.

Arranging samples in order of decreasing THAA-N/PN values, sample clusters are formed: chl-max particles > all particle traps > deeper suspended particles and surface sediment, which likely represents increasing degradation status (Fig. 6B). This order also generally reflects the amount of identifiable proteins in each sample and average sequence coverage of identified proteins in most samples. Fewer identifiable proteins and similar THAA-N/PN proxies from suspended particles suggest a similar “degraded” status for proteins compared to those found in the sediments. This may reflect the length of time since organic matter production (Hartnett et al., 1998) as well as the potential importance of sorption to sediment for protein preservation (Collins, 1995; Mayer, 1999). The enhanced sedimentation rates of large aggregates could control the fraction of proteins present in surface sediments.

In addition to the absolute number of identified proteins and THAAs, the diversity of different protein groups based on cellular function declined in deeper waters and with residence time in surface sediments. Metabolic proteins made up the largest group in all samples except for the 50 m suspended particle sample (Table 3). Within the metabolic protein category, photosynthetic and carbon fixation proteins represent the largest percentage of proteins remaining in sedimentary material. Recent work by Nunn et al. (2010) highlighted factors that might influence the preservation of such proteins over short time scales. Several characteristic traits were proposed to encourage protein stability and/or longevity including organelle compartmentalization, transmembrane-spanning domains, initial cellular abundance, glycan modifications, and aggregation. Several of these mechanisms can be considered in the context of Bering Sea protein preservation.

Compartmentalization and preservation potential

Proteins are not uniformly distributed in cells, but typically associated with various cellular compartments which might influence preservation and help explain the observed distribution shifts of protein cellular functions through water column loss. Gel electrophoresis has been shown to enhance liberation of membrane bound proteins (Coughenour et al., 2004) allowing improved identification of organelle proteins in addition to molecular weight separation. To examine the possibility of organelle preservation, protein compartments were assigned to sub-cellular locations based on the *T. pseudonana* proteome using the TargetP 1.1 Server (Emanuelsson et al., 2007) and uniprot.org (Jain et al., 2009).

The proportion of membrane compartmentalized proteins discovered in sediments (i.e. chloroplast and mitochondrial proteins) increased from post-bloom shelf sediment to both post-bloom basin and over-wintered shelf sediments, while the proportion of secretory proteins decreased. Similarly, the percentage of identified proteins with transmembrane regions, as modeled by TMHMM Server v. 2.0 (Krogh et al., 2001) increased in deeper particles and sediments (Table 4). These observations suggest that soluble secretory proteins, with no added organelle membrane protection, are more susceptible to microbial recycling during sinking to deep basin sediments or longer residence time in over-wintered shelf sediments compared to post bloom shelf sediments. Similar patterns were recently seen

in laboratory incubations (Nunn et al. 2010) with the preferential preservation of organelle enclosed proteins. This includes the important light harvesting FCP proteins which are enclosed in 4 membrane layers of the thylakoid and chloroplast (Westermann and Rhiel, 2005). Previous work has shown proteins enclosed in crude membrane extracts are degraded more slowly compared to soluble proteins (Nagata et al., 1998), and protein sequences derived from conserved membrane/envelope proteins were previously identified from Gulf of Mexico DOM (Powell et al. 2005). These lines of evidence point to physical protection through membrane associations as a factor in the survival of marine proteins.

Implications of identified proteins on THAA distribution

Although early reports found that the relative distribution of particulate amino acids show only minor changes with ocean depth (Wakeham et al., 1984; Müller et al., 1986), or as algae are subject to degradation (Nguyen and Harvey, 1997), amino acid distributions have been used as a metric for degradation state (Dauwe and Middelburg, 1998 and references therein). Given that the amino acid distribution of most proteins is very similar (Brooks et al., 2002), such changes are small. We can compare total THAAs among all sample types with amino acids tabulated from the sequences of identified proteins and those amino acids associated only with transmembrane regions of proteins (Fig. 4A–C). Grouped for ease of comparison into major functional groups, the distribution of amino acids tabulated from identified proteins shows remarkable similarity to THAAs among suspended, sinking, and sedimentary material. The proportion of hydrophobic amino acids was highest for transmembrane proteins among all sample types (71–73% non-polar), and may reflect hydrophobic interactions previously observed as stabilizing forces for proteins in particulate material and organic rich sediments (Nguyen and Harvey, 2001) and kerogens (Nguyen and Harvey, 2003).

Protein abundance and identification

The array of possible marine proteins is vast, as reflected by the breadth of the GOS protein database (Yooseph et al., 2007). Identification of proteins by data-dependent ion selection of peptides during HPLC-MS/MS is inherently biased to more abundant peptides in complex matrices and thus proteins in low concentrations may remain below detection limits. This suggests that the most abundant proteins present in diatom cells are more likely to be available for identification after long term microbial attack. To test this, proteins ranked in the top ~1% of abundance based on the proteome analysis of Nunn et al., (2009) were classified as high abundance proteins, while the remaining proteins in the *T. pseudonana* proteome were grouped as low abundance proteins. The proportion of high abundance proteins increases among identified proteins with depth from bloom material to sinking trap material to sediments (Table 4). The percentage of high abundance proteins was also greater in over-wintered shelf sediment than either post-bloom or deeper shelf sediment samples. This suggests that initial abundance of individual proteins in living cells influences the potential for their detection after substantial losses via degradation. Once a protein reaches the sediment, preservation mechanisms such as aggregation (Nguyen and Harvey, 2001; 2003), particle (Nagata and Kirchman, 1996), or mineral sorption (Mayer, 1994; 1999; Hedges and Keil, 1999), are likely to extend its longevity.

Protein molecular weight

An important caveat to the identification of proteins is that absolute molecular weight is not measured, and thus proteins which are retained in the system might represent non-native forms. Indeed, covalent modifications have been previously proposed as one mechanism for protein preservation in older sediments (Cronin and Morris, 1981; Benner et al, 1992; Nguyen and Harvey, 2003). Given the molecular weight distribution of low, intermediate, and high molecular weight proteins in the *T. pseudonana* proteome (Armbrust et al., 2004;

Nunn et al., 2009), the observed electrophoretic behavior among a subset of identified proteins suggests that changes to the original sequence (or charge) are common and can lead to higher than expected molecular weights based on mobility within a gel (Fig. 5B). While aggregation has been proposed previously as one mechanism (Nguyen and Harvey, 2001; 2003), the denaturing conditions used here suggest that covalent modifications or charge alterations are also operative. The fact that there were also a significant number of proteins which appear to have lower molecular weights than expected suggests that partial hydrolysis is active as well (i.e. Pantoja and Lee, 1999).

Bacterial proteins in sediment

In the Bering Sea as in other ocean environments, microbial processes act as the primary catalyst for organic matter recycling. Although estimated bacterial biomass present in sediments is far lower than that derived from primary production, proteins associated with active microbial populations undoubtedly are present. Mass spectra collected from Bering Sea shelf post-bloom sediments searched against the *T. pseudonana*/GOS Combined Assembly Protein database yielded only two bacterial protein identifications at the 90% confidence level: 1) a vacuolar proton inorganic pyrophosphatase and 2) translation elongation factor 1 alpha. The spectra that correlated to peptides from the GOS database from these two proteins also correlated with known *T. pseudonana* peptides, demonstrating that in many cases different species have homologous peptide sequences.

Challenges with identifying bacterial proteins noted in the soil literature include high diversity of known and unknown bacterial proteins resulting in incomplete bacterial protein databases and individual proteins being below detection limits (Graves and Haystead, 2002; Quince et al., 2008; Bastida et al., 2009). Furthermore, bacterial proteins may be masked by co-extracted sedimentary material (Criquet et al., 2002) confounding the issue of detection limits missing highly diverse low abundance proteins. Nevertheless, proteomic studies on soil organic matter have revealed functional information on microbial communities and particle bound material (Schulze et al., 2005; Benndorf et al., 2007). Bacteria appear principally as catalysts in this first examination of protein distributions during organic matter recycling in marine systems, with phytoplankton derived material as the confirmed source of proteins in Bering Sea sediments. Simple estimations based on typical bacterial cell abundance in marine sediments ($\sim 10^9$ cells g^{-1} ; Griffiths, et al., 1978; Deming and Colwell, 1982; Harvey, et al., 1984; Luna, et al., 2002; Kopke, et al., 2005) and average protein content per cell (24 fg cell $^{-1}$, Zubkov et al., 1999) indicate that bacteria likely contribute a small fraction to the total protein pool examined here.

CONCLUSIONS

This is the first study to apply an MS-based proteomics approach to follow the environmental fate of phytoplankton specific proteins present during bloom, transport, and initial incorporation into sediments. The survival of algal derived proteins appears selective, with compartmentalized and cell membrane proteins demonstrating greater longevity after genesis and short-term recycling in the water column. The correlation between identifiable proteins and THAA-N/PN suggests that proteins are not all rapidly hydrolyzed but may represent a predictable fraction of organic nitrogen present in organic matter. While database and detection limit challenges hinder the identification of bacterial proteins, phytoplankton proteins appear to be important contributors to Bering Sea sedimentary THAAs.

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APPENDIX 1

Summary list of all proteins identified in each sample. Includes identified species, biological function, cellular compartment (Comp): C = Chloroplast; S = Secretory; M = Mitochondria; N = Nucleus; U = Uncharacterized Compartment), molecular weight (MW), isoelectric point (pI) sequence coverage, percent sequence coverage (Seq Cov).

| Chl Max | | | | | | | | |
|--|--------------|--------------------------|-----------------------|------|--------|------|------|--|
| Protein | Annotation | Species | Function | Comp | MW | pI | SC | |
| 26S proteasome AAA-ATPase subunit RPT3 | jgi 24475 | Thalassiosira pseudonana | Photosynthesis | S | 42455 | 6.0 | 4.8 | |
| 30S ribosomal protein S1 | jgi 15259 | Thalassiosira pseudonana | Translation | S | 31770 | 4.6 | 7.7 | |
| 30S ribosomal protein S11 | gi 118411211 | Thalassiosira pseudonana | Translation | C | 13821 | 11.3 | 13.8 | |
| 30S ribosomal protein S18 | gi 118411132 | Thalassiosira pseudonana | Translation | C | 8155 | 10.8 | 31.9 | |
| 30S ribosomal protein S3 | gi 118411197 | Thalassiosira pseudonana | Translation | C | 24091 | 9.2 | 6.1 | |
| 30S ribosomal protein S7 | gi 118411217 | Thalassiosira pseudonana | Translation | C | 17730 | 10.5 | 21.2 | |
| 30S ribosomal protein S8 | gi 118411204 | Thalassiosira pseudonana | Translation | C | 14805 | 9.4 | 8.3 | |
| 3-deoxy-7-phosphoheptulonate synthase | jgi 2790 | Thalassiosira pseudonana | Biosynthesis | C | 53939 | 6.0 | 13.2 | |
| 3-phosphoshikimate 1-carboxyvinyltransferase | jgi 33008 | Thalassiosira pseudonana | Transport | S | 47333 | 4.6 | 5.6 | |
| 40S ribosomal protein S17 | jgi 37809 | Thalassiosira pseudonana | Translation | C | 14145 | 10.0 | 9.8 | |
| 40S ribosomal protein S5 | jgi 29955 | Thalassiosira pseudonana | Translation | S | 24397 | 6.9 | 6.0 | |
| 40S ribosomal protein S9 | jgi 268651 | Thalassiosira pseudonana | Binding rRNA | S | 21764 | 10.2 | 8.9 | |
| 40S ribosomal protein SA p40 | jgi 21871 | Thalassiosira pseudonana | Translation | S | 27261 | 5.9 | 18.9 | |
| 50S ribosomal protein L11 | gi 118411123 | Thalassiosira pseudonana | Translation | C | 14880 | 9.7 | 9.2 | |
| 50S ribosomal protein L14 | gi 118411201 | Thalassiosira pseudonana | Translation | C | 13433 | 10.3 | 27.3 | |
| 50S ribosomal protein L16 | gi 118411198 | Thalassiosira pseudonana | Translation | C | 15581 | 11.0 | 10.2 | |
| 50S ribosomal protein L2 | gi 118411193 | Thalassiosira pseudonana | Translation | C | 30675 | 10.9 | 6.5 | |
| 50S ribosomal protein L21 | gi 118411174 | Thalassiosira pseudonana | Binding RNA | C | 12433 | 10.1 | 8.6 | |
| 50S ribosomal protein L3 | gi 118411190 | Thalassiosira pseudonana | Translation | C | 22012 | 10.1 | 19.3 | |
| 60 kDa chaperonin | gi 118411188 | Thalassiosira pseudonana | Binding Protein | C | 57361 | 5.2 | 15.6 | |
| 60s Acidic ribosomal protein | jgi 3463 | Thalassiosira pseudonana | Translation | S | 27213 | 4.6 | 6.1 | |
| 6-phosphogluconate dehydrogenase | jgi 33343 | Thalassiosira pseudonana | Dehydrogenase | S | 53348 | 5.6 | 10.8 | |
| Abnormal wing discs CG2210-PA | jgi 6290 | Thalassiosira pseudonana | Biosynthesis | u | 17236 | 5.5 | 30.3 | |
| Acetyl-CoA carboxylase | jgi 6770 | Thalassiosira pseudonana | Metabolic Process | c | 228295 | 5.0 | 2.3 | |
| Acidic ribosomal phosphoprotein P0 | jgi 25812 | Thalassiosira pseudonana | Biosynthesis Ribosome | S | 34116 | 4.8 | 3.7 | |
| Actin A | jgi 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 19.9 | |
| Adenosinetriphosphatase | jgi 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 20.2 | |

| Chl Max | | | | | | | | | |
|---|-------------------|--------------------------|--------------------|-------------|-----------|-----------|-----------|--|--|
| Protein | Annotation | Species | Function | Comp | MW | pI | SC | | |
| ALA dehydratase | jgi 5240 | Thalassiosira pseudonana | Biosynthesis | S | 40419 | 5.0 | 7.4 | | |
| Aminotransferase AGD2 | jgi 31394 | Thalassiosira pseudonana | Transport | S | 44264 | 4.8 | 11.5 | | |
| Arginyl-tRNA synthetase | jgi 40028 | Thalassiosira pseudonana | translation | S | 66081 | 4.9 | 2.7 | | |
| | | Candidatus | | | | | | | |
| ArgJ family protein | gi 71083219 | Pelagibacter ubique | Biosynthesis | S | 43114 | 9.5 | 3.4 | | |
| Aromatic amino acid family biosynthesis-related protein | jgi 268552 | Thalassiosira pseudonana | Biosynthesis | C | 66486 | 5.0 | 3.8 | | |
| ATP binding / protein binding | jgi 23102 | Thalassiosira pseudonana | Binding Protein | S | 59170 | 5.3 | 5.3 | | |
| ATP synthase CF0 B chain subunit I | gi 118411110 | Thalassiosira pseudonana | Transport Proton | C | 20029 | 9.8 | 8.4 | | |
| ATP synthase CF0 B' chain subunit II | gi 118411109 | Thalassiosira pseudonana | Transport Proton | C | 17373 | 4.6 | 29.5 | | |
| ATP synthase CF1 alpha chain | gi 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 35.0 | | |
| ATP synthase CF1 beta chain | gi 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 51.1 | | |
| ATP synthase CF1 delta chain | gi 118411111 | Thalassiosira pseudonana | Transport Ion | C | 21077 | 9.2 | 8.0 | | |
| ATP/ADP translocator | jgi 39143 | Thalassiosira pseudonana | Transport | M | 32254 | 9.4 | 4.0 | | |
| ATPase, E1-E2 type | jgi 262679 | Thalassiosira pseudonana | Transport Cation | S | 99192 | 5.6 | 1.5 | | |
| ATP-dependent clp protease ATP-binding subunit | gi 118411220 | Thalassiosira pseudonana | Catalysis | C | 102150 | 6.5 | 1.5 | | |
| ATP-sulfurylase | jgi 1326 | Thalassiosira pseudonana | Metabolic Process | S | 45362 | 5.2 | 2.0 | | |
| BiP | jgi 27656 | Thalassiosira pseudonana | Cell Morphogenesis | C | 70451 | 4.7 | 27.6 | | |
| Catalytic | jgi 41733 | Thalassiosira pseudonana | Biosynthesis | C | 71455 | 5.4 | 9.3 | | |
| CbbX protein homolog | jgi 40193 | Thalassiosira pseudonana | Biosynthesis | C | 35036 | 5.3 | 25.1 | | |
| CDC48/ATPase | jgi 267952 | Thalassiosira pseudonana | Binding ATP | S | 89464 | 4.8 | 4.4 | | |
| cell division protein FtsH2 | jgi 31930 | Thalassiosira pseudonana | Binding Zn | C | 61956 | 5.1 | 11.9 | | |
| Cell division protein FtsH-like protein | gi 118411141 | Thalassiosira pseudonana | Proteolysis | C | 70206 | 5.1 | 15.9 | | |
| CG11154-PA, isoform A | jgi 41256 | Thalassiosira pseudonana | Transport Proton | U | 53388 | 5.1 | 50.8 | | |
| CG17332-PA, isoform A isoform 1 | jgi 263135 | Thalassiosira pseudonana | Transport Proton | U | 33233 | 5.7 | 5.4 | | |
| Chloroplast 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase precursor | jgi 29228 | Thalassiosira pseudonana | Biosynthesis | C | 75736 | 4.9 | 2.6 | | |
| Chloroplast clp protease P | jgi 1738 | Thalassiosira pseudonana | Proteolysis | C | 28223 | 4.8 | 11.1 | | |
| Chloroplast coproporphyrinogen III oxidase | jgi 31012 | Thalassiosira pseudonana | Biosynthesis | C | 34001 | 5.4 | 5.7 | | |
| Chloroplast cysteine synthase 1 precursor | jgi 31829 | Thalassiosira pseudonana | Metabolic Process | C | 33261 | 5.1 | 6.9 | | |
| Chloroplast light harvesting protein isoform 12 | jgi 270092 | Thalassiosira pseudonana | Photosynthesis | C | 18463 | 4.6 | 6.2 | | |
| Chloroplast light harvesting protein isoform 12 | jgi 33606 | Thalassiosira pseudonana | Photosynthesis | C | 26078 | 5.5 | 13.5 | | |

Chl Max

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|-------------------|--------------------------------|--------------------------|-------------|-----------|-----------|-----------|
| Chloroplast light harvesting protein isoform 15 | jgi 2845 | Thalassiosira pseudonana | Photosynthesis | C | 21873 | 5.1 | 5.4 |
| Chloroplast O-acetyl-serine lyase | jgi 267987 | Thalassiosira pseudonana | Metabolic Process | C | 38072 | 5.7 | 4.8 |
| Chorismate synthase | jgi 38964 | Thalassiosira pseudonana | Biosynthesis | C | 44051 | 5.5 | 4.9 |
| CPN60 protein | jgi 23329 | Thalassiosira pseudonana | Binding Protein | C | 59177 | 4.7 | 5.6 |
| Cytochrome b559 alpha chain | gi 118411160 | Thalassiosira pseudonana | Photosynthesis | C | 9514 | 5.6 | 25.0 |
| Cytochrome c-550 | gi 118411100 | Thalassiosira pseudonana | Electron Transport | C | 17841 | 7.7 | 11.0 |
| Cytochrome f | gi 118411137 | Thalassiosira pseudonana | Photosynthesis | C | 33988 | 8.2 | 28.3 |
| Cytosolic ribosomal protein S8 | jgi 29825 | Thalassiosira pseudonana | Translation | S | 22604 | 10.5 | 7.5 |
| D-3-phosphoglycerate dehydrogenase | jgi 25130 | Thalassiosira pseudonana | Oxidoreductase | C | 50144 | 6.4 | 4.3 |
| Diaminopimelate decarboxylase | gi 71083118 | Candidatus Pelagibacter ubique | Biosynthesis, amino acid | S | 45589 | 9.9 | 4.5 |
| DNA binding | jgi 29950 | Thalassiosira pseudonana | Binding DNA | C | 15300 | 11.3 | 8.1 |
| Domain specific binding protein 14-3-3 | jgi 26146 | Thalassiosira pseudonana | Binding Protein | S | 27869 | 4.6 | 23.1 |
| Elongation factor 2 | jgi 269148 | Thalassiosira pseudonana | Translation | S | 91887 | 6.0 | 4.2 |
| Elongation factor alpha-like protein | jgi 41829 | Thalassiosira pseudonana | Translation | S | 49969 | 8.7 | 10.6 |
| Endoplasmic reticulum membrane fusion protein | jgi 40348 | Thalassiosira pseudonana | Transcription | S | 74221 | 4.7 | 2.4 |
| Enolase | jgi 40771 | Thalassiosira pseudonana | Glycolysis | S | 46744 | 4.9 | 21.1 |
| Enolase 2 | jgi 40391 | Thalassiosira pseudonana | Glycolysis | S | 46547 | 4.8 | 21.1 |
| Enoyl-acyl carrier reductase | jgi 32860 | Thalassiosira pseudonana | Oxidation Reduction | S | 32813 | 5.1 | 25.0 |
| ENSANGP00000020417 | jgi 354 | Thalassiosira pseudonana | Binding, DNA | M | 41939 | 6.9 | 4.3 |
| Eukaryotic translation initiation factor 4A2 isoform 2 | jgi 9716 | Thalassiosira pseudonana | Binding DNA | S | 42405 | 5.6 | 19.5 |
| FOF1 ATP synthase subunit alpha | gi 33862007 | Prochlorococcus marinus | Transport Proton | S | 54306 | 4.9 | 4.6 |
| FOF1 ATP synthase subunit beta | gi 33861994 | Prochlorococcus marinus | Transport Proton | S | 51948 | 5.0 | 13.3 |
| FOF1 ATP synthase subunit beta | gi 71082935 | Candidatus Pelagibacter ubique | Transport Proton | S | 50696 | 4.9 | 9.7 |
| Ferredoxin component | jgi 29842 | Thalassiosira pseudonana | Oxidoreductase | C | 18511 | 8.9 | 6.7 |
| Ferredoxin-dependent glutamate synthase | jgi 269900 | Thalassiosira pseudonana | Metabolic Process | C | 178531 | 5.4 | 5.6 |
| FeS assembly protein SufD | jgi 268364 | Thalassiosira pseudonana | Binding Protein | S | 31963 | 5.2 | 5.8 |
| Formylglycineamide ribotide amidotransferase | jgi 30301 | Thalassiosira pseudonana | Catalysis | S | 143746 | 5.0 | 1.4 |
| Fructose-1,6-bisphosphate aldolase precursor | jgi 428 | Thalassiosira pseudonana | Glycolysis Metabolic | S | 39810 | 4.8 | 19.7 |
| Fructose-bisphosphatase | jgi 264556 | Thalassiosira pseudonana | Process Carbohydrate | C | 33667 | 5.3 | 5.1 |
| Fucoxanthin chlorophyll a/c protein | jgi 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 17.6 |

| Chl Max | | | | | | | | |
|--|-------------------|--------------------------|--------------------|-------------|-----------|-----------|-----------|--|
| Protein | Annotation | Species | Function | Comp | MW | pI | SC | |
| Fucoxanthin chlorophyll a/c protein | jgi 38715 | Thalassiosira pseudonana | Photosynthesis | C | 20718 | 4.9 | 19.3 | |
| Fucoxanthin chlorophyll a/c protein | jgi 38494 | Thalassiosira pseudonana | Photosynthesis | C | 20354 | 4.5 | 17.5 | |
| Fucoxanthin chlorophyll a/c protein | jgi 42962 | Thalassiosira pseudonana | Photosynthesis | C | 21515 | 5.1 | 18.4 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi 12097 | Thalassiosira pseudonana | Photosynthesis | C | 27330 | 4.8 | 8.2 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi 264921 | Thalassiosira pseudonana | Photosynthesis | c | 22205 | 4.6 | 8.6 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 17.1 | |
| Fucoxanthin chlorophyll a/c light-harvesting protein | jgi 33018 | Thalassiosira pseudonana | Photosynthesis | C | 21786 | 5.4 | 4.0 | |
| G protein beta subunit | jgi 26063 | Thalassiosira pseudonana | rRNA Processing | S | 35960 | 6.2 | 23.0 | |
| GDP-mannose dehydratase | jgi 40586 | Thalassiosira pseudonana | Catalysis | S | 40412 | 5.9 | 4.2 | |
| Geranyl-geranyl reductase | jgi 10234 | Thalassiosira pseudonana | Electron Transport | C | 47230 | 5.9 | 20.0 | |
| Glucose-6-phosphate isomerase | jgi 38266 | Thalassiosira pseudonana | Glycolysis | S | 61689 | 5.9 | 2.7 | |
| Glutamate 1-semialdehyde 2,1-aminomutase | jgi 575 | Thalassiosira pseudonana | Binding Phosphate | S | 43658 | 5.5 | 7.1 | |
| Glutamine synthetase | jgi 26051 | Thalassiosira pseudonana | Biosynthesis | C | 45620 | 5.2 | 5.8 | |
| Glyceraldehyde-3-phosphate dehydrogenase | jgi 28334 | Thalassiosira pseudonana | Glycolysis | C | 36574 | 6.1 | 8.4 | |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 29.6 | |
| Glycolaldehydetransferase | jgi 21175 | Thalassiosira pseudonana | Transport | M | 71708 | 5.0 | 25.6 | |
| Heat shock protein 60 | jgi 38191 | Thalassiosira pseudonana | Folding Protein | S | 58525 | 4.8 | 6.8 | |
| Heat shock protein 70 | jgi 269120 | Thalassiosira pseudonana | Folding Protein | S | 71187 | 4.8 | 10.1 | |
| Heat shock protein 83 | jgi 268500 | Thalassiosira pseudonana | Folding Protein | S | 86014 | 4.6 | 1.8 | |
| Heat shock protein Hsp90 | jgi 6285 | Thalassiosira pseudonana | Folding Protein | S | 80242 | 4.7 | 7.5 | |
| Histone H2A.1 | jgi 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 | |
| Histone H4 | jgi 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 41.7 | |
| Hsp70-type chaperone | gi 118411189 | Thalassiosira pseudonana | Transcription | C | 65339 | 4.8 | 7.0 | |
| HSP90-like protein | jgi 22766 | Thalassiosira pseudonana | Folding Protein | S | 80966 | 4.7 | 2.0 | |
| Hypothetical protein | jgi 26224 | Thalassiosira pseudonana | n.a. | S | 31116 | 8.9 | 7.7 | |
| Hypothetical protein | jgi 38221 | Thalassiosira pseudonana | n.a. | U | 14645 | 5.6 | 9.3 | |
| Hypothetical Protein | jgi 23918 | Thalassiosira pseudonana | n.a. | C | 31192 | 4.8 | 11.3 | |
| Hypothetical Protein | jgi 24512 | Thalassiosira pseudonana | n.a. | C | 41414 | 6.0 | 4.8 | |
| Hypothetical Protein | jgi 6441 | Thalassiosira pseudonana | n.a. | S | 26822 | 5.4 | 49.8 | |
| Hypothetical protein AN1993.2 | jgi 31424 | Thalassiosira pseudonana | Transport | S | 45198 | 6.2 | 3.8 | |

| Chl Max | | | | | | | | | |
|---|-------------------|--------------------------|-------------------------------|-------------|-----------|-----------|-----------|--|--|
| Protein | Annotation | Species | Function | Comp | MW | pI | SC | | |
| Hypothetical protein CBG01077 | jgi 22792 | Thalassiosira pseudonana | Transport | S | 22486 | 6.7 | 13.9 | | |
| Hypothetical protein CBG08717 | jgi 269322 | Thalassiosira pseudonana | Transport Proton | S | 58009 | 5.8 | 19.4 | | |
| Hypothetical protein DDB0218359 | jgi 24710 | Thalassiosira pseudonana | n.a. | C | 46717 | 4.6 | 3.8 | | |
| Hypothetical protein DEHA0F19712g | jgi 27352 | Thalassiosira pseudonana | Binding DNA | N | 13064 | 10.3 | 16.7 | | |
| Hypothetical protein FG01081.1 | jgi 25949 | Thalassiosira pseudonana | Translation | U | 20124 | 9.8 | 7.9 | | |
| Hypothetical protein LOC496448 | jgi 269540 | Thalassiosira pseudonana | Binding Protein | S | 192707 | 5.5 | 0.9 | | |
| Importin alpha 1 | jgi 43097 | Thalassiosira pseudonana | Transport Protein | S | 60533 | 4.9 | 3.2 | | |
| Inorganic diphosphatase/magnesium ion binding/pyrophosphatase | jgi 269348 | Thalassiosira pseudonana | Metabolic Process Phosphatase | S | 29982 | 4.8 | 5.5 | | |
| Integrin beta 4 binding protein | jgi 29782 | Thalassiosira pseudonana | Binding Ribosome | S | 27279 | 5.0 | 9.4 | | |
| Isocitrate/isopropylmalate dehydrogenase | jgi 5293 | Thalassiosira pseudonana | Oxidoreductase | S | 40667 | 4.6 | 12.5 | | |
| Ketol-acid reductoisomerase | jgi 23228 | Thalassiosira pseudonana | Oxidation Reduction | C | 58240 | 5.1 | 8.6 | | |
| L4/L1 | jgi 22610 | Thalassiosira pseudonana | Translation | S | 40991 | 10.3 | 7.7 | | |
| Magnesium-chelatase subunit I | gi 118411138 | Thalassiosira pseudonana | Photosynthesis | C | 39500 | 5.0 | 6.5 | | |
| Malate dehydrogenase | jgi 20726 | Thalassiosira pseudonana | Oxidoreductase | S | 36724 | 6.3 | 7.4 | | |
| Manganese superoxide dismutase | jgi 32874 | Thalassiosira pseudonana | Metabolic Process | M | 27061 | 5.5 | 14.8 | | |
| Molecular chaperone DnaK | jgi 269240 | Thalassiosira pseudonana | Morphogenesis, Cell | S | 72207 | 5.0 | 2.4 | | |
| Molecular chaperone DnaK2, heat shock protein hsp70-2 | gi 33862260 | Prochlorococcus marinus | Folding Protein | S | 68202 | 4.8 | 2.7 | | |
| Myo-inositol dehydrogenase precursor | jgi 1049 | Thalassiosira pseudonana | Biosynthesis | S | 48134 | 5.0 | 6.2 | | |
| Nucleoside diphosphate kinase | jgi 31091 | Thalassiosira pseudonana | Biosynthesis | C | 16597 | 5.8 | 17.2 | | |
| Nucleoside diphosphate kinase | jgi 12070 | Thalassiosira pseudonana | Biosynthesis | C | 16917 | 8.3 | 18.8 | | |
| Oxygen-evolving enhancer protein 1 precursor | jgi 34830 | Thalassiosira pseudonana | Photosynthesis | C | 29136 | 5.2 | 27.3 | | |
| PAaA | jgi 24864 | Thalassiosira pseudonana | Transport Proton | S | 29661 | 5.6 | 5.5 | | |
| phosphatase 1, catalytic subunit, beta isoform 1 | jgi 2538 | Thalassiosira pseudonana | hydrolase | S | 35512 | 5.0 | 4.7 | | |
| Phosphoadenosine-phosphosulphate reductase | jgi 24887 | Thalassiosira pseudonana | Metabolic Process | C | 49035 | 5.0 | 3.9 | | |
| Phosphofructokinase | jgi 22213 | Thalassiosira pseudonana | Glycolysis | C | 43797 | 5.7 | 2.7 | | |
| Phosphoglucomutase, cytoplasmic (Glucose phosphomutase) | jgi 268621 | Thalassiosira pseudonana | Binding Mg | S | 60470 | 4.8 | 2.5 | | |
| Phosphoglycerate kinase precursor | jgi 35712 | Thalassiosira pseudonana | Glycolysis | C | 42256 | 5.0 | 24.5 | | |
| Phosphoglycerate mutase 1 | jgi 27850 | Thalassiosira pseudonana | Glycolysis | C | 32465 | 6.1 | 4.1 | | |
| Phosphoribulokinase | jgi 4376 | Thalassiosira pseudonana | Biosynthesis | C | 42389 | 4.9 | 7.2 | | |
| Phosphoserine transaminase | jgi 3018 | Thalassiosira pseudonana | Metabolic Process | C | 55763 | 5.3 | 2.5 | | |

Chl Max

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|---------------------|-------------|-----------|-----------|-----------|
| Photosystem I ferredoxin-binding protein | gi 118411153 | Thalassiosira pseudonana | Photosynthesis | C | 15518 | 9.6 | 56.8 |
| Photosystem I protein F | gi 118411168 | Thalassiosira pseudonana | Photosynthesis | C | 20362 | 8.9 | 20.0 |
| Photosystem I protein L | gi 118411163 | Thalassiosira pseudonana | Photosynthesis | C | 15704 | 9.3 | 5.4 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II 11 kD protein | jgi 3258 | Thalassiosira pseudonana | Photosystem | C | 19602 | 9.6 | 6.3 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 14.5 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 4.7 |
| Photosystem II protein Y | gi 118411171 | Thalassiosira pseudonana | Photosynthesis | C | 4006 | 12.5 | 22.2 |
| Photosystem II reaction center protein D1 | gi 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 6.7 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 12.5 |
| Photosystem II stability/assembly factor HCF136 | jgi 38769 | Thalassiosira pseudonana | Photosystem | C | 40327 | 5.2 | 32.5 |
| Phytanoyl-CoA dioxygenase | jgi 2770 | Thalassiosira pseudonana | Oxygenase | S | 33971 | 6.6 | 4.4 |
| Phytoene dehydrogenase and related proteins | jgi 10233 | Thalassiosira pseudonana | Electron Transport | C | 75519 | 5.6 | 2.7 |
| Polyprenyl synthetase | jgi 268480 | Thalassiosira pseudonana | Biosynthesis | C | 36015 | 4.8 | 4.1 |
| Proteasomal ATPase | jgi 32037 | Thalassiosira pseudonana | Binding DNA | C | 45065 | 8.7 | 4.7 |
| Protein product unnamed | jgi 37976 | Thalassiosira pseudonana | Folding, Protein | U | 17068 | 8.8 | 6.7 |
| Pyridine nucleotide-disulphide oxidoreductase, class I | jgi 24399 | Thalassiosira pseudonana | Electron Transport | S | 52509 | 5.4 | 4.2 |
| Pyruvate dehydrogenase | | | | | | | |
| E1 component beta subunit | jgi 32983 | Thalassiosira pseudonana | Glycolysis | C | 37156 | 5.4 | 3.5 |
| Pyruvate kinase | jgi 4875 | Thalassiosira pseudonana | Glycolysis | C | 67221 | 5.2 | 4.5 |
| Quinone oxidoreductase | jgi 32955 | Thalassiosira pseudonana | Oxidation Reduction | C | 32992 | 5.9 | 10.9 |
| Ribosomal protein L12e | jgi 39424 | Thalassiosira pseudonana | Translation | S | 17412 | 9.1 | 14.6 |
| Ribosomal protein L14 | jgi 39499 | Thalassiosira pseudonana | translation | C | 14975 | 10.2 | 6.7 |
| Ribosomal protein L19 | jgi 268372 | Thalassiosira pseudonana | Translation | S | 21275 | 11.6 | 9.2 |
| Ribosomal protein L5 | jgi 802 | Thalassiosira pseudonana | Translation | C | 35283 | 8.6 | 3.9 |
| Ribosomal protein PETRP-like | jgi 33241 | Thalassiosira pseudonana | Translation | S | 17754 | 10.3 | 8.1 |
| Ribosomal protein S10 | jgi 19501 | Thalassiosira pseudonana | Translation | C | 11912 | 9.4 | 8.7 |
| Ribosomal protein S12 | jgi 37628 | Thalassiosira pseudonana | Binding RNA | C | 12611 | 6.2 | 21.7 |
| Ribosomal protein S18 | jgi 26893 | Thalassiosira pseudonana | Binding RNA | C | 17159 | 10.8 | 28.8 |
| Ribosomal protein S19 | jgi 28425 | Thalassiosira pseudonana | Translation | C | 16703 | 9.0 | 8.8 |

| Chl Max | | | | | | | | | |
|--|-------------------|--------------------------------|--------------------------------|-------------|-----------|-----------|-----------|--|--|
| Protein | Annotation | Species | Function | Comp | MW | pI | SC | | |
| Ribosomal protein S26e | jgi 20008 | Thalassiosira pseudonana | Translation | S | 10971 | 11.0 | 12.8 | | |
| Ribosomal protein S3 | jgi 28049 | Thalassiosira pseudonana | Binding RNA | C | 29161 | 9.3 | 9.6 | | |
| Ribosomal protein S9 | jgi 40312 | Thalassiosira pseudonana | Translation | C | 16088 | 10.2 | 5.6 | | |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 35.1 | | |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit | gi 118411103 | Thalassiosira pseudonana | Photosynthesis | C | 15843 | 5.1 | 69.8 | | |
| Rieske iron-sulfur protein precursor | jgi 38231 | Thalassiosira pseudonana | Electron Transport | C | 19151 | 5.5 | 5.0 | | |
| Rieske iron-sulfur protein precursor | jgi 26131 | Thalassiosira pseudonana | Electron Transport | C | 19305 | 5.1 | 8.8 | | |
| RsuA | jgi 269764 | Thalassiosira pseudonana | Binding RNA | S | 36568 | 6.2 | 4.0 | | |
| Rubisco expression protein | gi 118411164 | Thalassiosira pseudonana | Photosynthesis | C | 32381 | 5.9 | 22.3 | | |
| S-adenosyl methionine synthetase | jgi 21815 | Thalassiosira pseudonana | Transport | S | 50359 | 5.2 | 16.1 | | |
| S-adenosyl-L-homocysteinase protein | jgi 28496 | Thalassiosira pseudonana | Metabolic Process | S | 52309 | 5.1 | 10.6 | | |
| S-adenosyl-L-homocysteine hydrolase | gi 71082903 | Candidatus Pelagibacter ubique | Metabolism, one carbon | S | 47071 | 5.5 | 4.0 | | |
| Structural constituent of ribosome | jgi 26137 | Thalassiosira pseudonana | Translation | S | 20867 | 9.8 | 5.4 | | |
| Structural constituent of ribosome | jgi 262056 | Thalassiosira pseudonana | Translation | S | 14755 | 10.4 | 9.7 | | |
| Structural constituent of ribosome | jgi 31084 | Thalassiosira pseudonana | Translation | S | 13713 | 9.9 | 17.4 | | |
| Transaldolase | jgi 27187 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | S | 34855 | 4.8 | 11.0 | | |
| Translation elongation factor G | jgi 25629 | Thalassiosira pseudonana | Translation | c | 86389 | 5.0 | 16.6 | | |
| Translation elongation factor Tu | gi 118411218 | Thalassiosira pseudonana | Translation | c | 44458 | 4.9 | 28.9 | | |
| Triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 28239 | Thalassiosira pseudonana | Metabolic Process | S | 65308 | 5.6 | 4.9 | | |
| Tubulin alpha-2 chain | jgi 29304 | Thalassiosira pseudonana | Structural | S | 49904 | 5.0 | 8.4 | | |
| Tubulin beta chain | jgi 8069 | Thalassiosira pseudonana | Structural | S | 49497 | 4.9 | 3.3 | | |
| Tubulin beta chain | jgi 31569 | Thalassiosira pseudonana | Structural | S | 49670 | 4.9 | 12.6 | | |
| Ubiquinol-cytochrome-c reductase | jgi 36107 | Thalassiosira pseudonana | Oxidoreductase | M | 11977 | 5.4 | 9.3 | | |
| Ubiquitin | jgi 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 18.3 | | |
| Unknown | jgi 10417 | Thalassiosira pseudonana | n.a. | S | 22939 | 4.9 | 6.4 | | |
| Unknown | jgi 30683 | Thalassiosira pseudonana | Metabolic Process | u | 26039 | 6.0 | 6.3 | | |
| Unknown | jgi 39424 | Thalassiosira pseudonana | Binding GTP | u | 20905 | 6.8 | 25.6 | | |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 | | |
| Vacuolar ATP synthase subunit A | jgi 37123 | Thalassiosira pseudonana | Transport Proton | S | 68343 | 5.0 | 7.6 | | |
| Vacuolar ATPase B subunit | jgi 40522 | Thalassiosira pseudonana | Transport Proton | S | 56064 | 5.9 | 16.8 | | |

| Chl Max | | | | | | | | | |
|---|-----|-------------------|--------------------------|------------------|-------------|-----------|-----------|-----------|--|
| Protein | | Annotation | Species | Function | Comp | MW | pI | SC | |
| Vacuolar proton-inorganic pyrophosphatase | jgi | 39520 | Thalassiosira pseudonana | Transport Proton | S | 70120 | 5.0 | 2.7 | |
| Vacuolar sorting receptor homolog | jgi | 42545 | Thalassiosira pseudonana | Binding Calcium | S | 56362 | 4.9 | 3.1 | |

| 50m POC | | | | | | | | | |
|---|-----|-------------------|--------------------------------|--------------------|-------------|-----------|-----------|-----------|--|
| Protein | | Annotation | Species | Function | Comp | MW | pI | SC | |
| ABC transporter | gi | 71083646 | Candidatus Pelagibacter ubique | Transport | S | 25649 | 6.1 | 4 | |
| Actin A | jgi | 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 2.7 | |
| Adenosinetriphosphatase | jgi | 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 3.5 | |
| ATP synthase CF1 alpha chain | gi | 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 4.6 | |
| ATP synthase CF1 beta chain | gi | 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 6.1 | |
| Cytochrome c-550 | gi | 118411100 | Thalassiosira pseudonana | Electron Transport | C | 17841 | 7.7 | 11 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi | 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 14.8 | |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi | 31383 | Thalassiosira pseudonana | Glycolysis | C | 39587 | 5.3 | 4 | |
| Hypothetical Protein | jgi | 23918 | Thalassiosira pseudonana | n.a. | S | 31192 | 4.8 | 3.1 | |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi | 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 3.9 | |
| Tubulin beta chain | jgi | 8069 | Thalassiosira pseudonana | Structural | S | 49497 | 4.9 | 2.7 | |

| 100m POC | | | | | | | | | |
|--|-----|-------------------|--------------------------------|------------------|-------------|-----------|-----------|-----------|--|
| Protein | | Annotation | Species | Function | Comp | MW | pI | SC | |
| ABC transporter | gi | 71083646 | Candidatus Pelagibacter ubique | Transport | S | 25649 | 6.1 | 6.6 | |
| Adenosinetriphosphatase | jgi | 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 3.5 | |
| ATP synthase CF1 alpha chain | gi | 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 5 | |
| ATP synthase CF1 beta chain | gi | 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 8.4 | |
| CG11154-PA, isoform A | jgi | 41256 | Thalassiosira pseudonana | Transport Proton | U | 53388 | 5.1 | 3 | |
| DNA binding | jgi | 29950 | Thalassiosira pseudonana | Binding DNA | C | 15300 | 11.3 | 13.2 | |
| Fucoxanthin chlorophyll a/c protein | jgi | 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 6.8 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi | 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 6.2 | |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi | 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 4 | |
| Histone H2A.1 | jgi | 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 | |
| Histone H4 | jgi | 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 34 | |
| Hypothetical protein DEHA0F19712g | jgi | 27352 | Thalassiosira pseudonana | Binding DNA | N | 13064 | 10.3 | 12.5 | |

100m POC

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|----------------|--------------------------------|----------------------|-----------|-----------|-----------|
| Photosystem II chlorophyll A core antenna apoprotein | gi | 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 4.1 |
| Photosystem II reaction center protein D2 | gi | 118411148 | Thalassiosira pseudonana | Photosynthesis | C | 39064 | 5.6 6.3 |
| Protein product unnamed | jgi | 27435 | Thalassiosira pseudonana | Transcription | U | 18469 | 6.3 7.7 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi | 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 16.3 |
| Spermidine/putrescine-binding periplasmic protein | gi | 71084024 | Candidatus Pelagibacter ubique | Binding | S | 40556 | 5.0 8.8 |
| TRAP dicarboxylate transporter - DctP subunit | gi | 71082971 | Candidatus Pelagibacter ubique | Transport | S | 42131 | 9.2 6.2 |
| Tubulin alpha-2 chain | jgi | 29304 | Thalassiosira pseudonana | Structural | S | 49904 | 5.0 5.3 |
| Tubulin beta chain | jgi | 8069 | Thalassiosira pseudonana | Structural | S | 49497 | 4.9 12.9 |
| Ubiquitin | jgi | 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 8.5 |
| Vacuolar-type H+-pyrophosphatase | jgi | 32586 | Thalassiosira pseudonana | Transport Proton | S | 67969 | 4.6 1.7 |

40m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---------------------------------------|-------------------|----------------|--------------------------|-----------------------|-----------|-----------|-----------|
| 30S ribosomal protein S1 | jgi | 15259 | Thalassiosira pseudonana | Binding RNA | C | 31770 | 4.6 7.3 |
| 30S ribosomal protein S12 | gi | 118411216 | Thalassiosira pseudonana | Translation | C | 13914 | 11.6 6.5 |
| 30S ribosomal protein S18 | gi | 118411132 | Thalassiosira pseudonana | Translation | C | 8155 | 10.8 18.1 |
| 3-deoxy-7-phosphoheptulonate synthase | jgi | 2790 | Thalassiosira pseudonana | Biosynthesis | S | 53939 | 6.0 9.9 |
| 40S ribosomal protein S5 | jgi | 29955 | Thalassiosira pseudonana | Translation | R | 24397 | 6.9 6 |
| 40S ribosomal protein S9 | jgi | 268651 | Thalassiosira pseudonana | Binding rRNA | R | 21764 | 10.2 11.6 |
| 40S ribosomal protein SA p40 | jgi | 21871 | Thalassiosira pseudonana | Translation | R | 27261 | 5.9 13.2 |
| 50S ribosomal protein L4 | gi | 118411191 | Thalassiosira pseudonana | Translation | C | 24203 | 10.2 7.9 |
| 50S ribosomal protein L5 | gi | 118411203 | Thalassiosira pseudonana | Translation | C | 27571 | 9.7 5.9 |
| 60 kDa chaperonin | gi | 118411188 | Thalassiosira pseudonana | Binding Protein | C | 57361 | 5.2 5.3 |
| 6-phosphogluconate dehydrogenase | jgi | 33343 | Thalassiosira pseudonana | Dehydrogenase | S | 53348 | 5.6 8.4 |
| Acidic ribosomal phosphoprotein P0 | jgi | 25812 | Thalassiosira pseudonana | Biosynthesis Ribosome | R | 34116 | 4.8 3.7 |
| Actin A | jgi | 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 15.1 |
| Adenosinetriphosphatase | jgi | 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 7.4 |
| Aminotransferase AGD2 | jgi | 31394 | Thalassiosira pseudonana | Transport | M | 44264 | 4.8 3.7 |
| Argininosuccinate synthase | jgi | 42719 | Thalassiosira pseudonana | Biosynthesis | C | 45938 | 5.3 2.9 |
| Aromatic-ring hydroxylase | gi | 33861317 | Prochlorococcus marinus | Metabolic Process | S | 49438 | 8.9 3.1 |
| ATP binding / protein binding | jgi | 23102 | Thalassiosira pseudonana | Binding Protein | S | 59170 | 5.3 5.3 |
| ATP synthase CF0 B chain subunit I | gi | 118411110 | Thalassiosira pseudonana | Transport Proton | C | 20029 | 9.8 16.8 |

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| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|---------------------------------|-------------|-----------|-----------|-----------|
| ATP synthase CF0 B' chain subunit II | gi 118411109 | Thalassiosira pseudonana | Transport Proton | C | 17373 | 4.6 | 9.6 |
| ATP synthase CF1 alpha chain | gi 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 25.8 |
| ATP synthase CF1 beta chain | gi 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 36.5 |
| ATP/ADP translocator | jgi 39143 | Thalassiosira pseudonana | Transport | M | 32254 | 9.4 | 3.6 |
| ATP-dependent clp protease ATP-binding subunit | gi 118411220 | Thalassiosira pseudonana | Catalysis | C | 102150 | 6.5 | 1.5 |
| ATP-dependent clp protease ATP-binding subunit | gi 33861644 | Prochlorococcus marinus | n.a. | S | 93370 | 5.5 | 2.6 |
| ATP-sulfurylase | jgi 1326 | Thalassiosira pseudonana | Metabolic Process | M | 45362 | 5.2 | 4.9 |
| BiP | jgi 27656 | Thalassiosira pseudonana | Cell Morphogenesis | S | 70451 | 4.7 | 20 |
| CbbX protein homolog | jgi 40193 | Thalassiosira pseudonana | Biosynthesis | C | 35036 | 5.3 | 19.3 |
| CDC48/ATPase | jgi 267952 | Thalassiosira pseudonana | Binding ATP | S | 89464 | 4.8 | 3.2 |
| Cell division protein FtsH2 | jgi 31930 | Thalassiosira pseudonana | Binding Zn | C | 61956 | 5.1 | 16 |
| Cell division protein FtsH-like protein | gi 118411141 | Thalassiosira pseudonana | Proteolysis | C | 70206 | 5.1 | 9.8 |
| CG11154-PA, isoform A | jgi 41256 | Thalassiosira pseudonana | Transport Proton | U | 53388 | 5.1 | 29 |
| Chloroplast 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase precursor | jgi 29228 | Thalassiosira pseudonana | Biosynthesis | C | 75736 | 4.9 | 2.6 |
| Chloroplast ferredoxin dependent NADH oxidoreductase | jgi 25892 | Thalassiosira pseudonana | Transport Electron | C | 37819 | 5.9 | 2.4 |
| Chloroplast light harvesting protein isoform 12 | jgi 270092 | Thalassiosira pseudonana | Photosynthesis | C | 26078 | 5.5 | 11.2 |
| Chloroplast light harvesting protein isoform 15 | jgi 2845 | Thalassiosira pseudonana | Photosynthesis | C | 21873 | 5.1 | 5.4 |
| Chorismate synthase | jgi 38964 | Thalassiosira pseudonana | Biosynthesis | S | 44051 | 5.5 | 3.2 |
| Cobaltochelataase | jgi 26573 | Thalassiosira pseudonana | Biosynthesis | S | 148275 | 4.9 | 1 |
| CPN60 protein | jgi 23329 | Thalassiosira pseudonana | Binding Protein | M | 59177 | 4.7 | 5.1 |
| Cytochrome b559 alpha chain | gi 118411160 | Thalassiosira pseudonana | Photosynthesis | C | 9514 | 5.6 | 25 |
| Cytochrome c-550 | gi 118411100 | Thalassiosira pseudonana | Transport Electron | C | 17841 | 7.7 | 11 |
| Cytochrome f | gi 118411137 | Thalassiosira pseudonana | Photosynthesis | C | 33988 | 8.2 | 19.1 |
| DNA binding | jgi 29950 | Thalassiosira pseudonana | Binding DNA | C | 15300 | 11.3 | 8.1 |
| Domain specific binding protein 14-3-3 | jgi 26146 | Thalassiosira pseudonana | Binding Protein Domain Specific | S | 27869 | 4.6 | 7.3 |
| Elongation factor 2 | jgi 269148 | Thalassiosira pseudonana | Translation | S | 91887 | 6.0 | 4.2 |
| Enolase 2 | jgi 40391 | Thalassiosira pseudonana | Glycolysis | S | 46547 | 4.8 | 3.4 |
| Enoyl-acyl carrier reductase | jgi 32860 | Thalassiosira pseudonana | Oxidation Reduction | S | 32813 | 5.1 | 8 |
| Eukaryotic translation initiation factor 4A2 isoform 2 | jgi 9716 | Thalassiosira pseudonana | Binding Nucleic Acid | S | 42405 | 5.6 | 20.6 |
| F0F1 ATP synthase subunit alpha | gi 33862007 | Prochlorococcus marinus | Transport Proton | S | 54306 | 4.9 | 6.7 |
| | | Candidatus | | | | | |

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| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|-------------------|--------------------------|--------------------------------|-------------|-----------|-----------|-----------|
| F0F1 ATP synthase subunit beta | gi 71082935 | Pelagibacter ubique | Transport Proton | S | 50696 | 4.9 | 16.9 |
| FeS assembly protein SufD | jgi 268364 | Thalassiosira pseudonana | Binding Protein | S | 31963 | 5.2 | 5.8 |
| Fructose-1,6-bisphosphate aldolase precursor | jgi 428 | Thalassiosira pseudonana | Glycolysis | S | 39810 | 4.8 | 7.3 |
| Fructose-bisphosphatase | jgi 264556 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | M | 33667 | 5.3 | 5.1 |
| Fucoxanthin chlorophyll a/c protein | jgi 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 21.6 |
| Fucoxanthin chlorophyll a /c protein | jgi 38494 | Thalassiosira pseudonana | Photosynthesis | C | 20354 | 4.5 | 18.4 |
| Fucoxanthin chlorophyll a /c protein | jgi 42962 | Thalassiosira pseudonana | Photosynthesis | C | 21515 | 5.1 | 17.5 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 264921 | Thalassiosira pseudonana | Photosynthesis | C | 21263 | 5.0 | 5 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22205 | 4.6 | 15.3 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 30385 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 35.7 |
| GDP-mannose dehydratase | jgi 40586 | Thalassiosira pseudonana | Catalysis | S | 40412 | 5.9 | 3.3 |
| Geranyl-geranyl reductase | jgi 10234 | Thalassiosira pseudonana | Transport Electron | C | 47230 | 5.9 | 7.3 |
| Glucose-6-phosphate isomerase | jgi 38266 | Thalassiosira pseudonana | Glycolysis | C | 61689 | 5.9 | 4.9 |
| Glutamate 1-semialdehyde 2,1-aminomutase | jgi 575 | Thalassiosira pseudonana | Binding Phosphate | C | 43658 | 5.5 | 3.2 |
| Glutamine synthase | jgi 270138 | Thalassiosira pseudonana | Biosynthesis | C | 69172 | 5.2 | 1.8 |
| Glutamine synthetase | jgi 26051 | Thalassiosira pseudonana | Biosynthesis | C | 45620 | 5.2 | 3.4 |
| Glyceraldehyde-3-phosphate dehydrogenase | jgi 28334 | Thalassiosira pseudonana | Glycolysis | M | 36574 | 6.1 | 4.4 |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 27.2 |
| Glycolaldehydetransferase | jgi 21175 | Thalassiosira pseudonana | Transport | M | 71708 | 5.0 | 26.1 |
| Heat shock protein 60 | jgi 38191 | Thalassiosira pseudonana | Binding Protein | S | 58525 | 4.8 | 2.9 |
| Heat shock protein 70 | jgi 269120 | Thalassiosira pseudonana | Folding Protein | S | 71187 | 4.8 | 16.4 |
| Heat shock protein Hsp90 | jgi 6285 | Thalassiosira pseudonana | Folding Protein | S | 80242 | 4.7 | 7.1 |
| Histone H2A.1 | jgi 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 |
| Histone H4 | jgi 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 35 |
| Hsp70-type chaperone | gi 118411189 | Thalassiosira pseudonana | Transcription | C | 65339 | 4.8 | 2.3 |
| Hypothetical Protein | jgi 23918 | Thalassiosira pseudonana | n.a. | S | 31192 | 4.8 | 36.5 |
| Hypothetical protein CBG01077 | jgi 22792 | Thalassiosira pseudonana | Transport | S | 22486 | 6.7 | 9 |
| Hypothetical protein CBG08717 | jgi 269322 | Thalassiosira pseudonana | Transport Proton | S | 58009 | 5.8 | 19.4 |
| Hypothetical protein FG01081.1 | jgi 25949 | Thalassiosira pseudonana | Translation | U | 20124 | 9.8 | 7.9 |
| Hypothetical protein Synpcc7942_1497 | jgi 4382 | Thalassiosira pseudonana | n.a. | S | 30101 | 5.6 | 5.3 |
| Hypothetical protein UM03322.1 | jgi 28443 | Thalassiosira pseudonana | Translation | M | 24676 | 10.2 | 5.1 |

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| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|---------------------|-------------|-----------|-----------|-----------|
| Isocitrate/isopropylmalate dehydrogenase | jgi 5293 | Thalassiosira pseudonana | Oxidoreductase | S | 40667 | 4.6 | 5.9 |
| Ketol-acid reductoisomerase | jgi 23228 | Thalassiosira pseudonana | Oxidation Reduction | S | 58240 | 5.1 | 7.3 |
| L4/L1 | jgi 22610 | Thalassiosira pseudonana | Translation | R | 40991 | 10.3 | 5 |
| Malate dehydrogenase | jgi 20726 | Thalassiosira pseudonana | Oxidoreductase | M | 36724 | 6.3 | 3.4 |
| Mitochondrial glyceraldehyde-3-phosphate dehydrogenase | jgi 28241 | Thalassiosira pseudonana | Glycolysis | M | 36243 | 5.9 | 9.5 |
| Molecular chaperone DnaK2 | gi 33862260 | Prochlorococcus marinus | Folding Protein | S | 68202 | 4.8 | 4.9 |
| Myo-inositol dehydrogenase precursor | jgi 1049 | Thalassiosira pseudonana | Biosynthesis | S | 48134 | 5.0 | 4.2 |
| Nitrate reductase | jgi 25299 | Thalassiosira pseudonana | Transport Electron | S | 101408 | 5.9 | 1 |
| Oxidoreductase | jgi 8063 | Thalassiosira pseudonana | Metabolic Process | C | 36723 | 7.6 | 6.2 |
| Oxygen-evolving enhancer protein 1 precursor | jgi 34830 | Thalassiosira pseudonana | Photosynthesis | C | 29136 | 5.2 | 26.2 |
| Phosphoadenosine-phosphosulphate reductase | jgi 24887 | Thalassiosira pseudonana | Metabolic Process | C | 49035 | 5.0 | 3.9 |
| Phosphofructokinase | jgi 22213 | Thalassiosira pseudonana | Glycolysis | C | 43797 | 5.7 | 2.7 |
| Phosphoglycerate kinase precursor | jgi 35712 | Thalassiosira pseudonana | Glycolysis | S | 42256 | 5.0 | 26.8 |
| Phosphoglycerate mutase 1 | jgi 27850 | Thalassiosira pseudonana | Glycolysis | C | 32465 | 6.1 | 3.1 |
| Phosphoribosyl-pyrophosphate synthetase | jgi 26109 | Thalassiosira pseudonana | Biosynthesis | S | 33425 | 8.4 | 3.2 |
| Photosystem I ferredoxin-binding protein | gi 118411153 | Thalassiosira pseudonana | Photosynthesis | C | 15518 | 9.6 | 37.4 |
| Photosystem I p700 chlorophyll A apoprotein A | gi 118411096 | Thalassiosira pseudonana | Photosynthesis | C | 83642 | 7.3 | 4.1 |
| Photosystem I protein F | gi 118411168 | Thalassiosira pseudonana | Photosynthesis | C | 20362 | 8.9 | 8.1 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 20.2 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 12.1 |
| Photosystem II PsbD protein D2 | gi 33861713 | Prochlorococcus marinus | Photosynthesis | C | 39917 | 5.6 | 6.4 |
| Photosystem II reaction center protein D1 | gi 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 6.4 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 12.5 |
| Photosystem II stability/assembly factor HCF136 | jgi 38769 | Thalassiosira pseudonana | Photosystem | C | 40327 | 5.2 | 10.5 |
| Protein product unnamed | jgi 262083 | Thalassiosira pseudonana | n.a. | S | 103903 | 6.1 | 2.6 |
| Pyruvate kinase | jgi 40393 | Thalassiosira pseudonana | Glycolysis | C | 54650 | 5.9 | 2.5 |
| Ribosomal protein L12e | jgi 39424 | Thalassiosira pseudonana | Translation | R | 17412 | 9.1 | 14.6 |
| Ribosomal protein S13 | jgi 26221 | Thalassiosira pseudonana | Translation | C | 17054 | 10.4 | 8.6 |
| Ribosomal protein S18 | jgi 26893 | Thalassiosira pseudonana | Binding RNA | C | 17159 | 10.8 | 27.4 |
| Ribosomal protein S3 | jgi 28049 | Thalassiosira pseudonana | Binding RNA | C | 29161 | 9.3 | 8.9 |

40m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|--------------------------------|-------------|-----------|-----------|-----------|
| Ribosomal protein S9 | jgi 40312 | Thalassiosira pseudonana | Translation | C | 16088 | 10.2 | 7.7 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 32.2 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit | gi 118411103 | Thalassiosira pseudonana | Photosynthesis | C | 15843 | 5.1 | 19.4 |
| RsuA | jgi 269764 | Thalassiosira pseudonana | Binding RNA | S | 36568 | 6.2 | 4 |
| Rubisco expression protein | gi 118411164 | Thalassiosira pseudonana | Photosynthesis | C | 32381 | 5.9 | 4.9 |
| S-adenosyl methionine synthetase | jgi 21815 | Thalassiosira pseudonana | Transport | S | 50359 | 5.2 | 6 |
| S-adenosyl-L-homocysteinas protein | jgi 28496 | Thalassiosira pseudonana | Metabolic Process | S | 52309 | 5.1 | 12.7 |
| | | Candidatus | | | | | |
| S-adenosyl-L-homocysteine hydrolase | gi 71082903 | Pelagibacter ubique | Metabolic Process | S | 47071 | 5.5 | 4 |
| SDH1-1 | jgi 42475 | Thalassiosira pseudonana | Transport Electron | M | 68963 | 5.7 | 2.2 |
| Serine hydroxymethyltransferase | jgi 26031 | Thalassiosira pseudonana | Metabolic Process | S | 52999 | 6.5 | 1.9 |
| Transaldolase | jgi 27187 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | S | 34855 | 4.8 | 12.6 |
| Translation elongation factor 1 alpha | jgi 3858 | Thalassiosira pseudonana | Translation | S | 47815 | 7.2 | 2.5 |
| Translation elongation factor G | jgi 25629 | Thalassiosira pseudonana | Translation | S | 86389 | 5.0 | 9.2 |
| Translation elongation factor Tu | gi 118411218 | Thalassiosira pseudonana | Translation | C | 44458 | 4.9 | 17.8 |
| Tubulin alpha-2 chain | jgi 29304 | Thalassiosira pseudonana | Structure | S | 49904 | 5.0 | 11.9 |
| Tubulin beta chain | jgi 31569 | Thalassiosira pseudonana | Structure | S | 49497 | 4.9 | 18.5 |
| Tubulin beta chain | jgi 8069 | Thalassiosira pseudonana | Structure | S | 49670 | 4.9 | 3.3 |
| Ubiquitin | jgi 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 8.5 |
| Unknown | jgi 10417 | Thalassiosira pseudonana | n.a. | S | 22939 | 4.9 | 17.8 |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 |
| Vacuolar ATP synthase subunit A | jgi 37123 | Thalassiosira pseudonana | Transport Proton | S | 68343 | 5.0 | 3.5 |
| Vacuolar ATPase B subunit | jgi 40522 | Thalassiosira pseudonana | Transport Proton | S | 56064 | 5.9 | 23.9 |
| Vacuolar proton translocating ATPase A subunit | jgi 40728 | Thalassiosira pseudonana | Transport Proton | S | 92414 | 5.3 | 1.6 |
| Vacuolar-type H ⁺ -pyrophosphatase | jgi 32586 | Thalassiosira pseudonana | Transport Proton | S | 67969 | 4.6 | 1.7 |
| Vitamin B6 biosynthesis protein | jgi 42612 | Thalassiosira pseudonana | Biosynthesis | S | 35430 | 6.0 | 9 |

60m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|-------------------|--------------------------|-----------------|-------------|-----------|-----------|-----------|
| 30S ribosomal protein S1 | jgi 15259 | Thalassiosira pseudonana | Translation | R | 31770 | 4.6 | 3.8 |
| 3-deoxy-7-phosphoheptulonate synthase | jgi 2790 | Thalassiosira pseudonana | Biosynthesis | C | 53939 | 6.0 | 4.8 |
| 3-phosphoshikimate 1-carboxyvinyltransferase | jgi 33008 | Thalassiosira pseudonana | Transport | C | 47333 | 4.6 | 3.1 |

60m Trap

| Protein | | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-----|-------------------|--------------------------|--------------------------------|-------------|-----------|-----------|-----------|
| 6-phosphogluconate dehydrogenase | jgi | 33343 | Thalassiosira pseudonana | Dehydrogenase | S | 53348 | 5.6 | 2 |
| Actin A | jgi | 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 9 |
| Adenosinetriphosphatase | jgi | 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 3.5 |
| Aromatic-ring hydroxylase | gi | 33861317 | Prochlorococcus marinus | Photosynthesis | S | 49438 | 8.9 | 3.1 |
| ATP binding / protein binding | jgi | 23102 | Thalassiosira pseudonana | Binding Protein | S | 59170 | 5.3 | 5.3 |
| ATP synthase CF1 alpha chain | gi | 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 24.1 |
| ATP synthase CF1 beta chain | gi | 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 38.4 |
| ATP-sulfurylase | jgi | 1326 | Thalassiosira pseudonana | Metabolic Process | M | 45362 | 5.2 | 2.9 |
| BiP | jgi | 27656 | Thalassiosira pseudonana | Cell Morphogenesis | S | 70451 | 4.7 | 4.5 |
| CbbX protein homolog | jgi | 40193 | Thalassiosira pseudonana | Biosynthesis | C | 35036 | 5.3 | 7.1 |
| CG11154-PA, isoformA | jgi | 41256 | Thalassiosira pseudonana | Transport Proton | S | 53388 | 5.1 | 33 |
| CPN60 protein | jgi | 23329 | Thalassiosira pseudonana | Binding Protein | M | 59177 | 4.7 | 2.9 |
| Enolase 2 | jgi | 40391 | Thalassiosira pseudonana | Glycolysis | S | 46547 | 4.8 | 5.5 |
| Eukaryotic translation initiation factor 4A2 isoform2 | jgi | 9716 | Thalassiosira pseudonana | Binding DNA | S | 42405 | 5.6 | 17.6 |
| Fructose-1,6-bisphosphate aldolase precursor | jgi | 428 | Thalassiosira pseudonana | Glycolysis | S | 39810 | 4.8 | 12.4 |
| Fructose-bisphosphatase | jgi | 264556 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | M | 33667 | 5.3 | 5.1 |
| Fucoxanthin chlorophyl a/c protein | jgi | 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 13.2 |
| Fucoxanthin chlorophyll a /c protein | jgi | 38494 | Thalassiosira pseudonana | Photosynthesis | C | 20354 | 4.5 | 13.7 |
| Fucoxanthin chlorophyll a/c binding protein | jgi | 264921 | Thalassiosira pseudonana | Photosynthesis | C | 22205 | 4.6 | 8.6 |
| Fucoxanthin chlorophyll a/c binding protein | jgi | 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 27.6 |
| Glutamine synthetase | jgi | 26051 | Thalassiosira pseudonana | Biosynthesis | C | 45620 | 5.2 | 3.4 |
| Glyceraldehyde-3-phosphate dehydrogenase | jgi | 28334 | Thalassiosira pseudonana | Glycolysis | S | 36574 | 6.1 | 4.4 |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi | 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 10.4 |
| Glycolaldehydetransferase | jgi | 21175 | Thalassiosira pseudonana | Transport | S | 71708 | 5.0 | 4.4 |
| Heat shock protein 60 | jgi | 38191 | Thalassiosira pseudonana | Folding Protein | S | 58525 | 4.8 | 5.2 |
| Heat shock protein 70 | jgi | 269120 | Thalassiosira pseudonana | Folding Protein | S | 71187 | 4.8 | 10.3 |
| Histone H2A.1 | jgi | 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 |
| Hypothetical Protein | jgi | 23918 | Thalassiosira pseudonana | n.a. | S | 31192 | 4.8 | 9.6 |
| Hypothetical protein CBG08717 | jgi | 269322 | Thalassiosira pseudonana | Transport Proton | S | 58009 | 5.8 | 12.9 |
| Isocitrate/isopropylmalate dehydrogenase | jgi | 5293 | Thalassiosira pseudonana | Oxidoreductase | S | 40667 | 4.6 | 6.4 |
| L4/L1 | jgi | 22610 | Thalassiosira pseudonana | Translation | R | 40991 | 10.3 | 4.2 |

60m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|--------------------------------|-------------|-----------|-----------|-----------|
| Magnesium-chelatase subunit I | gi 118411138 | Thalassiosira pseudonana | Photosynthesis | C | 39500 | 5.0 | 5.1 |
| Mitochondrial glyceraldehyde-3-phosphate dehydrogenase | jgi 28241 | Thalassiosira pseudonana | Glycolysis | M | 36243 | 5.9 | 6.2 |
| Phosphoadenosine-phosphosulphate reductase | jgi 24887 | Thalassiosira pseudonana | Metabolic Process | C | 49035 | 5.0 | 3.9 |
| Phosphoglycerate kinase precursor | jgi 35712 | Thalassiosira pseudonana | Glycolysis | S | 42256 | 5.0 | 15 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 5.5 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 3.4 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 6.3 |
| Photosystem II stability/assembly factor HCF136 | jgi 38769 | Thalassiosira pseudonana | Photosystem | C | 40327 | 5.2 | 7.3 |
| Predicted translation elongation factor G | jgi 25629 | Thalassiosira pseudonana | Translation | S | 86389 | 5.0 | 6.6 |
| Putative aminotransferase AGD2 | jgi 31394 | Thalassiosira pseudonana | Transport | M | 44264 | 4.8 | 6.6 |
| Putative S-adenosyl-L-homocysteinase protein | jgi 28496 | Thalassiosira pseudonana | Metabolic Process | S | 52309 | 5.1 | 6.2 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 12.2 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit | gi 118411103 | Thalassiosira pseudonana | Photosynthesis | C | 15843 | 5.1 | 10.1 |
| S-adenosyl methionine synthetase | jgi 21815 | Thalassiosira pseudonana | Transport | S | 50359 | 5.2 | 3.2 |
| Transaldolase | jgi 27187 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | S | 34855 | 4.8 | 4.1 |
| Translation elongation factor Tu | gi 118411218 | Thalassiosira pseudonana | Translation | C | 44458 | 4.9 | 3.9 |
| Tubulin alpha-2 chain | jgi 29304 | Thalassiosira pseudonana | Structural | S | 49904 | 5.0 | 2.2 |
| Vacuolar ATPase B subunit | jgi 40522 | Thalassiosira pseudonana | Transport Proton | S | 56064 | 5.9 | 12.8 |

100m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|-------------------|--------------------------|--------------------|-------------|-----------|-----------|-----------|
| 30S ribosomal protein S12 | gi 118411216 | Thalassiosira pseudonana | Translation | C | 13914 | 11.6 | 6.5 |
| 3-deoxy-7-phosphoheptulonate synthase | jgi 2790 | Thalassiosira pseudonana | Transport Electron | C | 53939 | 6.0 | 1.9 |
| 40S ribosomal protein S17-like protein | jgi 37809 | Thalassiosira pseudonana | Translation | C | 14145 | 10.0 | 17.1 |
| 40S ribosomal protein S6 | jgi 269779 | Thalassiosira pseudonana | Translation | R | 27587 | 11.0 | 3.7 |
| 40S ribosomal protein SA p40 | jgi 21871 | Thalassiosira pseudonana | Translation | R | 27261 | 5.9 | 13.2 |
| 50S ribosomal protein L11 | gi 118411123 | Thalassiosira pseudonana | Translation | C | 14880 | 9.7 | 9.2 |
| 50S ribosomal protein L4 | gi 118411191 | Thalassiosira pseudonana | Translation | C | 24203 | 10.2 | 5.1 |
| 6-phosphogluconate dehydrogenase | jgi 33343 | Thalassiosira pseudonana | Dehydrogenase | S | 53348 | 5.6 | 6.9 |
| Actin A | jgi 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 11.7 |
| Adenosinetriphosphatase | jgi 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 3.5 |

100m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|-------------------|--------------------------|----------------------|-------------|-----------|-----------|-----------|
| Aromatic-ring hydroxylase | gi 33861317 | Prochlorococcus marinus | Metabolic Process | S | 49438 | 8.9 | 3.1 |
| ATP synthase CF1 alpha chain | gi 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 14.3 |
| ATP synthase CF1 beta chain | gi 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 14.1 |
| ATPase, E1-E2 type | jgi 262679 | Thalassiosira pseudonana | Transport Cation | S | 99192 | 5.6 | 1.5 |
| ATP-dependent clp protease ATP-binding subunit | gi 118411220 | Thalassiosira pseudonana | Catalysis | C | 102150 | 6.5 | 1.5 |
| BiP | jgi 27656 | Thalassiosira pseudonana | Cell Morphogenesis | S | 70451 | 4.7 | 6.7 |
| Cell division protein FtsH-like protein | gi 118411141 | Thalassiosira pseudonana | Proteolysis | C | 70206 | 5.1 | 1.9 |
| CG11154-PA, isoform A | jgi 41256 | Thalassiosira pseudonana | Transport Proton | S | 53388 | 5.1 | 11.6 |
| Chloroplast ferredoxin dependent NADH oxidoreductase | jgi 25892 | Thalassiosira pseudonana | Transport Electron | C | 37819 | 5.9 | 4.4 |
| Cyc07-like protein | jgi 26046 | Thalassiosira pseudonana | Translation | S | 28811 | 9.6 | 13.1 |
| Cytochrome b559 alpha chain | gi 118411160 | Thalassiosira pseudonana | Photosynthesis | C | 9514 | 5.6 | 10.7 |
| Cytochrome b6 | gi 118411154 | Thalassiosira pseudonana | Transport Electron | C | 23906 | 9.2 | 6 |
| Cytochrome c-550 | gi 118411100 | Thalassiosira pseudonana | Transport Electron | C | 17841 | 7.7 | 11 |
| Cytochrome f | gi 118411137 | Thalassiosira pseudonana | Photosynthesis | C | 33988 | 8.2 | 4.1 |
| DNA binding | jgi 29950 | Thalassiosira pseudonana | Binding DNA | C | 15300 | 11.3 | 13.2 |
| Elongation factor alpha-like protein | jgi 41829 | Thalassiosira pseudonana | Translation | S | 49969 | 8.7 | 2.2 |
| Eukaryotic translation initiation factor 4A2 isoform 2 | jgi 9716 | Thalassiosira pseudonana | Binding Nucleic Acid | S | 42405 | 5.6 | 6 |
| Fructose-1,6-bisphosphate aldolase precursor | jgi 428 | Thalassiosira pseudonana | Glycolysis | S | 39810 | 4.8 | 3 |
| Fucoxanthin chlorophyll a/c protein | jgi 38494 | Thalassiosira pseudonana | Photosynthesis | C | 20354 | 4.5 | 11.6 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 264921 | Thalassiosira pseudonana | Photosynthesis | C | 22205 | 4.6 | 8.6 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 11 |
| Fucoxanthin-chlorophyll a/c light-harvesting protein | jgi 33018 | Thalassiosira pseudonana | Photosynthesis | C | 21786 | 5.4 | 4.5 |
| GDP-mannose dehydratase | jgi 40586 | Thalassiosira pseudonana | Catalysis | S | 40412 | 5.9 | 3.3 |
| Glutamine synthetase | jgi 26051 | Thalassiosira pseudonana | Biosynthesis | C | 45620 | 5.2 | 5.8 |
| Glyceraldehyde-3-phosphate dehydrogenase | jgi 28334 | Thalassiosira pseudonana | Glycolysis | M | 36574 | 6.1 | 4.4 |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 8.8 |
| Glycolaldehydetransferase | jgi 21175 | Thalassiosira pseudonana | Transport | S | 71708 | 5.0 | 4.4 |
| Heat shock protein 70 | jgi 269120 | Thalassiosira pseudonana | Folding Protein | S | 71187 | 4.8 | 2 |
| Heat shock protein Hsp90 | jgi 6285 | Thalassiosira pseudonana | Folding Protein | S | 80242 | 4.7 | 2 |
| Histone H2A.1 | jgi 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 |
| Histone H4 | jgi 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 30.1 |

100m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|--------------------------------|-------------|-----------|-----------|-----------|
| Hypothetical protein | jgi 27167 | Thalassiosira pseudonana | n.a. | U | 27052 | 10.0 | 5.4 |
| Hypothetical Protein | jgi 23918 | Thalassiosira pseudonana | n.a. | S | 31192 | 4.8 | 33.1 |
| Hypothetical protein CBG08717 | jgi 269322 | Thalassiosira pseudonana | Transport Proton | S | 58009 | 5.8 | 6.5 |
| hypothetical protein FG01081.1 | jgi 25949 | Thalassiosira pseudonana | Translation | U | 20124 | 9.8 | 7.9 |
| Hypothetical proteinUM03322.1 | jgi 28443 | Thalassiosira pseudonana | Translation | R | 24676 | 10.2 | 10.6 |
| Inorganic diphosphatase/magnesium ion binding / pyrophosphatase | jgi 269348 | Thalassiosira pseudonana | Metabolic Process Phosphate | C | 29982 | 4.8 | 5.9 |
| Molecular chaperone DnaK2 | gi 33862260 | Prochlorococcus marinus | Folding Protein | S | 68202 | 4.8 | 2.5 |
| Nitrate reductase | jgi 25299 | Thalassiosira pseudonana | Transport Electron | S | 101408 | 5.9 | 1 |
| Oxygen-evolving enhancer protein 1 precursor | jgi 34830 | Thalassiosira pseudonana | Photosynthesis | C | 29136 | 5.2 | 8.4 |
| Phosphoglycerate kinase precursor | jgi 35712 | Thalassiosira pseudonana | Glycolysis | S | 42256 | 5.0 | 4.5 |
| Phosphoglycerate mutase 1 | jgi 27850 | Thalassiosira pseudonana | Glycolysis | S | 32465 | 6.1 | 3.1 |
| Phosphoribosyl-pyrophosphate synthetase | jgi 26109 | Thalassiosira pseudonana | Biosynthesis | S | 33425 | 8.4 | 3.2 |
| Photosystem I protein PsuD | gi 33862134 | Prochlorococcus marinus | Photosynthesis | C | 15665 | 6.4 | 8.6 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 2 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 8.7 |
| Photosystem II reaction center protein D1 | gi 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 6.7 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 3.7 |
| Photosystem II stability/assembly factor HCF136 | jgi 38769 | Thalassiosira pseudonana | Photosystem | C | 40327 | 5.2 | 3.8 |
| Predicted translation elongation factor G | jgi 25629 | Thalassiosira pseudonana | Translation | S | 86389 | 5.0 | 3.5 |
| Protein product unnamed | jgi 29007 | Thalassiosira pseudonana | Translation | M | 18378 | 10.5 | 5.6 |
| Putative ribosomal protein L12e | jgi 39424 | Thalassiosira pseudonana | Translation | R | 17412 | 9.1 | 9.1 |
| Putative S-adenosyl-L-homocysteinas protein | jgi 28496 | Thalassiosira pseudonana | Metabolic Process | S | 52309 | 5.1 | 2.5 |
| Pyruvate kinase | jgi 22345 | Thalassiosira pseudonana | Glycolysis | C | 57892 | 5.2 | 3.3 |
| Ribosomal protein S3 | jgi 28049 | Thalassiosira pseudonana | Binding RNA | C | 29161 | 9.3 | 13.3 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 17.3 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit | gi 118411103 | Thalassiosira pseudonana | Photosynthesis | C | 15843 | 5.1 | 10.1 |
| RsuA | jgi 269764 | Thalassiosira pseudonana | Binding RNA | S | 36568 | 6.2 | 4 |
| S-adenosyl methionine synthetase | jgi 21815 | Thalassiosira pseudonana | Transport | S | 50359 | 5.2 | 3.2 |
| Transaldolase | jgi 27187 | Thalassiosira pseudonana | Metabolic Process Carbohydrate | S | 34855 | 4.8 | 4.1 |
| Translation elongation factor 1 alpha | jgi 3858 | Thalassiosira pseudonana | Translation | S | 47815 | 7.2 | 2.5 |

100m Trap

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|--------------|--------------------------|----------------------|------|-------|-----|------|
| Translation elongation factor Tu | gi 118411218 | Thalassiosira pseudonana | Translation | C | 44458 | 4.9 | 6.1 |
| Triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 28239 | Thalassiosira pseudonana | Metabolic Process | S | 65308 | 5.6 | 2.3 |
| Tubulin alpha-2 chain | jgi 29304 | Thalassiosira pseudonana | Structure | S | 49904 | 5.0 | 2.2 |
| Tubulin beta chain | jgi 8069 | Thalassiosira pseudonana | Structure | S | 49497 | 4.9 | 5.6 |
| Ubiquitin | jgi 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 8.5 |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 |
| Vacuolar ATP synthase subunit A | jgi 37123 | Thalassiosira pseudonana | Transport Proton | S | 68343 | 5.0 | 2.4 |
| Vacuolar ATPase B subunit | jgi 40522 | Thalassiosira pseudonana | Transport Proton | S | 56064 | 5.9 | 3 |
| Vacuolar proton translocating ATPase A subunit, putative | jgi 40728 | Thalassiosira pseudonana | Transport Proton | S | 92414 | 5.3 | 1.6 |
| Vacuolar-type H ⁺ -pyrophosphatase | jgi 32586 | Thalassiosira pseudonana | Transport Proton | S | 67969 | 4.6 | 1.7 |

Post Bloom Shelf Sediment

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|--------------|--------------------------------|---------------------------------|------|--------|------|------|
| 3-deoxy-7-phosphoheptulonate synthase | jgi 2790 | Thalassiosira pseudonana | Transport Electron | S | 53939 | 6.0 | 2.5 |
| 6-phosphogluconate dehydrogenase | jgi 33343 | Thalassiosira pseudonana | Dehydrogenase | S | 53348 | 5.6 | 4.7 |
| Actin A | jgi 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 9.0 |
| Adenosinetriphosphatase | jgi 40156 | Thalassiosira pseudonana | Transport Proton | S | 39935 | 7.6 | 7.4 |
| ATP synthase CF0 B' chain subunit II | gi 118411109 | Thalassiosira pseudonana | Transport Proton | C | 17373 | 4.6 | 9.0 |
| ATP synthase CF1 alpha chain | gi 118411112 | Thalassiosira pseudonana | Transport Ion | C | 53989 | 5.0 | 10.1 |
| ATP synthase CF1 beta chain | gi 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 20.5 |
| ATP/ADP translocator | jgi 39143 | Thalassiosira pseudonana | Transport | M | 32254 | 9.4 | 3.6 |
| Cell wall surface anchor family protein | jgi 6962 | Thalassiosira pseudonana | Structure | S | 75600 | 9.7 | 4.9 |
| CG11154-PA, isoform A | jgi 41256 | Thalassiosira pseudonana | Transport Proton | U | 53388 | 5.1 | 8.0 |
| Chloroplast light harvesting protein isoform 15 | jgi 2845 | Thalassiosira pseudonana | Photosynthesis | C | 21873 | 5.1 | 5.4 |
| Cytochrome b6 | gi 118411154 | Thalassiosira pseudonana | Transport Electron | C | 23906 | 9.2 | 6.0 |
| DNA binding | jgi 29950 | Thalassiosira pseudonana | Binding DNA | C | 15300 | 11.3 | 13.2 |
| DNA-directed RNA polymerase beta prime chain | gi 71083809 | Candidatus Pelagibacter ubique | Translation | S | 154411 | 8.8 | 1.4 |
| Domain specific binding protein 14-3-3 | jgi 26146 | Thalassiosira pseudonana | Binding Protein Domain Specific | S | 27869 | 4.6 | 7.3 |
| Eukaryotic translation initiation factor 4A2 isoform2 | jgi 9716 | Thalassiosira pseudonana | Binding Nucleic Acid | S | 42405 | 5.6 | 2.7 |
| F0F1 ATP synthase subunit alpha | gi 33862007 | Prochlorococcus marinus | Transport Proton | S | 54306 | 4.9 | 4.6 |
| F0F1 ATP synthase subunit beta | gi 71082935 | Candidatus Pelagibacter ubique | Transport Proton | S | 50696 | 4.9 | 10.0 |

Post Bloom Shelf Sediment

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|---|-------------------|--------------------------|----------------------|-------------|-----------|-----------|-----------|
| Fucoxanthin chlorophyll a/c protein | jgi 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 13.2 |
| Fucoxanthin chlorophyll a /c protein | jgi 42962 | Thalassiosira pseudonana | Photosynthesis | C | 21515 | 5.1 | 6.5 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 12.9 |
| Glyceraldehyde-3-phosphate dehydrogenase precursor | jgi 31383 | Thalassiosira pseudonana | Glycolysis | S | 39587 | 5.3 | 9.1 |
| Heat shock protein Hsp90 | jgi 6285 | Thalassiosira pseudonana | Folding Protein | S | 80242 | 4.7 | 4.0 |
| Histone 3 | jgi 3183 | Thalassiosira pseudonana | Binding DNA | C | 15312 | 11.4 | 13.2 |
| Histone H2A.1 | jgi 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 18.5 |
| Histone H4 | jgi 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 42.7 |
| Hypothetical protein CBG01077 | jgi 22792 | Thalassiosira pseudonana | Transport | S | 22486 | 6.7 | 10.9 |
| Hypothetical protein CBG08717 | jgi 269322 | Thalassiosira pseudonana | Transport Proton | U | 58009 | 5.8 | 9.2 |
| Hypothetical protein DEHA0F19712g | jgi 27352 | Thalassiosira pseudonana | Binding DNA | N | 13064 | 10.3 | 12.5 |
| Hypothetical protein FG01081.1 | jgi 25949 | Thalassiosira pseudonana | Translation | U | 20124 | 9.8 | 7.9 |
| Manganese superoxide dismutase | jgi 32874 | Thalassiosira pseudonana | Metabolic Process | M | 27061 | 5.5 | 5.3 |
| Photosystem I p700 chlorophyll A apoprotein A | gi 118411096 | Thalassiosira pseudonana | Photosynthesis | C | 83642 | 7.3 | 3.5 |
| Photosystem I p700 chlorophyll A apoprotein B | gi 118411097 | Thalassiosira pseudonana | Photosynthesis | C | 82090 | 7.6 | 4.5 |
| Photosystem I protein F | gi 118411168 | Thalassiosira pseudonana | Photosynthesis | C | 20362 | 8.9 | 8.1 |
| Photosystem I protein L | gi 118411163 | Thalassiosira pseudonana | Photosynthesis | C | 15704 | 9.3 | 12.2 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 18.9 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 15.9 |
| Photosystem II reaction center protein D1 | gi 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 6.4 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 6.3 |
| Rab family GTPase Rab8 | jgi 33126 | Thalassiosira pseudonana | Transport | S | 20382 | 7.7 | 12.2 |
| RAB small monomeric GTPase | jgi 35818 | Thalassiosira pseudonana | Transport | S | 20626 | 6.6 | 11.1 |
| Ribosomal protein S18 | jgi 26893 | Thalassiosira pseudonana | Structure Ribosome | R | 17159 | 10.8 | 13.7 |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 25.3 |
| S-adenosyl methionine synthetase | jgi 21815 | Thalassiosira pseudonana | Transport | S | 50359 | 5.2 | 3.2 |
| Translation elongation factor 1 alpha | jgi 3858 | Thalassiosira pseudonana | Translation | S | 47815 | 7.2 | 2.5 |
| Tubulin alpha-2 chain | jgi 29304 | Thalassiosira pseudonana | Structure | S | 49904 | 5.0 | 2.9 |
| Tubulin beta chain | jgi 8069 | Thalassiosira pseudonana | Structure | S | 49497 | 4.9 | 11.5 |
| Ubiquitin | jgi 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 22.2 |

Post Bloom Shelf Sediment

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|------------|--------------------------|------------------|------|-------|-----|------|
| Unknown | jgi 39299 | Thalassiosira pseudonana | Binding GTP | U | 20905 | 6.8 | 25.1 |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 |
| Vacuolar proton-inorganic pyrophosphatase | jgi 39520 | Thalassiosira pseudonana | Transport Proton | S | 70120 | 5.0 | 2.4 |

Post Bloom Basin Sediment

| Protein | Annotation | Species | Function | Comp | MW | pI | SC |
|--|--------------|--------------------------------|-------------------------|------|--------|------|------|
| ATP synthase CF1 beta chain | gi 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 5.3 |
| DNA-directed RNA polymerase subunit gamma | gi 33862040 | Prochlorococcus marinus | Translation | S | 72335 | 6.6 | 1.7 |
| Fucoxanthin chlorophyll a/c protein | jgi 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 6.8 |
| Fucoxanthin chlorophyll a /c protein | jgi 38494 | Thalassiosira pseudonana | Photosynthesis | C | 20354 | 4.5 | 6.8 |
| Fucoxanthin chlorophyll a/c binding protein | jgi 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 6.2 |
| Histone H2A.1 | jgi 19793 | Thalassiosira pseudonana | DNA Binding | N | 13053 | 10.4 | 7.3 |
| Histone H4 | jgi 3184 | Thalassiosira pseudonana | DNA Binding | N | 11384 | 11.5 | 41.7 |
| Hypothetical protein DDB0187116 | jgi 25297 | Thalassiosira pseudonana | Metabolic Process Lipid | U | 369027 | 6.3 | 0.9 |
| Intracellular membrane-associated calcium-independent phospholipase A2 gamma | jgi 23984 | Thalassiosira pseudonana | Metabolic Process Lipid | S | 92973 | 5.4 | 2.3 |
| OmpA family protein | gi 71083303 | Candidatus Pelagibacter ubique | Membrane | S | 17499 | 9.6 | 5.7 |
| Oxygen-evolving enhancer protein 1 precursor | jgi 34830 | Thalassiosira pseudonana | Photosynthesis | S | 29136 | 5.2 | 7.6 |
| Photosystem I p700 chlorophyll A apoprotein A | gi 118411096 | Thalassiosira pseudonana | Photosynthesis | C | 83642 | 7.3 | 1.9 |
| Photosystem I p700 chlorophyll A apoprotein B | gi 118411097 | Thalassiosira pseudonana | Photosynthesis | C | 82090 | 7.6 | 3.4 |
| Photosystem II 10 kDa phosphoprotein | gi 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 |
| Photosystem II chlorophyll A core antenna apoprotein | gi 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 18.7 |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | gi 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 9.6 |
| Photosystem II reaction center protein D1 | gi 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 3.1 |
| Photosystem II reaction center protein D2 | gi 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 13.7 |
| TFIID subunit | jgi 3021 | Thalassiosira pseudonana | Transcription | N | 55578 | 6.6 | 4.4 |
| Transcription termination factor Rho | gi 71083054 | Candidatus Pelagibacter ubique | Transcription | S | 47060 | 8.4 | 2.6 |
| Translation elongation factor 1 alpha | jgi 3858 | Thalassiosira pseudonana | Translation | S | 47815 | 7.2 | 2.5 |
| Tubulin beta chain | jgi 8069 | Thalassiosira pseudonana | Structure | U | 49497 | 4.9 | 2.7 |
| Ubiquitin | jgi 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 11.8 |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 |

| Over Wintered Shelf Sediment | | | | | | | | | |
|---|-----|------------|--------------------------|----------------------|------|-------|------|------|--|
| Protein | | Annotation | Species | Function | Comp | MW | pI | SC | |
| Actin A | jgi | 25772 | Thalassiosira pseudonana | Binding Protein | S | 41791 | 5.0 | 7.2 | |
| ATP synthase CF1 beta chain | gi | 118411134 | Thalassiosira pseudonana | Transport Ion | C | 51143 | 4.7 | 8.0 | |
| DNA-directed RNA polymerase subunit gamma | gi | 33862040 | Prochlorococcus marinus | Translation | S | 72335 | 6.6 | 1.7 | |
| Fucoxanthin chlorophyl a/c protein | jgi | 38667 | Thalassiosira pseudonana | Photosynthesis | C | 21807 | 4.8 | 6.8 | |
| Fucoxanthin chlorophyll a /c protein | jgi | 42962 | Thalassiosira pseudonana | Photosynthesis | C | 21515 | 5.1 | 6.5 | |
| Fucoxanthin chlorophyll a/c binding protein | jgi | 268127 | Thalassiosira pseudonana | Photosynthesis | C | 22628 | 4.8 | 6.2 | |
| Heat shock protein 70 | jgi | 269120 | Thalassiosira pseudonana | Folding Protein | S | 71187 | 4.8 | 4.1 | |
| Histone H2A.1 | jgi | 19793 | Thalassiosira pseudonana | Binding DNA | N | 13053 | 10.4 | 7.3 | |
| Histone H4 | jgi | 3184 | Thalassiosira pseudonana | Binding DNA | N | 11384 | 11.5 | 40.8 | |
| Hypothetical protein UM00510.1 | jgi | 261141 | Thalassiosira pseudonana | Binging DNA | S | 29752 | 8.9 | 4.4 | |
| Photosystem I p700 chlorophyll A apoprotein A | gi | 118411096 | Thalassiosira pseudonana | Photosynthesis | C | 83642 | 7.3 | 1.9 | |
| Photosystem I p700 chlorophyll A apoprotein B | gi | 118411097 | Thalassiosira pseudonana | Photosynthesis | C | 82090 | 7.6 | 2.9 | |
| Photosystem I protein L | gi | 118411163 | Thalassiosira pseudonana | Photosynthesis | C | 15704 | 9.3 | 12.2 | |
| Photosystem II 10 kDa phosphoprotein | gi | 118411116 | Thalassiosira pseudonana | Photosynthesis | C | 7388 | 6.0 | 21.2 | |
| Photosystem II chlorophyll A core antenna apoprotein | gi | 118411113 | Thalassiosira pseudonana | Photosynthesis | C | 56408 | 6.5 | 5.9 | |
| Photosystem II chlorophyll A core antenna apoprotein CP43 | - | 118411149 | Thalassiosira pseudonana | Photosynthesis | C | 51845 | 7.7 | 6.4 | |
| Photosystem II reaction center protein D1 | gi | 118411180 | Thalassiosira pseudonana | Photosystem | C | 39699 | 5.3 | 3.1 | |
| Photosystem II reaction center protein D2 | gi | 118411148 | Thalassiosira pseudonana | Photosystem | C | 39064 | 5.6 | 6.3 | |
| Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi | 118411104 | Thalassiosira pseudonana | Photosynthesis | C | 54325 | 6.2 | 11.0 | |
| Translation elongation factor 1 alpha | jgi | 3858 | Thalassiosira pseudonana | Translation | S | 47815 | 7.2 | 2.5 | |
| Tubulin beta chain | jgi | 8069 | Thalassiosira pseudonana | Structure | u | 49497 | 4.9 | 5.4 | |
| Ubiquitin | jgi | 40669 | Thalassiosira pseudonana | Modification Protein | S | 17567 | 9.9 | 15.7 | |
| Vacuolar ATP synthase 16 kDa proteolipid subunit | jgi | 2233 | Thalassiosira pseudonana | Transport Proton | S | 16720 | 5.6 | 10.8 | |

APPENDIX 2

(A) Total hydrolyzable amino acid mole percent distribution of suspended particle, sediment trap, and sediment samples; (B) Tabulated amino acid mole percent distribution of identified proteins; (C) Tabulated amino acid mole percent distribution of identified protein transmembrane regions.

(A)

| | Chl Max POC | 50m POC | 100m POC | 40m Trap | 60m Trap | 100m Trap | PBS | PBB | OWS |
|---------|-------------|---------|----------|----------|----------|-----------|-------|-------|-------|
| Ala | 11.11 | 11.80 | 12.21 | 9.11 | 10.01 | 9.66 | 7.67 | 7.57 | 7.20 |
| Gly | 7.82 | 13.12 | 16.11 | 9.52 | 10.02 | 11.37 | 17.06 | 16.93 | 17.17 |
| Val | 4.62 | 4.47 | 4.01 | 5.93 | 6.18 | 5.65 | 4.71 | 4.94 | 5.18 |
| Leu | 6.25 | 6.41 | 4.43 | 7.31 | 7.66 | 6.46 | 3.39 | 3.44 | 3.12 |
| Ile | 4.04 | 2.57 | 1.61 | 4.53 | 4.50 | 3.88 | 3.68 | 4.06 | 3.76 |
| Thr | 3.80 | 2.06 | 2.77 | 3.96 | 3.79 | 4.03 | 5.83 | 5.13 | 5.43 |
| Pro | 5.12 | 6.07 | 5.75 | 4.83 | 5.19 | 5.28 | 4.42 | 4.78 | 4.43 |
| Asp/Asn | 8.73 | 6.82 | 6.50 | 8.30 | 7.12 | 8.50 | 10.05 | 10.07 | 10.30 |
| Phe | 3.09 | 1.77 | 0.88 | 3.73 | 3.13 | 2.46 | 1.92 | 1.89 | 1.92 |
| Glu/Gln | 12.74 | 4.99 | 3.75 | 7.80 | 5.60 | 6.49 | 6.48 | 5.68 | 6.94 |
| Lys | 4.38 | 1.80 | 4.15 | 3.33 | 2.53 | 2.07 | 2.04 | 1.94 | 2.35 |
| Tyr | 2.80 | 4.73 | 8.68 | 3.85 | 4.24 | 4.16 | 2.86 | 0.87 | 3.00 |

(B)

| | Chl Max POC | 50m POC | 100m POC | 40m Trap | 60m Trap | 100m Trap | PBS | PBB | OWS |
|-----|-------------|---------|----------|----------|----------|-----------|------|------|------|
| Leu | 8.20 | 8.12 | 8.28 | 8.29 | 7.93 | 8.12 | 8.86 | 9.40 | 9.22 |
| Gly | 8.46 | 8.65 | 9.48 | 8.57 | 9.02 | 8.64 | 8.87 | 8.60 | 9.50 |
| Ala | 9.26 | 8.93 | 10.12 | 9.22 | 9.51 | 8.93 | 9.32 | 8.10 | 8.72 |
| Phe | 3.72 | 4.29 | 4.73 | 3.88 | 3.79 | 3.93 | 4.39 | 4.88 | 5.38 |
| Ile | 6.14 | 6.19 | 6.16 | 6.30 | 6.32 | 6.37 | 6.55 | 5.96 | 6.65 |
| Val | 7.46 | 7.36 | 7.27 | 7.43 | 7.69 | 7.52 | 6.89 | 7.00 | 6.56 |
| Ser | 6.31 | 7.27 | 5.94 | 6.06 | 6.00 | 6.05 | 6.52 | 7.45 | 5.92 |
| His | 1.62 | 1.82 | 1.49 | 1.66 | 1.43 | 1.71 | 1.91 | 2.49 | 2.50 |
| Thr | 5.76 | 6.15 | 6.25 | 5.77 | 5.80 | 5.96 | 5.73 | 5.65 | 5.57 |
| Met | 2.78 | 2.65 | 2.94 | 2.84 | 2.91 | 2.79 | 2.71 | 2.73 | 2.93 |
| Trp | 0.87 | 1.20 | 1.12 | 0.90 | 0.91 | 1.01 | 1.28 | 1.57 | 1.93 |
| Tyr | 2.80 | 2.90 | 3.04 | 2.81 | 2.82 | 2.90 | 2.94 | 2.67 | 2.99 |
| Pro | 4.25 | 4.43 | 3.95 | 4.10 | 4.09 | 4.22 | 3.93 | 4.25 | 4.48 |

| (B) | Chl Max | 50m POC | 100m POC | 40m Trap | 60m Trap | 100m Trap | PBS | PBB | OWS |
|-----|---------|---------|----------|----------|----------|-----------|------|------|------|
| | Cys | 1.31 | 1.29 | 1.04 | 1.23 | 1.22 | 1.24 | 1.13 | 0.97 |
| Asn | 3.97 | 3.66 | 3.54 | 3.85 | 3.73 | 3.84 | 3.56 | 4.01 | 4.00 |
| Gln | 3.23 | 3.19 | 3.62 | 3.28 | 3.13 | 3.18 | 3.42 | 3.19 | 3.30 |
| Arg | 4.82 | 4.81 | 4.57 | 4.76 | 4.68 | 4.83 | 4.83 | 5.24 | 4.60 |
| Glu | 6.93 | 6.16 | 5.58 | 7.05 | 6.94 | 6.74 | 6.11 | 5.86 | 5.52 |
| Lys | 6.06 | 5.23 | 5.38 | 6.04 | 5.66 | 6.13 | 5.70 | 4.78 | 4.47 |
| Asp | 6.05 | 5.72 | 5.50 | 5.96 | 6.42 | 5.87 | 5.34 | 5.18 | 4.77 |

| (C) | Chl Max | 50m POC | 100m POC | 40m Trap | 60m Trap | 100m Trap | PBS | PBB | ows |
|---------|---------|---------|----------|----------|----------|-----------|-------|-------|-------|
| | Leu (L) | 13.80 | 14.38 | 14.33 | 14.61 | 14.16 | 14.16 | 14.37 | 14.30 |
| Gly (G) | 12.49 | 13.05 | 12.54 | 12.94 | 13.48 | 12.09 | 12.46 | 12.33 | 12.63 |
| Ala (A) | 13.42 | 13.45 | 15.64 | 12.71 | 11.24 | 12.42 | 12.06 | 13.05 | 12.29 |
| Phe (F) | 9.63 | 9.32 | 8.79 | 9.78 | 10.11 | 9.62 | 9.46 | 10.01 | 10.02 |
| Ile (I) | 10.50 | 9.72 | 9.28 | 10.64 | 8.76 | 9.82 | 9.92 | 9.56 | 9.85 |
| Val (V) | 9.70 | 8.92 | 9.45 | 8.17 | 8.99 | 10.42 | 8.94 | 7.77 | 7.58 |
| Ser (S) | 6.28 | 7.59 | 7.82 | 5.92 | 6.07 | 5.95 | 5.89 | 5.45 | 5.56 |
| His (H) | 1.68 | 2.66 | 1.95 | 3.22 | 4.27 | 2.07 | 4.15 | 5.90 | 5.64 |
| Thr (T) | 5.10 | 3.46 | 4.40 | 3.68 | 3.60 | 4.74 | 4.21 | 3.66 | 3.79 |
| Met (M) | 2.80 | 4.13 | 4.56 | 4.08 | 3.37 | 4.14 | 3.75 | 3.75 | 3.70 |
| Trp (W) | 2.18 | 2.93 | 2.61 | 2.82 | 4.49 | 2.40 | 3.17 | 4.02 | 3.87 |
| Tyr (Y) | 3.60 | 3.20 | 2.28 | 3.45 | 3.82 | 3.54 | 3.75 | 3.40 | 3.54 |
| Pro (P) | 2.86 | 2.26 | 2.28 | 2.59 | 3.15 | 2.54 | 2.37 | 2.06 | 2.10 |
| Cys (C) | 1.93 | 1.73 | 1.14 | 1.61 | 1.80 | 1.94 | 1.62 | 1.52 | 1.60 |
| Asn (N) | 1.18 | 0.80 | 0.81 | 1.27 | 0.90 | 1.14 | 1.04 | 1.07 | 1.01 |
| Gln (Q) | 0.87 | 0.53 | 0.65 | 0.92 | 0.22 | 1.07 | 0.75 | 0.63 | 0.67 |
| Arg (R) | 0.62 | 0.40 | 0.33 | 0.52 | 0.45 | 0.67 | 0.81 | 0.54 | 0.59 |
| Glu (E) | 0.62 | 0.53 | 0.49 | 0.46 | 0.45 | 0.40 | 0.63 | 0.36 | 0.42 |
| Lys (K) | 0.37 | 0.53 | 0.16 | 0.40 | 0.45 | 0.40 | 0.40 | 0.54 | 0.42 |
| Asp (D) | 0.37 | 0.40 | 0.49 | 0.23 | 0.22 | 0.47 | 0.23 | 0.09 | 0.17 |

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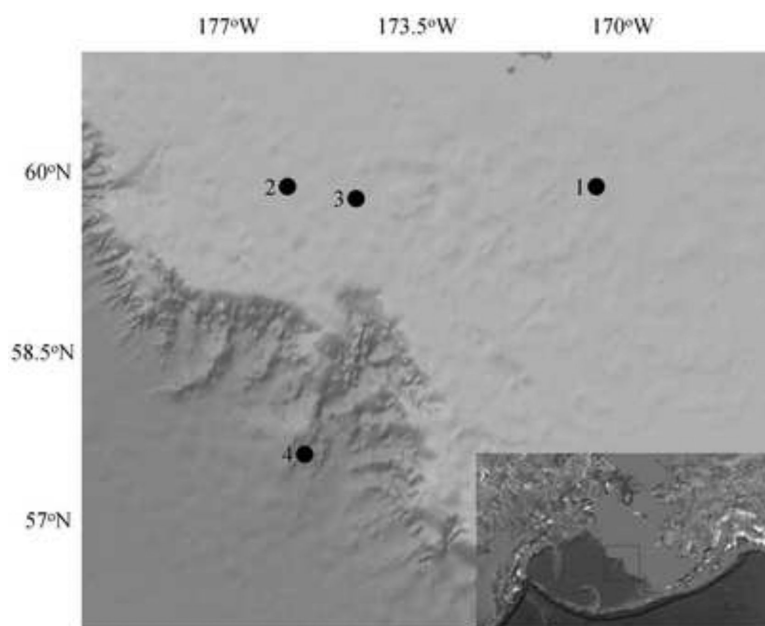


Figure 1. Map of Bering Sea and sample locations. Samples include: (1) shelf surface sediment during ice cover prior to the spring phytoplankton bloom; (2) water column suspended particles and sinking particle trap material during the spring phytoplankton bloom; (3) shelf sediments subsequent to the spring phytoplankton bloom and (4) basin surface sediments.

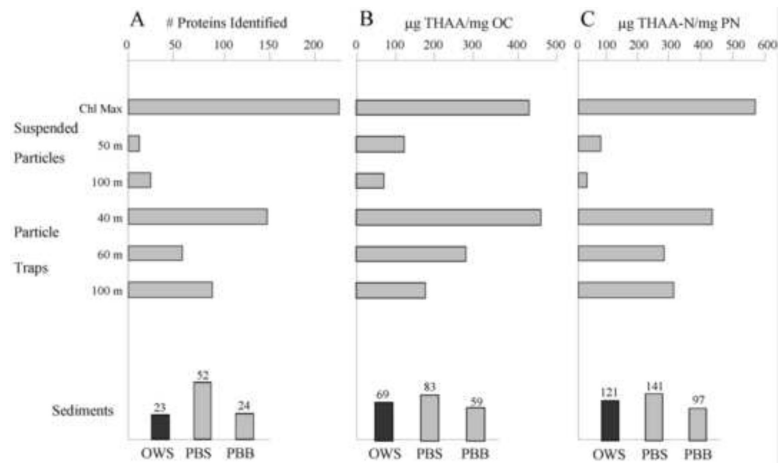


Figure 2. Profiles of (A) Number of proteins identified; (B) THAA/OC from each sample; (C) THAA-N/PN from each sample (Sediment samples graphed by residence time: OWS = Over-wintered Shelf; PBS = Post-bloom Shelf; PBB = Post-bloom Basin).

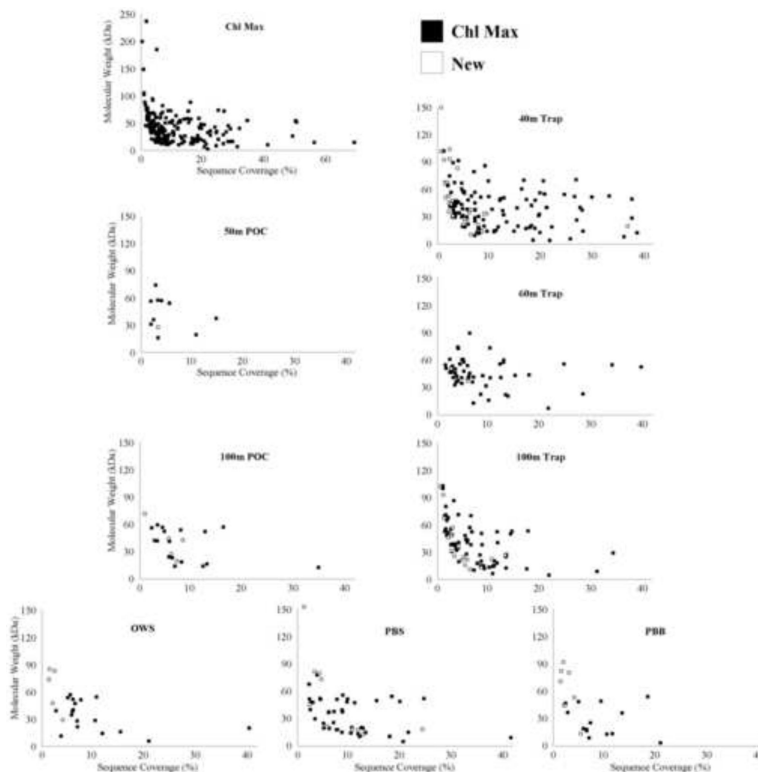


Figure 3. Protein molecular weight vs. sequence coverage plots for each sample. Solid data points represent proteins that were identified in chl-max, open data points represent proteins that were not identified in chl-max. One ~400 kDa protein (sequence coverage: 1%) in PBB plot has been excluded for ease of comparison.

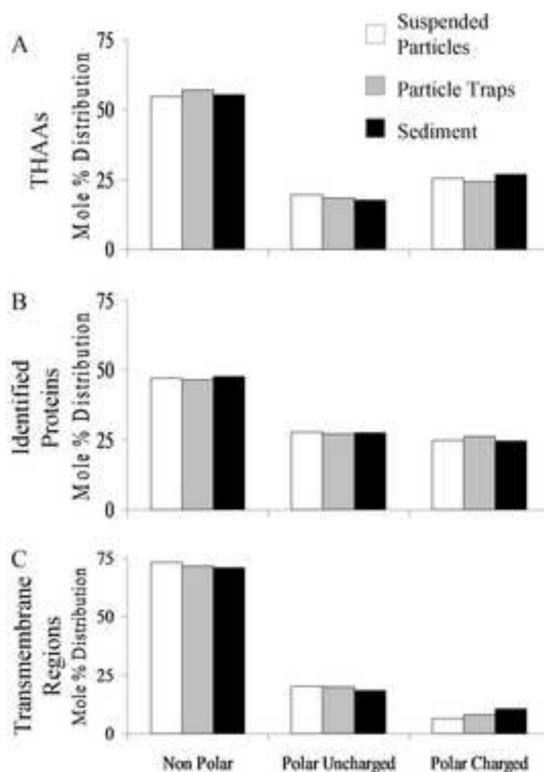


Figure 4. The distribution of non polar, polar uncharged, and polar charged amino acids among (A) total hydrolysable amino acids; (B) tabulated amino acids of identified proteins; (C) tabulated amino acids of TMHMM modeled transmembrane regions within identified proteins. Identified protein amino acids and THAAs show very similar distribution, while transmembrane regions have greater proportion of non polar amino acids.

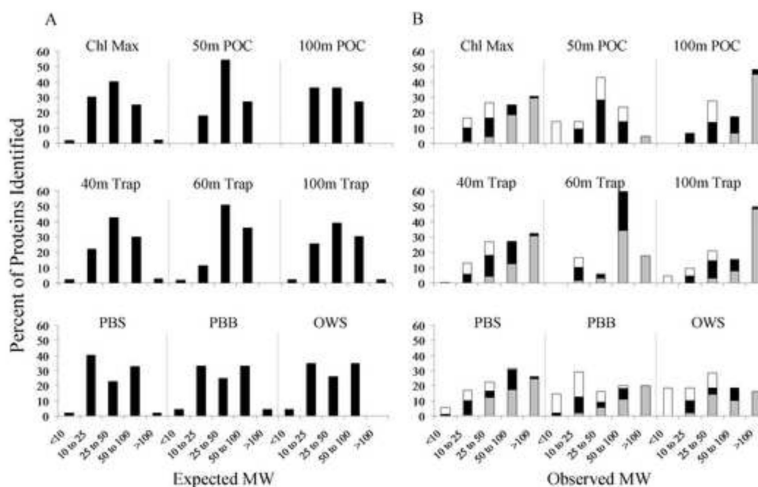


Figure 5. The percentage of identified proteins in each sample within molecular weight groups versus identified proteins with altered properties. A) The expected distribution of identified proteins in samples; (B) The distribution of proteins identified in each gel section: black bars represent the percentage of proteins identified in the expected gel section molecular weight range, grey bars represent “observed large” proteins, white bars represent “observed small” proteins.

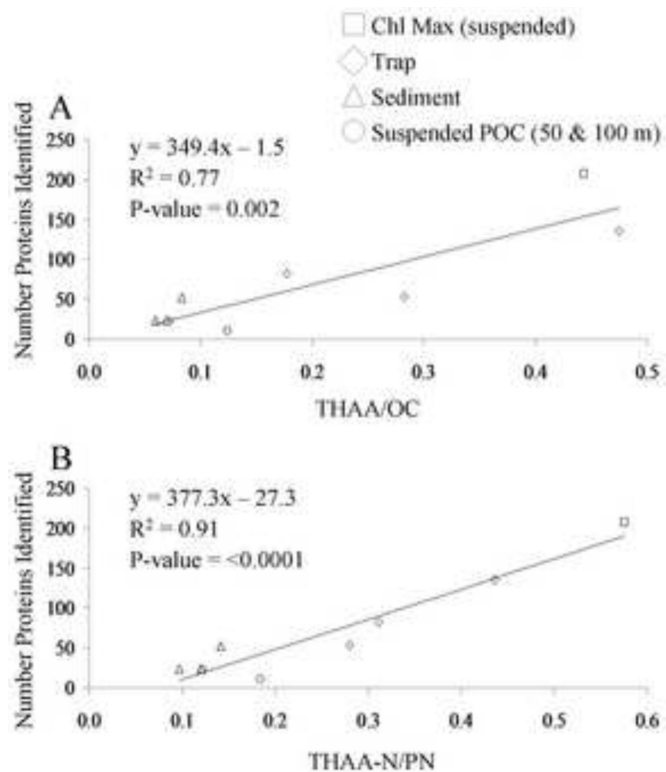


Figure 6. (A) The number of identified proteins plotted against THAA/OC; (B) Identified proteins plotted against THAA-N/PN with linear regressions displayed for each.

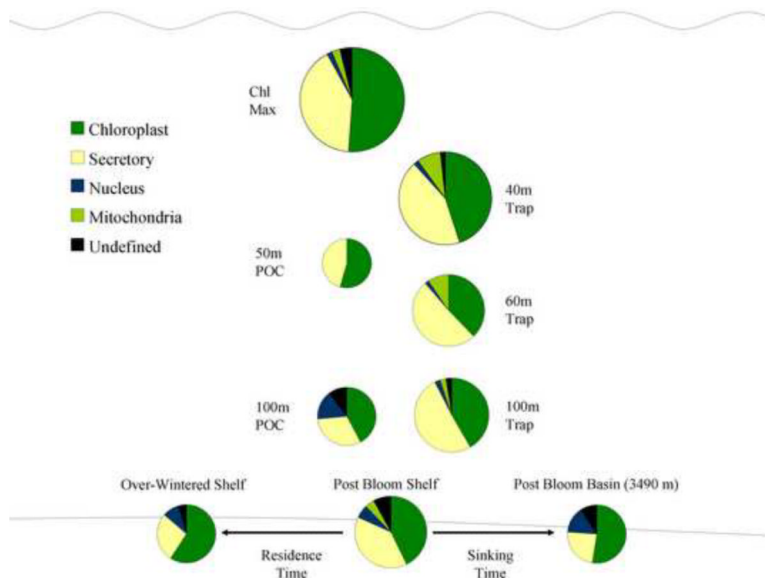


Figure 7. The relative distribution of proteins identified from the cellular compartments of diatoms. Each section shows the percent contribution of proteins originating from a specific compartment. Cellular compartments include: chloroplast, secretory, nucleus, mitochondria, and a group of proteins that are from undefined or unknown compartments. The sizes of each circle is scaled to the number of proteins identified in each sample.

Table 1

Station locations and bulk properties of suspended particles (POC), trap material and sediments of Bering Sea samples. Carbon and total hydrolysable amino acid (THAA) concentrations are $\mu\text{g/L}$ for suspended particles, $\mu\text{g/hr}$ for trap material, and $\mu\text{g/g}$ for sediments. PBS = Post-bloom Shelf; PBB = Post-bloom Basin; OWS = Over-wintered Shelf.

| Sample | Date | Lat (N) | Long (W) | Depth (m) | $^{\circ}\text{C}$ | C ($\mu\text{g/L}$) | C:N Ratio | THAA (μg) |
|-------------|-----------|---------|----------|-----------|--------------------|-----------------------|-----------|------------------------|
| Chl Max POC | 4/30/2009 | 59.9 | 176.1 | 4 | -0.79 | 1172 | 6.2 | 520.0 |
| 50m POC | 4/30/2009 | 59.9 | 176.1 | 50 | -0.05 | 114.4 | 3.5 | 14.2 |
| 100m POC | 4/30/2009 | 59.9 | 176.1 | 100 | 0.71 | 126.1 | 3.9 | 9.0 |
| 40m Trap | 4/30/2009 | 59.9 | 176.1 | 40 | -0.76 | 225 | 4.1 | 4.6 |
| 60m Trap | 4/30/2009 | 59.9 | 176.1 | 60 | 0.45 | 5314 | 4.0 | 4.0 |
| 100m Trap | 4/30/2009 | 59.9 | 176.1 | 1.00 | 1.00 | 365 | 8.1 | 2.9 |
| PBS | 7/5/2009 | 59.6 | 175.2 | 136 | 1.08 | 10200 | 7.9 | 846.9 |
| PBB | 6/26/2009 | 57.5 | 175.2 | 3490 | 3.67 | 11600 | 7.5 | 687.8 |
| OWS | 4/9/2009 | 59.9 | 171.6 | 101 | -0.15 | 10500 | 8.2 | 725.4 |

Table 2

The number of total proteins identified in suspended particles (POC), particle traps, and sediments. Species distribution is based on database identifications originating from diatoms, (*T. pseudonana*), an autotrophic bacteria (*P. marinus*), or the pelagic bacteria (*P. ubique*).

| Sample | Total Proteins Identified | <i>T. pseudonana</i> | <i>P. marinus</i> | <i>P. ubique</i> |
|-------------|---------------------------|----------------------|-------------------|------------------|
| Chl-max POC | 207 | 200 | 3 | 4 |
| 50m POC | 11 | 10 | 0 | 1 |
| 100m POC | 22 | 19 | 0 | 3 |
| 40m Trap | 136 | 129 | 5 | 2 |
| 60m Trap | 53 | 52 | 1 | 0 |
| 100m Trap | 82 | 79 | 3 | 0 |
| PBS | 52 | 49 | 1 | 2 |
| PBB | 24 | 21 | 1 | 2 |
| OWS | 23 | 22 | 1 | 0 |

Table 3

The distribution of proteins observed in particles and sediments categorized by major cellular function as defined by Gene Ontology (Metabolic, Structure/Binding, or Transport). Total proteins observed are categorized as percentage of each by subgroup.

| Chl-max POC IDs | | 207 | | | |
|-------------------------|--------------------|----------------------------|-------------------|--------------------|-------------------|
| % Metabolic | 131 (63.3%) | % Structure/Binding | 37 (17.9%) | % Transport | 27 (13.0%) |
| Translation | 35 (16.9%) | Binding, DNA/RNA | 13 (6.3%) | Ion Transport | 19 (9.2%) |
| Photosynthesis | 30 (14.5%) | Binding, Protein | 8 (3.9%) | Transport, General | 8 (3.9%) |
| Biosynthesis | 18 (8.7%) | Protein Folding | 7 (3.4%) | | |
| Cellular Processing | 29 (14.0%) | Binding, Molecule | 6 (2.9%) | | |
| Glycolysis | 11 (5.3%) | Structural | 3 (1.4%) | | |
| Oxidation Reduction | 8 (3.9%) | | | | |
| 50m POC IDs 11 | | | | | |
| % Metabolic | 3 (27.3%) | % Structure/Binding | 2 (18.2%) | % Transport | 5 (45.5%) |
| Photosynthesis | 2 (18.2%) | Binding, Protein | 1 (9.1%) | Ion Transport | 4 (36.4%) |
| Translation | 1 (9.1%) | Structural | 1 (9.1%) | Transport, General | 1 (9.1%) |
| 100m POC IDs 22 | | | | | |
| % Metabolic | 8 (36.4%) | % Structure/Binding | 7 (31.8%) | % Transport | 7 (31.8%) |
| Photosynthesis | 5 (22.7%) | Binding | 5 (22.7%) | Ion Transport | 5 (22.7%) |
| Cell Processing | 3 (13.6%) | Structure | 2 (9.1%) | Transport, General | 2 (9.1%) |
| 40m Trap IDs 136 | | | | | |
| % Metabolic | 82 (60.3%) | % Structure/Binding | 25 (18.4%) | % Transport | 24 (17.6%) |
| Photosynthesis | 24 (17.6%) | Binding, DNA/RNA | 9 (6.6%) | Ion Transport | 19 (14.0%) |
| Translation | 16 (11.8%) | Binding, Protein | 7 (5.1%) | Transport, General | 5 (3.7%) |
| Biosynthesis | 12 (8.8%) | Protein Folding | 3 (2.2%) | | |
| Glycolysis | 10 (7.4%) | Structure | 3 (2.2%) | | |
| Cellular Processing | 16 (11.8%) | Binding, Molecule | 3 (2.2%) | | |
| Oxidation Reduction | 4 (2.9%) | | | | |

| 60m Trap IDs 53 | | | | | |
|-------------------------------|-------------------|----------------------------|------------------|--------------------|-------------------|
| % Metabolic | 34 (64.2%) | % Structure/Binding | 8 (15.1%) | % Transport | 10 (18.9%) |
| Photosynthesis | 13 (24.5%) | Binding, DNA/RNA | 2 (3.8%) | Ion Transport | 6 (11.3%) |
| Glycolysis | 6 (11.3%) | Binding, Protein | 3 (5.7%) | Transport, General | 4 (7.5%) |
| Cellular Metabolism | 5 (9.4%) | Protein Folding | 2 (3.8%) | | |
| Translation | 4 (7.5%) | Structure | 1 (1.9%) | | |
| Biosynthesis | 3 (5.7%) | | | | |
| Cellular Processing | 3 (5.7%) | | | | |

| 100m Trap IDs 82 | | | | | |
|--------------------------------|-------------------|----------------------------|-------------------|--------------------|-------------------|
| % Metabolic | 39 (47.6%) | % Structure/Binding | 12 (14.6%) | % Transport | 18 (22.0%) |
| Translation | 15 (18.3%) | Binding | 7 (8.5%) | Ion Transport | 16 (19.5%) |
| Photosynthesis | 6 (7.3%) | Protein Folding | 3 (3.7%) | Transport, General | 2 (2.4%) |
| Glycolysis | 6 (7.3%) | Structure | 2 (2.4%) | | |
| Cellular Metabolism | 5 (6.1%) | | | | |
| Cellular Processing | 5 (6.1%) | | | | |
| Biosynthesis | 2 (2.4%) | | | | |

| Post-bloom Shelf IDs 53 | | | | | |
|---------------------------------------|-------------------|----------------------------|-------------------|--------------------|-------------------|
| % Metabolic | 21 (39.6%) | % Structure/Binding | 14 (26.4%) | % Transport | 17 (32.1%) |
| Photosynthesis | 14 (26.4%) | Binding, DNA/RNA | 6 (11.3%) | Ion Transport | 12 (22.6%) |
| Cellular Processing | 4 (7.5%) | Structure | 4 (7.5%) | Transport, General | 5 (9.4%) |
| Translation | 3 (5.7%) | Binding, Protein | 4 (7.5%) | | |

| Post-bloom Basin IDs 24 | | | | | |
|---------------------------------------|-------------------|----------------------------|------------------|--------------------|-----------------|
| % Metabolic | 17 (70.8%) | % Structure/Binding | 4 (16.7%) | % Transport | 2 (8.3%) |
| Photosynthesis | 11 (45.8%) | Binding, DNA/RNA | 2 (8.3%) | Ion Transport | 2 (8.3%) |
| Cellular Processing | 4 (16.7%) | Structure | 1 (4.2%) | | |
| Translation | 2 (8.3%) | Membrane | 1 (4.2%) | | |

| Over-wintered Shelf IDs | | 23 | | | |
|--------------------------------|-------------------|----------------------------|------------------|--------------------|-----------------|
| % Metabolic | 16 (69.6%) | % Structure/Binding | 5 (21.7%) | % Transport | 2 (8.7%) |
| Photosynthesis | 12 (52.2%) | Binding, DNA/RNA | 3 (13.0%) | Ion Transport | 2 (8.7%) |
| Translation | 2 (8.7%) | Binding, Protein | 1 (4.3%) | | |
| Cellular Processing | 2 (8.7%) | Structure | 1 (4.3%) | | |

Table 4

The average isoelectric point (pI), number and relative abundance of high abundance diatom proteins¹, number and percentage of transmembrane proteins, percent transmembrane amino acids from each sample, and number and percentage of transmembrane proteins located in the chloroplast. Transmembrane regions predicted by TMHMM server v. 2.0.

| Sample | pI | High Abundance Proteins | Membrane Proteins | Percent Transmembrane AAs | Transmembrane Proteins in Chloroplast |
|-----------|-----|-------------------------|-------------------|---------------------------|---------------------------------------|
| Chl Max | 6.5 | 59 (29%) | 25 (12%) | 2 | 17 (68%) |
| 50m POC | 5.6 | 8 (80%) | 2 (18%) | 16 | 2 (100%) |
| 100m POC | 6.8 | 13 (59%) | 6 (27%) | 8 | 4 (67%) |
| 40m Trap | 6.2 | 48 (37%) | 20 (15%) | 3 | 15 (75%) |
| 60m Trap | 5.5 | 30 (58%) | 5 (9%) | 2 | 5 (100%) |
| 100m Trap | 6.6 | 32 (41%) | 16 (20%) | 5 | 13 (81%) |
| PBS | 6.9 | 23 (47%) | 15 (28%) | 9 | 12 (80%) |
| PBB | 6.8 | 9 (43%) | 9 (38%) | 9 | 8 (89%) |
| OWS | 6.8 | 12 (55%) | 10 (44%) | 14 | 9 (90%) |

¹ high abundance proteins were defined as the top 1% of proteins based on proteome analysis (Nunn et al., 2009)