UNIVERSITY OF CALIFORNIA, SAN DIEGO

Comparative genomic analyses of transport proteins encoded within the red alga *Cyanidioschyzon merolae* and the green alga *Chlamydomonas reinhardtii.*

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Biology

by

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2015

The Thesis of Shounak Ghosh is approved and it is acceptable in quality and form for publication on microfilm and electronically:

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University of California, San Diego

2015

DEDICATION

This thesis is dedicated to those whom I consider most dear to me. Primarily, I would like to acknowledge my best friends – Victor, Lin, James, and David. They have been at my side for years and have helped keep me sane throughout my college career. Without them, I would not be where I am today. I would also like to thank Susie and Justin (without whom my thesis would not even exist) for their various forms of aid as I worked through my thesis and for joining the ranks of those I am fortunate to have met. I would also like to thank Jimmy for being a calm and down-to-earth companion through the last year, keeping me grounded through the stress. Lastly, I would like to acknowledge my parents, who have always supported me and done everything in their power to help me become better.

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ABSTRACT OF THE THESIS

Comparative genomic analyses of transport proteins encoded within the red algae, *Cyanidioschyzon merolae* and the green alga, *Chlamydomonas reinhardtii.*

by

Shounak Ghosh

Master of Science in Biology

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Cyanidioschyzon merolae is a thermo-acidophilic unicellular red alga that can be found living in volcanic environments. We bioinformatically analyzed the genome of *C. merolae* in order to identify and classify transport proteins related to its metabolic and extremophilic capabilities. These transport proteins were then compared with those of the green alga *Chlamydomonas reinhardtii* to characterize the extent of their divergence. As a more primitive alga, *C.* merolae has a smaller genome than *C.* reinhardtii and thus also exhibits fewer transport proteins. However, both algae contain large numbers of cation-specific transport systems and prioritize secondary carrier transport proteins. The

results presented in this thesis provide information about transport systems which will be relevant to furthering the studies of *Cyanidioschyzon merolae*, *Chlamydomonas reinhardtii*, and potentially other algae as well.

INTRODUCTION

The genome of any organism provides valuable insight into the way in which it has carved a niche for itself in the world. Various adaptations and the overall evolution of organisms required to survive can all be seen through changes within the genome, whether they be large modifications such as the addition or removal of a limb or smaller changes such as the production of a few proteins differing from their closest homologues by a single amino acid. All of these changes stem from the production of a unique combination of proteins, and thus the best way to understand the adaptations enabling an organism to survive in its chosen environment is to carefully consider its set of proteins.

Organisms that survive in conditions deemed intolerable by humans, such as extremely acidic areas, are highly unusual and therefore even more interesting to study. *Cyanidioschyzon merolae* (hereafter referred to as Cme), also known as the hot spring alga, is a prime example. It belongs to the class Cyanidiophyceae in the family Cyanidiaceae, a grouping of red algae (Yoon et al. 2005). Although Cme is a eukaryotic organism, it is a unicellular red alga and can be found inhabiting extremely acidic and warm areas, such as hot springs. For example, it can be found at the Phlegraean Fields, a volcanic area west of Naples, Italy (Eloranta et al. 2011). The pH of the springs in which it lives is extremely low, usually around 1.5, and the temperatures are around 45℃ (Matsuzaki et al. 2004). In order to survive in these extreme circumstances, organisms such as Cme must modify their genotypes and thus alter their phenotypes to out-compete neighboring species (Welch et al. 2014).

Cme is considered to be one of the most primitive photosynthetic eukaryotes (Cunningham et al. 2006). It is a small, club-shaped, unicellular alga with a 2µm diameter (Yagisawa et al. 2009). Due to its size, it lacks a rigid cell wall and only carries one nucleus, one mitochondrion, and one plastid in addition to one Golgi apparatus, one endoplasmic reticulum, and some polyphosphate-rich compartments (Yagisawa et al. 2009). This is a far smaller organelle composition than is generally present within animal or plant cells, and this minimal composition means that determining the behavior of organelles during mitosis and the rest of the cell cycle is very easy (Misumi et al. 2005). Its genome is also the smallest amongst photosynthetic eukaryotes but is highly specialized for its environment. The complete nucleotide sequence of the genome has been recorded, as has the sequence for its plastid genome (Ohta et al. 2003). Additionally, few genes within this alga contain introns, and they are in small numbers, unlike most other eukaryotes (Nozaki et al. 2007). Previous BLAST searches and annotation results determined that Cme has genes found both within plants and animals, implying that it is related to a common prokaryotic ancestor (Misumi et al. 2005). Due to its small genome and its classification as a primitive alga, it may be a good model organism for the study of the origin of eukaryotes and various types of endosymbiosis (Misumi et al. 2005).

Cme diverged from its closest cousin, *Galdieria sulphuraria*, about one billion years ago (Schonknecht et al. 2014). Due to its simplicity, Cme offers a unique opportunity for studies upon mitochondrial and plastid division. Its nucleus, mitochondrion, and plastid are spherical or disk-like in shape. Their division can be synchronized using light treatment (Terui et al., 1995). Cellular mechanisms studied using Cme are present in both higher animals and plants, making Cme a unique candidate for studying mitochondrial and plastid divisions (Kuroiwa et al., 1998)

Photosynthetic eukaryotes like *Chlamydomonas reinhardtii* are evolutionary intermediates between primitive algae like Cme and higher plants (Misumu et al. 2005). Although its nature as a multicellular green alga sets it apart from Cme, a large amount of background knowledge exists for Cre, as it has been very well characterized. Therefore, it is a good candidate with which to compare genomes and identify key differences allowing for the extremophilic nature of Cme as opposed to the more normal nature of Cre. Compared to Cme, Cre has several double membrane-bound organelles (nucleus, mitochondria, and plastids) as well as single membrane-bound organelles (endoplasmic reticulum, Golgi apparatus, microbodies, and lysosomes). Division of all of these organelles occurs at random and does not seem to be synchronized, in contrast to those of Cme. Cre does, however, offer a simple life cycle, easy isolation of mutants, and the ability to be manipulated easily to further molecular genetic studies (Harris 2001).

Of particular interest to the lab are the transporters present within Cme, which are used to regulate its internal ion concentrations and amino acid concentrations, among other things, in order to adapt to its environment. Transport proteins are integral to acquisition, waste removal, and signaling. They provide a method of understanding the connection between an organism's genome and its environment by showing how the organism has developed to utilize substances that may be toxic to others, such as ions present in large concentrations (Getsin et al. 2013). The characterization of these transport proteins will therefore help elucidate the physiology of Cme and the adaptations allowing it to specialize within its extreme environment as opposed to other red algae, which are not extremophiles. Understanding the difference between the

extremophile Cme and its non-extremophile relatives will provide insight into the processes that allowed it to branch away and become its own species.

MATERIALS AND METHODS

The proteomes of both Cme and Cre were retrieved from the protein database of the National Center for Biotechnology Information (NCBI; www.ncbi.nlm.nih.gov) website and then were screened by our genome BLAST (GBLAST) programs against transporters present in the Transporter Classification Database (TCDB; www.tcdb.org; Reddy and Saier 2012) as of January 1, 2015. Each putative open reading frame from the proteome was used as a query within the BLASTP software to compare against proteins in TCDB and thus find homologous proteins. A comparative e-value score cutoff of 0.001 was used. A low complexity filter was not used because it is normally used for larger datasets that include proteins with multiple repeat elements. The obtained information included suspected query transporters, their top TC hits, TC hit accession numbers, short descriptions, protein sequence match lengths, e-values, number of transmembrane segments (TMSs) in both the query and hit proteins, and the number of TMS overlaps. The number of TMSs was measured through the HMMTOP 2.0 program, used to scan each open reading frame and predict the number of putative TMSs (Tusnady and Simon 1998).

Both the Cme and Cre lists of putative transport proteins were screened for false positives, and those displaying 0 or 1 TMSs through the HMMTOP program were removed unless they displayed membrane insertion capabiltiies within their identified protein families. This was done to eliminate non-integral and non-multispanning membrane proteins, but still retain 0 TMS proteins such as **β**-barrel porins. When TMS numbers needed to be resolved between the query and hit, the Web-based Hydropathy, Amphipathicity, and Topology (WHAT) program was used with a window size of 19

residues and an angle of 100 degrees to display the protein's hydropathy plot. Though the WHAT program uses the HMMTOP program to highlight predicted TMS regions, the program cannot always predict completely accurately, and thus the user ultimately must judge the actual TMS numbers. The criterion used to determine a TMS was a hydrophobicity peak with a value greater than 1 (Zhai and Saier 2001). When the hydrophobicity plot was unclear, the TOPCONS web server program was used to find a consensus TMS prediction to apply to determine query and hit TMS counts. The current TOPCONS algorithm combines the predictions of five programs, including SCAMPI, OCTOPUS, **Δ** G-scale, ZPRED, and PRO/PROVID-TMHMM (Bernsel et al. 2009, Reddy et al. 2014).

When comparative e-value scores retrieved from the GBLAST program were low but TMS numbers and sequence locations were similar between a query and its hit, the Global Sequence Alignment Tool (GSAT) was used to check for statistical significant. The GSAT program utilizes the EMBOSS Needleman-Wunsch (NW) algorithm to provide a global alignment and gives a standard comparison score based on a user-defined number of shuffles (Reddy and Saier 2012). A last measure of verification is the use of NCBI's Conserved Domain Database (CDD) search, which produces a visualization of the conserved motifs within a query transporter which can be compared to the motifs in a hit protein family.

To find novel proteins, a GBLAST of the Cre and Cme proteomes was performed with a poorer e-value cutoff of 0.1, producing a larger list of putative transporters. Only proteins with comparative scores between 0.001 and 0.1 were analyzed to detect false positives, and verified candidate transporters were entered into TCDB. For each of the proteins in a verified list of transporters, substrates and mechanism of action were

identified through scientific literature searches, and listed with a UniProt accession number in Table 3. Proteins sequences with the same UniProt accession number were counted as a single entry, which is reflected in the total count of proteins in the two algal proteomes.

RESULTS

Statistical analysis of transport proteins found in Cre and Cme

The genomes of the red alga Cme and green alga Cre were scrutinized for transport proteins by using their proteomes as distinct queries for BLAST searches against the Transporter Classification Database using the GBLAST program (TCDB; www.tcdb.org; Saier et al. 2014). Table 3 contains all predicted TC classified transport-related proteins, while Table 1 displays a statistical summary of the results organized by TC class and subclass. Out of Cre's 14489 predicted proteins, 729 appear to be integral membrane transport proteins. This corresponds to approximately 4.9% of its genome being transport proteins. In comparison, Cme has 274 integral membrane transport proteins, but also has a much smaller complete proteome, containing 4803 proteins. Therefore, approximately 5.7% of Cme's proteome corresponds to transporters (Table 1). Even though Cre has a much larger genome, the percentage of its proteins that conform to the prediction of being integral membrane transport proteins is actually slightly less than that of Cme. Due to the sheer number of proteins within Cre versus those in Cme, the proportions of each TC class relative to the total number of transporters is a more comparable statistic than the absolute numbers. In terms of absolute numbers, Cre has more proteins in every class.

Class 1 proteins in TCDB include those that form either permanent or transient transmembrane channels. These generally utilize free diffusion to transport their substrates and are energy independent (Spencer and Rees 2002, Zeth and Thein 2010). When the numbers of Class 1 proteins between Cme and Cre are compared, the difference seen is large – whereas Cre has 139 Class 1 transport proteins, Cme has 30.

This corresponds to 19.3% and 10.9%, respectively, of their total transport protein numbers. This suggests that while these passive diffusion-mediating transporters are important, they are not responsible for Cme's ability to survive in extreme environments.

Channel proteins are further distinguished by their subclasses, where 1.A, 1.B, and 1.F are all relevant due to their presence in both algal genomes. Subclass 1.A transporters are characterized by their transmembrane α-helical secondary structure forming sequences. Herein lies the largest difference between Cme and Cre. Cre has 134 alpha-type channels, while Cme has 23. Subclass 1.B contains outer membrane porins, usually consisting of transmembrane β-barrels. These proteins exhibit very few predicted transmembrane segments (TMS), usually either 0 or 1. Cme and Cre both contain only one of these proteins. Subclass 1.F includes vesicle fusion pore proteins. Together, these proteins create a complex aiding in the interaction of vesicles with the cell membrane and create pores for solute exocytosis. While Cme has five of these proteins, Cre has four, so there is no significant difference between the two in this subclass. When comparing the percentage of each subclass relative to the total number of proteins within each alga, 1.A α-type channels show a difference of 8.3% and exhibit the largest difference between the algae. I.B and I.F show no significant differences (Figure 2).

Class 2 proteins function by secondary active transport, energized by electrochemical gradients of ions such as H^+ and Na^+. Only porters from subclass 2.A were found within either alga (Table 1). Cre and Cme respectively have 286 and 144 porters from this subclass, which includes uniporters, antiporters, and symporters. This accounts for 52.5% of the total number of transporters within Cme and 39.7% of the total number of transporters in Cre (Figure 2). The large number of 2.A proteins show that

these porters are key to the total transporter activities of both algae. The resulting 12.8% difference between Cre and Cme is the largest difference found of the various subclasses (Figure 2). Therefore, it appears that secondary active transporters are most important for algal growth and survival. The difference between the two organisms may be due to the fact that Cme is relatively poorly characterized, whereas Cre has been characterized extremely well. Additionally, the large percentage of 2.A transporters suggests that these transporters may be responsible for the ability of Cme to survive in extreme environments. The presence of greater numbers of secondary carriers compared with primarily active transporters also suggests that these algae use photosynthesis and electron transfer processes preferentially for energy generation compared with substrate level phosphorylation.

Class 3 proteins are primary active transporters and move solutes through membranes against larger concentration gradients than do secondary carriers. Proteins within this class often are subunits of transport complexes where only the channel-forming integral membrane constituents have been tabulated. The two algae possess similar percentages of these systems. Cre contains 156 of these transporters, whereas Cme contains 58 (Table 1). This accounts for 21.6% and 21.2% of their transporters, about half of the secondary carriers. The resulting 0.5% difference between the two organisms is probably not significant, but also indicates that transporters utilizing primary energy sources are not as important to survival for Cme, which has a much greater percentage of secondary carriers.

Of the Class 3 proteins, Cre contains transporters from 3.A, 3.B, 3.D, and 3.E whereas Cme contains all of those except 3.B. Subclass 3.A includes proteins energizing substrate transport by using pyrophosphate bond hydrolysis. Cre has 113

transporter proteins in this subclass, while Cme has 47 (Table 1). This accounts for 15.7% and 17.2% of the total number of proteins within their respective genomes. Subclass 3.B contains decarboxylation driven transporters, which drive solute uptake by decarboxylation of a cytoplasmic organocarboxylic acid. Cre only displays one protein from this subclass, while Cme displays none. Subclass 3.D includes ion transporters energized by redox reactions, and Cre and Cme have 34 and 7 of these proteins (4.7% and 2.6% of the total transporter count), respectively. Subclass 3.E includes transport systems using solar energy for transport, and Cre has double the number of these as Cme (8 and 4, respectively). However, this results in percentages of 1.1% and 1.5%. Therefore, out of the percentages of the class 3 subclasses, 3.D Oxidoreduction driven transporters display the greatest difference, with a 2.1% difference, while 3.A and 3.E have differences of 1.5% and 0.4% respectively (Figure 2). The sum total of these differences is probably not significant, suggesting that these organisms have comparable abilities to generate electro-chemical gradients using electron flow.

Class 4 proteins catalyze substrate transport by modifying various substrates in coupled processes. Small numbers of subclasses 4.C, 4.D, and 4.E were found in these two organisms. Subclass 4.C, which utilizes Coenzyme A to cause carboxylic acid thioesterification, was found in Cre but not Cme. The included Fatty Acid Transporter (FAT) Family proteins (TC #4.C.1) have been thought to allow coupled fatty acid uptake through the use of acyl-CoA synthetases (Schneider et al. 2014). Two of these transmembrane proteins were found in Cre (Table 1), but none were identified in Cme. One member of the Putative Vectorial Glycosyl Polymerization (VGP) Family, the 4.D subclass, was found in Cme, and but were seen in Cre. Within subclass 4.E, two proteins were found in Cre; none in Cme. The small numbers of these proteins in both organisms suggest that these transporters are not key to the survival of either Cre or

Cme. As a whole, Class 4 proteins are 0.5% and 0.4% of the total transporters in Cre and Cme respectively.

Class 5 proteins are responsible for electron transport from one side of a membrane to the other. Cre has 41 of these proteins, while Cme has 6. Proportionally, however, this results in 5.6% and 2.2% of their respective transporters. Cre contains proteins from both subclass 5.A and 5.B, while Cme only has proteins from 5.B. 5.A transporters are responsible for carrying electron pairs, whereas 5.B transporters carry single electrons. These electron flow processes must aid in survival and influence cellular energetics or regulation.

Class 8 contains auxiliary proteins that aid in substrate transport by enhancing the activities of transporters. Cre and Cme have seven and one of these transport proteins; Cme contains only one from subclass 8.A while Cre has five from 8.A and two from 8.B. The corresponding percentages are low, at 0.9% and 0.3% respectively (Figure 2). These auxiliary proteins also seem unlikely to be key factors in Cme's survival in extreme environments.

Finally, class 9 includes known and putative proteins known to be transporters, but their mechanisms are unknown. They are placed within the subclass 9.A; those for which evidence supporting transport is incomplete are placed within subclass 9.B. Cre has 86 proteins within class 9, while Cme has 34. Thus, Cre has 21 in 9.A (2.9% of its total transporter count) and 67 in 9.B (9.3%), while Cme has 7 (2.5%) and 27 (9.9%) respectively. These percentages are very similar for the two organisms, and the proteins seem to be present in approximately the same proportions.

Table 2 lists the substrates of transport systems found in the genomes of Cre and Cme based upon their entries in TCDB. The 650 systems found in Cre include a total of 721 transport proteins, and the 258 systems in Cme contain 274 transport proteins. Class 1 channels and pores within Cre seem to be largely used for inorganic ionic substrates and display an approximately 9:2 ratio for cations to anions (Table 2). In contrast, Cme displays a ratio of 15:4 (cation:anion), but also dedicates most of its Class 1 transporters to inorganic ions. Interestingly, both Cre and Cme have few proteins transporting other substrates – the largest portion of transporter substrates is inorganic, with these accounting for 92.6% and 73.1% of their Class 1 transporter counts. Other substrates transported by Class 1 proteins in the two organisms are sugars and polyols, nucleic acids, proteins, and vitamins. Due to Cme's smaller transporter count, these other substrates account for a larger percentage than in Cre (Table 2).

Cre contains about twice as many systems (286) within its class 2 secondary carriers than does Cme (144), but this number leads to a percentage of 39.6% versus 52.6%, respectively (Table 2). Cme has a higher proportion of transporters specific for cations and a similar proportion of those for anions. Additionally, a larger percentage of transporters are responsible for sugar and polyol transport as well as amino acid transport. Cre had higher percentages of transporters for carboxylates, organoanions, amines, lipids, and nucleic acids. Additionally, Cre is able to transport lipids and organoanions whereas transporters for these compounds in Cme were not found. Cme does not transport substrates that Cre cannot.

The superfamilies that confer upon both organisms their large numbers of transporters include 2.A.1, 2.A.7, and 2.A.29. 2.A.1 is the Major Facilitator Superfamily (MFS), which is the largest superfamily of carriers and diverse with respect to its various

substrate types. This accounts for 52 proteins in Cre and 15 in Cme (8% and 5.8% respectively). 2.A.7 is the Drug/Metabolite Transporter (DMT) Superfamily, and this is composed of 14 phylogenetic families, five of which include no functionally well-characterized members. Each DMT family is identified by their distinct topology, consisting of four, five, nine, or ten putative tramsmbrane α helical TMSs per polypeptide chain (Jack et al. 2001). Cre contains 40 of these proteins, and Cme contains 25. Though Cre has more proteins, Cme has a far larger proportion of its transporter count being filled by 2.A.7 proteins. Finally, 2.A.29 is the Mitochondrial Carrier (MC) Family. Cre has 35 of these proteins and Cme has 28. As expected, these transporters comprise a much larger percentage of Cme's total transporter count than of Cre's.

The 114 primary active transport proteins in Cre account for 17.5% of these proteins, while the 49 systems in Cme account for 19.3% (Table 2). Though present in low numbers, nucleoside and vitamin transporters in this class are unique to Cre (Table 2). Inorganic cation-specific systems account for 6.8% of the total transport systems in Cre and 7.8% in Cme; therefore, though Cre has more such transporters, the difference between the two organisms when considering percentages is less than expected. Cre has 6 electron transport systems in class 3, whereas Cme has only one. This accounts for 1% and 0.3% of their transporters. The biggest difference between the two algae concerns those responsible for protein and drug transport. Cre's primary active protein transporters represent 2% and its drug transporters are 3.6% of its total transporters, as compared to Cme's 2.7% and 3.1%. Otherwise, the two algae are similar in the percentage of primary active transporters.

Class 5 proteins, transmembrane electron carriers, are more numerous in Cre (14 systems containing 40 proteins) than in Cme (3 systems with 6 proteins). This is

clearly reflected in the percentages, where Cre contains more than double the relative proportion of Cme (5.5% and 2.2% of all transport proteins, respectively). These differences are almost exclusively within families 5.B.2 and 5.B.4. 5.B.2 is the Eukaryotic Cytochrome b561 (Cytb561) Family, which contains transmembrane proteins found in many eukaryotic cells. Some family members lack sequences coding for putative ascorbate-binding, and others exhibit transmembrane ferrireductase activity. While Cre has nine proteins in this family, Cme lacks them altogether. The 5.B.4 family, known as the Plant Phosphatase I Supercomplex (PSI) Family, generally features the movement of electrons driven by solar energy. As a supercomplex of reaction center and light harvesting proteins, PSI is able to generate the most negative redox potentials found in nature, at -1 V. Cme has one system, consisting of four proteins, representing the 5.B.4 family; Cre also has one system, but it consists of 28 proteins. Interestingly, this family is typically found only within plants and green algae. Despite this and its status as a primitive alga, Cme still contains only a few proteins from this family and thus may represent an evolutionary intermediate between primitive algae and higher plants (Misumi et al. 2005).

Very few auxiliary proteins were found in Cme and Cre. Of the seven available in Cre, five have an unknown function. The families found in Cre but not in Cme include the Immunophilin-like Prolyl:Peptidyl Isomerase Regulator (I-PPI) Family, The Plant/Algal/Chlorella Nitrate Transporter Accessory Protein (NAR2.1) Family, The Nedd4-Family Interacting Protein-2 (Nedd4) Family, and the Mitochondrial EF Hand Ca^{2+} Uniporter Regulator (MICU) Family. Both Cre and Cme contain one protein from the CDC50 P-type ATPase Lipid Flippase β-Subunit (CDC50) Family (8.A.27). These proteins are flippases and are responsible for drug import. They have been used in treatment of several protozoal and fungal diseases (Hanson et al. 2003).

Cre and Cme have 21 and 7 proteins within subclass 9.A and 67 and 27 in subclass 9.B. Of these proteins, 24 likely transport cations, four transport electrons, and ten transport sugars/polyols in Cre. Additionally, 11 transport proteins while three transport lipids and four transport vitamins, while 32 are of unknown function. Cme has nine proteins that utilize cations, one transporting anions, three for electrons, two for sugars/polyols, and three for amines. There are also two specific for peptides, one for lipids, two for cofactors, and six of unknown function. Cre contains more than double the number of these putative transporters than does Cme, at 88 versus 34.

Figure 3 presents the percentages of transport substrates in the two studied algae. The largest of the substrate groups in both organisms is inorganic molecules – 53% of Cre's transporters and 45% of Cme's are used for these substrates (Figure 3). Overall, Cre seems slightly more interested in transporting cations, anions, and nucleic acids, while Cme prioritizes sugars and polyols, amino acids, and peptides. However, both organisms have surprisingly similar proportions of many substrates.

Figure 4 summarizes how the transporter families within Cre and Cme are distributed and organizes them according to the frequency of occurrence in the two organisms. Both organisms, when combined, display 154 transporter families, of which 66 are unique to Cre and 10 are unique to Cme. The two organisms share 80 out of these 154 families, or 51.9% of the total number of transporter families. Therefore, Cme displays 58.4% of the transporter families represented in this data, while Cre has 94.8% of them.

Table 3 contains detailed information about the multispanning transport proteins found in the two studied algal species.

DISCUSSION

Cyanidioschyzon merolae (Cme) is a thermo-acidophilic single-celled red alga that resides in sulphate-rich, acidic, hot springs. It was originally isolated from the solfatane fumaroles in a large volcanic area located west of Naples, Italy, known as Campi Flegrei (De Luca et al. 1978). These environments can reach temperatures of up to 55° Celsius and have pH values as low as 1.5 (Zenvirth et al. 1985). In addition to surviving in these extreme conditions, Cme is one of the most primitive photosynthetic eukaryotes (Cunningham et al. 2007). It is thought to retain primitive features of cellular and genomic organization, and it has a mixed gene repertoire with representatives characteristic of plants and animals (Misumi et al. 2005). This suggests a possible relationship to prokaryotes even though the alga contains similar photosynthetic components as other algal phototrophs. Cme makes little phycoerythrin, the primary red algal pigment, and instead produces the light blue (red-absorbing) pigment phycocyanin and the green pigment (blue and red absorbing) chlorophyll. It thus appears blue-green, even though it is classified as a rhodophyte (Castenholz et al. 2010).

In contrast, *Chlamydomonas reinhardtii* (Cre) is a unicellular green alga found in many different environments throughout the world. It is motile, and its cells, though normally haploid, can become diploid in response to nitrogen deprivation. Though it is also photosynthetic, Cre can survive in total darkness if acetate is present (Merchant et al. 2010). The difference between the two algae can be, in part, understood by comparing the large number of transporters in Cre, no doubt suited for its various environments, against the relatively small number in Cme.

The extreme conditions in which Cme lives have put it under pressure for a long period of time, thus diminishing its physiological and morphological diversity. It survives entirely through obligate photoautotrophic growth, a feature common to most rhodophytes. This explains the presence of greater numbers of secondary carriers compared to primary active transporters found in Cme. In contrast, its closest relative, *Galdieria sulphuraria*, has a very diverse metabolism and grows photoautotrophically, heterotrophically, and mixotrophically (Barbier et al. 2005). In this way, Cme is considered primitive. Its genome contains almost no introns (only 26 genes contain introns) and it has a relatively low degree of genetic redundancy (Matsuzaki et al. 2004). Interestingly, Cme has a genome which contains a large variety of sugar kinases such as putative gluco-, galacto-, fructo-, glycero-, xylulo-, and ribokinases despite only using photoautotrophic growth (Barbier et al. 2005).

Cre has evolved via very different pathways, presumably reflecting the diverse environments in which it can survive and grow. It has been studied in the laboratory for over 60 years, and commonly used strains are derived from a soil isolate. Cre naturally inhabits an environment similar to that of land plants (Glaesener et al. 2013). It diverged from land plants such as *Arabidopsis* around 700 million years ago, which is when the last common ancestor between them can be found. One way in which Cre has significantly evolved from land plants is its ability to oxidize acetate and utilize bioenergetic routes such as hydrogen photoproduction and fermentation, along with several other metabolic differences (Grossman et al., 2007).

There are major differences in the amount of effort Cre and Cme put into transporting various substrates. The most transported substrates in both organisms are inorganic cations, where 35% of Cre’s transporters exhibit such specificities, while 31%

of Cme's transporters are the same. Many of the cation transporters in Cme are responsible for the transport of divalent heavy metal cations such as Mg^{2+}, Zn^{2+}, and Fe^{2+}. The vast majority of these transporters also utilize H^+ as the co- or counter-transporter cation. Due to the acidic nature of Cme's environment, H^+ is plentiful, which may be a contributing factor to Cme's ability to survive in these harsh locations. It has been found that Cme is able to maintain its intracellular pH in the range of 6.35 to 7.1 at an external pH ranging from 1.5 to 7.5 (Zenvirth et al. 1985), and the various cation transporters may therefore have a large effect in allowing Cme to retrieve critical nutrients while regulating its internal pH and ensuring its survival.

Cre devotes 4.5% of its transporters to moving nucleic acids, while Cme allocates 2.5%. However, a larger difference concerns the percentages responsible for amino acid transport – 13% for Cme, 5% for Cre (Figure 3b). All of the amino acid transporters are within the 2.A subclass. In spite of the large percentile difference, the numbers of proteins are fairly similar – Cre has 25 while Cme has 17. These transporters seem to be mostly from the AAAP, APC, and BASS families (2.A.3, 2.A.18, and 2.A.28).

It is important to note that TC subclass 2.A contains the most transport proteins, proportionally, for both algae. This subclass also includes several sugar transporters, in addition to the previously mentioned sugar kinases (Barbier et al. 2005). Proteins from this subclass alone comprise 55.8% of all transporters found in Cme and 39.7% in Cre. The emphasis both organisms place on these transporters shows that they are crucial to survival regardless of the environment in which the organism is found. However, the large difference between these percentages also implies that Cme utilizes proportionally

more transporters from this family in order to gain its ability to survive in extreme environments.

The most important difference between Cme and Cre is the sheer numbers of their transport proteins. In total, 274 transport proteins were identified in Cme and 721 in Cre. Cre also has a much larger overall genome than does Cme – 14489 proteins versus 4803. Despite this, the percentage of transporters present in their proteomes are fairly similar, at 5.0% (Cre) and 5.7% (Cme). The large number of transport proteins in Cre could allow growth in a diverse environment as opposed to the sulphate-rich hot springs where Cme is found.

The most studied variant of Cre is a soil isolate, but this alga can be found in fresh water as well (Merchant et al. 2010). Unlike Cme, it also has two flagella and more internal organelles (Harris 2001). The added complexity to its cell structure could have contributed to its relatively large genome and therefore to the increased number of transporters. In contrast, because of pressures from its extreme habitats, Cme may have narrowed its genome and transporter counts to adapt specifically to a nutrient poor. Thus, the transporter specificities in Cme and Cre, along with the large numerical difference between their transporters, would be explained by their environmental stress needs.

In our research, the impact of proteins from subclass 1.B (β-Barrel Porins) was not examined thoroughly. Future research would therefore include analyzing these proteins to see their effect upon both Cre and Cme. Additionally, analysis of the transporter repertoire of Cme along with its close relative, the extremophile, *Galdieria sulphuraria*, would provide further elucidation of the transporter families, allowing these two thermophilic, acidophilic algae to survive in similar environments when compared to

algae that live in neutral environments such as Cre. Finally, further research could also be done regarding the difference between Cre and Cme just as a function of their light absorbing pigment complements. As Cre is a green alga and Cme is classified as a red alga, there may be greater evolutionary divergence than has been recognized to date.

The characterization of their transport systems as reported here should provide new insight into these relationships. They may also be useful to compare Cme to red algae that live in neutral conditions, and to compare Cre with both close relatives and extremophilic green algae like *Dunaliella salina*, a halophilic green micro-alga found in such places as sea salt fields which is used in the cosmetic industry and provides dietary supplements because of its antioxidant activity (Ahmed et al. 2015). It is clear that this is a rich field for future study with possibilities in many areas of scientific study.

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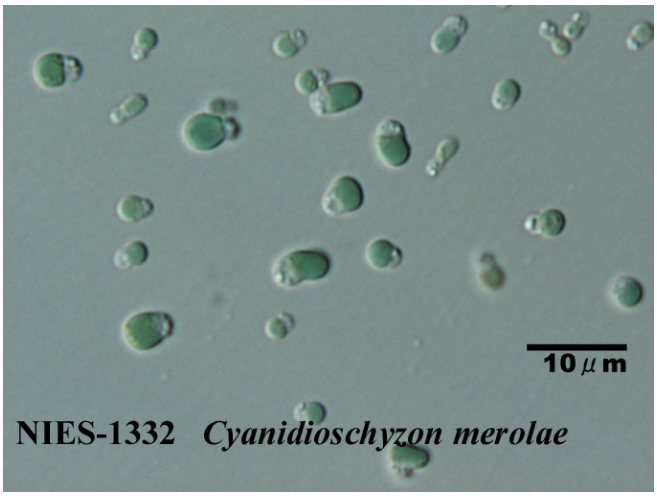
APPENDIX



"Cyanidioschyzon Merolae 1332." *Algal Resource Database*. National Bioresource Project, 1 July 2015. Web. 15 Aug. 2015.

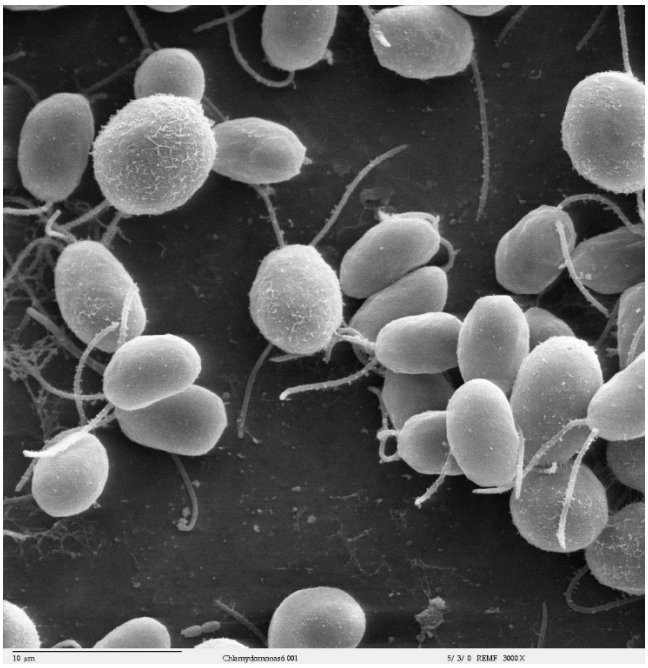


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Figure 1. The microalgae *Cyanidioschyzon merolae* (top) and *Chlamydomonas reinhardtii* (bottom).

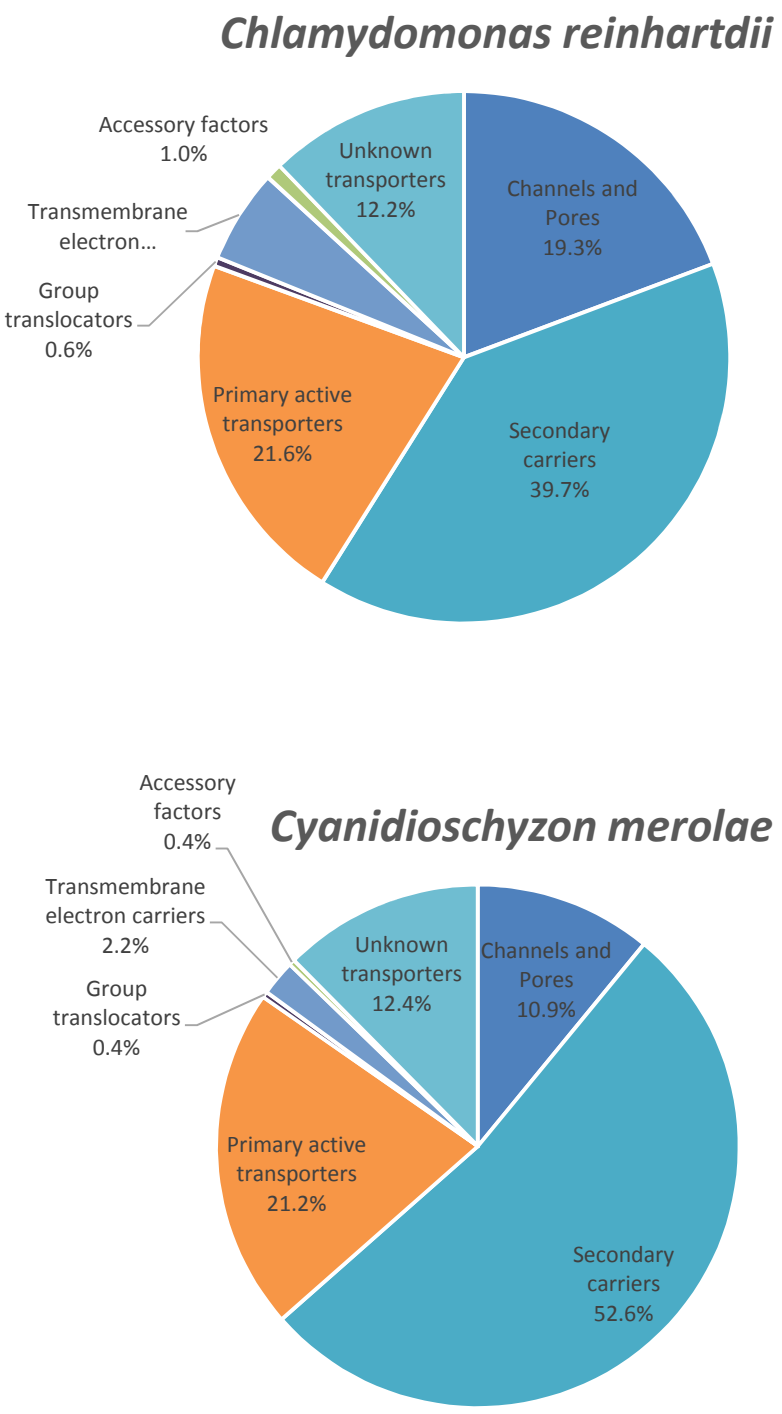

Figure 2a. Distribution of transporters based on TC classes in *Chlamydomonas reinhardtii* and *Cyanidioschyzon merolae*.

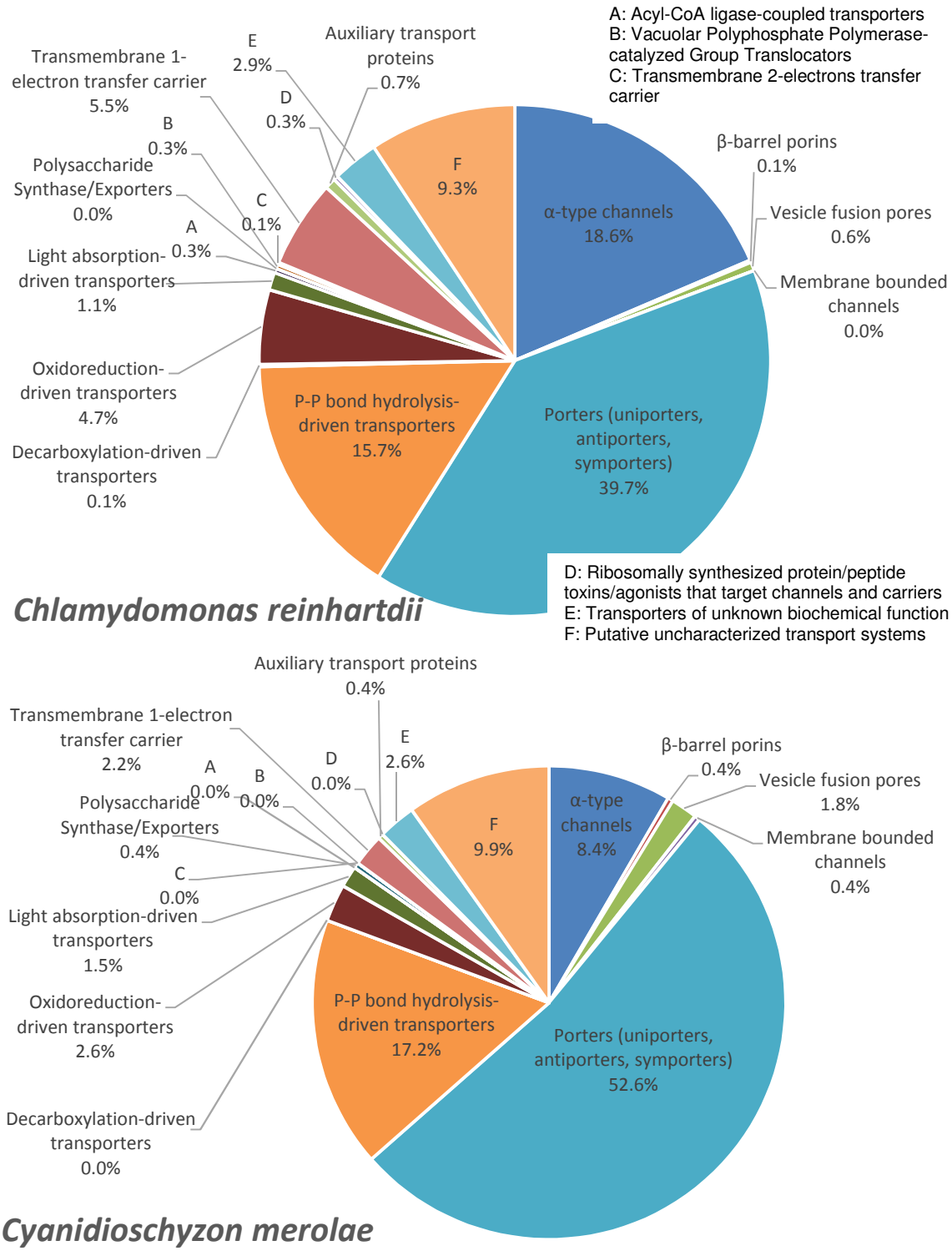

Figure 2b. Distribution of transporters based on TC subclasses in *Chlamydomonas reinhardtii* and *Cyanidioschyzon merolae*

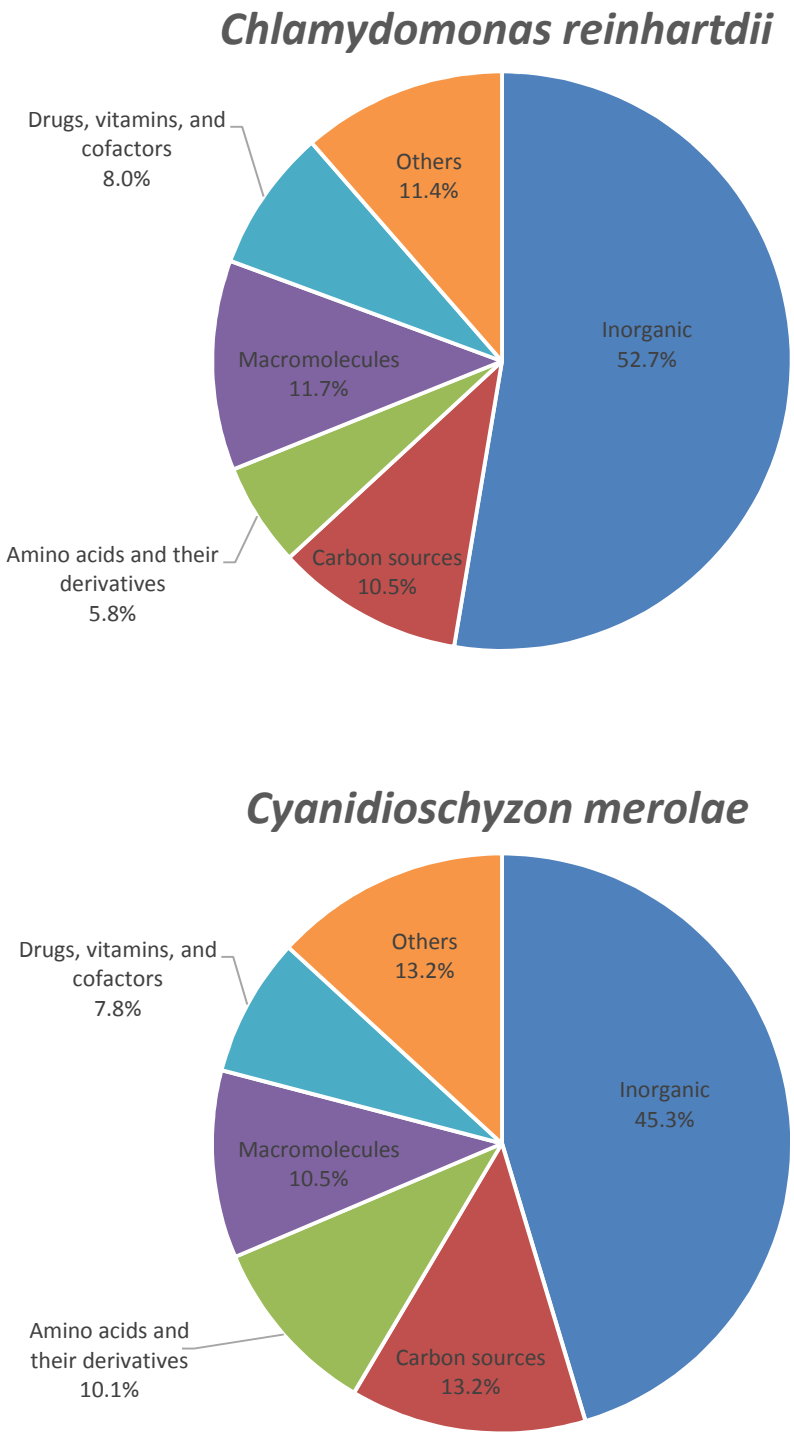

Figure 3a. Distribution of transporters based on TC substrate groups in *C. reinhardtii* and *C. merolae.*

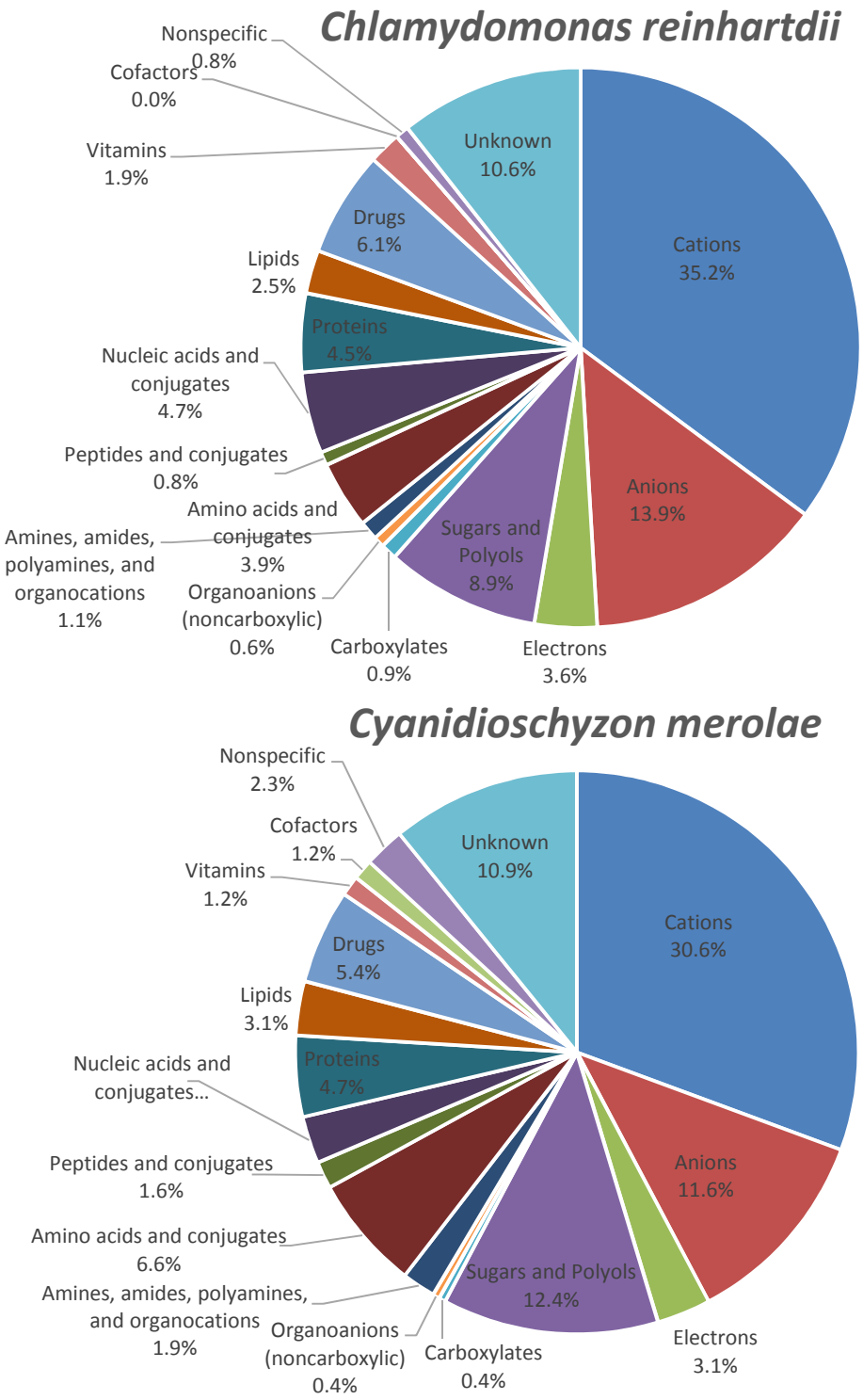

Figure 3b. Distribution of transporters based on TC substrate subgroups in *C. reinhardtii* and *C. merolae*.

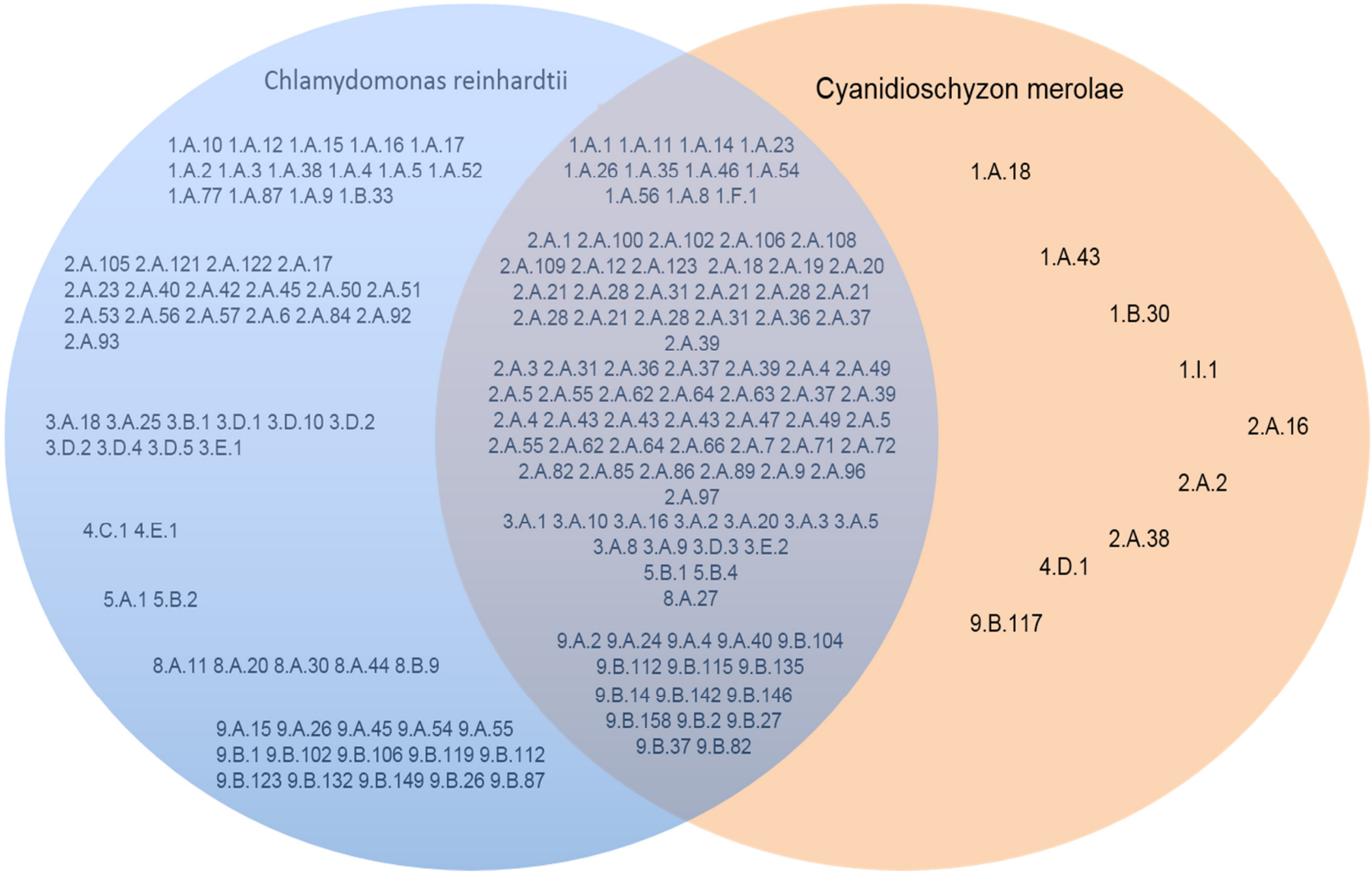

Figure 4. Recognized transporter families belonging to *C. reinhardtii* only, *C. merolae* only, or shared.

Table 1.
Overview of the *C. reinhardtii* and *C. merolae* transporter distribution based on TC class and subclass.

TC Class[a]	Class descriptions	No of transport proteins		TC subclass	Subclass description	No. of transport proteins	
		Cre	Cme			Cre	Cme
1	Channels and Pores	139	30	1.A	α-type channels	134	23
				1.B	β-barrel porins	1	1
				1.F	Vesicle fusion pores	4	5
				1.I	Membrane bounded channels	0	1
2	Secondary carriers	286	144	2.A	Porters (uniporters, antiporters, symporters)	286	144
3	Primary active transporters	156	58	3.A	P-P bond hydrolysis-driven transporters	113	47
				3.B	Decarboxylation-driven transporters	1	0
				3.D	Oxidoreduction-driven transporters	34	7
				3.E	Light absorption-driven transporters	8	4
4	Group translocators	4	1	4.C	Acyl-CoA ligase-coupled transporters	2	0
				4.D	Polysaccharide Synthase/Exporters	0	1
				4.E	Vacuolar Polyphosphate Polymerase-catalyzed Group Translocators	2	0
5	Transmembrane electron carriers	41	6	5.A	Transmembrane 2-electrons transfer carrier	1	0
				5.B	Transmembrane 1-electron transfer carrier	40	6
8	Accessory factors[b]	7	1	8.A	Auxiliary transport proteins	5	1
				8.B	Ribosomally synthesized protein/peptide toxins/agonists that target channels and carriers	2	0
9	Unknown transporters[c]	88	34	9.A	Transporters of unknown biochemical function	21	7
				9.B	Putative uncharacterized transport systems	67	27
Total no. of transport proteins		721	274				
Total no. of proteins in genome		14489	4803				
% transporters of genome		4.98%	5.71%				

a Detailed class and subclass descriptions can be found at www.tcdb.org. Transporter classes 6 and 7 have not been assigned in the TC system yet and therefore are absent from this table.
b Accessory factors facilitate transport via established transport systems and therefore are not counted as separate systems.
c Unknown transporters include families in TC subclass 9.A (known transporters of unknown biochemical function) and 9.B (putative uncharacterized transport systems), but not 9.C (functionally characterized transporters lacking identified sequences).

Table 2.
Substrates of transporter systems according to TC class identified in *C. reinhardtii* (left) and *C. merolae* (right). The total number of proteins contributing to each transport system for particular substrate subgroups are parenthesized.

Substrate Category	# of proteins of indicated type acting on substrate type in *C. reinhardtii*								# of proteins of indicated type acting on substrate type in *C. merolae*							
	Channels and Pores	Secondary carriers	Primary active transporters	Group translocators	TM electron carriers	Auxiliary proteins	Putative transporters	Total System #	Channels and Pores	Secondary carriers	Primary active transporters	Group translocators	TM electron carriers	Auxiliary proteins	Putative transporters	Total System #
Inorganic																
A. Cations	103	61	44(59)	2	1		24	225	15	34	20			9		79
B. Anions	23	59	7					89	4	23	2			1		30
C. Electrons			6(16)		14(40)		4	23	1		1(7)		3(6)	3		8
Carbon sources																
A. Sugars and Polyols	1	44	2				10	57		27	2	1		2		32
B. Carboxylates		6						6		1				1		1
C. Organoanions (noncarboxylic)		4						4						1		1
Amino acids and their derivatives																
A. Amines, amides, polyamines, and organocations		7						7		2				3		5
B. Amino acids and conjugates		25						25	1	16						17
C. Peptides and conjugates		2	2			1		5		2				2		4
Macromolecules																
A. Nucleic acids and conjugates	1(4)	23	4	2				30	1(5)	6						7
B. Proteins	1	4	13(29)				11	29		5	7(10)					12
C. Lipids		3	9			1	3	16			6			1	1	8
Drugs, vitamins, and cofactors																
A. Drugs		15	24					39		6	8					14
B. Vitamins	1	6	1				4	12	1	2						3
C. Cofactors								0							2	2
Others																
A. Nonspecific	3	2						5	2	1					3	6
B. Unknown	3	25	3			5	32	68	1	19	3				6	29
Total systems	136	286	114	4	15	7	88	650	26	144	49	1	3	1	34	258
Total proteins	139	286	156	4	41	7	88	721	30	144	58	1	6	1	34	274

Table 3.
TC classification and functional prediction of transport-related proteins found in *Chlamydomonas reinhardtii* and *Cyanidioschyzon merolae*. Sequences were retrieved using GBLAST with e-values of 0.1 or less. Comparative e-value scores are written next to each entry in the comments section.

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
1.A α-Type Channels												
1.A.1	Voltage-gated Ion Channel (VIC) Superfamily	1.A.1.2.1	P17970	8	K^+	bidirectional	A8IB39	4	8.5E-40			
							A8JC32	4	1.4E-18			
		1.A.1.2.11	Q14721	6	K^+	bidirectional	A8IH70	4	2.1E-40			
		1.A.1.2.12	Q09470	6	K^+	bidirectional	A8HPX4	4	1.2E-36			
		1.A.1.3.1	Q03720	7	K^+	bidirectional	A8J0X8	4	9.0E-23			
		1.A.1.3.2	Q62976	7	Ca^{2+}, K^+	bidirectional				M1V5T2	9	3.1E-15
		1.A.1.4.1	Q38998	5	K^+	bidirectional	A8J968	4	2.0E-17			
		1.A.1.4.3	Q8VX27	6	K^+	bidirectional	A8HPD4	19	9.3E-49			
							A8HPD6	7	1.6E-47			
		1.A.1.5.9	A3EYY6	24	K^+	bidirectional	A8IH98	4	4.0E-33			
		1.A.1.5.11	Q9Y3Q4	6	K^+/Na^+ channel	bidirectional	A8HZS1	6	3.6E-56			
							A8J7I2	6	2.9E-17			
		1.A.1.5.16	Q10V66	6	K^+ channel	bidirectional	A8J0U9	7	2.9E-25			
		1.A.1.10.2	P90670	22	Na^+	bidirectional	A8JF90	19	1.4E-99			
		1.A.1.10.3	Q14524	18	Na^+	bidirectional	A8JF89	18	8.2E-109			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		1.A.1.10.5	Q15858	22	Na^+	bidirectional	A8JIU8	21	8.3E-84			
							A8IQ59	16	4.4E-82			
		1.A.1.10.7	P35498	25	Na^+	bidirectional	A8JF52	18	1.8E-93			
		1.A.1.10.12	Q99250	20	Na^+	bidirectional	A8J6D9	18	7.9E-76			
		1.A.1.11.2	P07293	18	Ca^{2+}	bidirectional	A8ISH7	16	1.4E-105			
		1.A.1.11.5	O95180	16	Ca^{2+}	bidirectional	A8IVU6	19	4.6E-86			
		1.A.1.11.20	A8PYS5	19	Ca^{2+}	bidirectional	A8IHW3	18	8.4E-97			
		1.A.1.20.2	O54853	5	K^+	bidirectional	A8IYN1	6	8.2E-53			
							A8IYM3	6	5.0E-46			
							A8IRB5	5	1.5E-40			
		1.A.1.20.6	Q02280	7	K^+	bidirectional	A8I214	4	1.5E-38			
		1.A.1.24.4	B7K3R7	6	K^+	bidirectional				M1VA18	6	2.7E-31
1.A.2	Inward Rectifier K Channel (IRK-C) Family	1.A.2.1.9	Q14500	3	K^+	bidirectional	A8ILZ7	2	1.2E-39			
		1.A.2.1.10	P48051	3	K^+	inward rectifying	A8HM49	4	1.1E-20			
		1.A.2.1.14	A7UVG1	1	K^+	bidirectional	A8I5R9	1	1.6E-59			
							A8JID7	3	3.7E-50			
							A8JGQ3	1	1.1E-16			
1.A.3	The Ryanodine-Inositol 1,4,5-triphosphate Receptor Ca^{2+} Channel (RIR-CaC) Family	1.A.3.2.2	P29993	6	Ca^{2+}	efflux	A8JF83	6	1.7E-28			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
1.A.4	The Transient Receptor Potential Ca^{2+} Channel (TRP-CC) Family	1.A.4.1.7	Q9UL62	9	Ca^{2+}, Sr^{2+}	bidirectional	A8JCM1	6	6.8E-13			
		1.A.4.1.9	Q27GV1	9	Ca^{2+}	bidirectional	A8I051	9	4.4E-09			
		1.A.4.2.7	Q9R186	7	Ca^{2+}, Sr^{2+}, Ba^{2+}	bidirectional	A8IAT9	7	1.6E-12			
		1.A.4.6.5	Q18297	4	Ca^{2+}	bidirectional	A8IV32	2	8.0E-03			
1.A.5	The Polycystin Cation Channel (PCC) Family	1.A.5.4.1	A9LE42	8	Ca^{2+}	bidirectional	A8JDA6	7	0.0E+00			
			A9LE42	8	Ca^{2+}	bidirectional	A8I2S1	5	4.1E-15			
			A9LE42	8	Ca^{2+}	bidirectional	A8IS33	5	3.1E-12			
1.A.8	The Major Intrinsic Protein (MIP) Family	1.A.8.8.15	B5L019	6	H_2O, small neutral solutes	bidirectional				M1V5D1	8	8.0E-12
		1.A.8.10.5	Q9M8W5	6	H_2O, small neutral solutes	bidirectional	A8HMD0	2	2.4E-05			
		1.A.8.11.1	P25794	6	H_2O, small neutral solutes	bidirectional	Q5VLJ9	6	4.7E-24			
		1.A.8.18.2	E3UMZ6	7	glycerol, urea, boric acid	bidirectional	A8IR22	5	E-10			
1.A.9	The Neurotransmitter Receptor, Cys loop, Ligand-gated Ion Channel (LIC) Family	1.A.9.5.2	O95166	1	Cl^-	bidirectional	A8JB85	1	2.3E-37			
1.A.10	The Glutamate-gated Ion Channel (GIC) Family of Neurotransmitter Receptors	1.A.10.1.8	Q61625	1	K^+	GluR δ2 subunit	A8HUF9	2	5.9E-14			
		1.A.10.2.2	A3I049	5	K^+	Glutamate receptor GluR	A8IVT4	4	7.4E-08			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			A3I049	5	K^+	Glutamate receptor GluR	A8IVS7	4	2.9E-07			
		1.A.10.2.3	Q3B5G3	4	K^+	part of glutamate receptor GluR (probable)	A8ISB5	3	3.1E-13			
1.A.11	The Ammonia Channel Transporter (Amt) Family	1.A.11.2.1	P54144	11	NH_4^+, NH_3, H^+	cotransporter (NH_3, H^+), pore receptor (NH_4^+)	Q8RUT6	11	1.6E-115			
							A8J1H0	11	2.0E-105			
							A8JFM1	6	3.5E-53			
		1.A.11.2.6	Q9SVT8	12	NH_4^+, H^+	symporter, uptake				M1V5E0	9	2.9E-48
		1.A.11.2.8	E2CWJ2	11	NH_4^+, H^+	symporter, uptake	A8HSA2	11	8.7E-114	M1V7W3	11	4.4E-84
							A8IUV9	11	1.2E-101			
							A8JFV7	9	7.0E-100			
		1.A.11.2.9	Q9BLG3	11	NH_4^+, H^+	symporter, uptake	Q6QBS6	11	2.1E-79			
							Q6PPG2	10	9.4E-76			
							Q6QBS7	11	3.2E-73			
		1.A.11.4.2	Q9H310	12	NH_3+/NH_4^+	uptake	Q8RUE9	11	9.1E-68			
							Q94CJ2	11	1.0E-67			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
1.A.12	The Intracellular Chloride Channel (CLIC) Family	1.A.12.2.2	Q8F2Y8	1	glutathione	antioxidant, transferase	A8JBB4	2	1.5E-05			
1.A.14	The Testis-Enhanced Gene Transfer (TEGT) Family	1.A.14.1.1	P55061	6	Ca^{2+}	bidirectional, part of GluR glutamate receptor	A8JCT0	6	3.7E-35	M1UXV9	6	2.7E-25
		1.A.14.3.2	E9CCY6	7	Ca^{2+}	bidirectional, part of GluR glutamate receptor	A8HM37	7	5.0E-45			
			E9CCY6	7	Ca^{2+}	bidirectional, part of GluR glutamate receptor	A8HYH9	6	3.8E-40			
		1.A.14.3.6	Q9HC24	7	Ca^{2+}	bidirectional, part of GluR glutamate receptor				M1VAG9	7	3.3E-30
1.A.15	The Non-selective Cation Channel-2 (NSCC2) Family	1.A.15.2.1	Q99442	2	non-specific cations	bidirectional	A8I8A8	2	3.3E-14			
1.A.16	The Formate-Nitrite Transporter (FNT) Family	1.A.16.2.1	P35839	8	HCO_2^-	uptake	A8HPB4	6	8.9E-28			
		1.A.16.2.4	Q9LE25	8	NO_2^-	uptake	A8J4Q0	8	0.0E+00			
							Q75NZ3	6	1.9E-60			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8IYW1	6	2.6E-59			
							Q6IYG1	6	5.5E-36			
							Q6IYG4	6	6.0E-33			
1.A.17	The Calcium-Dependent Chloride Channel (Ca-ClC) Family	1.A.17.5.9	Q9SY14	10	Cl^-	bidirectional	A8JGH0	11	1.3E-54			
							A8JGH3	9	2.0E-53			
							A8J1F3	10	3.1E-53			
							A8JGH2	9	1.9E-48			
							A8JGH4	8	1.1E-39			
							A8HT24	10	4.8E-29			
							A8I130	9	3.5E-21			
							A8JCC3	11	7.0E-17			
1.A.18	The Chloroplast Envelope Anion Channel-forming Tic110 (Tic110) Family	1.A.18.1.2	M1V6H9	3	nonselective anions	TIC110 family				M1V6H9	3	0.0E+00
1.A.23	Small Conductance Mechanosensitive Ion Channel (MscS) Family a	1.A.23.4.3	P0AEB5	4	nonselective osmolytes and ions	inner membrane protein				M1VA20	4	6.5E-57
										M1UW96	6	1.6E-39
		1.A.23.4.4	Q56X46	5	uncharacterized	uncharacterized (putative)	A8JCR4	4	1.4E-27			
		1.A.23.4.7	F4IME2	5	cations	opens in response to stretch	A8IJY5	6	3.0E-24			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		1.A.23.4.9	F9X0Q3	6	Ca^{2+}	bidirectional, putative	A8I071	3	4.2E-22			
		1.A.23.6.1	A3KE12	6	nonselective ions	bidirectional, anions preferred over cations	A8IHD4	5	0.0E+00			
							A8HM43	4	2.6E-27			
							A8HM47	2	1.3E-23			
1.A.26	Mg2+ Transporter-E (MgtE) Family	1.A.26.1.2	Q5SMG8	5	Mg^{2+}, Co^{2+}	uptake				M1V9W9	5	4.6E-34
		1.A.26.1.4	Q52398	4	Mg^{2+}, Co^{2+}	uptake	A8J2E0	5	3.8E-28			
1.A.35	CorA Metal Ion Transporter (MIT) Family	1.A.35.3.3	O31543	2	divalent metal cations	uptake	A8HRI6	1	4.4E-16			
		1.A.35.5.2	Q9SAH0	2	Mg^{2+}	uptake	A8I4S8	2	1.4E-61	M1V5R2	2	1.2E-32
							A8HQP6	2	9.6E-19	M1VGZ9	2	2.7E-31
		1.A.35.5.3	Q058N4	2	Mg^{2+}	uptake	A8IF03	2	2.0E-22	M1VC54	2	1.0E-18
		1.A.35.5.4	Q93ZD7	2	Mg^{2+}	uptake				M1V5P1	2	1.6E-29
										M1V910	2	3.3E-18
		1.A.35.5.5	Q02783	2	Mg^{2+}	uptake				M1VGU3	2	3.5E-31
		1.A.35.5.6	Q9ZPR4	2	Mg^{2+}	uptake	A8IUC0	3	1.3E-32			
1.A.38	Golgi pH Regulator (GPHR) Family	1.A.38.1.1	B2ZXD5	9	Cl^-	bidirectional	A8J3B4	9	5.5E-72			
1.A.43	Camphor Resistance (CrcB) Family	1.A.43.2.8	F6XSK1	6	Uncharacterized	uncharacterized				M1USA6	9	8.7E-18

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
1.A.46	The Anion Channel-forming Bestrophin (Bestrophin) Family	1.A.46.1.1	O76090	4	NO_3^-, I^-, Br^-, Cl^-	substrates in preferential order (most to least)				M1V654	6	1.0E-17
		1.A.46.1.3	Q8NFU1	7	Cl^-	uptake				M1VK72	5	1.2E-15
		1.A.46.1.4	Q6H1V1	5	SCN^-, I^-, Cl^-	substrates in preferential order (most to least)				M1VK75	4	3.6E-19
		1.A.46.3.5	Q9M2D2	2	anions	putative, chloroplastic	A8J8S2	3	2.9E-44			
							A8JFR7	3	3.5E-35			
							A8JIN0	3	6.2E-33			
							A8JFV1	3	6.9E-28			
							A8HMB1	4	7.6E-28			
							A8J8U0	1	6.7E-26			
							A8JJD2	2	2.3E-14			
1.A.52	The Ca^{2+} Release-activated Ca^{2+} (CRAC) Channel (CRAC-C) Family	1.A.52.2.1	Q012G5	4	Ca^{2+}	efflux	A8HQ39	4	1.9E-61			
							A8J8H4	4	2.1E-46			
1.A.54	The Presenilin ER Ca^{2+} Leak Channel (Presenilin) Family	1.A.54.1.2	P49810	9	Ca^{2+}	efflux	A8IAG6	9	7.7E-30			
		1.A.54.3.4	A7KX19	9	Ca^{2+}	bidirectional	A8IGT6	7	1.5E-61	M1UQC0	9	2.1E-44
							A8HNU4	8	5.5E-23			
1.A.56	The Copper	1.A.56.1.16	M2VZF5	8	Cu^+	uptake				M1UX17	7	7.5E-53

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	Transporter (Ctr) Family	1.A.56.3.1	Q4U0V9	3	Cu^{+}	uptake	Q4U0V9	3	0.0E+00			
							Q0ZB35	5	4.0E-65			
1.A.77	The Mg2+ /Ca2+ Uniporter (MCU) Family	1.A.77.1.3	A8J6W0	2	Mg^{2+},Ca^{2+}	uniporter	A8J6W0	2	8.8E-178			
		1.A.77.1.13	A9V8N9	6	Mg^{2+},Ca^{2+}	uniporter	A8J0V5	1	2.3E-72			
		1.A.77.3.21	P08443	2	Mg^{2+},Ca^{2+}	uniporter	A8HNA8	3	1.9E-08			
		1.A.77.4.2	Q86H82	4	Mg^{2+},Ca^{2+}	uniporter	A8J3D7	7	2.5E-26			
1.A.87	The Mechanosensitive Calcium Channel (MCA) Family	1.A.87.2.2	Q2QQC1	1	Mg^{2+},Ca^{2+}	uniporter	A8JF93	1	6.5E-16			
							A8IF89	1	1.4E-15			
		1.A.87.2.3	Q9LSR8	2	Ca^{2+}	efflux	A8HQ26	1	1.3E-19			
							A8HQ35	1	3.1E-18			
							A8HQ33	1	3.9E-18			
							A8HMH1	2	1.2E-13			
		1.A.87.2.4	Q80YS4	2	Ca^{2+}	uptake	A8J8L4	1	1.6E-35			
							A8JF67	2	1.7E-20			
							A8I2K1	1	5.9E-20			
							A8J3K7	1	1.0E-19			
							A8J7F3	3	3.0E-19			
							A8JAU8	1	3.2E-19			
							A8I6F3	1	4.3E-18			
							A8JEH7	1	6.6E-18			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8I6T9	1	2.7E-17			
							A8I222	1	2.0E-16			
							A8JBK6	1	1.1E-15			
							A8I662	1	3.2E-15			
							A8IYK0	1	6.6E-15			
							A8J9A2	1	1.7E-14			
							A8IGG5	1	3.5E-14			
							A8JC91	2	3.9E-14			
							A8I8U7	3	8.6E-14			
							A8JKC3	1	1.2E-13			
							A8JDZ1	1	1.5E-13			
		1.A.87.3.2	P0CW97	2	heavy metal cations, Ca^{2+}	efflux	A8JCC0	2	9.5E-16			
1.B β-Barrel Porins												
1.B.30	The Plastid Outer Envelope Porin of 16 kDa (OEP16) Family	1.B.30.3.1	B8BRM2	4	cationic solutes amino, acids	bidirectional				M1VEB9	3	3.3E-06
1.B.33	Outer Membrane Protein Insertion Porin (OmpIP) Family	1.B.33.2.1	Q43715	1	specific proteins	bidirectional	A8IE32	1	6.1E-85			
1.F Vesicle Fusion Pores												

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
1.F.1	Synaptosomal Vesicle Fusion Pore (SVF-Pore) Family	1.F.1.1.1	Q16623	1	1.F.1 subunits form one system involved in vesicular efflux	syntaxin subunit, part of a complex	A8HUY7	1	9.0E-24	M1V562	1	9.3E-20
			Q9BV40	1		synaptobrevin subunit, part of a complex	A8IT48	2	3.2E-13	M1VI02	1	2.7E-16
							A8J924	2	1.4E-17	M1V7K3	1	9.9E-09
			P63027	1		synaptobrevin subunit, part of a complex				M1UQC6	1	1.8E-07
		1.F.1.1.2	P33328	1		synaptobrevin subunit				M1V3V8	1	2.3E-07
		1.F.1.1.3	P34815	2			A8J5W3	1	3.1E-20			
1.I Membrane-bounded Channels												
1.I.1	The Nuclear Pore Complex (NPC) Family [formerly 1.A.75]	1.I.1.1.1	P08067	1	e^-	part of a complex				M1VJ85	1	7.7E-60
2.A Porters (uniporters, symporters, antiporters)												
2.A.1	Major Facilitator Superfamily (MFS)	2.A.1.1.56	Q9SFG0	12	sugar, H^+	symporter				M1V8A2	11	1.2E-25
		2.A.1.1.102	Q56ZZ7	12	sugar, H^+	symporter	A8IX73	12	1.8E-106			
		2.A.1.2.10	P0A0J7	12	quinolone, H^+	antiporter	A8IM52	8	5.9E-06			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.1.2.30	Q5SR56	12	drugs	efflux	A8J8G2	11	3.5E-19			
		2.A.1.2.39	Q5JAK9	12	tetracycline	efflux				M1UWV2	10	2.9E-17
		2.A.1.2.53	Q96BI1	12	drugs, H^+	antiporter	A8J6G6	9	1.4E-18			
		2.A.1.2.77	Q8NKG7	12	drugs	efflux	A8JG41	12	1.0E-98			
		2.A.1.2.80	M2VXR7	11	tetracycline, H^+	antiporter				M1VA10	12	1.1E-41
		2.A.1.4.6	Q9Z7N9	10	sugar phosphates, P_i	antiporter	A8JBA2	10	1.8E-76	M1VKR7	12	3.4E-105
							A8JBA1	10	2.3E-76			
							A8IGJ1	9	5.0E-26			
		2.A.1.4.8	Q8TED4	12	sugar phosphates, P_i	antiporter	A8IJH7	13	1.9E-117			
		2.A.1.6.4	P0C0L7	12	amino acids, H^+/Na^+	symporter	A8HVM9	12	8.1E-63			
		2.A.1.7.4	Q80T22	12	glucose, Na^+	symporter	A8J7M6	10	4.9E-10	M1V5C4	11	2.3E-08
							A8J3N0	11	1.7E-08			
		2.A.1.8.6	Q39608	12	NO3-, NO_2^-	antiporter	A8IZY8	11	0.0E+00			
							A8J4P5	12	0.0E+00			
		2.A.1.8.7	A8J4P3	11	NO3-, NO_2^-	uptake	A8J4P3	11	0.0E+00	M1VBA4	12	1.4E-77
							A8I3C4	9	1.5E-64			
		2.A.1.9.4	Q01MW8	12	P_i	uptake	A8ISD6	12	4.6E-47			
							Q8LP70	12	8.8E-47			
							A8ISD7	12	1.8E-46			
							Q8LP69	12	3.0E-45			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							Q8LP71	12	1.9E-44			
		2.A.1.9.6	A5H2U6	11	PO_4	uptake				M1VIM0	12	2.0E-39
										M1V932	11	5.3E-38
		2.A.1.9.7	P25346	13	PO_4	uptake				M1VI98	13	5.5E-35
										M1VMK7	13	1.1E-33
		2.A.1.14.3	P70786	12	tartrate, D-galactonate, polyols	symporter	A8J1H5	5	1.5E-32			
							A8IGS9	4	3.2E-25			
		2.A.1.14.22	O82390	12	Na^+, PO_4	symporter	A8IZ81	10	1.3E-128	M1V680	12	2.6E-128
							A8IRP0	11	2.0E-83			
							A8JFB8	12	1.3E-82			
							A8J006	12	3.5E-76			
							A8J3L0	11	2.6E-67			
							A8J0K6	12	5.6E-65			
							A8J9M5	12	1.5E-64			
							A8JHW9	13	1.2E-58			
							A8HPZ2	9	5.7E-22			
		2.A.1.19.43	Q9LHQ6	12	carnitine, organocations	uptake	A8J114	10	5.1E-64			
		2.A.1.19.47	D8U9F6	9	uncharacterized	uncharacterized	A8J288	11	5.7E-79			
							A8I4V0	5	1.5E-15			
		2.A.1.25.1	O00400	12	acetyl-CoA, CoA	antiporter	A8ITI8	10	4.6E-55	M1VIQ1	12	5.6E-62

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.1.31.1	Q44591	12	Ni^{2+}	efflux	A8INK8	11	7.9E-09			
							A8INL7	12	2.2E-07			
		2.A.1.35.1	P52067	11	drugs	efflux				M1VFK7	11	E-06, entered into TCDB as 2.A.1.79.1
		2.A.1.40.2	Q5R542	13	molybdate (putative)	uptake	A8JBM0	13	5.4E-57	M1VJN5	13	9.5E-60
							A8HTT3	11	9.2E-52			
		2.A.1.49.1	Q9GQQ0	12	sphingolipid-1-phosphate/sphingolipid	uptake	A8IZN8	12	5.1E-09			
		2.A.1.49.3	F4IKF6	13	sphingolipid-1-phosphate/sphingolipid	uptake	A8INM9	12	1.3E-94			
		2.A.1.53.3	A6NID9	12	uncharacterized	uncharacterized				M1V8F4	14	3.9E-53
		2.A.1.59.2	B2JBG5	12	uncharacterized	uncharacterized	A8J4Z9	10	1.7E-34			
		2.A.1.63.4	P47159	10	uncharacterized	uncharacterized	A8J425	10	7.1E-49			
		2.A.1.65.11	A8IDJ5	20	uncharacterized	uncharacterized	A8IDJ5	20	0.0E+00			
		2.A.1.66.5	S7W5W5	12	uncharacterized	uncharacterized	A8IM58	6	E-13			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.1.75.4	D2W1L7	12	uncharacterized	uncharacterized	A8HMG5	12	2.4E-13			
		2.A.1.81.1	D5AKT2	12	Cu^{2+}	uptake	A8IW87	8	2.8E-11			
		2.A.1.82.1	F2CRE4	11	Cu^{2+}	uptake	A8I9M1	11	9.9E-38			
		2.A.1.82.5	D8UG81	12	uncharacterized	uncharacterized	A8JCF2	5	5.2E-103			
							A8JCF3	3	2.3E-42			
		2.A.1.83.1	B6EN82	11	1-arseno-3-phosphoglycerate	efflux	A8JFT2	12	2.5E-69			
2.A.2	The Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family	2.A.2.4.6	Q9FE59	12	sucrose, H^+	symporter				M1V620	13	2.5E-37
2.A.3	The Amino Acid-Polyamine-Organocation (APC) Superfamily	2.A.3.3.3	Q84MA5	14	cationic amino acids	bidirectional	A8HMJ8	15	8.2E-104			
							A8IHE7	16	4.1E-92			
		2.A.3.3.14	Q8W4K3	14	cationic amino acids	bidirectional				M1UPE2	14	1.2E-60
		2.A.3.4.2	Q9Y860	12	amino acid	bidirectional	A8IU08	7	2.5E-18			
		2.A.3.4.7	Q9KZF1	12	amino acid	bidirectional	A8IT81	11	1.3E-59			
							A8I3P4	9	1.9E-39			
		2.A.3.12.1	Q5C8V6	12	polyamine	bidirectional				M1VL23	12	6.7E-49
		2.A.3.12.5	Q6Z8D0	12	polyamine	bidirectional	A8JFN6	4	2.3E-37			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.4	The Cation Diffusion Facilitator (CDF) Family	2.A.4.3.2	Q99726	6	Zn^{2+}	bidirectional				M1V735	5	1.8E-48
		2.A.4.3.4	Q9ZT63	6	Zn^{2+}	bidirectional	A8J339	6	3.4E-34			
		2.A.4.4.5	Q8NEW0	5	Zn^{2+}	bidirectional				M1VMR2	15	1.0E-32
		2.A.4.5.1	A4ZUV2	5	Mn^{2+}	bidirectional	A8J7C6	7	1.4E-34	M1VER5	5	6.2E-40
							A8J7C5	6	1.8E-34			
		2.A.4.5.1	A4ZUV2	5	Mn^{2+}	bidirectional	A8J7C7	4	5.9E-22			
		2.A.4.6.1	Q6PML9	5	uncharacterized	uncharacterized	A8J2F6	4	1.6E-53			
2.A.5	The Zinc (Zn^{2+})-Iron (Fe^{2+}) Permease (ZIP) Family	2.A.5.1.3	O81123	8	Zn^{2+}, Fe^{2+}	uptake	A8HSY2	9	1.5E-29			
							A8JFU8	7	1.2E-27			
		2.A.5.1.5	A3BI11	9	Zn^{2+}	uptake	A8JFU7	8	3.3E-25			
							A8JD29	11	2.1E-16			
		2.A.5.1.6	Q9M7J1	8	Zn^{2+}, Cd^{2+}	uptake	A8IUA1	7	3.5E-14			
		2.A.5.1.8	O94639	8	Zn^{2+}	uptake				M1VLV8	7	1.7E-35
		2.A.5.3.1	Q9NP94	8	Zn^{2+}	uptake	A8INX4	8	7.3E-18	M1V7A1	6	2.0E-08
		2.A.5.4.12	P40544	7	Zn^{2+}	uptake				M1VK97	6	1.2E-22
		2.A.5.5.5	B2UL32	8	Zn^{2+}	uptake	A8J232	15	9.8E-08	M1VAT6	6	1.3E-26
							A8IRU0	8	5.6E-34			
							A8JCU2	7	1.4E-28			
							A8IW07	9	5.4E-23			
							A8J059	8	1.8E-19			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.6	The Resistance-Nodulation-Cell Division (RND) Superfamily	2.A.6.6.1	O15118	13	lipids, cholesterol	efflux	A8I9H8	11	2.5E-25			
2.A.7	The Drug/Metabolite Transporter (DMT) Superfamily	2.A.7.1.1	P14319	4	cationic drugs	efflux				M1UNX5	3	7.6E-06
		2.A.7.3.29	O34416	10	uncharacterized drug or metabolite	uncharacterized (efflux)	A8IK88	9	5.3E-12			
		2.A.7.3.51	M1V7G4	10	uncharacterized	uncharacterized				M1V9H1	10	7.6E-18
										M1VEA9	11	9.0E-13
		2.A.7.3.52	K7QW88	10	uncharacterized	uncharacterized				M1VB48	9	4.3E-29
		2.A.7.3.53	K0RU20	10	uncharacterized	uncharacterized				M1V7G4	10	0.0E+00
										M1V9U7	10	5.1E-18
		2.A.7.9.1	P49133	8	triose-P/glycerate-3-P, P_i	antiporter	A8HN02	8	2.9E-83			
		2.A.7.9.2	P52178	6	glucose-P/triose-P/glycerate-P, P_i	antiporter				M1VB76	8	7.6E-08
		2.A.7.9.3	P93642	6	phosphoenolpyruvate, P_i	antiporter	Q84XW3	10	1.3E-106	M1UU87	9	5.0E-74
							Q7XJ66	6	1.3E-103			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.7.9.5	B5AJT1	8	PO_4/triose-PO_4 (putative)	antiporter				M1V611	8	1.6E-104
										M1US62	9	8.1E-71
		2.A.7.9.6	Q94B38	7	Glucose-6-P/P_i	antiporter	A8JFB4	8	1.2E-70			
		2.A.7.9.11	Q6ICL7	10	thiamine pyrophosphate	antiporter	A8JE46	9	5.2E-28			
							A8IJ64	10	3.1E-24			
							A8IHU0	9	2.8E-19			
		2.A.7.9.12	Q9SRE4	10	UDP-galactose, UDP-glucose and UDP-fructose	antiporter	A8J0T5	9	1.6E-53			
		2.A.7.9.13	Q9LPU2	10	nucleotide-sugar (probable UDP-galactose)	antiporter	A8J762	10	4.1E-66			
							A8J1R8	9	4.7E-62			
		2.A.7.9.15	Q7Z769	10	triose phosphate	antiporter	A8IR29	6	5.8E-31	M1VC58	10	1.5E-54
										M1VHP9	8	2.1E-46
										M1VGP7	8	7.8E-38
		2.A.7.9.16	Q9NQQ7	10	triose phosphate	antiporter				M1VD27	10	6.5E-23
										M1VAY9	9	1.0E-19

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.7.9.17	Q9SKJ7	10	sugar-phosphate/ phosphate (probable)	antiporter	A8I424	10	2.8E-88			
							A8IZ39	10	6.6E-86			
							A8IFX8	9	2.0E-83			
							A8J502	8	8.5E-78			
							A8IUJ9	8	2.7E-25			
							A8I041	6	6.3E-25			
							A8IQ71	6	4.5E-19			
		2.A.7.10.2	Q969S0	10	UDP-xylose and UDP-N-acetylglucosamine	antiporter				M1V660	6	7.7E-19
		2.A.7.11.1	P78383	8	UDP-galactose:UMP	antiporter				M1V603	8	2.8E-36
		2.A.7.11.4	O64503	9	UDP-galactose/ UDP-glucose, UDP	antiporter	A8HQM1	8	3.1E-82			
		2.A.7.11.5	Q9H1N7	10	3’ phosphoadenosine 5’ phosphosulfate	antiporter, translocation from cytosol to Golgi lumen	A8I7Y4	9	3.3E-33			
		2.A.7.11.7	Q6NM25	10	UDP-galactose	antiporter	A8HXL0	9	1.1E-93	M1VD92	8	2.0E-68

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8J3P3	8	1.7E-67			
		2.A.7.12.3	Q9C5H6	9	UDP-galactose	antiporter	A8JEJ7	6	2.3E-46			
		2.A.7.12.13	Q8N357	10	sugar-nucleotide (putative)	antiporter				M1VAQ2	9	2.0E-32
		2.A.7.13.3	Q941R4	10	GDP-mannose, GDP	antiporter	A8ILL7	10	9.3E-73			
							A8ILL9	10	1.1E-72			
							A8ILM1	4	4.5E-43			
		2.A.7.13.4	Q84L09	10	GDP-mannose	antiporter	A8I318	9	4.2E-56			
		2.A.7.13.5	Q9S845	9	sugar-nucleotide (putative)	antiporter	A8JBZ1	10	3.7E-51			
							A8IN18	9	2.8E-43			
							A8J1R9	7	1.4E-31			
		2.A.7.15.2	Q18779	10	UDP-glucuronate/UDP-galactose	antiporter				M1V5X7	9	1.1E-24
		2.A.7.15.3	Q95YI5	10	UDP-sugar	antiporter	A8IQ34	5	3.4E-15	M1V5S2	8	1.9E-27
		2.A.7.15.4	Q9NTN3	10	UDP glucuronate/ UDP-N-acetylgalactosamine	antiporter	A8JF68	7	2.5E-17			
		2.A.7.16.1	Q96A29	7	GDP-fucose	antiporter				M1VMP4	10	2.2E-65

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.7.20.2	Q9GSB0	12	chloroquine, H^+	antiporter	A8HQH0	11	1.4E-10	M1V4Z5	10	1.3E-57
										M1V8Z8	10	4.1E-18
		2.A.7.24.4	Q9SFT8	8	amino acids, carbohydrates	antiporter	A8JFS6	5	8.5E-27			
		2.A.7.24.6	Q03730	10	uncharacterized	uncharacterized vacuolar membrane protein, antiporter (putative)				M1V6F9	8	6.1E-39
		2.A.7.25.5	Q9LIR9	9	divalent cations	primarily Mg^{2+}, lesser transport for other divalent cations	A8IY94	9	3.3E-92			
							A8J5R4	9	3.1E-19			
		2.A.7.25.6	Q7RWT8	7	uncharacterized	uncharacterized	A8JGA6	7	9.7E-16			
		2.A.7.26.4	A9T501	4	Multidrug resistance	efflux	A8J859	3	9.6E-22			
		2.A.7.28.11	Q7V7U0	10	uncharacterized	uncharacterized	A8JFV5	9	E-11			
2.A.9	The Membrane Protein Insertase	2.A.9.1.2	Q15070	4	proteins	cytoplasm to membrane	A8JB75	3	7.7E-15	M1V6L4	4	6.8E-39

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	(YidC/Alb3/Oxa1) Family	2.A.9.2.1	Q8LBP4	6	proteins	insertion of chlorophyll binding proteins into thylakoid membrane	A8HYK7	2	9.3E-90	M1V7G8	4	6.3E-75
2.A.12	The ATP:ADP Antiporter (AAA) Family	2.A.12.1.2	Q9S6V3	12	ATP, ADP	antiporter	A8IQU4	12	1.6E-83			
		2.A.12.1.16	Q39002	12	ATP, ADP	antiporter	A8JID6	12	0.0E+00			
							A8HTX0	12	3.2E-105			
		2.A.12.2.1	Q39002	12	ATP, ADP	antiporter				M1V528	13	7.0E-159
2.A.16	The Tellurite-resistance/Dicarboxylate Transporter (TDT) Family	2.A.16.4.2	A3R044	10	SO_3^{2-}	efflux				M1UX85	10	9.5E-62
2.A.17	The Proton-dependent Oligopeptide Transporter (POT/PTR) Family	2.A.17.3.2	P46032	11	Histidine/peptide, H^+	symporter	A8IT46	6	4.9E-64			
2.A.18	The Amino Acid/Auxin Permease (AAAP) Family	2.A.18.5.2	P47082	11	amino acids	symporter	A8IF06	10	1.8E-31			
		2.A.18.6.3	Q99624	11	glutamine/histidine/asparagine/alanine, Na^+ and H^+	sym/antiporter, 1 amino acid + 2 Na^+ cotransported against 1 H^+ antiported out	A8J0W7	12	4.6E-16			
							A8I356	10	1.1E-13			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.18.6.4	Q9JHE5	12	neutral amino acids, Na^+	symporter	A8J0W8	11	4.3E-16			
		2.A.18.6.13	Q9NVC3	11	neutral amino acids, Na^+	symporter	A8HWZ1	11	9.8E-25			
							A8HWZ3	9	8.1E-20			
		2.A.18.6.16	Q9HBR0	9	neutral amino acids, Na^+	symporter	A8I2S6	12	1.9E-27			
		2.A.18.8.7	Q7Z2H8	10	amino acids, H^+	symporter				M1V4R7	11	3.4E-26
2.A.19	The Ca^{2+}:Cation Antiporter (CaCA) Family	2.A.19.2.2	Q99385	11	Mn^{2+}/Ca^{2+}, H^+	antiporter				M1VKS5	9	5.6E-29
		2.A.19.2.4	Q39254	11	Ca^{2+}/heavy metal cation, H^+	antiporter	A8J9J9	3	9.6E-31			
		2.A.19.2.6	B6ZCF4	11	Ca^{2+}/Na^+, H^+	antiporter	A8J629	11	0.0E+00			
							A8J4L6	10	2.4E-116			
		2.A.19.3.5	Q9UPR5	11	Na^+, Ca^{2+}	antiporter	A8J755	9	1.2E-94			
2.A.20	The Inorganic Phosphate Transporter (PiT) Family	2.A.20.2.4	Q38954	11	P_i, H^+	symporter, P_i uptake				M1V7V0	10	2.3E-32
		2.A.20.2.8	A7U4W2	10	Na^+, P_i	symporter	A8J0U0	10	1.0E-123			
						symporter	A8J993	12	1.4E-123			
						symporter	A8J0U1	10	2.5E-123			
						symporter	A8J0U2	10	1.4E-120			
						symporter	A8J0U4	10	3.4E-119			
						symporter	A8J994	11	4.8E-118			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
						symporter	A8J399	11	1.3E-103			
						symporter	Q8LP67	12	2.9E-98			
						symporter	A8JH07	12	8.6E-98			
						symporter	A8ILI7	10	1.7E-64			
						symporter	A8ILT7	14	1.5E-51			
						symporter	A8JJL0	5	5.4E-42			
2.A.21	The Solute:Sodium Symporter (SSS) Family	2.A.21.2.5	M1TZ79	13	proline	uptake	A8HSY0	15	2.0E-22			
		2.A.21.3.5	P31637	14	myoinositol, Na^+	symporter				M1V4C4	13	3.8E-90
		2.A.21.6.2	Q9FHJ8	15	Na^+, urea	symporter	A8JGG6	15	1.4E-167			
						symporter	A8JGG7	15	2.9E-163			
						symporter	A8IPZ9	13	9.0E-140			
		2.A.21.6.5	Q7SE83	11	uncharacterized	uncharacterized	A8J6F4	12	5.3E-27			
		2.A.21.8.2	Q9GZV3	13	choline, Na^+, Cl^-	symporter, chloride and sodium dependent	A8JCW9	11	1.3E-15			
2.A.23	The Dicarboxylate/Amino Acid:Cation (Na^+ or H^+) Symporter (DAACS) Family	2.A.23.2.2	P31596	9	Glutamate/aspartate, Na^+	symporter	A8I0J4	8	2.0E-81			
2.A.28	The Bile Acid:Na Symporter (BASS) Family	2.A.28.2.2	E0D3H5	9	pyruvate,Na^+	symporter	A8IVU1	10	5.5E-59	M1VC91	10	7.3E-31
		2.A.28.2.3	Q1EBV7	8	pyruvate,Na^+	symporter				M1V8I5	10	1.8E-75

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
										M1VLH8	11	4.5E-55
2.A.29	The Mitochondrial Carrier (MC) Family	2.A.29.1.2	P12235	6	acetyl-CoA	transport from peroxisomes to mitochondria, carnitine dependent				M1VJ11	5	3.9E-122
		2.A.29.1.5	P31167	4	ADP	antiporter	P27080	4	1.5E-132			
		2.A.29.1.10	P12236	6	ADP/ATP	antiporter	A8IZX0	1	1.5E-35			
							A8IMU0	2	2.5E-31			
		2.A.29.2.5	Q99297	1	2-oxodicarboxylates, malate	antiporter	A8HZM9	3	1.8E-38			
							A8J0L0	2	5.9E-36			
		2.A.29.2.6	Q8SF04	4	2-oxodicarboxylates, malate	antiporter	A8J3F7	4	4.4E-97			
		2.A.29.2.13	Q02978	6	2-oxodicarboxylates, malate	antiporter				M1UNU0	6	1.5E-80
		2.A.29.3.3	O65623	3	H^+	oxidative phosphorylation uncoupler	A8J1X0	3	1.8E-116			
							A8JHJ5	3	2.7E-49			
							A8HXY9	3	3.9E-38			
							A8I975	4	8.2E-12			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.29.4.3	P23641	6	PO_4	can also transport fatty acids to completely inhibit phosphate transport				M1VML7	6	3.8E-70
										M1V636	6	2.2E-33
		2.A.29.4.6	Q9FMU6	7	PO_4	ATP dependent, uptake	Q84X74	4	2.1E-131			
							A8IEH0	4	7.5E-131			
		2.A.29.5.2	P23500	6	Fe^{2+}	uptake, pH dependent				M1V6U8	5	2.2E-49
		2.A.29.5.6	Q96DW6	6	glycine, 5-aminolevulinate	uptake	A8J2A1	4	6.1E-33	M1VGG5	4	7.2E-45
		2.A.29.6.2	O04200	5	NAD/AMP	antiporter, uptake of NAD	A8IUD0	3	3.0E-33			
		2.A.29.8.4	Q12289	5	carnitine, acylcarnitine	antiporter				M1VAS8	6	1.8E-07
		2.A.29.8.6	Q84UC7	6	arginine, lysine/ornithine/arginine/histidine	antiporter	A8JI17	3	4.1E-45			
		2.A.29.8.9	Q8N8R3	2	basic amino acids	antiporter	O24451	5	2.7E-44			
							A8IT08	5	5.1E-44			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8IPJ0	4	2.1E-40			
		2.A.29.10.3	Q4A3R4	4	folate derivatives	mediates folate import into chloroplast	A8J9I5	3	8.1E-58	M1V7R7	5	5.1E-50
		2.A.29.10.8	P39953	6	NAD/NADP, ADP/AMP	antiporter				M1V5E6	5	1.2E-47
										M1VBC7	5	8.5E-35
		2.A.29.10.11	O22261	4	NAD /NADP	symporter	A8JEQ5	5	4.3E-67			
		2.A.29.11.4	Q9SUV1	2	ATP, ADP	symporter				M1V5Q4	5	1.4E-46
		2.A.29.12.6	Q9SZI9	6	CoA		A8JHG0	6	1.7E-65			
		2.A.29.13.1	P33303	2	succinate, fumarate	antiporter	A8HXK7	2	3.7E-45			
		2.A.29.14.1	O75746	3	aspartate, glutamate	antiporter				M1V3G1	2	6.6E-58
		2.A.29.14.4	Q12482	2	aspartate, glutamate	antiporter				M1VIP3	4	2.0E-43
										M1VEZ1	6	2.3E-34
		2.A.29.14.7	Q96H78	5	uncharacterized	uncharacterized	A8I9C1	3	6.8E-28			
		2.A.29.14.8	Q9BZJ4	4	uncharacterized	uncharacterized				M1UX89	3	2.0E-33
		2.A.29.16.1	Q9HC21	6	deoxynucleotides, thiamin pyrophosphate	uniporter	A8JBP5	6	9.6E-49	M1V731	4	2.7E-50

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.29.18.1	P38921	4	S-adenosylmethionine, S-adenosylhomocysteine	antiporter				M1V6P2	5	1.1E-60
										M1VAJ9	6	2.4E-21
		2.A.29.18.2	Q94AG6	5	S-adenosylmethionine, S-adenosylhomocysteine	uptake (importer)	A8J2A5	7	2.5E-75	M1V5R9	3	1.8E-38
							A8I5X7	4	1.9E-25	M1V633	5	2.0E-36
							A8ISG2	3	1.0E-23	M1V5A7	3	8.1E-33
							A8JIR6	6	1.0E-11	M1UX72	1	3.4E-32
										M1VM35	1	9.1E-32
										M1VI47	1	1.5E-27
										M1VMR4	5	5.1E-23
		2.A.29.20.2	Q8VZS0	6	ATP, ADP, NAD+	antiporter (ATP, AMP)	A8I9M5	4	6.0E-27			
		2.A.29.23.3	Q9M024	4	ATP, AMP	antiporter	A8HW48	3	6.6E-60			
							A8IYD6	2	3.0E-22			
		2.A.29.23.4	O04619	5	AMP, ADP, ATP	prefers AMP/ADP to ATP	A8IXI7	2	1.2E-112	M1VJT6	4	6.1E-48
							A8J1N8	4	1.1E-27			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.29.23.5	Q9BV35	4	ATP, Mg, P_i, Ca^{2+}	mitochondrial carrier				M1VD17	4	4.4E-44
										M1VGS9	2	6.5E-24
		2.A.29.23.8	Q6NUK1	4	ATP, Mg, P_i, Ca^{2+}	antiporter (ATP + Mg^{2+} for P_i)	A8IIQ2	3	5.5E-67			
		2.A.29.26.1	Q5UPV8	6	dATP, dTTP, TTP, UTP, ADP	mitochondrial carrier-like protein	A8JF47	4	4.7E-05			
		2.A.29.29.1	Q04013	2	citrate, oxoglutarate, succinate, fumarate	symporter (any two)				M1UUW1	2	2.3E-81
2.A.31	The Anion Exchanger (AE) Family	2.A.31.2.6	Q9VM32	12	HCO_3^-, Cl^-	antiporter, Na^+ dependent				M1V6M5	10	1.6E-94
		2.A.31.3.1	Q8VYR7	11	B^-	efflux	A8II11	12	1.4E-94			
		2.A.31.4.1	Q8NBS3	13	B^-	efflux				M1UX91	13	1.4E-64
										M1VGR9	13	1.9E-64
2.A.36	The Monovalent Cation:Proton Antiporter-1 (CPA1) Family	2.A.36.1.9	Q9Y2E8	12	Na^+, H^+	efflux				M1UU62	12	9.7E-104
		2.A.36.1.14	Q92581	13	Na^+, H^+	efflux	A8ISJ2	9	3.6E-38			
		2.A.36.1.19	Q8IVB4	12	Na^+, H^+	efflux	A8J0T9	9	1.2E-30			
		2.A.36.4.1	Q99271	13	Na^+/K^+, H^+	antiporter	A8J222	9	5.0E-49			
		2.A.36.5.2	B1PLB6	12	Na^+, H^+	antiporter	A8J5G2	11	9.1E-69			
							A8J1K5	9	7.1E-34			
		2.A.36.6.7	Q2XWL3	13	Na^+, H^+	antiporter				M1VH31	11	1.3E-23
		2.A.36.7.6	Q9LKW9	11	Na^+, H^+	antiporter				M1VHF6	13	1.9E-43

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
										M1UWU5	13	8.0E-43
2.A.37	The Monovalent Cation:Proton Antiporter-2 (CPA2) Family	2.A.37.1.4	Q9ZTZ7	14	K^+	efflux				M1UWZ0	13	8.8E-115
		2.A.37.1.6	Q9M0Z3	13	K^+	efflux	A8ISE8	13	1.6E-168	M1USG1	12	1.3E-84
		2.A.37.1.7	O65272	14	K^+	efflux	A8IST1	9	1.4E-172			
		2.A.37.1.8	Q8VYR9	13	K^+	efflux	A8JDR2	10	2.9E-39			
2.A.38	The K^+ Transporter (Trk) Family	2.A.38.2.3	P28584	10	K^+	efflux				M1VHM6	10	3.2E-46
2.A.39	The Nucleobase:Cation Symporter-1 (NCS1) Family	2.A.39.3.4	P94575	12	allantoin	bidirectional	A8J166	12	3.7E-94			
		2.A.39.3.9	M2X8U9	14	uncharacterized	uncharacterized				M1V777	15	3.8E-11
2.A.40	The Nucleobase/Ascorbate Transporter (NAT) or Nucleobase:Cation Symporter-2 (NCS2) Family	2.A.40.4.1	Q07307	12	uric acid, xanthine	bidirectional	A8IB03	12	2.5E-114			
							A8IB05	13	3.7E-114			
							A8II76	12	1.9E-111			
							A8II65	12	1.6E-109			
		2.A.40.6.2	Q9UGH3	12	L-ascorbate, Na^+	symporter, Ca^{2+}/Mg^{2+} dependent	A8JD83	12	2.6E-108			
		2.A.40.7.3	Q9SRK7	13	purine	bidirectional	A8HXH6	12	1.2E-125			
							A8HZI7	9	6.0E-63			
2.A.42	The Hydroxy/Aromatic Amino Acid Permease (HAAAP) Family	2.A.42.1.1	P0AAD4	11	tyrosine	bidirectional	A8HSM1	11	8.2E-25			
2.A.43	The Lysosomal Cystine Transporter	2.A.43.3.1	Q60441	5	H^+, cystine	symporter	A8J6H4	6	4.4E-18	M1VM60	7	7.8E-22
										M1VL43	6	6.8E-16

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	(LCT) Family											
2.A.45	The Arsenite-Antimonite (ArsB) Efflux Family	2.A.45.1.1	P30329	11	As(III)/Sb(III), H^+	antiporter	A8J0C5	13	6.5E-23			
2.A.47	The Divalent Anion:Na^+ Symporter (DASS) Family	2.A.47.2.2	P27514	12	PO_4	efflux	A8HYL9	14	1.1E-148	M1V628	12	2.4E-92
		2.A.47.3.1	Q41364	14	2-oxoglutarate, malate	antiporter	A8JDE3	13	4.2E-172			
							A8JDE6	13	9.4E-172			
							A8HXJ4	12	1.3E-110			
		2.A.47.4.3	A8IJF8	13	Na^+, SO_4^{2-}	symporter	A8IHV3	13	0.0E+00			
							A8IJF8	13	0.0E+00			
		2.A.47.4.4	A8IHV5	13	Na^+, SO_4^{2-}	symporter	D2K6F1	13	0.0E+00			
		2.A.47.4.5	Q9K7H7	14	Na^+, SO_4^{2-}	symporter	A8J7D0	11	2.9E-75	M1VIP9	11	4.3E-76
2.A.49	The Chloride Carrier/Channel (ClC) Family	2.A.49.2.9	M1UVK6	9	Cl^-					M1UVK6	9	0.0E+00
		2.A.49.3.1	Q96325	13	NO_3^-, H^+	antiporter	A8HMC7	13	5.1E-139			
		2.A.49.3.2	Q9XF71	13	nonselective anion		A8J1N2	11	1.1E-63			
		2.A.49.3.3	P51798	10	Cl^-, H^+	antiporter	A8J6W6	13	1.2E-73			
		2.A.49.3.4	O35454	8	Cl^-, H^+	antiporter	A8HSY5	13	1.9E-60			
		2.A.49.6.3	Q8GX93	10	Cl^-		A8HM87	8	1.3E-32	M1VDK2	10	3.9E-58
2.A.50	The Glycerol Uptake (GUP) Family	2.A.50.1.1	P53154	11	glycerol, H^+	symporter	A8HNT6	6	6.0E-52			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.51	The Chromate Ion Transporter (CHR) Family	2.A.51.1.2	Q55027	12	chromate	uptake	A8JH92	9	1.2E-15			
2.A.53	The Sulfate Permease (SulP) Family	2.A.53.1.8	A8J6J0	14	H^+, SO_4^{2-}	symporter	A8J6J0	14	0.0E+00			
		2.A.53.5.2	A6YCJ2	9	molybdate	efflux	A6YCJ2	8	0.0E+00			
2.A.55	The Metal Ion (Mn^{2+}-iron) Transporter (Nramp) Family	2.A.55.2.4	Q9SAH8	12	H^+, divalent metal cations	antiporter (NRAMP-1)				M1VCH5	12	1.7E-34
		2.A.55.2.5	Q6ZG85	12	Me^{2+}, (Fe^{2+} Co^{2+} Mn^{2+})	uptake				M1VDK0	12	9.5E-82
		2.A.55.2.6	Q89K67	11	Mn^{2+}	putative	Q8LKG7	11	1.5E-127			
							A8I780	11	9.9E-123			
							A8I688	11	1.7E-85			
		2.A.55.2.10	Q553K4	10	H^+, divalent metal cations	antiporter (NRAMP-2)				M1VME5	12	1.0E-102
2.A.56	The Tripartite ATP-independent Periplasmic Transporter (TRAP-T) Family	2.A.56.1.7	Q930W3	11	malonate	uptake	A8J0V4	1	2.4E-44			
2.A.57	The Equilibrative Nucleoside Transporter (ENT) Family	2.A.57.1.3	O54698	11	nucleosides	uptake	A8JAG2	7	1.5E-15			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.62	The NhaD Na^+:H^+ Antiporter (NhaD) Family	2.A.62.1.2	Q56EB3	14	(Na^+/ Li^+), H^+	antiporter	A8J0C8	11	3.0E-29	M1V814	12	1.7E-31
2.A.64	The Twin Arginine Targeting (Tat) Family	2.A.64.2.1	Q9SJV5	6	proteins	antiporter (TatC)	A8J2Y6	4	5.6E-76	M1VCX5	1	7.1E-11
			Q9XH75	1	proteins	antiporter (TatC)				M1V3J6	1	1.1E-06
			Q9SJV5	6	proteins	antiporter (TatC)				Q85FW9	6	2.4E-42
2.A.66	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	2.A.66.1.11	Q9SIA5	12	drugs, Cd^{2+}	antiporter	A8HZ39	10	E-19			
		2.A.66.1.14	Q9SIA5	12	H^+, cationic drugs	antiporter	A8IXA0	10	E-30			
			Q945F0	9	H^+, cationic drugs	antiporter	A8IDR3	11	3.0E-30			
		2.A.66.1.16	Q96FL8	13	organic cations, H^+	antiporter	A8HPG3	12	3.4E-60	M1VH38	12	1.1E-38
		2.A.66.1.18	Q96FL8	13	organic cation, H^+	antiporter	A8HNF6	10	5.4E-51			
			Q3V050	13	organic cation, H^+	antiporter	A8J5R0	9	1.7E-16			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.66.1.19	Q8K0H1	13	Multidrug and toxin extrusion	antiporter	A8IIZ1	12	1.7E-51			
							A8HQ95	7	8.8E-37			
			B7ZGM0	12	nicotine, anabasine, other alkaloids, H^+	antiporter	A8IHW0	12	2.5E-70			
		2.A.66.1.8	B7ZGM0	12	drugs, Cd^{2+}	antiporter	A8IV68	12	4.5E-44			
							A8JD26	10	4.5E-39			
		2.A.66.1.24	Q9SFB0	12	citrate	antiporter	A8IQZ6	9	1.7E-36	M1V5T5	14	1.1E-24
							A8J9U8	10	3.0E-24			
			S6APG9	10	citrate	antiporter	A8J477	7	7.9E-12			
		2.A.66.3.3	Q6V5B3	13	Man5GlcNAc2PP-Dol	flippase	A8JEF4	12	4.5E-50			
		2.A.69.2.3	B8MZ51	10	auxin	efflux	A8J3V3	10	6.4E-13			
		2.A.69.2.4	C4MAS5	11	auxin	efflux				M1VB74	9	7.2E-06
2.A.71	The Folate-Biopterin Transporter (FBT) Family	2.A.71.2.1	O68867	12	uncharacterized	uncharacterized				M1VEP5	12	7.4E-117
		2.A.71.2.2	Q9SKZ5	12	folate, biopterin	uptake	A8IM62	12	6.5E-66			
		2.A.71.2.3	Q55721	12	folate, biopterin	uptake	A8JAS5	10	8.5E-74			
2.A.72	The K^+ Uptake Permease (KUP) Family	2.A.72.3.1	O22397	13	K^+	uniporter				M1V740	13	1.2E-88
		2.A.72.3.7	Q6VVA6	12	K^+	uniporter	A8JDC7	5	5.7E-62			
							A8JDC6	3	8.9E-47			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		2.A.72.3.9	Q9M7K4	13	K^+	uniporter	A8JDC2	11	8.1E-135			
							A8JHM1	11	5.9E-129			
2.A.82	The Organic Solute Transporter (OST) Family	2.A.82.1.3	Q9Y519	7	uncharacterized	uncharacterized (putative)	A8IJF1	6	2.6E-59	M1VM62	7	5.1E-44
							A8I469	7	8.6E-29			
2.A.84	The Chloroplast Maltose Exporter (MEX) Family	2.A.84.1.1	Q9LF50	10	maltose	efflux	A8IL44	10	8.0E-42			
2.A.85	The Aromatic Acid Exporter (ArAE) Family	2.A.85.11.1	M2Y600	11	uncharacterized	uncharacterized, GSAT zscore 30				M1V3W7	12	1.7E-11
		2.A.85.11.1	M2Y600	11	uncharacterized	uncharacterized, GSAT zscore 16				M1V6F5	12	6.4E-11
		2.A.85.11.2	M2VZN8	13	uncharacterized	uncharacterized, GSAT zscore 24	A8JC73	11	4.8E-07	M1V7I9	13	1.2E-12
2.A.86	The Autoinducer-2 Exporter (AI-2E) Family (formerly the PerM Family, TC #9.B.22)	2.A.86.1.10	M2VTE1	8	Auto Inducer 2	bidirectional	A8I5F5	6	2.5E-51	M1VHQ8	8	2.4E-108
2.A.89	The Vacuolar Iron Transporter (VIT) Family	2.A.89.1.2	Q9ZUA5	5	Fe^{2+}	uptake				M1VIJ3	5	8.1E-57
		2.A.89.3.8	Q9P6J2	5	Fe^{2+}, Mn^{2+}	uptake	A8I501	5	5.3E-37			
							A8I3U7	5	1.3E-36			
2.A.92	The Choline Transporter-like (CTL) Family	2.A.92.1.2	Q8BY89	11	choline	bidirectional	A8HPW6	9	1.2E-63			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.93	The Unknown BART Superfamily-1 (UBS1) Family	2.A.93.1.1	Q0GE19	10	Na^+, bile acid	symporter	A8JEL6	9	7.9E-50			
		2.A.93.1.6	Q01E11	12	cysteine	uptake	A8J0Z4	10	5.4E-46			
							A8IZU2	9	3.1E-43			
							A8HYT2	8	3.5E-43			
2.A.96	The Acetate Uptake Transporter (AceTr) Family	2.A.96.1.1	P0AC98	6	acetate, succinate	uptake	A8IQI1	5	5.6E-21	M1V8U8	6	2.8E-14
							A8IQH3	6	1.1E-19			
							A8IQ56	5	1.8E-19			
							A8IQ53	5	4.6E-19			
							A8IQG4	6	2.2E-18			
2.A.97	The Mitochondrial Inner Membrane K^+/H^+ and Ca^{2+}/H^+ Exchanger (LetM1) Family	2.A.97.1.1	O95202	1	cations, Ca^{2+}	antiporter (exchanger)				M1UTQ6	2	4.8E-61
		2.A.97.1.2	Q08179	2	Ca^{2+}, H^+	antiporter				M1VBT8	2	2.7E-07
		2.A.97.1.3	P91927	2	Ca^{2+}, H^+	antiporter	A8JEE6	2	1.2E-42			
		2.A.97.1.4	Q06493	2	K^+, H^+ antiporter	antiporter				M1V4U5	2	2.8E-13
2.A.100	The Ferroportin (Fpn) Family	2.A.100.1.3	O80905	12	Fe^{2+}	efflux	A8ISE1	9	4.4E-13			
		2.A.100.1.4	Q9NP59	11	H^+, Fe^{2+}/Mn^{2+}	antiporter				M1V7E3	12	4.4E-23
2.A.102	The 4-Toluene Sulfonate Uptake Permease (TSUP) Family	2.A.102.4.9	M2X4H1	9	uncharacterized	uncharacterized	A8J7K5	8	2.3E-16	M1US33	8	5.1E-31
										M1V759	8	5.0E-08
		2.A.102.5.1	Q5ZAL4	8	uncharacterized	uncharacterized				M1VEW9	9	5.2E-13
										M1V5F7	9	1.6E-06

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
2.A.105	The Mitochondrial Pyruvate Carrier (MPC) Family	2.A.105.1.4	Q949R9	2	uncharacterized	uncharacterized	A8I311	2	1.2E-40			
2.A.106	Ca^{2+}:H^+ Antiporter-2 (CaCA2) Family	2.A.106.1.1	P52876	6	Ca^{2+}, H^+	antiporter	A8I8C6	6	4.9E-34	M1VG38	6	1.8E-24
		2.A.106.2.2	Q9HC07	5	Ca^{2+}, H^+	antiporter	A8JFF7	6	6.5E-50	M1VF40	7	2.5E-30
							A8J8M6	5	8.8E-31			
							A8J8M8	6	4.6E-28			
		2.A.106.2.4	Q10320	7	uncharacterized	uncharacterized				M1UX04	6	1.9E-43
2.A.108	The Iron/Lead Transporter (ILT) Family	2.A.108.1.6	Q8LL16	7	Fe^{2+}	uptake	Q8LL16	7	0.0E+00	M1V928	8	2.2E-17
										M1VFY3	8	2.2E-17
		2.A.108.2.3	P75901	6	Fe^{2+}	uptake				M1VHL7	11	1.2E-22
		2.A.108.2.3	P75901	6	Fe^{2+}	uptake				M1VD58	11	2.0E-22
		2.A.108.2.4	Q0P7X0	1	Fe^{2+}	uptake				M1V4R2	1	3.0E-30
2.A.109	The Tellurium Ion Resistance (TerC) Family	2.A.109.1.6	I1HMH4	7	uncharacterized	uncharacterized	A8JDF6	7	1.9E-77	M1VE00	8	6.5E-64
2.A.121	The Sulfate Transporter (CysZ) Family	2.A.121.3.3	Q5BPL5	7	uncharacterized	uncharacterized	A8HQM9	5	3.3E-43			
2.A.122	The LrgB/CidB holin-like auxilary protein (LrgB/CidB) Family	2.A.122.2.4	A8IZX1	10	uncharacterized	uncharacterized	A8IZX1	10	0.0E+00			
2.A.123	The Sweet; PQ-loop;	2.A.123.1.9	Q8L9J7	7	glucose	bidirectional				M1V748	7	4.7E-11

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	Saliva; MtN3 (Sweet) Family	2.A.123.1.16	M2X865	7	uncharacterized	uncharacterized	A8HVE3	7	1.9E-35			
							A8HVV8	7	1.2E-30			
							A8ITL9	6	6.5E-21			
							A8ICN5	6	5.5E-20			
3.A P-P-bond-hydrolysis-driven transporters												
3.A.1	ATP-binding Cassette (ABC) Superfamily	3.A.1.6.7	Q6QJE2	6	sulfate	uptake (chloroplastic)	Q6QJE2	6	0.0E+00	Q85G63	7	6.8E-42
			Q8RVC7	6	sulfate	uptake (chloroplastic)	Q8RVC7	6	0.0E+00	Q85G64	6	2.6E-41
			Q6QJE0	1	sulfate	uptake (chloroplastic)	Q6QJE0	1	0.0E+00			
		3.A.1.7.1	P0AG82	1	PO_4	uptake	A8HMR8	1	2.2E-15			
							A8HMV9	1	1.2E-14			
		3.A.1.27.2	Q8L4R0	5	trigalactosyl diacyl glycerol	transfer from endoplasmic reticulum to thlakoid membrane (chloroplastic)	A8HWE7	5	4.7E-94	Q85G49	1	3.3E-11

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			Q9LTR2	1	trigalactosyl diacyl glycerol	transfer from endoplasmic reticulum to thlakoid membrane (chloroplastic)	A8JBK4	1	6.2E-46	Q85FS1	6	4.3E-42
		3.A.1.109.1	P08716	8	α-Hemolysin	efflux				M1V5Y5	9	2.6E-61
		3.A.1.120.6	P43672	1	ATP, DNA	uncharacterized	A8ISZ1	1	1.4E-32			
		3.A.1.139.2	P77307	7	Fe^{2+}	efflux				M1UX52	6	4.5E-38
		3.A.1.201.1	P08183	12	12 multidrugs (xenobiotics, long-chain fatty acids, tetramethylrosamine analogues, peptides, phospholipids, cholesterols)	efflux				M1VAN7	7	5.6E-116
		3.A.1.201.7	O80725	12	indole acetic acid, indole-3propionic acid, vanillic acid, auxin	efflux	A8J6M4	14	0.0E+00			
							A8J6M5	14	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.201.17	Q9NRK6	6	multidrugs (peptides, auxins, xenobiotics)	efflux				M1V9C8	6	5.1E-118
		3.A.1.203.1	P28288	5	long chain fatty acyl-CoA	uptake	A8JEC6	4	4.1E-36	M1V3V5	6	9.3E-166
		3.A.1.203.8	Q6NLC1	5	long chain fatty acyl-CoA	uptake	A8IIQ5	5	4.3E-154	M1VAX4	6	6.5E-142
										M1UUW8	5	5.1E-114

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.204.1	P10090	5	multidrugs (3-hydroxykynurenine, sterols, mitoxantrone, falvopiridol, methotrexate, 7hydroxymethotrexate, methotrexate diglutamate, topotecan, resveratrol, folates, mitoxantrone, daunorubicin, doxorubicin, glutathione, phospholipids, calceinAM, bodipy-verapamil, bodipyvinblastine)	efflux	A8IYC3	7	1.2E-87	M1UUG3	5	5.6E-67

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.204.2	Q9UNQ0	7	similar substrates as 3.A.204.1	efflux	A8IEX1	6	2.6E-87	M1V7E4	6	5.8E-105
							A8IHK0	6	6.3E-81	M1VLD5	7	4.9E-103
		3.A.1.204.4	Q9C8K2	6	similar substrates as 3.A.204.1	efflux				M1VC06	8	8.0E-47
		3.A.1.204.8	Q8RXN0	7	similar substrates as 3.A.204.1	efflux	A8I2E4	6	1.1E-142	M1VGV2	6	5.1E-92
		3.A.1.204.11	A9SCA8	7	similar substrates as 3.A.204.1	efflux	A8JIS8	6	1.9E-132	M1VJB6	6	1.3E-58
		3.A.1.204.13	Q55DW4	5	similar substrates as 3.A.204.1	efflux	A8ISU4	5	1.1E-47			
		3.A.1.204.15	I0DHI9	6	similar substrates as 3.A.204.1	efflux	A8IVZ2	6	2.1E-89			
							A8J5E7	2	2.4E-51			
							A8HQF7	8	2.5E-22			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.205.10	Q9M9E1	15	multidrugs (anilinopyrimidine, benzimidazole, phenylpyrrole, phenylpyridylamine, strobirulin, azoles, dicarboximides, quintozene, acriflavin, rhodamine 6G, camptothecin, stilbene phytoalexin, resveratrol, brefeldin, actinomycin D,cerulenin, cytochalasin B	efflux	A8JA59	6	1.2E-45			
		3.A.1.205.17	H6WS94	16	similar substrates as 3.A.1.205.10	efflux	A8IT35	11	0.0E+00			
							A8IT38	12	0.0E+00			
							A8IZY4	14	0.0E+00			
							A8J8F1	14	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8J6J3	12	4.9E-151			
		3.A.1.205.21	Q949G3	16	similar substrates as 3.A.1.205.10	efflux	A8IYV1	8	3.3E-68			
							A8J6T8	15	1.0E-49			
		3.A.1.208.2	Q92887	16	Hepatic canalicular conjugate exporter	efflux	A8HNZ4	3	2.9E-59			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.208.5	Q42093	15	multidrugs (folates, antifolates, dianionic bile salts, cysteinyl leukotrienes, anthracyclines, epipodophyllotosin e, cisplatin, methotrexate, protease inhibitors, cyclic nucleotides, purines, prostaglandins, estradiols, nucleobases, arsenicals, antimonals, mercurials)	efflux	A8HRK2	12	0.0E+00			
		3.A.1.208.7	O15439	10	similar substrates as 3.A.1.208.5	efflux	A8J479	3	5.4E-36			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.208.8	P33527	17	similar substrates as 3.A.1.208.5	efflux	A8J481	2	6.3E-50			
		3.A.1.208.11	P39109	14	cadmium-glutathione conjugates, glutathione S-conjugated leucotriene C_4, organic glutathione S-conjugates, selenodigluthation e, unconjugated bilirubin, reduced glutathione, and diazaborine	efflux	A8I4J0	10	1.6E-118			
		3.A.1.208.16	Q10185	16	glutathione S-conjugates	involved in vacuolar sequestration	A8IE86	12	0.0E+00			
		3.A.1.208.19	A8I268	10	$HCO3^-$	putative	A8IW55	12	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8I268	10	0.0E+00			
		3.A.1.208.31	Q5T3U5	17	similar substrates as 3.A.1.208.5		A8HNZ2	5	7.8E-35			
		3.A.1.209.2	Q9NP78	9	broad spectrum of peptides	cytosol to lysosomal lumen	A8I872	7	6.1E-102			
							A8JBH0	5	3.6E-98			
		3.A.1.210.3	Q9ZDW0	8	Fe^{2+}, Cd^{2+}, Ni^{2+}, Co^{2+}, phytochelins	efflux				M1UXB5	6	4.0E-137
		3.A.1.210.4	O75027	5	similar substrates as 3.A.1.210.3	efflux				M1UVM8	7	3.3E-178
		3.A.1.210.6	Q9NP58	10	similar substrates as 3.A.1.210.3	efflux	Q6VTH1	13	1.8E-156			
		3.A.1.210.7	Q9XUJ1	10	similar substrates as 3.A.1.210.3	efflux	A8II54	6	5.7E-146			
		3.A.1.210.8	Q9LVM1	7	similar substrates as 3.A.1.210.3	efflux	A8J6S4	6	0.0E+00	M1VEA4	6	3.0E-136

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.1.211.7	Q8T5Z7	7	lipids and protein surfactants, sterols, vitamin A derivatives, phosphatidylethanolamine	efflux	A8JAP1	7	1.7E-83			
		3.A.1.211.11	Q84M24	15	similar to 3.A.1.211.7	efflux	A8IRY0	9	5.2E-35			
		3.A.1.211.12	Q9FLT8	7	similar to 3.A.1.211.7	efflux	A8HNY7	8	0.0E+00	M1V516	8	2.0E-88
							A8J6E9	1	8.1E-126			
3.A.2	H+- or Na+translocating F-type, Vtype and Atype ATPase (F-ATPase) Superfamily	3.A.2.1.2	P21903	6	Na^+	efflux, A subunit				Q85FR3	5	1.4E-21
		3.A.2.1.3	P00854	7	H^+	efflux, A subunit	Q8RVB8	6	3.2E-20			
			P61829	2	H^+	efflux, C subunit	A8JFE2	2	9.6E-14			
							A8JFE3	2	9.7E-14			
		3.A.2.1.5	Q59166	2	Na^+					Q85FR2	2	1.3E-15
		3.A.2.2.5	P59227	4	H^+	efflux, C1/C3/C5 subunit	A8HXZ5	4	1.9E-73	M1VKU0	4	2.4E-53
		3.A.2.2.6	Q9Z1G4	9	H^+	A subunit form 1	A8IST3	8	0.0E+00	M1V7B0	4	3.1E-45
							A8J1K0	6	0.0E+00			
							A8J9X3	9	4.0E-165			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			Q91V37	5	H^+	efflux, C subunit	A8J588	5	1.5E-47			
		3.A.2.2.7	P30628	7	H^+					M1V6S0	7	1.2E-172
3.A.3	The P-type ATPase (P-ATPase) Superfamily	3.A.3.1.1	P05023	8	Na^+, K^+	α1 subunit, Na^+ efflux, K^+ uptake	A8HX15	8	0.0E+00			
		3.A.3.2.10	Q9LF79	12	Ca^{2+}	efflux	A8J0V2	8	0.0E+00			
		3.A.3.2.11	Q37145	12	Ca^{2+}	efflux	A8HM60	6	7.5E-111			
		3.A.3.2.13	P92939	10	Ca^{2+}/Mn^{2+}	efflux	A8I542	9	0.0E+00			
							A8JJH7	2	3.6E-35			
		3.A.3.2.14	Q9LU41	10	Ca^{2+}	efflux	A8IJV9	10	0.0E+00	M1V6J3	10	4.2E-169
		3.A.3.2.17	P54678	8	Ca^{2+}	efflux	A8IZL7	10	2.6E-178			
							A8IS11	10	1.8E-170			
		3.A.3.2.19	Q9SY55	12	Ca^{2+}/Mn^{2+}	efflux	A8JC12	2	1.4E-88			
		3.A.3.2.29	D5C355	10	Ca^{2+}	efflux	A8J4M6	10	0.0E+00			
							A8J4M4	9	0.0E+00			
		3.A.3.2.32	Q49LV5	11	Ca^{2+}	efflux, calcium transporting ATPase activity				M1VI70	10	0.0E+00
										M1V8V6	10	6.2E-177
		3.A.3.2.33	H9CZN9	8	Ca^{2+}	efflux	A8JEM4	6	1.8E-49			
		3.A.3.3.2	P11718	10	H^+, K^+/ Mg^{2+}	antiporter	A8IFK0	10	0.0E+00			
							A8IFH0	8	0.0E+00			
		3.A.3.3.8	Q9SH76	10	H^+	efflux	Q93Z22	10	0.0E+00	M1VKQ8	10	0.0E+00
		3.A.3.5.6	Q04656	9	Cu^+, Cu^{2+}	efflux	A8JBB5	6	1.1E-178			
		3.A.3.5.11	Q9SZC9	8	Cu^+	efflux	A8IC93	8	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
		3.A.3.5.12	Q7Y051	8	Cu^{+}	efflux	A8ICL1	2	2.0E-70			
		3.A.3.5.32	Q9S7J8	8	Cu^{+}, Cu^{2+}	efflux	A8J829	8	9.7E-174	M1VFS2	9	3.1E-94
		3.A.3.6.6	Q9M3H5	7	Cu^{+}, Zn^{2+}, Cu^{2+}, Cd^{2+}, Co^{2+}, Ca^{2+}	efflux	A8J6D5	5	9.2E-47	M1VM24	5	4.4E-78
		3.A.3.8.1	Q29449	7	phosphilipids	efflux				M1VLE5	10	0.0E+00
										M1VC09	10	2.3E-128
		3.A.3.8.6	Q9XIE6	9	phospholipids	efflux	A8IVJ6	9	0.0E+00			
							A8IVJ3	10	0.0E+00			
		3.A.3.8.8	P98200	7	phosphatidylserine flippase	efflux	A8J8G9	10	0.0E+00			
		3.A.3.10.1	B9RHM6	12	Mn^{2+}, Ca^{2+}	efflux	A8JI26	12	0.0E+00			
		3.A.3.10.2	Q7SXR0	12	Mn^{2+}, Ca^{2+}	efflux				M1V5Q8	12	0.0E+00
		3.A.3.10.9	Q54X63	13	Mn^{2+}, Ca^{2+}	efflux	A8I9J2	11	2.8E-103			
		3.A.3.16.1	Q23QW3	7	Mn^{2+}, Ca^{2+}	efflux				M1V6X8	11	1.3E-47
3.A.5	The General Secretory Pathway (Sec) Family	3.A.5.1.1	P10408	1	proteins	efflux	A8J682	1	2.7E-135			
		3.A.5.4.1	P0A4H1	10	unfolded proteins	uptake, SecY	A8IS14	10	1.7E-86			
							A8J7G8	10	4.1E-21			
		3.A.5.5.1	P46249	10	unfolded proteins	uptake				Q85FU6	8	1.1E-67
		3.A.5.7.2	Q8U051	3	unfolded proteins	uptake	A8IS72	1	1.4E-54			
		3.A.5.9.1	Q9H9S3	10	unfolded proteins	Sec61 α2 subunit	A8IEL6	10	0.0E+00	M1VLT8	1	8.3E-17

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			Q9UGP8	3	unfolded proteins	Sec63 subunit	A8J8J1	3	2.3E-45	M1VKP0	3	2.1E-31
		3.A.5.9.1	P60059	1	unfolded proteins	uptake, Sec61 γ subunit	A2PZD3	1	1.3E-18	M1VHV4	12	5.5E-160
			P60468	1	unfolded proteins	Sec61 β subunit	A8I6P9	1	6.2E-08			
3.A.8	The Mitochondrial Protein Translocase (MPT) Family	3.A.8.1.1	P39515	4	proteins	Tim17 subunit, uptake (mitochondrial)	A8I032	3	1.5E-35	M1V617	3	2.2E-12
			P32897	3	proteins	Tim23 subunit, uptake (mitochondrial)	A8IJZ0	1	2.7E-33	M1VHJ2	3	4.2E-11
			Q12328	4	proteins	Tim22 subunit, uptake (mitochondrial)	A8HPV7	3	4.8E-14			
			Q02776	1	proteins	Tim50 subunit, uptake (mitochondrial)	A8I7G3	1	1.3E-12			
3.A.9	The Chloroplast Envelope Protein Translocase (CEPT or Tic-Toc) Family	3.A.9.1.1	Q9SC41	1	proteins	Tic40 subunit, uptake (chloroplastic)	A8IK91	1	3.3E-44			
			O49931	3	proteins	Tic55 subunit, uptake (chloroplastic)	A8J6L3	3	1.8E-33			
							A8J6L5	2	1.0E-30			
							A8J8W2	3	3.0E-30			
							Q9ZWM5	1	3.4E-28			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			Q8SKU2	2	proteins	Tic62 subunit, uptake (chloroplastic)	A8JBZ2	2	6.9E-32			
							A8IU49	2	1.2E-30			
							A8JH47	1	6.7E-20			
							A8J1Z2	1	2.4E-13			
		3.A.9.1.2	Q8LPR9	2	proteins	Tic110 subunit, uptake (chloroplastic)	A8I023	1	2.2E-43	M1UWP3	5	5.4E-07
			Q8GZ79	5	proteins	Tic20-I subunit, uptake (chloroplastic)	A8IZ79	4	E-17			
3.A.10	The H^+, Na^+-translocating Pyrophosphatase (M^+-PPase) Family	3.A.10.1.2	Q93Y49	16	H^+	bidirectional	A8J0B0	16	0.0E+00			
		3.A.10.2.3	Q56ZN6	17	H^+	efflux				M1VJH8	16	0.0E+00
3.A.16	The Endoplasmic Reticular Retrotranslocon (ER-RT) Family	3.A.16.1.1	Q9BUN8	4	misfolded luninal ER proteins	efflux, Derlin-1 subunit				M1V547	5	5.9E-23
		3.A.16.1.2	E7NGV2	1	misfolded luninal ER proteins	efflux, Ubc6p	A8JBR3	1	4.2E-32			
		3.A.16.1.3	Q8ILM8	7	misfolded proteins	uncharacterized subunit, efflux	A8JEP8	6	1.3E-35	M1V8D2	6	6.7E-29
			Q8IJ82	4	misfolded proteins	uncharacterized subunit, efflux	A8J5Q5	5	1.8E-25	M1UQ95	6	4.4E-34

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			C7SP48	5	misfolded proteins	uncharacterized subunit, efflux	A8JDW9	3	2.0E-22			
3.A.18	The Nuclear mRNA Exporter (mRNA-E) Family	3.A.18.1.1	Q53GS7	1	mRNA	efflux	A8INQ8	2	1.6E-19			
3.A.20	The Peroxisomal Protein Importer (PPI) Family	3.A.20.1.1	O75381	1	peroxisomes	Pex14 subunit, uptake				M1V5S5	1	8.2E-05
		3.A.20.1.2	Q9FZF1	3	proteins	Pex11A subunit, uptake	A8IYU9	2	2.6E-42			
			Q9M841	4	proteins	Pex12 subunit, uptake	A8HX31	1	1.7E-41			
3.A.25	The Symbiont-specific ERAD-like Machinery (SELMA) Family	3.A.25.2.1	P46468	1	ATP	putative	A8J6C7	2	1.2E-53			
							A8IL08	2	2.0E-52			
3.B Decarboxylation-driven transporters												
3.B.1	The Na^+-transporting Carboxylic Acid Decarboxylase (NaT-DC) Family	3.B.1.1.2	Q57079	1	Na+	α subunit	A8JH46	1	2.3E-69			
3.D Oxidoreduction-driven transporters												
3.D.1	The H^+ or Na^+-translocating NADH Dehydrogenase (NDH) Family	3.D.1.6.4	P20113	15	Na^+	NuoM subunit	P20113	15	0.0E+00			
			P08739	17	H^+	NuoL subunit	P08739	17	0.0E+00			
			P08740	11	H^+	NuoN subunit	P08740	11	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			Q6V9B2	1	H^+	NuoF subunit	A8ICJ1	1	0.0E+00			
			Q6V506	1	H^+	uncharacterized 39 kDa subunit	Q6V506	1	0.0E+00			
			P11658	8	H^+	NuoH subunit	P11658	8	7.2E-167			
			Q6V502	3	H^+	NuoA subunit	Q6V502	3	2.0E-163			
			Q84K56	5	H^+	NuoK subunit	Q84K56	5	8.9E-131			
			Q6QAY4	4	H^+	uncharacterized 23 kDa subunit	Q6QAY4	4	4.6E-126			
			Q6QIW0	1	H^+	uncharacterized 17 kDa subunit	A8J843	1	2.4E-97			
			Q6V9B0	1	H^+	NuoB subunit	Q6V9B0	1	7.5E-95			
			P10329	4	H^+	NuoJ subunit	P10329	4	6.7E-87			
			Q6UP32	1	H^+	B16.6 subunit	Q6UP32	1	1.3E-79			
			Q6UP28	2	H^+	uncharacterized 20.9 subunit	Q6UP28	2	2.0E-68			
			Q6QIV4	1	H^+	uncharacterized subunit	Q6QIV4	1	2.4E-33			
			Q6QIV8	1	H^+	uncharacterized subunit	Q6QIV8	1	4.8E-28			
		3.D.1.8.1	O80634	2	e^-	electron shuttle in photosynthetic chain and chloroplast respiratory chain	A8IKE6	1	3.9E-25			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
3.D.2	The Proton-translocating Transhydrogenase (PTH) Family	3.D.2.3.1	P11024	16	H^+	bidirectional	A8JCP5	15	0.0E+00			
3.D.3	The Proton-translocating Quinol:Cytochrome c Reductase (QCR) Superfamily	3.D.3.2.1	P13272	1	3.D.3 subunits form one system involved in bidirectional e- and H^+ transport	UCRI subunit	A8JJ26	1	1.5E-118			
		3.D.3.3.1	P07143	2		Cytochrome C	A8JIU5	2	5.5E-68	M1UV57	2	9.9E-91
			P08067	1		Rieske subunit	Q8HEB4	1	9.8E-54			
		3.D.3.5.1	P26287	2		CYF subunit	P23577	2	4.3E-102	Q85FX0	2	4.3E-78
		3.D.3.5.2	P56773	5		Cytochrome b6	Q00471	5	1.0E-113	M1V7X1	1	3.4E-54
			P56774	3		Cytochrome b6/f complex subunit 4	P23230	3	2.7E-73	M1UVM3	1	2.7E-53
			Q9ZR03	1		Rieske subunit	P49728	1	5.5E-60	M1VET8	1	2.1E-52
			O23166	1		HCF164 subunit, chloroplastic	A8IQA9	1	3.5E-38	Q85G15	3	2.7E-66
			P56773	5		Cytochrome b6				Q85G16	4	5.7E-112
3.D.4	The Proton-translocating Cytochrome Oxidase (COX) Superfamily	3.D.4.7.1	P00415	6	e^-	COX3 subunit, efflux	Q9FV97	7	1.9E-42			
		3.D.4.8.1	P00401	12	3.D.4 subunits form one system involved in bidirectional H^+ transport	Cytochrome c oxidase subunit 1	P08681	12	1.1E-163			
			P19516	1		COX11 subunit, efflux	A8JCS0	1	2.1E-44			
			P00410	2		Cytochrome c oxidase subunit 2, efflux	Q9AU05	3	5.9E-23			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			P53266	2		SHY1 subunit	A8JF96	1	3.8E-15			
3.D.5	The Na^+-translocating NADH:Quinone Dehydrogenase (Na-NDH) Family	3.D.5.1.1	Q56584	2	Na^+	bidirectional	A8J308	2	1.0E-09			
3.D.10	The Prokaryotic Succinate Dehydrogenase (SDH) Family	3.D.10.1.1	Q65GF4	1	e^-	SdhA subunit	A8HP06	1	5.1E-70			
							A8J5A6	1	2.6E-45			
3.E Light absorption-driven transporters												
3.E.1	The Ion-translocating Microbial Rhodopsin (MR) Family	3.E.1.7.1	Q93WP2	10	H^+	Chanelrhodopsin-1	A8JAJ2	10	0.0E+00			
		3.E.1.7.2	Q8RUT8	4	monovalent and divalent cations	Chanelrhodopsin-2	Q8RUT8	4	0.0E+00			
3.E.2	The Photosynthetic Reaction Center (PRC) Family	3.E.2.1.1	Q02761	10	3.E.2 subunits form one system involved in H+ efflux	photosynthetic reaction center	Q36954	9	3.3E-91			
			P04997	8		photosystem II D1	P07753	8	0.0E+00	Q85G26	7	0.0E+00
							P07753	8	0.0E+00	Q85G59	8	0.0E+00
			P11005	6		photosystem II D2	P06007	6	0.0E+00			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
			P11004	6		photosystem II CP43	P10898	7	0.0E+00			
		3.E.2.2.2	P09193	8		photosystem II CP43	P37255	6	5.5E-15	Q85G27	6	0.0E+00
										Q85FZ5	6	1.9E-15
4.C Acyl CoA ligase-coupled transporters												
4.C.1	The Proposed Fatty Acid Group Translocation (FAT) Family	4.C.1.1.4	P69451	2	fatty acids	uptake	A8HZR1	3	2.2E-25			
							A8JCQ8	1	1.2E-23			
4.D: Polysaccharide Synthase/Exporters												
4.D.1	The Putative Vectorial Glycosyl Polymerization (VGP) Family	4.D.1.3.3	B3EBP1	1	glycosyl	putative				M1VGI4	1	6.8E-09
4.E Vacuolar Polyphosphate Polymerase-catalyzed Group Translocators												

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
4.E.1	The Vacuolar (Acidocalcisome) Polyphosphate Polymerase (V-PPP) Family	4.E.1.1.4	P40046	3	ATP, ADP	cytoplasm to vacuolar lumen	A8IKM0	3	E-13			
							A8J7Z7	3	E-12			
5.A Transmembrane 2-electron transfer carriers												
5.A.1	The Disufide Bond Oxidoreductase D (DsbD) Family	5.A.1.2.4	Q8S3X4	6	e^-	uptake	A8JI93	6	9.8E-172			
5.B Transmembrane 1-electron transfer carriers												
5.B.1	The gp91phox Phagocyte NADPH Oxidase-associated Cytochrome b558 (Phox) Family	5.B.1.3.1	O81209	5	e^-	export	A8IRR3	6	2.0E-21	M1VG56	11	1.5E-23
							A8IRR2	6	1.2E-20	M1UWF8	9	6.6E-19
		5.B.1.4.2	A2I2U7	11	e^-, Fe^{3+}	putative	A2I2U7	11	0.0E+00			
5.B.2	The Eukaryotic Cytochrome b561 (Cytb561) Family	5.B.2.1.2	Q9WUE3	6	e^-	import	A8J1Z7	6	E-12			
		5.B.2.2.1	G7ZYU6	5	e^-	import	A8IUR9	5	2.2E-07			
							A8JJD8	3	4.4E-05			
		5.B.2.2.2	Q0WRW8	5	e^-	import	A8J3G0	8	E-12			
							A8J3G1	5	E-12			
			Q0WRW8	6	e^-	import	A8J2S1	5	2.5E-16			
							A8IY98	5	1.4E-15			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8JEX2	5	5.0E-14			
							A8JDH5	5	3.0E-11			
5.B.4	The Plant Photosystem I Supercomplex (PSI) Family	5.B.4.1.1	Q9SYW8	1	5.B.4 subunits form one system involved in e-uptake	Lhca2 subunit	Q9ZSJ4	3	6.1E-33	Q85FP8	3	3.0E-26
							Q8S3T9	2	7.0E-32	Q85FS9	3	2.0E-43
							A8J270	2	7.2E-32	Q85FY6	12	0.0E+00
							A8J264	2	6.0E-31	Q85FY7	13	0.0E+00
							Q93WE0	3	6.4E-31			
							Q9AXF6	3	7.0E-31			
							Q93WD2	2	6.1E-20			
							A8J431	2	7.6E-11			
							P93664	2	7.7E-12			
							A8ISG0	3	3.1E-49			
							A8IKC8	3	2.7E-36			
			Q43381	3		Lhca3 subunit	Q9FEK6	3	3.6E-31			
							Q93WL4	3	3.7E-31			
							A8J287	2	7.0E-31			
							A8JF10	3	3.8E-84			
							A8I0C6	3	1.4E-48			
			Q6YWJ7	1		Lhca4 subunit	Q75VY6	1	8.2E-55			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8I000	3	3.3E-54			
							Q75VY7	3	3.9E-47			
							Q75VY8	3	4.5E-47			
							A8J249	2	4.7E-30			
							A8ITV3	1	5.5E-36			
			P56766	11		PsaA subunit, uptake	P12154	11	0.0E+00			
			P56767	10		PsaB subunit	P09144	10	0.0E+00			
			Q9S7N7	1		PsaG subunit	A8JHN9	2	6.8E-16			
			Q9SUI5	2		PsaK subunit	P14225	2	5.0E-22			
			Q9SUI4	2		PsaL subunit	A8IL32	2	9.6E-41			
			Q9SHE8	3		Photosystem I reaction center subunit III, chloroplastic	P12356	2	1.6E-51			
8.A Auxiliary transport proteins												
8.A.11	The Immunophilin-like Prolyl:Peptidyl Isomerase Regulator (I-PPI) Family	8.A.11.1.1	Q9LDC0	2	auxin	efflux	A8I9C7	1	1.3E-50			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
8.A.20	The Plant/Algal/Chlorella Nitrate Transporter Accessory Protein (NAR2.1) Family	8.A.20.2.1	A8J4P7	2	associated with NO_3- transport	accessory protein	A8J4P7	2	7.5E-154			
8.A.27	The CDC50 P-type ATPase Lipid Flippase β-Subunit (CDC50) Family	8.A.27.1.4	Q9LTW0	2	associated with lipid transport capability	accessory protein	A8J1W0	2	1.6E-76	M1V7M7	2	2.5E-33
8.A.30	The Nedd4-Family Interacting Protein-2 (Nedd4) Family	8.A.30.1.3	C3XWE5	3	uncharacterized	accessory protein	A8ID60	1	3.6E-07			
8.A.44	The Mitochondrial EF Hand Ca^{2+} Uniporter Regulator (MICU) Family	8.A.44.1.6	A8JGI1	1	associated with Ca2+ transport	accessory protein, uniporter	A8JGI1	1	0.0E+00			
8.B Ribosomally synthesized protein/peptide toxins/agonists that target channels and carriers												
8.B.9	The Triflin Toxin (Triflin or CRISP) Family	8.B.9.1.5	P11670	1	possibly involved in plant defense against pathogens	accessory protein	A8HMY0	1	2.9E-13			
							A8J8Z3	1	7.0E-13			
9.A Recognized transporters of unknown biochemical mechanism												
9.A.2	The Endomembrane	9.A.2.1.2	Q9LIC2	10	copper ions	uptake	A8IIL1	10	0.0E+00	M1VAU9	10	6.8E-157

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	protein-70 (EMP70) Family						A8JDP0	9	1.6E-134			
		9.A.2.1.5	Q84LF6	10	copper ions	uptake	A8HQ21	9	0.0E+00			
							A8JBC9	10	0.0E+00			
		9.A.2.1.7	O04091	9	copper ions	uptake	A8JAK4	9	0.0E+00			
9.A.4	The YggT or Fanciful K^+ Uptake-B (FkuB; YggT) Family	9.A.4.2.1	Q81WE1	2	uncharacterized	uncharacterized				M1V3W2	2	2.4E-06
		9.A.4.2.2	M2WYR6	2	K^+	uptake	A5H8I0	3	9.0E-12			
							A8IS78	2	1.0E-06			
		9.A.4.2.3	M2WX31	3	K^+	uptake	A8JGZ1	1	6.1E-15			
							A8IAN4	1	5.0E-07			
9.A.15	The Autophagy-related Phagophore-formation Transporter (APT) Family	9.A.15.1.1	P43601	2	phosphatidylinositol 3,5-bisphosphate	efflux	A8I0Q7	1	6.7E-39			
9.A.24	The Mitochondrial Cholesterol/Porphyrin Uptake Translocator Protein (TSPO) Family	9.A.24.1.1	Q6ICF9	4	cholesterol, porphyrin	uptake (mitochondrial)				M1V785	5	1.2E-10
		9.A.24.1.2	Q3J192	4	cholesterol, porphyrin	uptake (mitochondrial)	A8IE17	4	E-14			
9.A.26	The Lipid-translocating Exporter (LTE) Family	9.A.26.1.3	P53047	7	protoporphyrin	uptake (mitochondrial)	A8HP05	7	2.5E-16			
9.A.40	The HlyC/CorC (HCC) Family of Putative	9.A.40.2.2	Q0PBV6	4	auxiliary protein to CorA channels	accessory protein				M1URQ2	6	1.2E-46

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	Transporters	9.A.40.3.1	Q3TWN3	5	divalent metal cations	uptake	A8JIJ6	3	4.7E-53	M1VMB9	5	1.8E-45
							A8IEJ9	3	7.7E-52	M1UQW3	4	4.3E-45
							A8IIC2	3	2.2E-43	M1VES5	4	5.5E-33
							A8HSS9	3	8.3E-38			
							A8J0V3	2	1.0E-37			
9.A.45	The Magnesium Transporter1 (MagT1) Family	9.A.45.1.6	Q7ZV50	4	Mg^{2+}	uptake	A8JBD0	4	5.0E-09			
9.A.54	The Lysosomal Cobalamin (B_{12}) Transporter (L-B_{12}T) Family	9.A.54.1.4	B9SQ26	9	cobalamin (Vitamin 12)	putative, uncharacterized	A8HPZ9	9	1.2E-107			
		9.A.54.3.1	Q22WA5	9	uncharacterized	uncharacterized	A8I062	3	1.9E-10			
9.A.55	The TMEM205 (TMEM205) Family	9.A.55.1.4	A8J716	2	sugars	bidirectional	A8J716	2	1.9E-75			
9.B Putative transport proteins												
9.B.1	The Integral Membrane CAAX Protease (CAAX Protease) Family	9.B.1.2.5	Q8GW19	8	protein, protein fragment	uncharacterized	A8HMM6	6	5.2E-34			
9.B.2	The Integral Membrane CAAX Protease-2 (CAAX	9.B.2.1.8	F9DWD5	6	protein, protein fragment	uncharacterized				M1VKX6	8	5.1E-04

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	Protease2) Family	9.B.2.1.10	Q99Z60	8	protein, protein fragment	uncharacterized	A8JDF8	7	E-6			
9.B.12	The Sensitivity to Sodium or Salt Stress-induced Hydrophobic Peptide (Sna) Family	9.B.12.2.2	I1CTU6	2	uncharacterized	uncharacterized	A8IWT4	2	1.5E-15			
9.B.14	The Putative Heme Handling Protein (HHP) Family	9.B.14.3.2	Q7VCA3	8	heme	efflux (putative)				Q85G53	8	3.6E-50
		9.B.14.3.3	P48269	9	heme	efflux (putative)	P48269	9	0.0E+00			
9.B.26	The Regulator of ER stress and autophagy TMEM208 (TMEM208) Family	9.B.26.1.1	Q9BTX3	4	ER stress, autophagy (both putative)	uncharacterized	A8I2C0	2	1.4E-17			
9.B.27	The DedA or YdjX-Z (DedA) Family	9.B.27.1.1	P76219	6	selenite, oxalate (putative)	uncharacterized	A8HMR2	6	2.6E-22	M1UV71	5	1.5E-17
							A8JD31	4	6.7E-19			
							A8HXB2	5	6.2E-12			
		9.B.27.1.3	M3A107	5	selenite, oxalate (putative)	uncharacterized				M1VFH3	6	8.7E-12
		9.B.27.2.3	P0ABP6	6	Ca^{2+}, Mg^{2+}	putative	A8J0C3	5	1.4E-50			
9.B.37	The Huntington-interacting Protein 14	9.B.37.1.1	Q8IUH5	6	divalent metal cations	efflux	A8HZ94	4	4.8E-52	M1UR71	5	2.0E-28

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
	(HIP14) Family	9.B.37.1.2	Q9VUW9	6	divalent metal cations	efflux	A8JCX6	4	1.0E-13	M1V4K4	5	5.1E-17
							A8IBL5	5	1.9E-12			
		9.B.37.2.1	Q8R173	4	divalent metal cations	efflux	A8IX50	2	4.9E-06	M1VAM4	4	1.3E-14
										M1UX09	4	8.5E-13
										M1V742	4	1.6E-08
		9.B.73.1.1	Q37050	5	H^+ (putative)	efflux (putative)	Q37050	5	0.0E+00			
		9.B.73.1.2	P75028	4	H^+ (putative)	efflux (putative)	A8HXK4	4	7.3E-33	Q85FP7	4	3.9E-76
9.B.82	Endoplasmic Reticulum Retrieval Protein1 (Putative Heavy Metal Transporter) (Rer1) Family	9.B.82.1.3	O48670	4	proteins	export	A8IYQ8	3	6.1E-56	M1VC93	4	6.5E-42
9.B.87	The Selenoprotein P Receptor (SelP-receptor) Family	9.B.87.1.6	B8LPX7	2	uncharacterized	uncharacterized	A8JEJ5	1	7.7E-91			
9.B.102	The YedE/YeeE (YedE/YeeE) Family	9.B.102.5.3	M2VZH1	9	prodigiosin (putative)	efflux (putative)	A8HZF2	10	6.0E-43			
							A8JAC9	9	4.8E-37			
							A8I0T2	7	6.2E-30			
9.B.104	The Rhomboid Protease Family	9.B.104.1.3	F0Z2G1	6	proteins	efflux	A8J380	7	2.8E-14	M1UNE5	7	1.1E-20
							A8I5H3	4	1.4E-10	M1UT47	6	7.3E-17
		9.B.104.1.5	Q8F2A9	5	proteins	efflux				M1VA02	6	5.2E-09
		9.B.104.4.1	Q8TEB9	4	proteins	efflux	A8IXD5	4	8.6E-23	M1VE62	6	3.7E-18

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
							A8HNC7	6	7.6E-20			
							A8J351	4	9.7E-18			
9.B.106	The Pock Size-determining Protein (PSDP) Family	9.B.106.3.3	C5L569	2	uncharacterized	uncharacterized	A8IA03	1	6.2E-26			
							Q6UPR1	1	2.9E-24			
							A8JG78	1	7.9E-24			
							A8J1L4	1	2.2E-20			
							A8J0E1	1	4.3E-20			
							A8J6I9	1	1.5E-19			
							A8J3B8	1	4.3E-19			
							A8I1C2	2	2.7E-18			
							A8HNM7	1	1.4E-17			
							A8JI35	1	1.2E-16			
							A8I9Y4	1	3.4E-16			
							A8J0D7	1	4.0E-16			
							A8J0P4	1	2.9E-15			
							A8IB58	1	3.4E-15			
							A8J8E9	2	5.1E-15			
							A8HQX8	1	2.0E-14			
							A8HS22	1	1.7E-13			
							A8IZ83	1	7.4E-13			
							A8IYZ5	1	8.1E-13			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
9.B.112	The Stress-inducible Transmembrane Protein (TMPIT1) Family	9.B.112.1.1	G0ZL54	4	uncharacterized	uncharacterized	A8J188	4	4.2E-28	M1VGR6	5	8.5E-22
9.B.115	The Putative Integral Membrane Steroid 5α-reductase (SαR) Family	9.B.115.1.1	M2X3K0	7	e^-	accessory protein (putative)				M1UPF6	7	1.2E-46
		9.B.115.1.2	F0M2Z7	8	e^-	accessory protein (putative)	A8J7X5	5	2.9E-40			
		9.B.115.1.3	B2HS04	8	e^-	accessory protein (putative)	A8I7P2	5	1.7E-16			
		9.B.115.1.4	A8ILY4	6	e^-	accessory protein (putative)	A8ILY4	6	0.0E+00			
		9.B.115.1.5	B8C953	5	e^-	accessory protein (putative)				M1UUE5	6	1.2E-42
		9.B.115.1.6	D7VS98	5	murein hydrolase	accessory protein (putative), export	A8J316	3	1.4E-07			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
9.B.117	The DUF4190 (DUF4190)Family	9.B.117.1.1	C6EAH0	5	murein hydrolase	accessory protein (putative), export				M1V5M9	11	9.8E-14
			E8VD44	5	uncharacterized	uncharacterized				M1VGX0	10	3.2E-11
9.B.119	The Glycan Synthase, Fks1 (Fks1) Family	9.B.119.1.2	Q3B724	15	1,3-β-D-glucan	synthase	A8IWZ7	11	2.9E-114			
							A8INK5	18	9.8E-74			
							A8IRK0	5	7.5E-73			
							A8IRI5	5	1.2E-72			
		9.B.119.1.3	Q9LUD7	14	callose	synthase	A8HT27	16	4.5E-106			
							A8JH88	1	2.3E-39			
		9.B.119.1.4	A8JK32	3	glycosoyl	bidirectional	A8JK32	3	0.0E+00			
9.B.123	The Lysosomal 7-TMS (TM7SF1) Family	9.B.123.2.2	B8B6I6	7	uncharacterized	uncharacterized	A8IL75	8	4.6E-66			
9.B.132	The Post-GPI Attachment Protein-3 (P-GAP3) Family	9.B.132.1.1	Q7K0P4	8	proteins	accessory protein	A8I9U6	6	1.6E-38			
9.B.135	The Membrane Trafficking Yip (Yip) Family	9.B.135.1.1	P53039	5	proteins	accessory protein	A8J1K4	5	5.3E-15	M1V6L7	5	2.5E-19
		9.B.135.1.2	O64614	5	uncharacterized	accessory protein	A8IHQ2	5	4.0E-32			
		9.B.135.2.2	Q60EM1	5	uncharacterized	accessory protein	A8J6H6	5	1.2E-16			

Table 3 Continued

Transporter Classification							Chlamydomonas reinhardtii			Cyanidioschyzon merolae		
Family TC #	Family Name	Hit TCID #	Hit Accession #	Hit TMS	Substrate	Comments	Accession #	Query TMS #	Comment	Accession #	Query TMS #	Comment
9.B.142	The Integral membrane Glycosyltransferase family 39 (GT39) Family	9.B.142.2.1	C6NTX4	13	glycosyl moeity (putative)	efflux (putative)				M1VEV7	14	4.4E-35
		9.B.142.3.3	B3S136	13	glycosyl moeity (putative)	efflux (putative)	A8IH85	13	0.0E+00	M1V604	13	0.0E+00
		9.B.142.3.4	B4DJ24	12	glycosyl moeity (putative)	efflux (putative)	A8J119	4	1.2E-73			
		9.B.142.5.1	I1WBQ5	11	glycosyl moeity (putative)	efflux (putative)				M1V6S7	11	7.1E-09
9.B.146	The Putative Undecaprenyl-phosphate N-Acetylglucosaminyl Transferase (MurG) Family	9.B.146.1.5	M2X0J8	12	e^-	bidirectional	A8J8T5	10	6.1E-97	M1VKF6	12	E-98
9.B.149	The M50 Peptidase (M50-P) Family	9.B.149.1.9	O58089	8	uncharacterized	uncharacterized	A8JBT7	7	2.6E-18			
							A8HNA2	8	6.6E-15			
9.B.158	The 4 TMS Putative DMT2 (DMT2) Family	9.B.158.1.5	Q1HPG8	3	uncharacterized	uncharacterized				M1V6D1	4	2.5E-06
		9.B.158.1.7	M2XLC6	4	uncharacterized	uncharacterized				M1V3K0	3	2.1E-11
		9.B.158.2.2	R0I828	4	uncharacterized	uncharacterized	A8ICM7	4	6.4E-16			