

STUDIES ON THE PHOTOSYNTHETIC MICROORGANISM  
*SYNECHOCYSTIS PCC6803* AND  
HOW IT RESPONDS TO THE EFFECTS OF SALT STRESS

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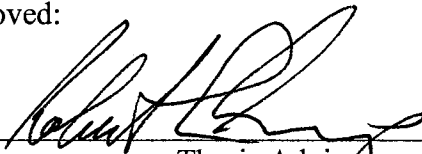
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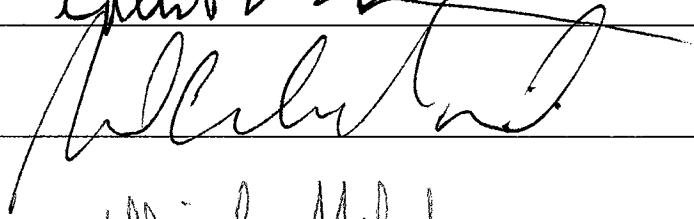
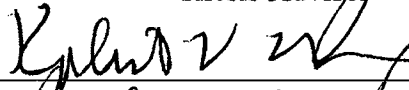
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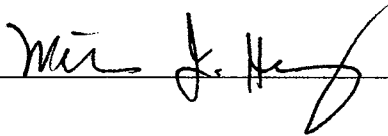
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## TABLE OF CONTENTS

Chapter	Page
I. Functional and Comparative Genomics of Cyanobacteria.....	1
Cyanobacterial Systems.....	2
Genomics.....	7
Functional Genomics in a Cyanobacterium.....	22
Outlook and Prospective.....	43
Bibliography.....	47
II. The Construction and Use of Bacterial DNA Microarrays Based on an Optimized Two-stage PCR Strategy.....	52
Abstract.....	53
Introduction.....	55
Materials and Methods.....	57
Results and Discussion.....	65
Bibliography.....	77
III. Optimization of Fusion PCR for <i>In Vitro</i> Construction of Gene Knockout Fragments.....	78
Introduction.....	79
Methods, Results and Discussion.....	79
Bibliography.....	90
IV. Global gene expression profiling and physiological analysis of salt stress and acclimation in <i>Synechocystis</i> sp PCC6803.....	91
Abstract.....	92
Introduction.....	92
Materials and Methods.....	100
Results.....	110
Discussion.....	146
Bibliography.....	151

TABLE OF CONTENTS CONTINUED.

Summary.....	154
Bibliography.....	159
Appendix.....	161
Vitae.....	247

## LIST OF TABLES

1.1 Statistical summary and comparison of cyanobacterial genome sequencing efforts.....	12
1.2 Abbreviated list of web based genomic information services.....	19
1.3 Representative genes induced after one and five hours salt shock from 2mM to 684 mM NaCl in <i>Synechocystis</i> PCC6803 as determined through analysis with sub-genomic DNA microarrays.....	33
1.4 <i>Synechocystis</i> genes regulated by salt stress after 5 hours of treatment revealed through microarray differential expression profiling.....	34-35
1.5 Hypothetical genes differentially expressed before and after salt shock.....	37
2.1 Construction of DNA microarray.....	66
2.2 Synthesis and hybridization of fluorescently labeled cDNA derived from sample RNA.....	72
3.1 Primer sequences for PCR mutagenesis.....	81
4.1 Genes induced after acclimation to high salt conditions.....	113
4.2 Genes repressed after acclimation to high salt conditions.....	120
A-1 Gene expression profiles for <i>Synechocystis</i> PCC6803 after acclimating to high salt conditions.....	161
A-2 Gene expression profiles in response to 650 mM NaCl shock treatment By <i>Synechocystis</i> PCC6803.....	202

## LIST OF FIGURES

1.1 Venn diagram presentation of genome homology clustering with various genome sequencing projects.....	15
1.2 Functional genomics strategy for <i>Synechocystis PCC6803</i> .....	24
1.3 PCR amplification strategy used to develop full genome arrays.....	38
2.1 Overall strategy for the production of bacterial DNA microarrays.....	59
2.2 Design and use of chimeric bipartite oligonucleotides for PCR amplification of each open reading frame of the genome from <i>Synechocystis PCC6803</i> .....	67
2.3 Thermal cycling conditions and resultant products from first and second round amplifications.....	69
2.4 Scatter-plot of differential hybridization of fluorescently labeled cDNA from a 3-hour salt shock treated culture versus an untreated sample.....	74
3.1 Comparison of fusion PCR strategies for <i>in vitro</i> construction of gene knockout fragments developed in this study and elsewhere.....	82
3.2 Optimization of fusion PCR steps for <i>in vitro</i> construction of gene knockout fragments.....	84
3.3 Colony PCRs of <i>Synechocystis</i> with <i>Taq</i> or <i>Herculase</i> DNA polymerases.....	88
4.1 The effect of an upshift in salt concentration (18 mM→650 mM NaCl) On the autotrophic growth of Wild-type <i>Synechocystis PCC6803</i> .....	111
4.2 Hierarchical clustering of gene expression profiles.....	129-132
4.3 Polarographically measured rates of photosynthesis and respiration following salt shock of <i>Synechocystis PCC6803</i> cells.....	136
4.3 PAM Fluorometer measurements of PSII activity.....	138
4.5 Salt shock reduces quantum efficiency of PSII.....	139
4.6 Impact of salt shock on P700 content and P700 <sup>+</sup> re-reduction kinetics.....	142

LIST OF FIGURES CONTINUED

4.7 Salt shock induced superoxide production.....143

4.8 Superoxide production during salt shock requires PSII activity during  
autotrophic growth.....145



## NOMENCLATURE

DNA	deoxyribonucleic acid
RNA	ribonucleic acid
DCMU	3-(3,4-dichlorophenyl)-1,1-dimethylurea
DCBQ	2,5-dichloro-1,4-benzo-quinone
PSI	photosystem I
PSII	photosystem II
DEPC	diethyl pyrocarbonate
DTT	dithiothreitol
ATP	adenosine triphosphate
GTP	guanosine triphosphate
TTP	thymidine triphosphate
CTP	cytidine triphosphate
aa-dUTP	amino-allyl deoxyuridine triphosphate

**CHAPTER I**  
**LITERATURE REVIEW**

Bradley L. Postier and Robert L. Burnap  
**Functional Genomics of Plants and Fungi**

## CYANOBACTERIAL SYSTEMS

Some of earth's oldest fossils derive from cyanobacteria-dominated mats that filled the shallow Archaean seas over 3.5 billion years ago (52). A significant factor in the ecological success of the cyanobacteria was likely to have been the evolutionary invention, presumably within the cyanobacteria or their evolutionary antecedents, of the photosynthetic H<sub>2</sub>O-splitting mechanism. This enzymatic innovation enabled the use of H<sub>2</sub>O as a source of electrons to satisfy the demand for reductant that is required for the biosynthetic processes and thus, for organismal growth and proliferation. Prior to this innovation, reductant for assimilatory metabolism must have been obtained from other external sources such as the Fe<sup>2+</sup>, H<sub>2</sub>S or abiotically generated reduced organic compounds postulated to have been accumulated via chemical and photochemical processes occurring early in earth's history. The consequence of the innovation of using H<sub>2</sub>O as a source of electrons was the gradual accumulation of oxygen in the early earth's atmosphere due to the release of molecular oxygen, O<sub>2</sub>, which is the principal waste product of the light-driven H<sub>2</sub>O-splitting reaction. The rise of oxygenic photosynthesis thereby transformed the earth's atmosphere from that of a reducing environment containing trace levels of geochemically generated oxygen to one in which oxygen became freely available. With the ability to tap into a virtually limitless supply of electrons (H<sub>2</sub>O) to sustain anabolic metabolism, the prokaryotic oxygenic photosynthesis, perhaps due largely to the cyanobacteria, became the base of ecosystem productivity in the Archaean world and at the same time set the stage for the advent of aerobic respiratory metabolism as the dominant mode of heterotrophic existence. To this day, cyanobacteria remain one of the largest and most diverse groups of eubacteria and

accordingly occupy a variety of key positions within the biosphere. Furthermore, if one considers the likelihood that the chloroplasts of all extant and extinct plant and algal species are indeed the specialized descendents of endosymbiotic cyanobacteria of the Cambrian epoch, the centrality of the cyanobacterial lineage to past and current global primary productivity can be appreciated. From a practical perspective, the genetic affinities between cyanobacteria and chloroplasts, has rendered cyanobacteria as models of plant-like photosynthesis, with the noted exception of the lack of enzymes to synthesize chlorophyll *b* in most cyanobacteria. As discussed below, this has provided a genetic resource for the elucidation of metabolic pathways that have proven otherwise difficult to clarify using traditional genetic and biochemical approaches in the more complex plant systems.

As prokaryotes, cyanobacteria do not contain *bona fide* membranous sub-cellular organelles. However, cyanobacteria generally exhibit a high degree of sub-cellular structure when viewed with an electron microscope. The ability of some species to differentiate into different cell types, such as the nitrogen-fixing heterocyst cell-type of the filamentous genera, extends the range of internal complexity (61). Cyanobacterial cells typically possess an extensive internal membrane system, termed thylakoids, observed in a variety of species-specific arrangements, often appearing in thin section electron micrographs as concentric rings of appressed membrane pairs that are immediately beneath the cytoplasmic membrane and surround the central cytoplasm (21). The pairs of appressed membranes enclose the thylakoid lumen, analogous to the situation found in higher plant chloroplasts. As in higher plants, the thylakoid

membranes contain the photosynthetic machinery, but unlike higher plants the thylakoid membranes also contain an extensive set of multi-protein complexes associated with respiratory metabolism including NADH dehydrogenase and cytochrome *c* oxidase. The production of the thylakoid increases the total cellular membrane surface area several fold and permits increased numbers of membrane-bound photosynthetic complexes to form. Recent evidence suggests that the thylakoids are formed, or at least expanded, by fusion of vesicles originating from the surrounding cytoplasmic membrane. On the cytoplasmic surface of the thylakoid membranes, are numerous structures, termed phycobilisomes, which are large pigment-protein complexes composed of water-soluble phycobiliproteins and serve as light-harvesting antennae for the photosynthetic reaction centers. Phycobilisomes are found in all cyanobacterial groups with the exception of the genus *Prochlorococcus*, which, as discussed below, have replaced the phycobilisome with intrinsic, membrane-bound, light-harvesting antennae<sup>1</sup>. Another photosynthetic structure visible by electron microscopy is the polyhedral body, termed the carboxysome, which is the site of carbon fixation and, accordingly, is composed primarily of the major carbon-fixing enzyme, ribulose biphosphate carboxylase-oxygenase (36). Other sub-cellular inclusions visible in electron micrographs are cyanophycin granules composed of a copolymer of aspartate and arginine. Cyanophycin and phycocyanin are both used extensively as nitrogen reserve molecules, with the latter often comprising up to 50% of the total cellular protein content (4). In broad morphological terms, cyanobacteria occur either as unicellular or as multicellular, filamentous forms. In addition to being major

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<sup>1</sup> While Prochlorophytes do not assemble phycobilisomes, genomic sequence analyses indicate the presence of intact phycobiliprotein genes. Features such as this supports the close taxonomic affinities between the phycobilisome-containing cyanobacteria and the Prochlorophytes deduced from rRNA sequence analyses. As discussed below, this contrasts with earlier expectations that the Prochlorophytes represent a separate prokaryotic group that split from the cyanobacterial line and subsequently produced representatives that gave rise to green plant and algal chloroplasts.

contributors to the fixation of carbon through photosynthesis, cyanobacteria occupy key positions in many ecosystems owing to the ability of some species to fix nitrogen. Examples of nitrogen fixation are found in both morphological forms, with some filamentous cyanobacteria differentiating specialized cell types (heterocysts) to isolate the  $O_2$ -sensitive N-fixing enzyme (nitrogenase) from the  $O_2$ -yielding photosynthetic reactions and the unicellular forms achieving the separation temporally by performing N-fixation at night or at periods of low light to avoid  $O_2$  poisoning of the nitrogenase (9).

While oxygenic photosynthesis is their primary source of energy, a number of cyanobacterial species are capable of utilizing external carbon such as glucose, glycerol and amino acids to supplement their endogenous photosynthetic and metabolic capabilities. In some cases, these capabilities have been utilized to enhance the genetic and biochemical analysis of these organisms. For example, the endogenous or selected capability of using glucose as an exogenous energy and carbon source has been used to rescue otherwise lethal mutations in the photosynthetic apparatus. The photosynthetic mechanisms involving the light-driven electron transport reactions and  $CO_2$  fixation via the Calvin cycle are highly homologous to the corresponding processes in higher plants and algae and, accordingly, the corresponding genes reflect these deep similarities.

While amino acid sequence identities between core photosynthetic proteins of higher plants and cyanobacteria are generally very high and in the range of 60-90% sequence identity, the more peripheral components of the mechanism are typically less conserved or even entirely different. The light-harvesting antennae of the reaction

centers are a good example of this divergence. In the case of higher plants, virtually all light harvesting is carried out by the intrinsic light-harvesting chlorophyll protein complexes (LHCs), whereas in cyanobacteria and red algae this function is generally carried out by very large peripheral membrane protein complexes termed phycobilisomes. On the other hand, another genus of cyanobacteria, the *Prochlorococcus*, lacks phycobilisomes and, like higher plants, relies upon intrinsic membrane protein complexes that contain chlorophyll *b*. Initially, this similarity was thought to indicate that the Prochlorophytes descended from the same line that gave rise to modern green algal and higher plant chloroplasts and, conversely, that phycobilisome-containing cyanobacteria gave rise to the chloroplasts of red algae. However, closer analysis of the chlorophyll pigment-protein complexes revealed that the genes of the membrane-bound chlorophyll-protein complexes bore little resemblance to the higher plant complexes and indeed, were most closely related to a stress-induced protein termed *isiA* (iron-stress induced) found in the phycobilisome-containing cyanobacteria (57). These findings and consideration of the enzymatic simplicity of producing chlorophyll *b* from chlorophyll *a*, has led to the conclusion that the appearance of chlorophyll *b* probably occurred independently in several species lines during the course of evolution and, perhaps, occurred following the endosymbiosis event that led to modern plant chloroplasts. This 'post-endosymbiosis' hypothesis for the evolution of the modern higher plant and green algal type of LHCs is consistent with phylogenetic analyses which find the phycobilisome-containing endosymbionts/chloroplasts of the taxonomically enigmatic *Cyanophora paradoxa* as sharing the last common ancestor of both the cyanobacteria and chloroplasts. This has implications regarding the similarities and

contrasts between the higher plants and cyanobacteria discussed below, since it is therefore incorrect to assume that closer homologs to higher plant genes would be found in the Prochlorophytes rather than in other cyanobacteria.

## GENOMICS

According to the National Center for Biotechnology Information (NCBI) at the National Institutes of Health, over 800 full genome sequences including 172 Eukaryota, 112 Bacterial, and 13 Archaeal are complete, or "in process" and have been submitted to their database as of the summer of 2001. In this increasingly data-rich environment, the ability to efficiently analyze and find meaningful patterns to specific research problems is obviously a critical task. One important consideration regarding the utility of the cyanobacterial sequences obtained is the phyletic diversity of genomes analyzed. While the choice of genomes to be sequenced inevitably reflects consideration of its use as a model system in the scientific community, happily these choices are also reflecting fundamental scientific issues in regard to the type of information that can be obtained due to phyletic position. The choice of the first sequenced cyanobacterium (for example see (34)), *Synechocystis* sp. PCC 6803 (hereafter referred to as *Synechocystis*) depended, to a large measure, on its widespread, although not exclusive use as a cyanobacterial model system for the study of the oxygenic photosynthetic mechanism (22, 62). On the other hand, choices for the subsequent cyanobacterial genomes that have been sequenced and those in process also reflect additional evolutionary and physiological considerations. In the case of the six cyanobacterial genomes now available and discussed below, comparative information will undoubtedly be developed based upon these additional



considerations. Moreover, the utilization of diverse sequences will enable not only better comparisons within the currently sequenced cyanobacterial genomes, but also with other prokaryotes as well as higher organisms such as the fully sequenced plant model *Arabidopsis thaliana* and the green algal model *Chlamydomonas reinhardtii*, which is being sequenced. It is apparent, for example, that the cyanobacterial genomes contain significant numbers of genes for two-component regulatory systems and ABC-type transporters (35) that may be meaningfully compared with better characterized genes in other bacteria in order to infer testable hypotheses regarding function (42). At the same time, the recently sequenced *Arabidopsis* genome contains both two-component regulatory genes and ABC transporters, the latter of which occur in large numbers. This raises the question as to the extent that the cyanobacterial models can be used to explore hypotheses regarding the function of genes such as these in making inferences regarding the function of the higher plant homologs.

Currently, six cyanobacterial genomic sequences are available at least in part: the freshwater unicellular species *Synechocystis* mentioned above, the marine species *Synechococcus marinus*, two ostensibly similar marine strains of *Prochlorococcus* isolated from different depths, and two filamentous *Nostoc* species capable of differentiation and nitrogen fixation. As mentioned above, *Synechocystis* has been extensively used for detailed molecular analysis of the enzymes and regulatory features underlying oxygenic photosynthesis. Important for this purpose, *Synechocystis* is capable of photoheterotrophic growth which allows the construction and rescue of otherwise lethal mutations in the photosynthetic mechanism (62). Additionally, *Synechocystis* is

easily transformable with exogenous DNA and undergoes homologous double cross-over recombination (62). This has permitted a number of genetic strategies such as replacement of Wild-type alleles with copies that are mutated in-vitro, allowing the study of structure-function relationships of target proteins (22, 30, 38, 40, 46, 59, 62). When combined with isotopic labeling, this has allowed the detailed analysis of the function of specific parts of the photosynthetic reaction centers down to the level of individual atoms comprising catalytic amino acid side chains (8, 15, 18, 27, 44). Additionally *Synechocystis* is capable of growth under a variety of conditions including high and low salt, light, and temperature (5). As with other photoautotrophic strains, it must respond to the environment and adapt the photosynthetic and metabolic machinery to balance energy production with CO<sub>2</sub> fixation and other energetically demanding activities such as the maintenance of transmembrane ion homeostasis. Considering the relative ease of protein and genetic manipulation in addition to its diverse mechanisms of adaptation identifies this strain as a valuable prokaryote for functional genomics.

Marine *Synechococcus* strains occupy a variety of important niche positions in oceanic and coastal marine environments and figure prominently in the marine food webs (60). A few *Synechococcus* strains are well studied for their enigmatic mechanism of motility. They are capable of traveling in a gliding motion at up to 25  $\mu\text{m sec}^{-1}$  and use no microscopically obvious extracellular machinery for this activity. Most importantly it is taxis, not to light, but to trace metals and nutrients at concentrations  $10^{-9}$  to  $10^{-10}$  M in accordance with the paucity and/or patchiness of nutrients often existing in its marine habitat. Compared with freshwater species, the obligate marine *Synechococcus marinus*

strain requires high  $\text{Na}^+$ ,  $\text{Cl}^-$ ,  $\text{Mg}^{2+}$ , and  $\text{Ca}^{2+}$  concentrations for growth, which, when considered together with the other features, makes it a model for nutrient sensing and chemo-tactic motility as well as for the study of photosynthetic capacity in marine environments (6, 7).

*Prochlorococcus* strains may contain the smallest genomes, around 2 Mb, of all known photoautotrophic organisms. They dominate the temperate and tropical oceans and are speculated to contribute a significant fraction of the photosynthesis in the world's oceans making them an important factor in global carbon cycling and the Earth's atmospheric fluxes of carbon dioxide and oxygen (10, 58). In addition to chlorophyll *b*, they also contain an unusual combination of divinyl derivatives of chlorophyll *a*,  $\beta$ -carotene, zeaxanthin, and a type of phycoerythrin. Two ecotypes of *Prochlorococcus* have been sequenced. According to the Department of Energy's Joint Genome Institute (DOE JGI), strain MED4 is observed at greater depths than the strain MIT9313. While these two strains representing the two ecotypes have been sequenced, annotation of only MED4 is complete. At first glance, the two genomes differ in several respects including a 0.3 Mb range in size from 1.8 to 2.1 Mb and a highly contrasting G+C content.

*Nostoc punctiforme* and *Anabaena* are two representatives of the filamentous Nostocales, which are capable of differentiating into four cellular types. The vegetative state is most common and is responsible for asexual reproduction and general metabolism under normal conditions. Heterocysts are specialized cells capable of fixing dinitrogen. Akinetes are spore-like bodies, which develop under growth-limiting conditions.

Finally, hormogonia are short fragments of filaments capable of motility. Nostocs are found in freshwater and tropical, temperate, and polar terrestrial systems, and can also be found rarely in marine samples (47).

### *Sequence Comparisons and Statistics*

*Synechocystis* was the first cyanobacterium to have its complete genome sequenced. When the sequence was first completed, 3168 potential proteins were identified, of which nearly 40% still are not linked to characterized proteins with specified biological activity as seen in Table 1.1. Table 1.1 is a compilation of data from several database resources including the DOE-JGI (<http://www.jgi.doe.gov/>), Integrated Genomics database "ERGO" (<http://integratedgenomics.com/>), and Cyanobase (<http://www.kazusa.or.jp/cyano/cyano.html>). Many of the genes coding for metabolic functions could be categorized, and *Synechocystis* has already been a valuable resource for the study of photosynthesis, respiration and the biosynthesis of prosthetic groups and the like. In addition, 80 genes for two-component signal transduction have been identified. These have become interesting targets for knock-out mutagenesis and phenotypic analysis, as *Synechocystis* is known for its capacity to acclimate to changing environments, possibly using two-component regulatory systems (54).

First comparisons of these five genomes reveal a number of distinguishing characteristics. *Prochlorococcus* strains appear as good examples of what may prove to be among the smallest genomes of photoautotrophic organisms. These strains have developed a niche in which they are highly competitive and are postulated to be the most

	<i>Prochlorococcus marinus</i> (MED4)		<i>Synechococcus marinus</i>		<i>Synechocystis PCC6803</i>		<i>Anabaena</i>		<i>Nostoc punctiforme</i>	
	Total	% Total	Total	% Total	Total	% Total	Total	% Total	Total	% Total
Length, Mb	1.67	---	2.75	---	3.57	---	7.20	---	9.22	---
Coding sequence, Mb	1.4	85.9	2.1	75.2	3.1	86.7	5.8	79.8	7.2	77.9
G+C content	---	30.90	---	58.46	---	47.20	---	41.20	---	41.50
total orfs	1645	---	2447	---	3356	---	5826	---	7569	---
orfs with assigned function	1128	68.6	1358	55.5	1978	58.9	3281	56.3	3158	41.7
hypothetical orfs	70	4.3	46	1.9	1262	37.6	191	3.3	83	1.1
Orfs with no assignment	447	27.2	1043	42.6	116	3.5	2354	40.4	4328	57.2

**Table 1.1 Statistical summaries and comparisons of cyanobacterial genome sequencing efforts.** Data for this table was compiled from 3 database resources; ERGO, Cyanobase, and the DOE JGI as referenced in table 1.2.

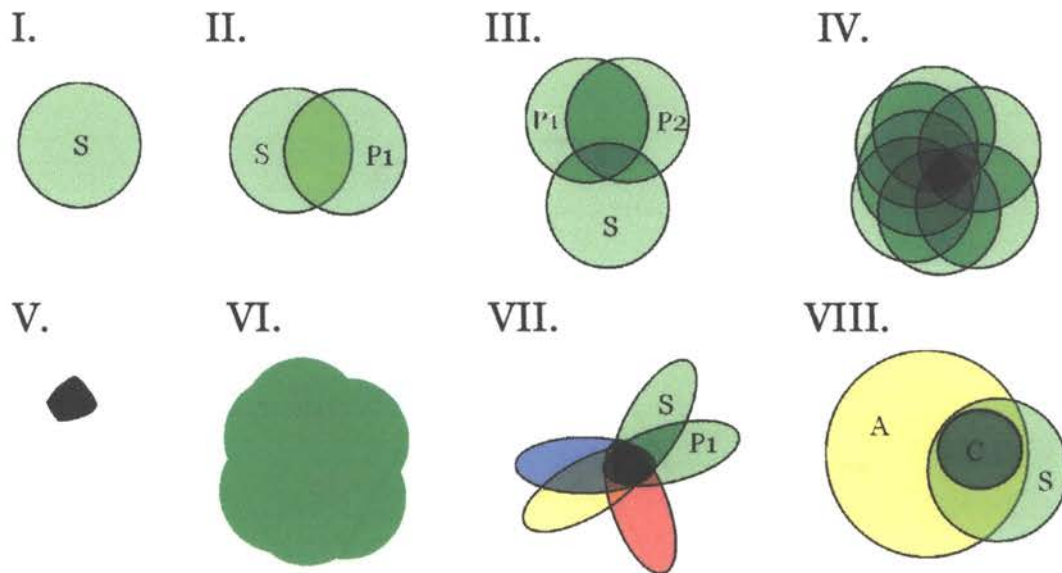
abundant photosynthetic organisms on earth and contribute a large fraction of the ocean's primary productivity (45). However, they lack the ability to survive well outside of it, possibly due to their streamlined genome which accompanies their exceedingly small cellular dimension ( $<1 \mu\text{M}$ ). Notice the linear relationship between genome length and the number of open reading frames. The two *Nostoc* genomes are nearly five times greater in length and in number of open reading frames maintaining a similar coding sequence percentage. Each of these genomes are densely packed with coding information, averaging from one open reading frame per thousand bases, in the finished *Prochlorococcus* MED4 strain, to at most one open reading frame in 1218 bases in *Nostoc punctiforme*. Interestingly, the two *Prochlorococcus* strains have widely different G+C contents (data not shown), with that of MIT9313 falling closer to the *Synechococcus* strain. *Synechocystis* has a larger proportion of hypothetical genes (genes with no functional assignment) than the other organisms. This may be due to the differences in orf prediction matrices used to analyze the genomes and their default functional assignment cutoff values or to the fact that when it was sequenced, fewer genome sequences were available for comparison. Also, it is likely that different definitions of "hypothetical" are used between the various databases. Cyanobase annotates all genes with slight to no apparent sequence similarity to previously characterized genes from Genebank as hypothetical genes. ERGO however defines them as unknown genes and assigns a hypothetical class to them if they are loosely associated to another characterized gene. Differences such as these also might contribute to the discrepancy between the total number of open reading frames assigned by each of the databases, as ERGO includes an additional 188 open reading frames. Interestingly, the two *Nostoc* strains

have a larger supply of genes with no known homologs. This makes them excellent resources for novel genes and protein products. Other obvious findings include the development in the organisms with larger genomes, of more functional divergence such as cell differentiation, filamentation, and nitrogen fixation. All of these presumably require additional genetic information.

### *Comparative Genomics*

Comparative genomics is literally the study of comparing two or more genomes either through nucleic acid or amino acid sequence similarity and dissimilarity or through mapping gene positions, analysis of gene function, and studies on evolution. A principal aim is to study all of these aspects and develop an understanding of how to link genotype with phenotype (12), and understand the evolution of entire ensembles of genes which may move *en block* across species barriers through 'horizontal' gene transfer mechanisms. An example of this type of analysis with cyanobacteria, still in its early stages, was presented recently by Chisholm et al. at the latest Cyanobacterial Workshop (49). This work requires the sequencing and analysis of complete genomes for the DOE JGI focusing on two *Prochlorococcus* genomes. Nearing completion of the sequencing and analysis of the second strain, direct comparisons of gene amino acid sequence similarity enables the clustering of genes based simply on their presence or absence from each of the two organisms or from other cyanobacterial genomes such as *Synechocystis* PCC6803.

Figure 1.1 illustrates several examples of how genes are clustered in this manner. This analysis begins with the first completed sequenced genome as depicted by I. Once a



**Figure 1.1 Venn diagram presentation of genome homology clustering with various genome sequencing projects.** Each circle represents a sequenced genome. The overlapping areas of two or more circles represents the amount of homology between those genomes. Parts I-VI represent the accumulating results of sequencing efforts on cyanobacterial genomes. Parts VII and VIII depict the relationships between all cyanobacteria and other sequenced organisms such as other bacterial species or *Arabidopsis* and it's chloroplast genome. A) *Arabidopsis* genome, C) Chloroplast genome, P1) *Prochlorococcus* genome 1, P2) *Prochlorococcus* genome 2, S) *Synechocystis* genome



second genome is complete, the total contents of both are compared through homology of each gene's amino acid sequence to its counterpart's genome and scored for hits based on a predetermined level of sequence similarity required to specify two genes as orthologs. Example II could represent the genomes of *Synechocystis* PCC6803 and *Prochlorococcus* MED4, with the area of overlap representing the number of orthologous genes present. These two cyanobacteria are moderately related and a large number of genes may show homology as shown here with two overlapping circles. Some examples of orthologous genes might encode for the photosynthetic complexes or for common metabolic pathways such as lipid biosynthesis or conserved regulatory genes. Clearly, this analysis depends on the sequence similarity cut-off values employed to score pairs of genes as orthologous. Extending this analysis to include three genomes, now including the *Prochlorococcus* strain, MIT9313, is shown in hypothetical example III. The two strains of *Prochlorococcus* represented by the top two circles show much more extensive homology with each other than either show toward *Synechocystis*. In addition, *Synechocystis* has many more genes showing no homology to either *Prochlorococcus* strain, even while there are still many examples of non-orthologous genes between the two *Prochlorococcal* strains, denoted here by the light green areas of each circle. As a result of increasing the stringency for scoring hits, the amount of overlap between *Synechocystis* and *Prochlorococcus* MED4 would be less than that depicted in II. Patterns such as this might aid in phylogenetic analysis and, in principal, should tend to reflect phylogenetic trees based upon rRNA sequence analysis if the extent of horizontal gene transfer is minimal. However this is probably not a valid assumption when considering prokaryotic systems. Possibly, more cases of horizontal gene transfer would

become apparent as more genomes from cyanobacteria are sequenced and it becomes possible to develop a situation such as that represented by IV. Two important components of IV are the focus of V which represents the core set of genes found in all cyanobacterial strains and VI which represents the total genetic variation of all cyanobacterial strains. As a result, IV might also suggest which strains are more susceptible to horizontal gene transfer and which are incapable. Additionally, two distantly related cyanobacterial strains shown in green in VII are depicted as they would relate to other organisms whose genomes have been sequenced. This demonstrates how they each have evolved by building on the successes of a small class of genes. This highly conserved class might be well represented by DNA replicase, ribosomal proteins, and tRNAs. In a more complex variation, VIII depicts the relationship between a cyanobacterium, *Arabidopsis*, and its chloroplast. It would be intriguing to find out how the set of highly conserved "core" genes compare to chloroplast and plant genomes, unfortunately we must better define that "core" before those hypotheses can be made.

A common result from every sequencing project thus far has been the assignment, depending upon the stringency criteria applied, of roughly 25% of each genome with no discernable sequence homology to gene sequences already deposited in the databases<sup>2</sup>. These genes are typically characterized as hypothetical, unknown, or unique genes. On the surface it would appear as if every genome therefore carries a large portion of novel and therefore uncharacterized genes. However, it is possible that some amino acid

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<sup>2</sup> The following argument was first brought to the attention of the authors during a presentation by Prof. Don Bryant of the Pennsylvania State University. The analysis of the proteases is based upon a talk given by Prof. W. Pearson and given in the World Wide Web address: [http://www.people.virginia.edu/~wpr/talk95/prot\\_talk12-95\\_17.html](http://www.people.virginia.edu/~wpr/talk95/prot_talk12-95_17.html)

sequences have diverged to the extent that statistically significant sequence homologies are no longer detectable and yet still retain a high degree of tertiary structure homology. In short, a protein's structural conservation might be enough to maintain function even in the face of quite radical sequence divergence and evolution. As a result, many of the genes with no sequence homology may actually have functional homology to known and well characterized genes. For example, three members of the serine protease superfamily are clearly homologous at the tertiary structure level and in terms of the catalytically active residues of the active site. Nevertheless, two of the structurally homologous proteases, bovine chymotrypsin and *Staphylococcus griseus* trypsin, share strong sequence similarity (expectations values smaller than  $\sim 10^{-20}$ ) while the third related sequence, *Staphylococcus griseus* protease A, has a very low sequence similarity score compared to the others (expectation values greater than 10). Given these considerations, it is possible that a large proportion of the hypothetical genes from related species are truly orthologous and in fact are still functionally related despite the loss of coherent similarity at the primary amino acid sequence level. As a result it will be impossible to determine evolutionary links or protein function through sequence analysis for many of these genes.

#### *Gene analysis tools: Beyond the Blast*

There are already a great variety of bioinformatic tools available on the Internet that one can use to identify biologically important genes or proteins. Table 1.2 is a partial list of sites used frequently for such analyses. The availability of these databases and

<b>Provider/service</b>	<b>Web link</b>
National Center for Biotechnology Information	<a href="http://www.ncbi.nlm.nih.gov">http://www.ncbi.nlm.nih.gov</a>
The Institute for Genomic Research	<a href="http://www.tigr.org">http://www.tigr.org</a>
Kyoto Encyclopedia of Genes and Genomes	<a href="http://www.genome.ad.jp/kegg/">http://www.genome.ad.jp/kegg/</a>
DOE Joint Genome Institute	<a href="http://www.jgi.doe.gov/">http://www.jgi.doe.gov/</a>
Pedant	<a href="http://pedant.gsf.de/">http://pedant.gsf.de/</a>
Mips	<a href="http://mips.gsf.de/">http://mips.gsf.de/</a>
Integrated Genomics	<a href="http://www.integratedgenomics.com/">http://www.integratedgenomics.com/</a>
SDSC Biology Workbench	<a href="http://workbench.sdsc.edu/">http://workbench.sdsc.edu/</a>
Cyanobase (KDRI)	<a href="http://www.kazusa.or.jp/cyano/cyano/html">http://www.kazusa.or.jp/cyano/cyano/html</a>

**Table 1.2 Abbreviated list of web based genomic information services.**

their powerful techniques are designed for use without an extensive background in writing computational algorithms. This allows the biologist to investigate without the need for programming skills. Tools are currently available for sequence alignments, hydrophathy profiles, and domain analysis. Also available are protein motif and secondary structure assignment algorithms.

Prokaryotic organisms possess an operonic structure for transcriptional expression of genes linked to the same metabolic pathway, thus enabling the regulation of entire pathways with one promoter. Even where polycistronic mRNAs are not produced, functionally connected genes sometimes remain physically connected at the same chromosomal region, perhaps shuffled in order. As a result, the gene order or proximity of functionally related genes for a particular pathway may be preserved. Therefore, the existence of patterns of gene clustering and gene order alignments allow the generation of hypotheses on unknown gene function on the basis of physical association with better defined genes. Importantly, there are multi-genomic bioinformatic approaches exploiting this type of conserved gene clustering. The motivation for these tools is to provide clues to the function of unknown genes even if they themselves are not clustered with functionally related genes in the species they are found in. Integrated Genomics Inc. offers a database called ERGO available at their website referenced in Table 1.2. After selecting a gene of interest in the database, it is possible to use a query tool providing analysis of regions of conserved gene order and clustering among related species. This clustering tool, allows ready access to information regarding the clustering of orthologous genes around the query gene. These so-called "pinned regions" may be conserved

operons found across more than one species and thus consist of stretches of genomic sequence from two or more organisms containing more than one orthologous gene when the corresponding stretches of DNA from the different species are compared. In some cases, gene order is preserved, whereas in other cases, the gene order is rearranged, yet the clustering remains. In other cases, one or more of the genes present in the operon of one species has been lost from the corresponding region in the other species. These typically are found in closely related organisms, but in the case of several ribosomal protein complex genes, are common to many of the prokaryotes.

Researchers in many areas of plant biology are utilizing the cyanobacterial databases to search for homologous proteins with specific enzymatic activities. This is particularly important for proteins involved in chloroplast structure and function, e.g., chloroplast envelope proteins, protein translocation systems, phytochromes, vitamin synthesis, and ion uptake. For example, Shintani and Della Penna describe the introduction of the *Synechocystis* gene  $\gamma$ -tocopherol methyltransferase ( $\gamma$ -TMT), important in the metabolic processing of  $\alpha$ -tocopherol (vitamin E), into *Arabidopsis* seeds increasing vitamin E production (53). Here they have used the sequence from a cloned carrot gene called *p*-hydroxyphenylpyruvate dioxygenase (HPPDase) known to be involved in the metabolic pathway of vitamin E synthesis. From the sequence of the carrot HPPDase gene, they identified the *Synechocystis* ortholog slr0090. Through gene clustering, they were able to identify a candidate open reading frame slr0089 for  $\gamma$ -TMT, which was immediately upstream of the ortholog to carrot HPPDase. This gene ( $\gamma$ -TMT) was capable of increasing vitamin E production once cloned and expressed in

*Arabidopsis* seeds. Currently, only a few examples exist for using cyanobacterial genes for metabolic enhancement of other organisms. However, given the diversity of genes in the five sets of genomic sequences from cyanobacterial strains, efforts in these areas will undoubtedly continue for some time.

### FUNCTIONAL GENOMICS IN A CYANOBACTERIUM

Recent advances in technology have given rise to techniques that take advantage of the availability of full genome sequences and provide vast amounts of information in a short period of time. With the development of the Internet-based databases, the wealth of genomic sequences, and the diverse set of bioinformatic tools available, it is now possible to make a large number of hypotheses concerning the functions of the multitude of genes revealed through sequencing efforts. Assignment of gene function, referred to as 'annotation', is a predictive tool and thus, the annotations are essentially a set of hypotheses. This is fundamentally different from the initial stages of molecular database formation. In the early stages, individual gene sequences were typically deposited by one research group that had isolated the gene following extensive characterization (e.g. enzymatic activities) or on the basis of the physical characterization of mutants for which detailed phenotypic information had been developed. Consequently, the reliability of the deposited gene annotation had the strength of the associated biochemical and genetic characterizations preceding it. The genomic sequence era now inverts this process and at the same time builds upon the earlier and concurrent biochemical and genetic characterizations to generate the hypothetical gene function assignments. While bioinformatic approaches are excellent at predicting biological function and generating hypotheses, it is obviously important to test these hypotheses. In the case of

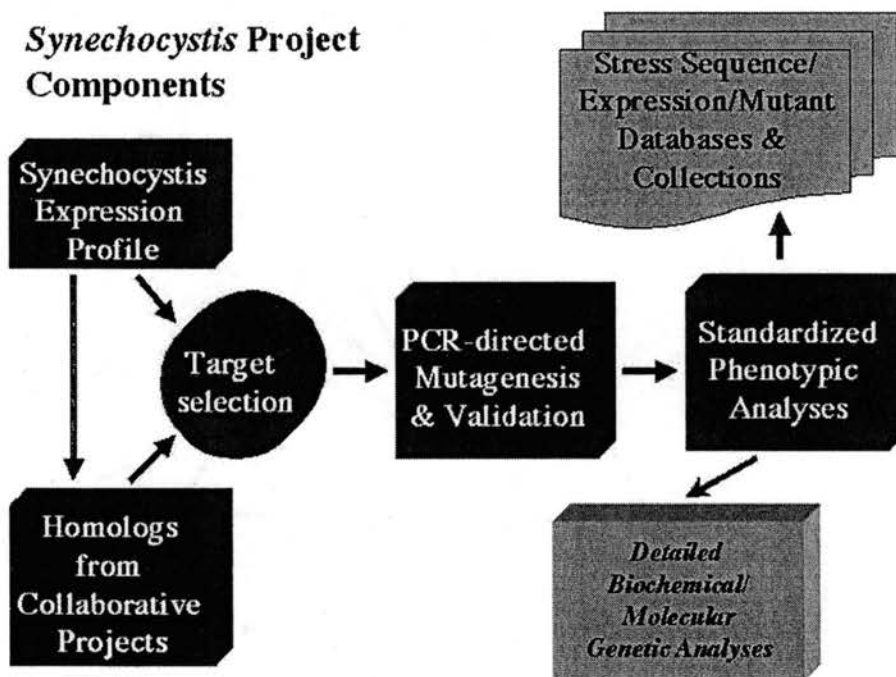
*Synechocystis* sp. PCC 6803, one such strategy combines the use of various technologies including gene expression arrays, PCR-mediated knock-out strategies, and high-throughput screening of mutants for functional analysis of the *Synechocystis* genome as is demonstrated below. The strategy diagramed in figure 1.2 exemplifies the types of technologies necessary to perform molecular biological analysis on a genomic scale. An explanation with illustrations of the techniques used and some of the information gathered help develop the concepts.

*Application of functional genomics to a physiological problem:*

*Salt stress in cyanobacteria*

Salt stress in cyanobacteria remains poorly understood at the molecular level, although classical mutational approaches have recently identified a set of structural genes important for coping with this stress. *Synechocystis* represents an excellent model for osmoregulation since it tolerates up to 1.2 M NaCl. From a physiological point of view, salt stress adaptation in cyanobacteria is a rich phenomenon with a characteristic sequence of events that ensue immediately following an initiation of salt shock and proceeding over the course of 24 to 48 hours as the cells adapt to the new regime. The physiological adjustments to hypertonic and hypersaline environments are multifold and include changes in the expression of photosynthesis- and respiration-related enzymes and the induction of several categories of stress proteins (1, 14, 19, 20, 26, 31, 32). These changes can be followed using fluorescence and spectroscopic methods, which are capable of reporting on a variety of parameters ranging from the relative concentrations and activities of the photosystems to changes in the soluble pools of reduced substrate in





**Figure 1.2 Functional genomics strategy for *Synechocystis* PCC6803** This concept will be expanded further in later chapters.

the cytoplasm. This allows for real-time detection of several physiological changes in a non-invasive manner.

Acquisition of tolerance is, in part, effected through the accumulation of the osmolyte glucosylglycerol, by *de novo* synthesis (23). Mutant analysis has provided insight regarding the role of two genes expressed in response to salt shock. *StpA* encodes glucosylglycerol-P phosphatase involved in the salt-induced accumulation of glucosylglycerol. *GgtA*, *B*, *C*, and *D* encode subunits of an ABC-type transporter which permits the maintenance of high levels of solutes in the cytoplasm by recovering leaked glucosylglycerol (24, 25, 41). At this stage, clear functional homologs to the *Omp* system of genes have not been identified (nor have *envZ* homologs) in *Synechocystis*, although multiple members of the conserved OmpR subfamily of regulatory molecules are present in the genomic sequence.

As mentioned above, many of these genes were identified through time-consuming random mutagenesis, screening and cloning projects. Now with multiple genomic sequences available it is possible to identify their orthologs in other cyanobacteria with sequence comparison algorithms such as Blast (2). It seems likely that this procedure will not identify novel proteins, yet it still remains one of the most useful tools when comparing two or more genomes. Moreover, this strategy is prone to difficulties in accurately predicting functions of the homologs. Predicted regulatory proteins such as the approximately 80 two-component histidine kinase proteins found in *Synechocystis* show very high deduced amino acid sequence similarity, but are activated

by quite different environmental and physiological signals. Thus, the similarity analysis provides only a very superficial assessment of function (56).

Another example where sequence similarity may be confusing is in the case of  $\text{Na}^+/\text{H}^+$  antiporters. Here, very high sequence similarity is observed, but each functions quite differently as each is responsible for ion homeostasis under different conditions. One transporter may be responsible for maintaining cytoplasmic ion concentrations under high-salt or low-pH conditions, while another is responsible for low-salt or high-pH conditions. Only through direct molecular and biochemical techniques is it possible to decipher how subtle differences in sequence determine functionality (37).

Nevertheless, genomic sequence data can be exploited to facilitate these direct approaches, since the genomic data can be used to create mutants in the interesting genes, with great efficiency in some cases as discussed below. One important point, in regard to the transporters, is the relationship between the number of paralogous genes in the genome and the biological niche of the organism. The cyanobacteria colonizing soil or aquatic habitats that are more prone to fluctuations in ionic composition, compared to those inhabiting a marine environment, may contain more ion homeostasis genes. For example, *Synechocystis* and the two *Nostocs* contain more  $\text{Na}^+/\text{H}^+$  transporters than the *Synechococcus* or *Prochlorococcus* strains. It could be argued that since *Prochlorococcus* and *Synechococcus* are strictly marine and since marine conditions are largely invariant with respect to ionic composition, these species may not require as many ion transporters for maintaining ion homeostasis. This type of situation may, in turn,

account for the apparently small genome size in the *Prochlorococcus* and *Synechococcus* strains.

The goal of one current project taken up by the authors of this work is to develop techniques to investigate the role of any or all genes of the genome of *Synechocystis* PCC6803 as they pertain to salt stress. We have begun by identifying targets of interest in two manners. The sequences of known salt-responsive genes in higher organisms such as *Saccharomyces* and *Arabidopsis* were used in a Blast search against the entire genome of *Synechocystis*. A list of homologs or potential targets was generated from the results of the Blast search. In addition sub- and full-genome microarrays for differential gene expression were developed as described below. These arrays were used to screen total RNA from cultures before, and at various time points after salt shock for differential expression. The resulting differentially expressed genes are also added to the list of potential target sequences and those unaffected by salt shock were either removed from the list or put on a waiting list. The resulting list of genes was targeted for knock-out mutagenesis using a PCR-mediated method developed to eliminate cloning steps. The resulting strains were then subjected to a battery of tests in a microtitre dish format to investigate their relative physiological fitness compared to Wild-type strains. The information gathered in this manner is used to develop a database of the expression and physiological characteristics of each gene listed.

*DNA Microarrays*

With the growing availability of complete genomic sequences for scores of prokaryotic organisms, efforts have turned to the development of experimental approaches to measure transcription from a global perspective. DNA microarrays have emerged as a particularly effective tool for genome-wide transcript profiling, especially for studies examining eukaryotic organisms (16, 17, 48, 51). Information on the temporal patterns of accumulation and disappearance of transcripts for specific groups of genes is suggestive of cellular programs orchestrating these changes. A combination of knock-out mutagenesis of known or suspected regulatory loci coupled with microarray analysis should help elucidate the signal circuitry giving rise to programmatic changes in gene expression. Unfortunately, reports on the successful use of DNA microarrays for transcriptional profiles in prokaryotes have been sparse. As discussed below, this lag in the development of microarray technology for prokaryotes can be largely traced to technical issues associated with generating the high signal-to-noise ratio probes from non-poly (A) RNA (28). However, workable techniques are now available as demonstrated by the recent report from the Blattner lab as well as experience in other labs (R. Burnap et al.; A. Grossman et al., unpublished observations) (48).

DNA microarray technology uses microscopic, high-density arrays of DNA target elements immobilized to solid surfaces such as microscope slides. The DNA target elements typically represent specific gene sequences or sub-sequences that hybridize to cognate sequences in samples under investigation. There are currently two major types of DNA microarrays: oligonucleotide microarrays and DNA fragment microarrays.

Oligonucleotide microarrays generally utilize *in situ* oligonucleotide synthesis techniques that directly build individual DNA targets on the surface of the array. Such an approach is epitomized by the proprietary manufacturing methods of the Affymetrix Corporation, a successful, but extremely expensive, implementation. Alternatively, oligos on the average of 60 to 70 bases in length can be printed onto the surface in the same manner as printing larger PCR products or clones. The second type of array, the DNA fragment microarray, was initially pioneered for *Saccharomyces* by Brown at Stanford University and for *Escherichia coli* by Blattner at the University of Wisconsin. These arrays consist of PCR-amplified fragments either from Expressed Sequence Tagged (EST) project libraries or from sequencing information. This latter approach is more broadly accessible to academic and commercial labs and has been used to produce full genomic and sub-genomic microarrays for cyanobacteria.

Once constructed, microarrays are interrogated with fluorescently labeled DNA or RNA mixtures from biological sources, washed to remove background fluorescence, and scanned using laser confocal microscopy. A key advantage of the glass slide microarrays, compared to membrane-based, high density arrays hybridized with radioactive probe, is the ability to hybridize more than one fluorescently labeled probe to the same microarray. Typically, this capability is used to compare control and treated (e.g. un-induced and induced) samples. This feature allows a direct qualitative comparison of hybridization intensities on the same DNA, thus controlling for potential disparities in a given immobilized DNA spot between two replica microarrays. The magnitude of the fluorescence emission intensities from the control and treated samples

hybridized to a given DNA spot is then used to compute the corresponding hybridization signal ratio theoretically reflecting the relative abundance of the mRNA species in each sample. Obviously, this raises questions about how well the cDNA product of the labeling procedure reflects the population of mRNA that it is meant to represent and to what extent the labeling reaction generates non-specific background signal, which diminishes the sensitivity of the procedure. For reasons discussed below, these issues are especially acute for prokaryotic systems. What has probably been the greatest detractor in publication of microarray data is its reproducibility. Microarray hybridizations are very sensitive, and are susceptible to even the slightest differences in protocol. Most obviously, RNA purity can have a major impact on the final output. The production and hybridization of two target cDNA pools requires many steps where error can be introduced. Automated machines and molecular biology kits developed for just such a purpose have recently been developed and market decreasing user interface and therefore increased reproducibility. The greatest impact on results might be the experiment itself. The extent to which apparently subtle differences in cell culture result in significant variations in global transcriptional patterns remains to be evaluated. Preliminary indications suggest these variations may be quite pronounced (Prof. H. Pakrasi, personal communication). Therefore, the preliminary data presented here should be considered tentative, and accordingly, treated with caution.

Improved labeling, hybridization, and normalization techniques could solve most of the current problems with analysis of prokaryotic gene expression with DNA microarrays. One of the most difficult challenges relates to the lack of polyadenylated

mRNA. In the case of prokaryotic microorganisms, typical labeling conditions for production of cDNA involve the use of random oligos. The final result is a cDNA pool, which is rich in ribosomal RNA complement. The abundance of ribosomal cDNA nonspecifically binds across the surface of the array. This prevents the analysis of many genes present at low concentrations in the pool including important regulatory proteins, which may or may not respond to a change in conditions. New techniques are being developed to circumvent such problems. One such attempt uses arbitrary primers, or a small nonrandom pool of specific primers capable of preferential binding to only mRNA sequences during cDNA production, thus eliminating the production of labeled ribosomal cDNA (55). Unfortunately, without a large pool of oligos it is difficult at best to determine the amount necessary to gain an excess coverage of all transcripts and still not bind to rRNA. Alternatively, all oligos annealing to the 3' end of the open reading frame used for the original amplification of fragments for the array could be pooled and used in the reverse transcription reaction. However, this is not possible if oligonucleotide arrays were produced.

### *Cyanobacterial Microarrays*

The first cyanobacterial microarrays, "Cyanochips", were produced for *Synechocystis* in Japan via a commercial arrangement. The microarrays were used by Ikeuchi et. al. to follow global patterns of gene expression as a function of time in response to changing light regimes and by the Murata group to investigate cold-responsive genes. The latter study included the parallel comparative analysis of Wild-type and mutant cells that have a deletion in a histidine kinase gene previously shown to



control the expression of cold-responsive lipid desaturase genes. The Ikeuchi work provides an evaluation of the sources and level of errors in their experiments, and they were able to generate data on a large fraction of genes. Their results agree with other published works for the most part, and have validated the use of microarrays for gene expression in cyanobacteria. Sub-genomic DNA microarrays for *Synechocystis* sp. PCC 6803 have been utilized to explore salt stress and provide some interesting parallels to the studies of the Ikeuchi and Murata groups. During the early stages of the response, the photosynthetic complexes are repressed, followed shortly after acclimation with an accumulation to near pre-stress levels. During this acclimation phase many events happen. The membrane becomes more rigid due to the expression and activity of lipid desaturase genes. Many chaperonins and dnaK proteins are also up-regulated. The production of compatible osmolytes is induced. This is not measurable using microarrays however, as this is a post-translational regulation event. Eventually the cellular ionic homeostatic environment is secured and under the protection of increased levels of Reactive Oxygen Species (ROS) protecting enzymes such as superoxide dismutase and glutathione peroxidase, and with the help of many chaperonins, the photosynthetic apparatus is reintroduced to the thylakoid membrane and cellular proliferation resumes. Many of these events can be monitored through gene expression. Table 1.3 demonstrates the temporal expression of several representative genes after one and five hours exposure to salt stress relative to pre-stress expression levels. After exposure for one hour to salt shock, a large fraction of the induced genes belong to regulatory complexes. Four hours later, the effect of increased expression of regulatory proteins on the pool of RNA, is seen as several transcripts encoding structural proteins are increased in number. Table 1.4

Genes Induced after 1 Hour Salt Stress		Genes Induced after 5 Hour Salt Stress	
<u>Orf</u>	<u>Annotated function</u>	<u>Orf</u>	<u>Annotated Function</u>
slr0210	Sensory transduction histidine kinase	slr2075	10kD chaperonin (groES)
sll1590	Sensory transduction histidine kinase	ssl1633	CAB/ELIP/HLIP superfamily
slr0395	Transcriptional activator protein NtcB (ntcB)	sll1441	Delta 15 desaturase (desB)
slr1324	Hybrid sensory kinase	slr1171	Glutathione peroxidase
slr0533	Sensory transduction histidine kinase	sll0170	DnaK protein (dnaK)
slr1871	Transcriptional regulator	ssr1169	Salt-stress induced hydrophobic peptide (ESI3)
sll0248	Flavodoxin (isiB)	sll0430	Heat shock protein (htpG)
slr1774	Hypothetical protein	ssr2595	High light inducible protein
ssl1633	CAB/ELIP/HLIP superfamily	ssl0452	Phycobilisome degradation protein NblA (nblA)

**Table 1.3 Representative genes induced after one and five hours salt shock from 2mM to 684mM NaCl in *Synechocystis* PCC6803 determined through analysis with sub-genomic DNA microarrays.** 480 gene arrays were produced from PCR products representing 300 to 2000 base fragments from selected genes from the *Synechocystis* PCC6803 genome. Each product was verified on an agarose gel, purified, and printed on Clontech Type I slides in 3X SSC with a Cartesian Pixsys 6000 microarrayer. These slides were subject to UV crosslinking with 300 mJ of energy and subsequent hybridization to cy3 labeled cDNA from control or time 0 hr. and cy5 labeled cDNA from 1 or 5 hr 684 mM NaCl shocked cells. cDNA pools synthesized from 20 ug total RNA were labeled using 10 ug random hexamers and Superscript II from BRL according to the manufacturer's specifications. Incorporation of the appropriate Cyanine dye (Amersham Pharmacia) was achieved through substitution with a 3:2 ratio of dTTP to cydUTP. The resulting products were purified on Microcon 30 concentrators (Amicon), then combined, mixed with 0.5 ug denatured salmon sperm DNA and an equal volume of Sigma Perfect Hyb solution (Sigma Corp.). The hybridization was performed under a polypropylene coverslip at 65° C for 16-18 hrs in a 40 ul volume. The array was washed once in 0.2 X SSC and 0.2%SDS, twice in 0.2 X SSC and once in 0.1X SSC. The slides were dried and scanned using a Scannarray 3000 from GSI Lumonics. The average signal ratio from each gene listed above are significantly different by two standard deviations from control spots whose *in-vitro* transcribed RNA products were spiked in the experimental and control samples at the same concentration.

**Table 1.4 *Synechocystis* genes regulated by salt stress after 5 hours of treatment revealed through microarray differential expression profiling.** These data were derived from the same experiments described in Table 3.1

Genes induced by 5 hours salt stress		Genes repressed by 5 hours salt stress	
orf	gene designation	orf	gene designation
slr0741	negative regulator	slr0640	sensory transduction histidine kinase
sll0895	ammonium transport protein	slr2076	60kD chaperonin 1
slr1214	atA protein	slr0074	ABC transporter
ssl1633	CAB/ELIP/HLIP superfamily	slr0075	ABC transporter
slr0797	cadA	sll0336	accD or ycf11
slr0798	cadA	slr2067	allophycocyanin a
slr0822	cation transporting	slr1986	apcB
sll0698	dfr	sll0928	apcD
slr0449	DNR protein	slr0335	apcE
sll1383	extragenic suppresso	slr1459	apcF
sll0567	fur	sll1317	apocytochrome f
sll1085	glpD or glyD	sll1874	AT103
slr1672	glpK	sll1326	ATP synthase
slr1776	high affinity sulfate transporter	slr1329	ATP synthase
sll0623	hypothetical protein	sll1325	ATP synthase
sll1387	hypothetical protein	slr1330	ATP synthase
slr1403	hypothetical protein	sll1327	ATP synthase
slr1557	hypothetical protein	sll1323	ATP synthase
slr0616	hypothetical protein	sll1324	ATP synthase
slr2031	SibG	sll1028	carbon dioxide concen.
slr1509	Na <sup>+</sup> ATPase subunit J	sll1029	carbon dioxide concen.
slr0415	Na <sup>+</sup> /H <sup>+</sup> antiporter	sll1030	carbon dioxide concen.
ssl0452	nblA	sll1031	carbon dioxide concen.
slr1529	nitrogen assimilation	sll0934	carboxysome formation
slr1305	nitrogen fixation	sll1579	cpcC
slr1041	patA	sll1580	cpcC
slr1594	patA	slr2051	cpcG
sll1435	pet112	slr1379	cydA or cyd
slr1443	pknA	sll0258	cytochrome c550
sll0199	plastocyanin (petE)	sll1796	cytochrome c553
sll0779	PleD gene product	sll1441	desB
slr0302	pleD	sll1479	devB
slr1657	pleD	slr0150	ferredoxin (petF)
sll1592	regulatory component	ssl0020	ferredoxin (petF)
slr1037	regulatory component	sll1009	frpC
slr1042	regulatory component	sll1342	gap2
slr1693	regulatory component	sll0404	glcD
slr1760	regulatory component	slr2075	groES
slr1982	regulatory component	sll0247	iron stress
slr1983	regulatory component	sll0248	isiB

Table 1.4 Continued

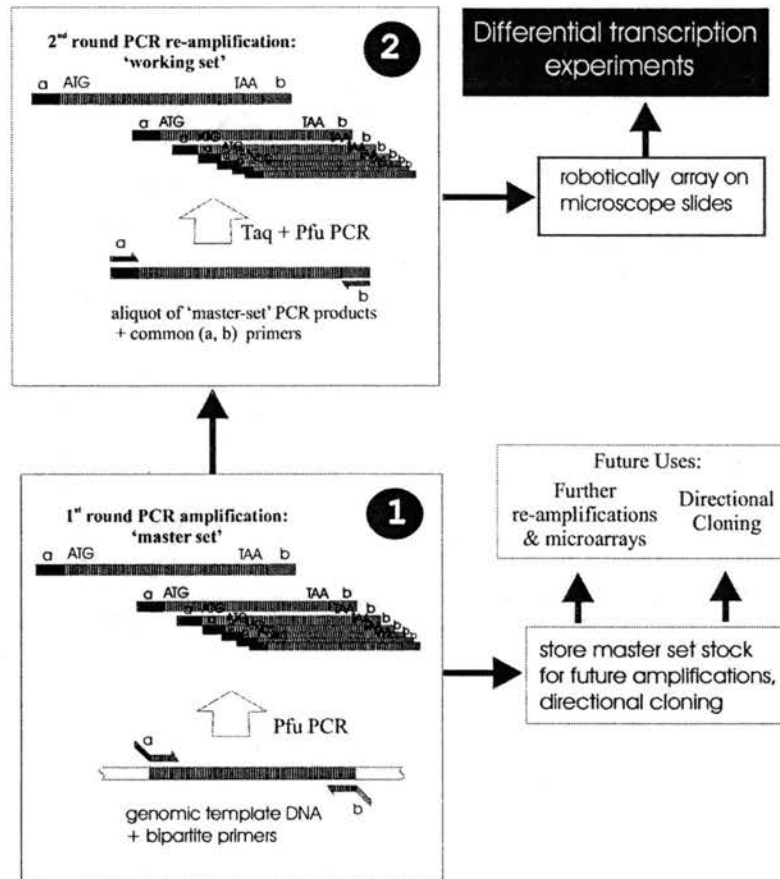
Genes induced by 5 hours salt stress		Genes repressed by 5 hours salt stress	
orf	gene designation	orf	gene designation
sll1205	regulatory protein P	sll0689	Na <sup>+</sup> /H <sup>+</sup> antiporter
slr1234	protein kinase C inhibitor	slr1595	Na <sup>+</sup> /H <sup>+</sup> antiporter
sll0474	sensory transduction	slr0343	petD
sll0790	sensory transduction	smr0003	petM
sll0798	sensory transduction	sll1525	phosphoribulokinase
sll1003	sensory transduction	sll1194	photosystem II 12 kD
sll1475	sensory transduction	slr1181	photosystem II D1
sll1590	sensory transduction	sll0427	photosystem II manganese
sll1871	sensory transduction	slr0906	photosystem II P680
slr0210	sensory transduction	sll1578	phycocyanin a subunit
slr0311	sensory transduction	sll1577	phycocyanin b subunit
slr0533	sensory transduction	slr1434	pntB
slr1147	sensory transduction	ssl0563	psaC
slr1393	sensory transduction	slr0737	psaD
slr1414	sensory transduction	sll0819	psaF
slr1759	sensory transduction	smr0004	psaI
slr1805	sensory transduction	sll0629	psaK
slr2098	sensory transduction	slr1655	psaL
sll1575	serine/threonine protein kinase	ssr3451	psbE
slr0152	serine/threonine protein kinase	slr1239	pyridine nucleotide
sll2014	sfsA	sll1292	regulatory component
slr0724	sohA or PrIF	slr0194	ribose 5 phosphate I
slr1213	umQ gene product	slr0009	ribulose bisphosphat
sll1002	ycf22	slr0012	ribulose bisphosphat
ssr1425	ycf34	sll1594	rubisco operon trans
sll0584	ycf36	slr0783	triosephosphate isomerase
sll1218	ycf39	sll1057	trx
sll0226	ycf4	slr1139	trxA or trx
ssr0102	ycf40	slr0623	trxA
sll0194	ycf43	sll1685	ycf10
slr0692	ycf45	ssr2142	ycf19
slr0480	ycf46	sll1281	ycf9
ssr2595	high light inducible protein	sll0998	ysR transcriptional
		sll1594	rubisco operon trans

includes a larger list of genes whose expression is affected, either induced or repressed, after five hours acclimation to 684 mM salt. This list was developed from the analysis of several hybridizations between sub-genomic arrays and (2) labeled total cDNA pools (control and experimental samples). In concert with the more well-annotated genes, is the regulation of a number of uncharacterized open reading frames currently annotated only as "Hypothetical". Table 1.5 lists the ten most highly regulated hypothetical genes from the same sub-genomic array experiments. The inclusion of hypothetical genes in our sub-genome array arose only through their identification as homologs to salt-regulated genes from either *Saccharomyces* or *Arabidopsis*. This result confirms the method for selection criteria of sub-genomic array constituents. Similar responses in the light adaptation experiment cannot be confirmed however, as the results of all hypothetical genes were not reported.

Full genome arrays are being developed as part of a National Science Foundation project in the following manner. Each gene or sequence was used to determine primers which could PCR amplify products representing the entire open reading frame, but with a cut-off of 2000 bases in length, such that the longer genes have products that are truncated at 2000 bp. The amplification process has been diagrammed in figure 1.3. Oligonucleotides were produced in individual tubes and transferred in cognate pairs of primer to 96-well format allowing for high-throughput amplification and analysis. In addition to the gene-specific sequences, each oligo was designed to include universal ends which allow second round amplifications using the first round products as template and universal oligos for priming. This second round amplification proved critical in

Hypothetical genes most induced by salt	Hypothetical genes most repressed by salt
slr1403	sll1663
sll0623	sll1945
slr1557	slr0442
sll1387	sll0242
sll1373	sll1686

**Table 1.5 Differentially expressed hypothetical open reading frames.** This list contains the most induced or repressed hypothetical orfs from transcriptional profiles using sub-genomic arrays to analyze 5-hour exposures of *Synechocystis* PCC6803 to high salt shock. The data for this list were derived from the same experiments described in Table 1.3



**Figure 1.3 PCR amplification strategy used to develop full genome arrays.**

maximizing yield without sacrificing accuracy. In addition, the universal portions of the oligos were designed to introduce restriction sites so that successfully amplified products could be digested with an endonuclease to directionally clone each of the products. Using universal oligos and template from first round amplifications produced elements of relatively equal and robust yield and had an unexpected leveling effect on the yield of the approximately 3200 genes being amplified. That is, the yield of products from the first round of amplification using the gene-specific sequences and chromosomal DNA template was comparatively much more heterogeneous than the yields on the second round of amplification using the universal primers. In the extreme case, some first round primers yield no detectable product as judged by ethidium stained agarose gels, whereas as good yield was obtained using the same poor-yielding first round product as template for the second round reactions primed with the universal primers. Furthermore the yield of such reactions was comparable to the second round reactions based upon first round template that had been produced in abundance. Amplified products were purified in 96-well format, then combined and transferred to 384-well plates under the appropriate conditions for robotic deposition on modified glass slides.

Sub-genomic arrays are identical in concept to full-genomic arrays with one exception. They only contain a small number of genes. This makes it easier to analyze and coordinate the production of arrays on smaller scales, thus making them less expensive, and more reliable. In addition, arrays can be printed with more replicates in the same space allowing for better statistical averaging and thus more reliable data. Our sub-genome arrays contain 480 *Synechocystis* genes from the networks of photosynthesis



and respiration complexes, known stress-responsive genes, regulatory genes, and homologues to salt-induced genes from *Arabidopsis* and *Saccharomyces*.

A determination of differential transcriptional profiles associated with abiotic stresses is expected to be a key component of an overall understanding of the adaptive mechanisms of cyanobacteria challenged with environmental stress. We are focusing on salt stress, paying close attention to the function, regulation, and protection of the photosynthetic apparatus. Already, cyanobacterial microarrays are being utilized by several laboratories to analyze global patterns of transcript abundance during time course experiments and are being used to monitor their adaptation to various abiotic stresses (28, 54). These studies are likely to be followed by comparative analyses of mutants with alterations in their stress response. Additionally, the microarrays have already begun to contribute to an understanding of the biogenesis and regulation of the photosynthetic apparatus. In accord with our project on the structure and assembly of the photosystem II (PSII) complex in cyanobacteria, we also envision utilizing the microarrays to help dissect the processes governing the biogenesis and repair of the easily damaged and constantly turning-over PSII complex.

The results from our sub-genomic arrays have already presented us with valuable information regarding the response of many cyanobacterial genes to salt stress. Table 1.3 lists genes whose expression was significantly regulated by the induction of a salt-shock response. In this example, total RNA from time zero and three hours after the addition of 684mM NaCl were labeled with fluorescent molecules cyanine 3(cy 3) and cyanine 5(cy

5) respectively in a first-strand reverse transcriptase reaction. The resulting cDNA was hybridized to our sub-genomic arrays overnight. The arrays were washed, dried, and scanned. Two false-colored images were overlaid and normalized using positive control spots whose transcripts were spiked into the labeling reaction at equal concentrations. Analysis of the resulting images produced results similar to previously described, published works. Specifically, the repression of PSII gene expression and activity early in the stress response is predicted to be a protective measure against the production of reactive oxygen species. The induction of known salt-responsive genes such as *esi3* and *stpA* was observed. And, interestingly, a few regulatory genes such as *sibG* and *pata* were also up-regulated. The result of these experiments has contributed to the targeted mutagenesis of several genes using a PCR-mediated procedure. In addition to those mentioned, mutants of several other up-regulated genes are now under close inspection (all Na<sup>+</sup>/H<sup>+</sup> antiporters, and several cation ATPases).

Other uses for DNA arrays besides measuring differential transcription include comparative genomics assays, including single nucleotide polymorphism analysis and the development of arrays for clinical identification of strains (11, 13, 33, 39, 50). As of yet, however, no applications for cyanobacterial strains have been developed.

#### *Mutational Analysis*

Knock-out mutants have been used extensively by many researchers already and are a proven strategy. In the case of *Synechocystis*, gene knock-outs can be constructed by relying upon this organism's natural competence and chromosomal transformation by

integration of foreign DNA via homologous recombination. The vast majority of recombinants produced by this procedure occur by double cross-over events in a manner at least superficially analogous to chromosomal transformation in *Saccharomyces*. Typical protocols require cloning of chromosomal DNA followed by enzymatic insertion of an antibiotic-resistance cassette within the chromosomal fragment, transformation, and selection based upon the antibiotic resistance provided by the cassette. The utilization of efficient procedures and cloning vectors specialized for the cloning of PCR products has greatly simplified the knock-out procedure as does advanced knowledge of the restriction sites available for the disruption of the gene using an antibiotic-resistance cassette.

Alternatively, it is possible to use one of several PCR mediated knock-out strategies which require no cloning (3, 43). These strategies take advantage of double-crossover homologous recombination and the requirement for only short stretches (>200 bp) of flanking homologous sequence on each end of an antibiotic cassette. Such strategies are much less time consuming, and may be less expensive in the long run. In most cases, a final PCR product can be manufactured through fusion PCR reactions involving two flanking regions and a selectable marker gene. The resulting fragment is capable of transforming the Wild-type strain and inserting the selectable marker directly into the targeted gene, either interrupting it or replacing it completely. Using the two most distal oligonucleotides designed for amplifying the two flanking regions, it is possible to screen mutants for complete loss of the Wild-type genotype directly from cultured cells without purification of DNA (29). Coupling PCR-knockout strategies with

whole-cell PCR screens to confirm gene deletion or disruption make these protocols very fast and efficient.

Having the capacity to clone each PCR product synthesized for array production, including virtually every identified gene in the genome, into one vector increases the capabilities of the study several fold. Cloned products can be over-expressed in *Escherichia coli*, and/or histidine-tagged to simplify purification. Site-directed mutagenesis is also a viable strategy taking advantage of the cloned products. Including this step in the aforementioned strategy increases the capabilities several-fold.

### OUTLOOK AND PROSPECTIVE

At the time of this writing, several additional cyanobacterial sequencing projects are underway as well as numerous other genome sequencing projects that will continue to be initiated and finished in the years to come. The subjects of the cyanobacterial sequencing projects include the genetically amenable marine strain *Synechococcus* sp. PCC7002, the thermophilic species *Synechococcus vulcanus* (also referred to as *Thermosynechococcus elongatus*), the long-used *Synechococcus* sp. PCC7942, and the evolutionarily interesting *Gloeobacter violaceus*. *Gloeobacter* remains largely unstudied, but from the little information available, it is clear that it exhibits unusual and ostensibly primitive cellular properties. This organism is interesting from the evolutionary perspective since analysis of rRNA sequences place this organism near the root of the cyanobacterial phyletic radiation. Among other things, the features of the photosynthetic apparatus in this organism are most likely to hold clues as to the

evolutionary transition from anoxygenic to oxygenic photosynthesis and the availability of the full genome sequence will likely revolutionize this analysis. The analysis of the *Synechococcus vulcanus* genome also ought to prove interesting information, due not only to its thermophilicity, but also because there are preliminary indications that it may hold some interesting gene clustering features. The genes for cytochrome  $c_6$  and cytochrome  $c_{550}$ , heme proteins which serve quite distinct and non-overlapping functions in photosynthesis, are not usually physically associated with each other in other cyanobacteria. However, not only are these genes found in tandem in the *Synechococcus vulcanus* genome, but an additional and apparently non-functional cytochrome gene (pseudo-gene) is also found at this locus. This gene arrangement is highly suggestive of gene duplication and divergence events that started from unequal crossovers. The retention of the intact gene family cluster is intriguing since it raises the as yet unanswered question of whether or not additional ancient relics for other clustered paralogs are more common in this organism in comparison to those whose sequences have been finished. If this turns out to be the case it will provide an unprecedented window on gene family evolution in the cyanobacteria. It is likely that as microarray analysis proceeds, the regulatory networks governing the coordinate expression of functional classes of proteins will be revealed. Given the large number of candidate regulatory proteins found in these organisms, this will remain an awesome task. In the case of *Synechocystis*, for example, there are over 80 histidine kinase genes and some may participate in multiple regulatory pathways. This is evidenced by the finding that the histidine kinase designated HK33, functioning in the regulation of the lipid desaturation pathway, has also been found to govern the expression of high-light

inducible proteins (HLIPs) which function as part of the high-light stress response-mechanism. Consistent with this apparent multiple-function role, analysis of the HK33 protein has lead to the identification of multiple-sensing domains. Thus, the regulatory networks may prove to be highly ramified through the existence of multiple regulatory interactions.

This brings up the issue of how to go beyond the sequence data and evaluate the nature of protein-protein and protein-ligand interactions that underlie this network. This will require the analysis of the proteins through, perhaps, the proteomics approaches already utilized for other organisms. Since the advent of genomic sequence availability, several advancements have been made toward the development of technologies focusing on the expression and activity of proteins. Included in these are protein over-expression tools, improved purification methods using, for example, hexahistidine-tagging methods, 2-D gel electrophoresis, and MALDI-TOF characterization of protein complexes. The success of each of these technologies has required or at least has been enhanced by the availability of sequence data. Through MALDI-TOF (Matrix Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry), proteins and fragments thereof can be identified by comparing accurate experimental molecular masses with databases of deduced peptides, using computationally intensive algorithms. While protein over-expression and 2-D gel electrophoresis have been available for some time, they can be technically difficult to master and therefore their use to this point has been limited, but rewarding. At least one group at the Kazusa DNA Research Institute has developed the techniques to use 2-D gels and some of their data are available on the Cyanobase website.

Unfortunately, to date, this single case is the only published example of proteomics research in a cyanobacterium. Expressing a protein modified to include a six amino acid linker (six histidines) allows for chromatographic purification along with any other protein(s) of which might make up a complex this practice is referred to as His-Tagging. Coupling two or more of these technologies such as 2-D gel electrophoresis or six histidine tagging with MALDI-TOF mass spectrometry sequencing has just begun to redefine the field. The ability to purify protein complexes and identify their constituents is a very powerful tool. Within this decade, it is likely that these technologies will move to the forefront of molecular biology as they become more widely understood, accepted, and used by cyanobacteriologists and plant scientists exploiting the cyanobacterial models and databases.

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## **Chapter II**

# **The construction and use of bacterial DNA microarrays based on an optimized two-stage PCR strategy**

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**Abstract:**

DNA microarrays are a powerful tool with important applications such as global gene expression profiling. Construction of bacterial DNA microarrays from genomic sequence data using a two-stage PCR amplification approach for the production of arrayed DNA is attractive because it allows, in principal, the continued re-amplification of DNA fragments and facilitates further utilization of the DNA fragments for additional uses (e.g. over-expression of protein). The purpose of this work is to describe the successful construction and use of DNA microarrays using a two-stage amplification approach, and to discuss the technical challenges that were met and resolved during the project.

Chimeric primers that contained both gene-specific and shared, universal sequence allowed the two-stage amplification of the 3,168 genes identified on the genome of *Synechocystis* sp. PCC6803, an important prokaryotic model organism for the study of oxygenic photosynthesis. The gene-specific component of the primer was of variable length to maintain uniform annealing temperatures during the first round of PCR synthesis, and situated to preserve full-length ORFs. Genes were truncated at 2 kb for efficient amplification, so that about 92% of the PCR fragments were full-length genes. The two-stage amplification had the additional advantage of normalizing the yield of PCR products and this improved the uniformity of DNA features robotically deposited onto the microarray surface. Also described herein are the techniques developed through optimizing hybridization conditions for improved signal-to-noise ratios. The inter-lab transportability was demonstrated by the virtual error-free amplification of the entire

genome complement of 3,168 genes using the universal primers in partner labs. The printed slides have been successfully used to identify differentially expressed genes in response to a number of environmental conditions, including salt stress.

The technique detailed here minimizes the cost and effort to replicate a PCR-generated DNA gene fragment library and facilitates several downstream processes (e.g. directional cloning of fragments and gene expression as affinity-tagged fusion proteins) beyond the primary objective of producing DNA microarrays for global gene expression profiling.

## Introduction

DNA microarrays have proven to be a particularly effective tool for genome-wide transcript profiling, and they can generate information on the accumulation and disappearance of thousands of specific transcripts in a single experiment (3, 4, 8-10). Because such an array generates vast quantities of data, it is desirable to improve the statistical reliability of the data through experimental repetitions. Additionally, it is useful to perform time course experiments involving multiple time points to enable the application of cluster analysis to classify groups of genes exhibiting similar temporal patterns of regulation in response to shifts in environmental conditions. Therefore, a robust experimental design may involve the consumption of many individual DNA microarrays. Given these considerations, it is important to have methods for improving the efficiency and economy of microarray production.

Since the bacterial genes are typically not cloned at a genome-wide scale as non-redundant, ordered sets, as with eukaryotic cDNA libraries, it is not possible to use 'universal primers' (e.g. T3, T7 sequences) and therefore PCR amplification requires design and synthesis of PCR primers for all target genes. In this context, the construction of bacterial DNA microarrays from genomic sequence data using a 'two-stage' approach, is attractive because it allows the continued re-amplification of DNA fragments and facilitates further utilization of the DNA fragments for additional uses (e.g. over-expression of protein) (7). This approach involves the use of chimeric primers containing both gene-specific and engineered sequences (adaptamers). These primers are used to synthesize PCR products directly from genomic DNA, which serves as template during



the first stage of PCR amplification. This amplification can be performed for thousands of genes during a given production run using well-established procedures that include microtiter plates and multichannel pipetting techniques to afford efficient parallel processing of the samples. The products of this first stage of amplification are gene sequences flanked by the arbitrary adaptamer sequences engineered into the first stage PCR primers. The adaptamer sequences become the basis for re-amplification of the gene sequences in a second stage amplification. During the second stage of amplification, the first stage PCR products serve as template, whereas a single pair of primers recognizing the flanking adaptamer sequence can be used to re-amplify all products of the first stage PCR.

In this report, we describe the procedures for the production and use of DNA microarrays for the cyanobacterium *Synechocystis* PCC6803 (hereafter referred to as *Synechocystis*). This organism is a widely used experimental model for the study of gene expression and plant-like oxygenic photosynthesis (1). *Synechocystis* was predicted to contain 3,168 open reading frames (prior to May 2002) (<http://www.kazusa.or.jp/cyano/index.html>) (5). Of these, over 50% (>1700 ORFs) have been characterized as hypothetical or having no similarity to known sequences. Thus, differential gene expression via microarray analysis will represent an important functional genomics approach and we describe the two-stage PCR strategy that led to the successful production of full-genome microarrays for *Synechocystis*.

## Materials and Methods

### *Growth conditions and RNA isolation*

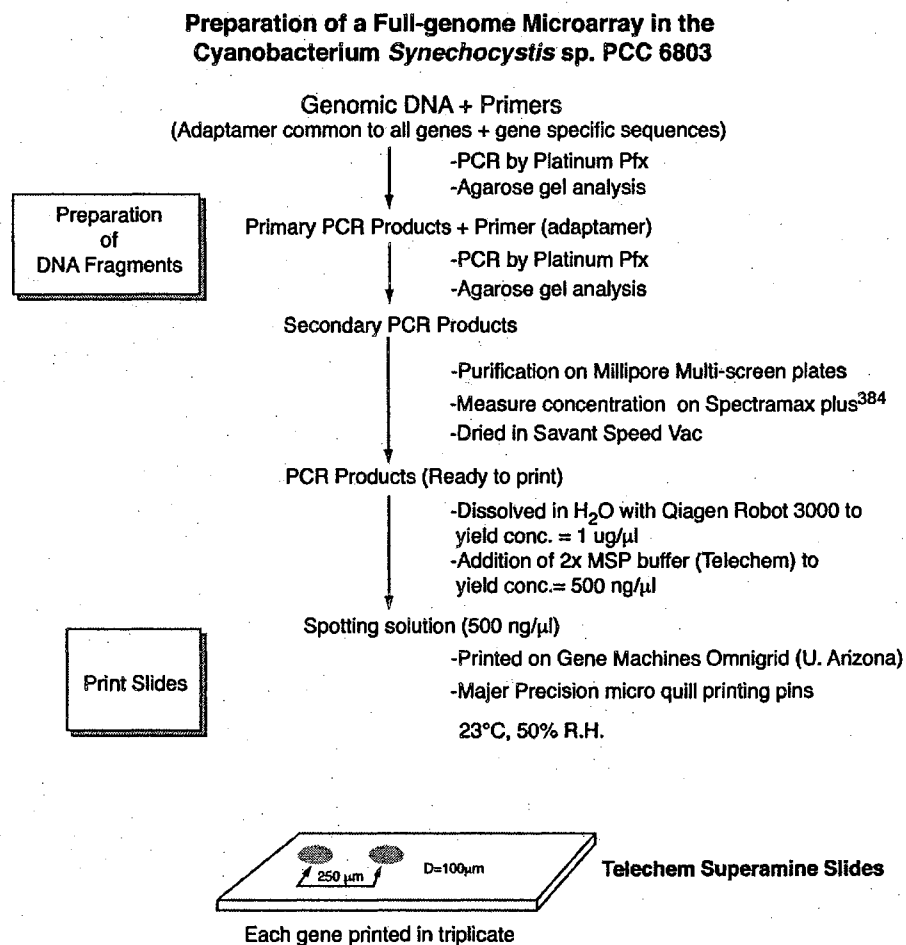
*Synechocystis* cultures were grown autotrophically in BG-11 medium essentially as described by Williams (11). Specifically, 500 ml cultures were grown in flat (4 cm across the light path) Bellco tissue culture flasks at 30°C under white light fluorescent illumination (Cool White<sup>®</sup>, General Electric) with an incident intensity of 80  $\mu\text{moles photons m}^{-2} \text{ s}^{-1}$ . Aeration was provided by bubbling with air enriched with 3% CO<sub>2</sub> at a rate of 300 ml min<sup>-1</sup>. RNA was isolated using hot phenol in conjunction with vigorous agitation with glass beads as described by Bhaya et al. (2).

### *Chimeric oligonucleotide design and PCR amplification*

Figure 2.1 provides a flow chart of the preparation of the full-genome *Synechocystis* microarray. Oligonucleotides, synthesized by Sigma Genosys (<http://www.sigmagenosys.com/>), were designed to amplify the complete coding region of each open reading frame from the sequenced genome of *Synechocystis*. The only exceptions were instances for genes with a predicted length extending beyond 2 kb. Of the 3,168 open reading frames, fewer than 10% (261) of the genes were truncated at the 3'-end to the 2 kb limit. Each of the oligos is a chimeric sequence designed for first round synthesis and, as such, contained two components: a 5' universal sequence and a 3' gene-specific sequence as shown in Figure 2.2. The oligonucleotides gene-specific region begins at the first or last base of the open reading frame and continues inside until the T<sub>m</sub> of the oligo was in the range of 58-62°C (25-45 nt, including the universal sequence). An algorithm (Sigma Genosys) based upon Primer3 (Whitehead Institute)

was used for this purpose and resulted in a high frequency of successful amplification as discussed below. Importantly, the universal sequences were designed to include *SapI* restriction sites in order to facilitate downstream applications, including cloning into an expression vector. Aliquots of the oligonucleotides were transferred and mixed as primer pairs to separate locations of 96-well plates prior to delivery from the commercial source, which facilitated amplification in the 96-well format. The remaining products from the synthesis reaction were stored in individual tubes at -20°C.

First round amplifications were performed in 96-well microtiter dish format using PTC-100 Thermocyclers from MJ Research Inc. Five microliters of 20 µM premixed primer pairs were transferred to 0.2 ml Thermo-Fast® 96-well plates (Marsh cat. No. AB-0600) and mixed with 95 µl of Reaction mix one (For 110 reactions; 55 µl of 500 µg/ml chromosomal DNA, 1.1 ml Pfx Buffer®, 1.1 ml Pfx Enhancer reagent®, 220 µl 50 mM MgSO<sub>4</sub>, 165 µl 10 mM premixed dNTPs [Amersham Pharmacia cat. No. 93-77212], 88 µl Pfx DNA Polymerase® [Invitrogen cat. No. 11708-039] and 7.722 ml sterile, deionized water). Plates were sealed using Microseal™ 'A' film (MJ Research cat. No. MSA-50001) during thermal cycling. Step-down thermo-cycling conditions consisted of 2 min at 94°C initial denaturation followed by 10 rounds of 94°C for 30 s, 62°C(-1°C/cycle) for 45 s, and 68°C for 3 min. The step down cycling was followed immediately by 24 cycles of 94°C for 30 s, 52°C for 45 s and 68°C for 3 min. Five microliters of each sample were mixed with an equal volume of 20% glycerol and loaded on 0.7% agarose/TAE gels stained with ethidium bromide and separated by electrophoresis in Bio-Rad Sub-cell® model 192 units. Gels were analyzed using an



**Figure 2.1. Overall strategy for the production of bacterial DNA microarrays using the two-stage PCR approach for the production DNA microarray elements.**

Alpha Imager™ 2000 workstation and software for image capture and Total Lab v. 1.10 (Phoretix) software for image analysis. Second round products were generated with universal primers and products of the first round of amplification. Specifically, 5 µl of the original 100 µl reaction was transferred to new plates and mixed with 95 µl reaction mix two (For 110 reactions; 1.1 ml 10X Buffer, 220 µl 50mM MgSO<sub>4</sub>, 165 µl premixed 10mM dNTP's, 550 µl 20 µM universal primer pair, 1.1 ml Pfx Enhancer reagent, 88 µl Pfx enzyme, and 7.227 ml sterile, deionized water). Amplifications were carried out by denaturation for 2 min at 94°C followed by 35 cycles of the following conditions: 94°C for 15 s, 55°C for 45 s, and 68°C for 2 min. After completion of all 35 cycles, an additional extension period at 68°C for 20 min was added to polish the ends. Five microliters of each sample were loaded into 0.7% agarose gels and analyzed as described above. Oligonucleotides for unsuccessful products after the second round reaction were redesigned, resynthesized, and used for reamplification. PCR fragments were compared to a known size marker (Cat. No. 10068-013, Invitrogen). Products were scored successful if their length, as defined by gel analysis, was +/- 15% of their predicted length, contained only a single band, and were of adequate density.

#### *Purification, preparation, and printing DNAs*

Upon verification of successful amplification by gel analysis, each plate of second round PCR products was purified using Multiscreen-PCR plates from Millipore according to the manufacturers specifications, except that a pre-wash was incorporated to remove potential surfactant type agents present in at least some batches of the filtration units. The resulting products were resuspended in 50 µl sterile deionized water at room

temperature on a rotary shaker for 30 minutes. The yield of each product was measured by calculating concentration from  $A_{260}$  values using Corning Incorporated's Costar UV transparent 96 well plates with the Molecular Devices Spectramax 384 Plus spectrophotometer. The products were then dried in a Savant DNA110 Speed Vac. Using a Qiagen Bio-Robot 3000™, each product was resuspended in water to  $1.0 \mu\text{g}\cdot\mu\text{l}^{-1}$ . To each sample, an equal volume of 2X Microspotting solution (Cat. No. MSS-1, Telechem) was added. Ten microliters of each product was transferred to two sets of 384 Micro Array plates (Cat. No. X7020, Genetix Limited). Using a Omnigrid arrayer (Gene Machines) and 16 Microquill 2000 pins (Majer Precision), arrays were printed in triplicate on Superamine slides (cat. No. SMM-25, Telechem), using 250 micron spacing, in 18x15 spot subgrids. To improve spot morphology, blotting was increased to 30 spots per dip, and pins were re-dipped into the sample after every 50 slides. Cross-contamination between successively spotted samples is a potentially severe problem and was found to be minimized by increasing the stringency of pin washing procedures beyond the manufacturer's recommendations by increasing sonication in the washing solution for five seconds at the highest power setting. Relative humidity was maintained at 50% and temperature at  $23^{\circ}\text{C}$  throughout the arraying procedure.

#### *Array process verification*

At the end of printing, one or two slides were used to verify the quality of printing such as spot morphology and intensity. Slides were baked at  $80^{\circ}\text{C}$  for one hour, washed with 0.1% SDS and rinsed in deionized water. The slide was then stained with a 100 nanomole aqueous Syto-61 (Molecular Probes) solution, washed twice with a 0.1%

solution of SDS, rinsed once in deionized water and scanned for fluorescence at 550 nm in the ScanArray 3000. Each wash or rinse was carried out at room temperature for five minutes. The scanned images were analyzed for spot morphology and intensity and the results of the analysis were used to optimize the printing process during each run. This includes cleaning pins when necessary, and designing the overall layout of the arrays.

### *Labeled cDNA production*

Fluorescently labeled cDNA was produced using a two-step procedure involving cDNA production from target RNA using a reverse transcriptase reaction incorporating aminoallyl-modified deoxynucleotide (aadUTP), followed by the second step involving chemical coupling of fluorescent dye (either Cy3 or Cy5) to the introduced amino moieties of the newly synthesized cDNA. The cDNA was synthesized from 16  $\mu$ g total RNA using 5  $\mu$ g random 8-base oligonucleotides (Sigma GenoSys) and Superscript II<sup>TM</sup> reverse transcriptase (Invitrogen). RNA samples (control and experimental) were each mixed with random octamers in a total volume of 25  $\mu$ l DEPC (diethylpyrocarbonate) treated water, heated to 65°C for five minutes and then transferred to 42°C. Subsequently, 25  $\mu$ l of a premix containing two  $\mu$ l of 100 mM DTT (dithiothreitol), 10  $\mu$ l 5X Superscript II buffer, one  $\mu$ l 50X aadNTP mix (25 mM dA, C, and GTP, 8.4 mM dTTP, and 16.6 mM aadUTP [Sigma Cat. No.A-5660]), 10  $\mu$ l DEPC treated water, and two  $\mu$ l Superscript II was added to each tube. Following a two hour incubation at 42°C, 4  $\mu$ l of 50 mM EDTA and 2  $\mu$ l of 10 N NaOH was added to each tube and incubated at 65°C for 20 minutes to degrade RNA. The reaction was neutralized by the addition of 4  $\mu$ l of 5 M acetic acid. The cDNA was purified using Millipore Microcon 30 centrifugal

filter devices by diluting the reaction mix with sterile deionized water to a volume of 500  $\mu\text{l}$  according to the manufacturer's specifications. Each of the two samples was washed five times using 500  $\mu\text{l}$  deionized water and the final retentate adjusted to approximately 50  $\mu\text{l}$  to facilitate handling. The resultant solutions were dried at room temperature in the Speed Vac, and the pellets were resuspended in 20  $\mu\text{l}$  0.1 M  $\text{Na}_2\text{CO}_3$  (pH 9.0) and mixed with 10  $\mu\text{l}$  of previously prepared Cy3 or Cy5 dye. Preparation of the dyes was performed in advance and involved dissolving one tube of powdered Cy3 or Cy5 dye from Amersham Pharmacia Biotech Cat. No. PA23001, or PA 25001 respectively, in 55  $\mu\text{l}$  dimethyl sulfoxide and storing at  $-20^\circ\text{C}$  until use. The coupling reaction was carried out at room temperature in the dark for one hour. The reaction was quenched by adding 4.5  $\mu\text{l}$  of 4 M hydroxylamine, followed by incubation for an additional five min. The Cy3- or Cy5 dye-coupled cDNA samples were combined and purified using a Qiagen PCR product purification kit according to the manufacturer's specifications. Samples were adjusted to 14.75  $\mu\text{l}$  using SpeedVac and remainder of the hybridization components containing 2.5  $\mu\text{l}$  of 10  $\mu\text{g}/\mu\text{l}$  salmon sperm DNA, 8.75  $\mu\text{l}$  20X SSC, 0.25  $\mu\text{l}$  10% SDS, and 8.75  $\mu\text{l}$  formamide were added. The mixture was then heated for two minutes at  $99^\circ\text{C}$ , briefly centrifuged at high speed, and maintained at  $42^\circ\text{C}$  until the hybridization with the DNA microarray was begun.

#### *Hybridization and wash conditions*

Printed slides were baked at  $80^\circ\text{C}$  for one hour, washed twice for two minutes each at room temperature in 0.1% SDS and once in deionized water to remove unbound material. The slides were boiled in deionized water for three minutes to denature the



printed DNA, dried using low speed centrifugation in a specialized microscope slide-accommodating rotor (Telechem). The DNA on the microarray was then subjected to a UV-cross-linking at a dose of 150 mJ/cm<sup>2</sup>. Prehybridization was performed by incubating the slide in a fresh mixture of 100 ml of 25% formamide, 5X SSC, 0.1% SDS, and 1% BSA for 45 min. at 42°C in a Coplin jar. The slide was then rinsed under distilled water and dried using low speed centrifugation.

The slide was preheated at 42°C in a Telechem hybridization chamber by placing in a static 42°C incubator. The pre-warmed sample was pipetted and spread uniformly onto a 24 x 60 mm glass cover-slip (Fisher Scientific, Cat. No., 12-548-5P) and the pre-warmed slide was inverted and placed with the arrayed surface contacting the sample on the cover-slip surface. Deionized water (10 µl) was added to each of the reservoirs of a Telechem Hybridization Chamber, and the slide was transferred to and enclosed within the chamber. The slide was incubated in a static incubator at 42°C for 12-16 h, and washed by placing in a 250 ml solution of 2X SSC and 0.1% SDS at 42°C for five minutes with gentle agitation provided by rotation of a magnetic stir bar. The slide was transferred quickly to a solution of 0.1X SSC, and 0.1% SDS, incubated for 10 minutes at room temperature with gentle agitation, and washed five additional times in 0.1X SSC for one minute at room temperature. The slide was then rinsed briefly with deionized water and dried by low speed centrifugation. The slides were stored in the dark until scanned.

## Results and Discussion

The goal of this project was to develop a DNA microarray as part of an overall strategy for functional genomics in the unicellular model cyanobacterium, *Synechocystis*. The two-stage amplification strategy (6) was adopted as a means to facilitate replication of the arrays as needs dictated (Figure 2.1). In general terms, the optimization of this technical approach required particular attention to the design of the adaptamers, the choice and use of the thermostable DNA polymerase, and the thermocycling conditions. Other technical factors, such as the array printing conditions, were found to conform to observations that are well-described in the literature. Overall, the rate-limiting production steps following the reaction optimization were those involving the analysis of the products. Figure 2.1 outlines the main features of this successful construction project and Table 2.1 highlights some of the key parameters that we tested during the array construction.

Critical design features of the chimeric first round primers were the inclusion of the directional cloning and expression features, plus the inclusion of a good common template sequence for the subsequent second round amplification. The adaptamers included the introduction of G+C rich sequences at the 5' termini to stabilize the end structure of the first round PCR products. Another important design aspect that proved critical, according to our preliminary tests, was incorporation of an additional five base G+C rich overhang in the universal primers used for the second round PCR (Figure 2.2). The absence of the additional sequences resulted in very poor PCR performance compared to the excellent performance observed with their inclusion.

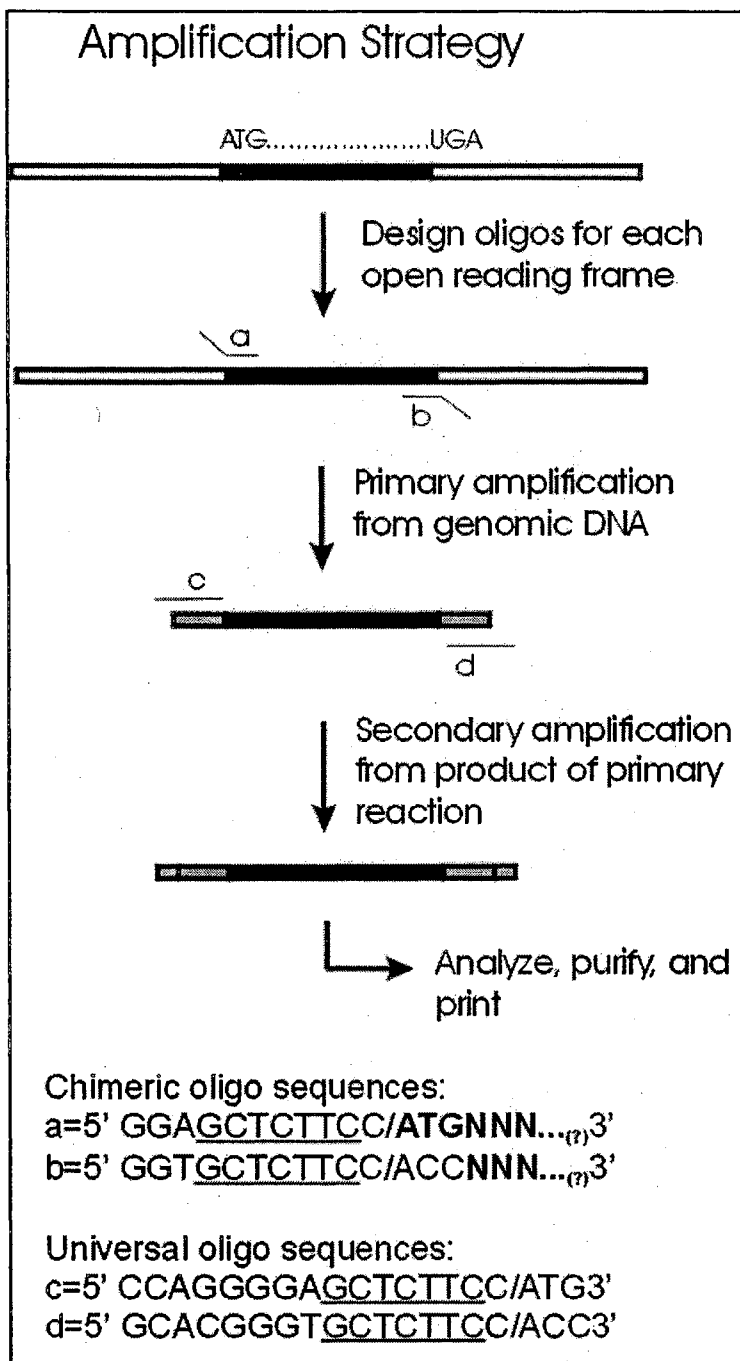
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**Table 2.1: Construction of DNA microarray**

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Microarrays are constructed by synthesizing oligonucleotides on glass slides, by spotting PCR-amplified cDNA clones from EST data (eukaryotes), or by spotting PCR products from genomic DNA template (prokaryotes) using a set of gene-specific primers. The method described in this paper has the advantage of being both more cost effective and less labor intensive for the construction of microarrays from prokaryotic organisms. The procedure is most useful for those laboratories working with organisms for which commercial microarrays are unavailable. The salient features of our approach include:

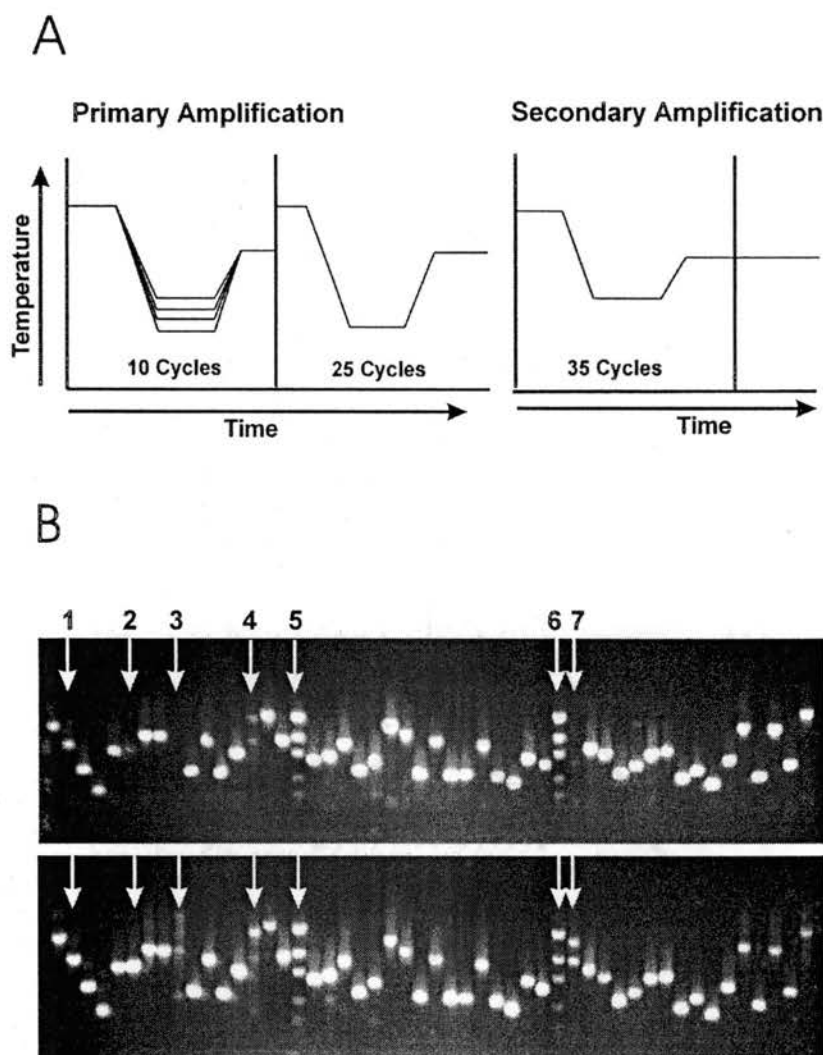
- **Bipartite Primer:** The use of a bipartite primer for the amplification of genes has several advantages (see text). Importantly, it permits the use of a common primer for the amplification of all genes in the second and subsequent amplification steps. This simple modification in primers alleviates the problem of primer-limitation and therefore, is particularly valuable in constructing many arrays for a multi-investigative, collaborative effort.
  - **Two stage amplification:** The use of the two-stage amplification process increases the signal-to-noise ratio by diminishing the hybridization signal resulting from contaminating genomic DNA used for amplification of PCR fragments. Additionally, it also yields relatively uniform quantities of PCR products.
  - **Purification and Quantitation:** For efficient binding of the amplified products and to reduce the background signal, it is essential to purify the products. The results of ethanol precipitation were found to be unsatisfactory, whereas the use of Multiscreen filter plates gave excellent results. One drawback with this technique is the relatively lower percentage recovery of smaller fragments. Therefore, following purification, fragments were quantified and normalized to an equal concentration.
  - **Printing:** We checked the suitability of various slide surfaces (poly-Lysine and amine) and the spotting buffers from a number of commercial vendors to ensure reproducible and uniform spot morphology and maximal retention of DNA. After experimenting with several variations, the combination of Telechem's Superamine slides and MSP spotting buffer gave satisfactory results.
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**Figure 2.2 Design and use of chimeric bipartite oligonucleotides for PCR amplification of each open reading frame of the genome from *Synechocystis* PCC6803.** Bipartite oligos (a and b) were designed to include: 1) a gene specific sequence at their 3' end of variable length to maintain a constant  $t_m$  of 58-62°C; and 2) universal sequence at their 5' to introduce a common sequence to all primary products. These primary products were then re-amplified by universal oligonucleotides (c and d) introducing more universal sequence. The re-amplification of products using universal oligonucleotides allows amplification of all products under optimized conditions, thus improving the success rate and product yields. The final products of the second amplification are analyzed for size, yield, and lack of multiplicity on agarose gels, then purified, resuspended in printing buffer, and printed on modified surface glass slides. This strategy minimizes the cost and effort to replicate the PCR-

generated DNA gene fragment library and facilitates several downstream processes beyond the primary objective of producing DNA microarrays.

Importantly, the two-stage amplification had the unanticipated advantage of normalizing the yield of PCR products across the entire set of genes, such that lower than average yielding products from the first round PCR (using the gene specific sequence and chromosomal DNA as template) often had a robust yield during the second round of amplification using the common adaptamer sequences. Although the primers were deliberately designed so that oligo  $T_m$ 's fell in narrow range (58-62° C), it was determined after a number of trials that it was necessary to use 'touchdown' PCR conditions for the first round amplification. Nevertheless, the percentage of successful products after the first round synthesis appeared quite low, based on yield as visualized in the ethidium stained electrophoretic gels. Some lanes showed little to no product or multiple products after the first round amplification with the chimeric primers. However, these products generally resulted in successful amplification after their use as template in the second round amplification when the universal sequences introduced as overhangs of the chimeric primers during the first round amplification were used. Thus, the universal primers in the second round amplification provided the additional benefit of generating consistent yields across most of the genes (see Figure 2.3). Apparently, the amount of correct template produced by the first round PCR, albeit often invisible during gel analysis, was usually sufficient to give high yields during the second round of amplification using the common adaptamer sequences. Thus 86% of the products were successfully amplified during our initial round of two-stage PCR. Primers for the remaining 14% were redesigned and synthesized, so that essentially all of the annotated genes were successfully amplified. As a result, it is apparent that this two-stage



**Figure 2.3 Thermal cycling conditions and resultant products from first and second rounds of amplifications.** Panel A illustrates the thermal cycling conditions for the primary and secondary amplifications. During the first round amplification (Panel A, left side) with gene-specific chimeric primers, step-down thermal cycling PCR conditions involve decreasing the annealing temperature by 1°C per cycle beginning at 62°C for 10 cycles and the subsequent 24 cycles have a set annealing temperature of 52°C. The graph on the right depicts the conditions for constant annealing temperature of 55 °C for the second round amplification using a common set of adaptamers primers complementary to the entire set of first round products (Panel A, right side). Panel B illustrates one half (48 reactions) of the results from the primary (above) and secondary (below) amplification of one 96-well plate. Lanes 2 and 6 (arrows 1 and 2) illustrate the product ‘leveling effect’ on the yields of product due to the secondary amplification with adaptamer primers. Lanes 9, 14, and 35 (arrows 3, 4, and 7) illustrate missing or double products which are scored as bad and have new primers designed for subsequent use in another PCR run. Lanes 17 and 34 (under arrows 5 and 6, respectively) contain molecular weight markers.

amplification strategy is highly successful, robust and efficient for the purpose of PCR amplifying multiple products for genome scale applications. The use of adapter sequences with identical  $T_m$ 's for the 2<sup>nd</sup> round of amplification optimized the yields, despite different product lengths and different template concentrations (which were dependent on the yield from the first round reactions). The enzyme and thermocycling conditions were also optimized. The choice of Platinum *Pfx* (Invitrogen) as the polymerase was determined to be crucial as was its use in conjunction with the proprietary reaction enhancer solution supplied with the buffer. Tests with alternatives, including mixes of *Taq* and *Pfu*, yielded less satisfactory results. All the images for the analysis of the PCR amplification are available at: <http://microbiology.okstate.edu/faculty/burnap/index.html>.

Organization and quality control were emphasized throughout production of the microarrays to ensure uniformity and accuracy. A semi-automated gel analysis procedure scored products on the basis of size and absence of multiplicity. All PCR products were documented by digital photography and the images quantitatively analyzed using *TotalLab*<sup>TM</sup> Phoretics gel analysis software (Nonlinear Dynamics, Durham, North Carolina). This application was found to be most accurate, user-friendly, and efficiently handled dual tier gels. Furthermore, as with other packages, it allowed simple export of the numerical results to Excel spreadsheets. A database was developed to integrate information, including gene sequences, oligonucleotide design, PCR product length, etc. In addition, Excel macros were developed to transform the aforementioned information to produce lists for each plate, which were then used to track and identify the location of the

arrayed elements under any condition, including the use of different array configurations. The scoring system, described in the Materials and Methods section, was set up to identify successful PCR amplified products.

DNA purification was simply and efficiently performed using filtration-type purification plates. Early issues with variation in printed spot morphology were resolved by pre-rinsing the filters: apparently this removes material acting as a surfactant and affects the spot morphology and/or drying characteristics. Alternatives such as ethanol or isopropanol precipitations were explored, but for the chosen PCR conditions, produced less reliable results and appeared to cause the co-precipitation of non-DNA material that interfered with downstream operations. The nature of this material remains undefined, although it may be due to constituents of the PCR reaction proprietary enhancer that is supplied with the *Pfx* polymerase. The concentrations of the purified DNA fragments were determined (Molecular Devices Spectramax Plus) and a Qiagen Bio-Robot 3000 was used to dilute the DNA samples to 500 ng/ $\mu$ l in 2X spotting solution. Tests showed that the combination of Superamine slides and MSP printing buffer solution from Telechem provided the best combination of spot morphology, retention of DNA after processing of slides and signal-to-noise ratio after hybridization. Alternately, Clontech type II slides in combination with the Telechem spotting buffer also gave good results in terms of printing and hybridization results. Tests with other buffer systems, e.g. 6X SSC and 50% DMSO, gave less satisfactory results under the specified printing conditions. The synthesis and hybridization of the fluorescently labeled cDNA derived from sample RNA is outlined in Table 2.2.



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**Table 2.2: Synthesis and hybridization of fluorescently labeled cDNA derived from sample RNA**

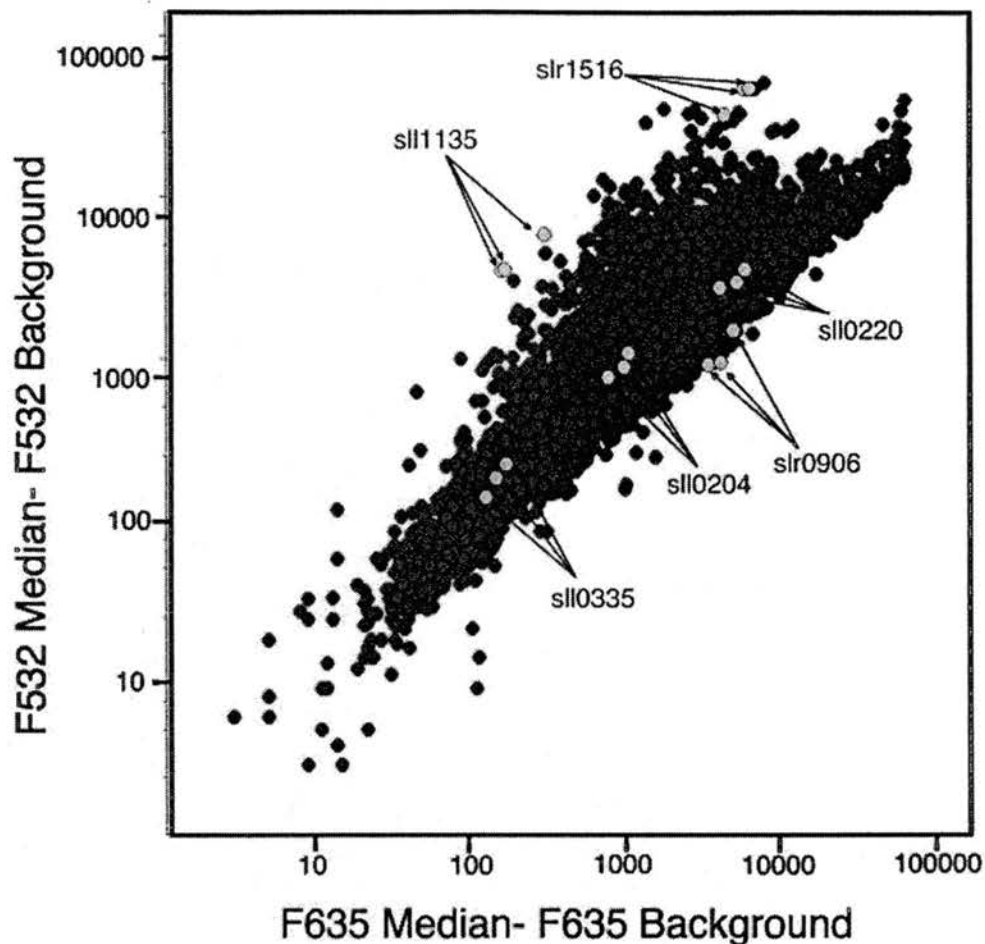
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Hybridization of the microarray with sample representing the mRNA population is accomplished by synthesizing complementary DNA (cDNA) using reverse transcriptase. Microarray experiments in prokaryotic organisms cannot utilize the poly(A) tails found in eukaryotic mRNA; thus, alternatives to the highly successful methods employed for generating fluorescent cDNA using oligo-dT to prime the reverse transcription labeling reaction have to be employed.

- cDNA synthesis Tests comparing random hexamers and random octamers gave essentially indistinguishable results. On the other hand, critical parameters for maximizing signal-to-noise were: 1.) high level of incorporation of fluorescent dye by using a high ratio of amino allyl dUTP in the reverse transcription reaction and saturating amount of reactive dye during the coupling of activated dye; and 2.) the use of two purification steps relying on independent physical separation principals applied to the test sample: first after cDNA synthesis and second, after the coupling of fluorescent dye. Direct chemical labeling of RNA, while attractive, did not allow as high signal-to-noise during our tests. Similarly, pilot experiments using pooled 3' gene-specific oligos as cDNA primers did not give better results.
  - Hybridization: While increases in signal-to-noise were associated with optimization of fluorescent sample production (above), a fairly wide range of standard microarray pre-hybridization and hybridization protocols were found to give comparable results. However, critical aspects of the described method were keeping the microarray slide warm during the addition of sample to the surface following pre-hybridization and ensuring that the slide remains hydrated prior to the final drying immediately before scanning.
-

In order to generate uniform spot morphology and to maximize DNA concentration and consistency for each spot across the array, all products were printed at the same concentration. This was accomplished using the Qiagen Bio-robot 3000™ to resuspend each of the purified PCR products to the same concentration, based on the results of the Spectramax UV analysis. These products were then mixed with an equal volume of 2X MSP printing buffer from Telechem and two aliquots were transferred via the Bio-robot to separate printing plates. The use of this robotic transfer reduced the chance for human error, increased the rate of transfer (thus reducing the exposure of the products to desiccation), and increased the reproducibility of the transfer. Syto-61 staining was regularly used to maintain a high level of quality control during the printing process.

Several internal and external comparisons were analyzed to demonstrate the effective use of the arrays. Internally, the use of triplicate spotting of all array elements and distribution of the triplicate elements in different regions of the array allows the comparison of hybridization uniformity across the array, as depicted in Figure 2.4. Initially, we determined the effectiveness of printed slides by hybridization with total RNA from control and salt-stressed cells. The results were compared with that of the published report from Kanasaki et al. (6). Similar patterns of regulation of specific transcripts were observed and several examples of the differentially regulated genes are indicated in Figure 2.4. Qualitatively similar results using a direct RNA-dye coupling procedure can be achieved using the Micromax™ ASAP RNA Labeling Kit (Perkin Elmer Life Sciences, Inc. cat. No. MPS544) following the manufacturer's suggested



**Figure 2.4** Scatter-plot of differential hybridization of fluorescently labeled cDNA from a 3-hour salt shock treated cell culture versus an untreated sample. Log phase cultures were subjected to an upshift in NaCl concentration from ~25 mM to 650 mM. *Synechocystis* is halotolerant and grows at concentrations up to approximately 1.2 M NaCl. Fluorescently labeled (Cy-3) cDNA derived from total RNA extracted from cells exposed for three hours to the higher salt concentration was co-hybridized with Cy-5-labelled cDNA derived from the culture immediately prior to the upshift (control cells). The full genome *Synechocystis* sp. PCC 6803 high-density microarrays contain DNA features printed in triplicate on glass slides. The gene names according to original annotation are behind the arrows. As indicated with arrows, signals from the replicated elements exhibited similarity in the estimated expression ratio. Each data point corresponds to a different gene address on the microarray and each gene is replicated at three separate and spatially distant addresses. The X and Y axes correspond to the normalized fluorescence intensity of fluorescence-labeled cDNA of the control sample (Y-axis, Cy-3, 532 nm fluorescence) and the 650 mM NaCl three hour time point (X-axis, Cy-5, 635 nm fluorescence).

protocol. While it is significantly quicker and requires less manipulation, the direct chemical labeling kit is more expensive, and produces a final RNA product which is less stable than cDNA. Specifically, direct labeling has thus far not provided a hybridization signal-to-noise ratio which compares to that of the indirect approach of coupling dyes to cDNA.

Substantial effort was devoted to ensure spot uniformity, high signal-to-noise ratio, and good statistical reproducibility. It is apparent that these arrays meet these objectives, and relate favorably to the best of current prokaryotic and eukaryotic arrays. The strengths of these *Synechocystis* arrays include: 1.) consistent and high DNA concentrations in each of over 11,000 spots per array; 2.) three replicates per probe per slide; and 3.) high signal-to-noise ratio. This last parameter is due to the quality of the slides, the hybridization procedures utilized and the quality of the products printed. These arrays have been used to develop a set of robust statistical tools for the analysis of the microarray data. The analysis involves an ANOVA model that makes excellent use of the technical replicates designed into each slide and a loop design (Singh, McIntyre and Sherman, unpublished results). The availability of large quantities of DNA, the ability to print many slides and the statistical tools will enable us to analyze transcriptional changes under many environmental conditions and for many mutants. The two-stage amplification procedure also provides full gene copies for techniques like PCR-fusion mutagenesis. This will permit many comparisons among different conditions and should greatly facilitate functional genomics. In conclusion, the two-stage PCR

amplification strategy detailed here is demonstrated to be highly useful and undoubtedly can be applied to other bacterial species.

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## **Chapter III**

# **Optimization of Fusion PCR for *In Vitro* Construction of Gene Knockout Fragments**

Hong-Liang Wang, Bradley L. Postier, and Robert L. Burnap

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## Introduction

Some eukaryotic and prokaryotic organisms such as *Saccharomyces cerevisiae* and *Synechocystis PCC6803* (hereafter referred to as *Synechocystis*) spontaneously take up foreign DNA and can integrate this DNA into their genomes via homologous recombination (5). This property provides the opportunity to knock out genes in these model organisms by transformation with linear DNA in which a selectable marker is flanked by chromosomal sequence surrounding the targeted gene. For this reason, a fusion PCR strategy has been developed to rapidly construct this kind of fragment *in vitro* (1). This report describes efforts made to optimize the fusion PCR for the construction of gene knockout fragments in the widely-used cyanobacterial model organism *Synechocystis* sp. PCC 6803.

## Methods, Results and Discussion

The genomic sequences of *Synechocystis* were obtained through CyanoBase (<http://www.kazusa.or.jp/cyano/cyano.html>) in this study. All primers were designed to amplify the gene-flanking segments through a web-based program (<http://genome-www2.stanford.edu/cgi-bin/SGD/web-primer>) (Table 3.1). Each primer was 23-26 bases in length, with a 58-62°C melting temperature. The plasmids serving as a source of template used to amplify the selectable cassettes of chloramphenicol (*Cm*), kanamycin (*Km*) and streptomycin/spectinomycin (*Sm/Sp*), respectively, were members from the set of plasmids produced by the Wolk group (2).

For the amplification of flanking regions of a target gene, the primers distal from the selectable marker insertion site were simple primers complementary to the target

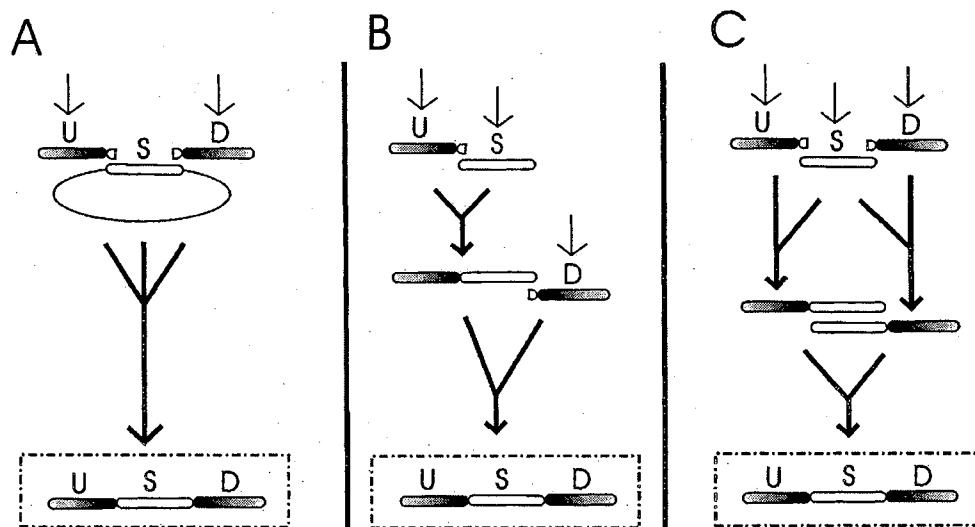


sequence; the primers proximal to the insertion site were chimeric: their 5' end was complementary to the primers used to amplify the selectable gene and their 3' end is complementary to the target sequence. The products of this primary amplification were purified by electrophoresis through 1% low-melting agarose. Target bands were excised and stored in 1.5 mL Eppendorf tubes at  $-20^{\circ}\text{C}$  prior to usage. The frozen gel slices were centrifuged and the resulting supernatants were used as templates in the following fusion PCR experiments exhibiting differential performance, depending on the combinations of templates (Figure 3.1).

To assure the fidelity of the amplified sequence, a proofreading DNA polymerase was generally employed for all amplifications for the synthesis of the mutagenic fragment (1). As mentioned above, the sequences mediating the fusion are added to the 5' end of one primer of each primer pair for the amplification of flanking regions. This additional sequence may cause PCR difficulty. In some cases, the desired PCR products are not even abundant enough to be visible on the gel, despite extreme care in the design of the primers and execution of the reaction. One solution is to use PCR enhancers such as betaine, DMSO, formamide or glycerol to improve the match of primer and template during the annealing. Therefore, effort was expended to evaluate the effects of these PCR enhancers on the production of the chimeric PCR products. Platinum *Pfx* DNA polymerase in combination with its enhancer (Life Technologies, Rockville, MD, USA) was identified as an ideal candidate for the application. The enzyme is supplied with an enhancer, a co-solvent purported to have no negative effect on the proofreading capacity of *Pfx* DNA polymerase based on the manufacturer's tests (3). The additional, but important advantage is that the enzyme produces a high-yield of PCR products as

Primer	Sequence (5' → 3') <sup>a</sup>
<i>sll0247</i> <sup>b</sup>	
upstream	ATCAATTACTTCCAGCACCACGTC GTTTGTTCGCCAGCTTCTGTATGATAGGTTTGCACAGAATTGCCTC
<i>slr1595</i> <sup>b</sup>	
upstream	AATACCATCACCGACCCATTTAAGG GAAGACGAAAGGGCCTCGTGATACTATTGGTGTCCATCGTTGTGATGC
downstream	GATGAATGGCAGAAATTCGAAAGCCCCAGCCATTAATAATCCATTA CATTACCCTGGCGACTATTTACCAA
streptomycin/ spectinomycin	CATACAGAAGCTGGGCGAACAAAC TTGTGTAGGGCTTATTATGCACGC
chloramphenicol	GTATCACGAGGCCCTTTCGTCTTC GCTTTCGAATTTCTGCCATTCATC

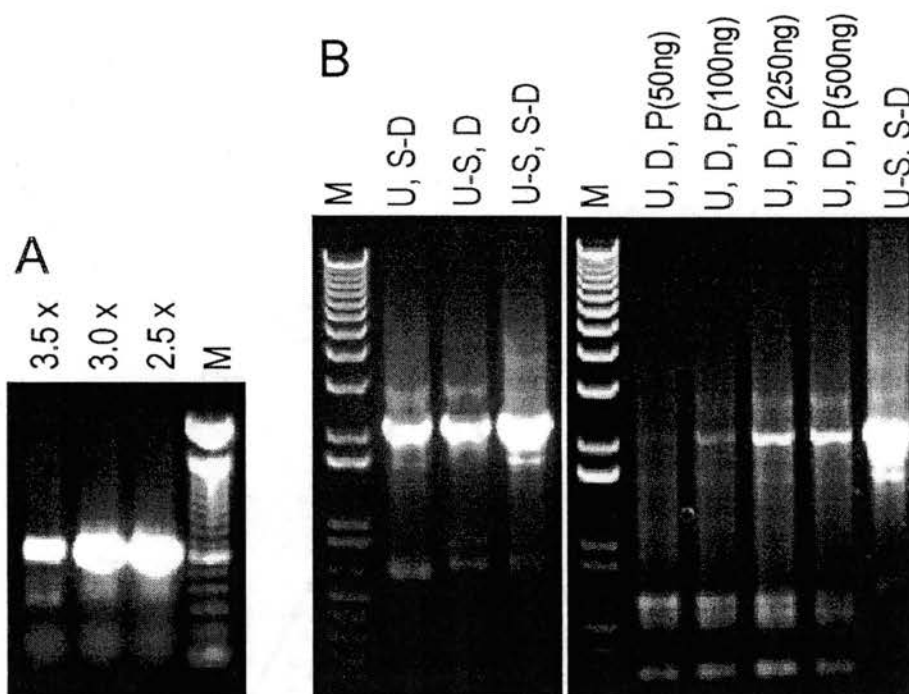
**Table 3.1 Sequences of primer pairs used to amplify flanking regions of target genes in *Synechocystis* sp. PCC 6803 and selectable markers. a. Boldface indicates homology to selectable marker. b. Gene identification numbers as in CyanoBase (<http://www.kazusa.or.jp/cyano/cyano.html>)**



**Figure 3.1 Comparison of fusion PCR strategies for *in vitro* construction of gene knockout fragments developed in this study and elsewhere.** The gene knockout fragment consists of three parts. Two PCR amplified products, having sequences homologous to the flanking regions of the targeted gene to be replaced, flanking a selectable marker gene such as an antibiotic resistance cassette (U and D, up- and downstream flanks of target gene respectively; S, selectable marker). The flanking regions include ~24 bases of sequence introduced through amplification with bipartite primers having homology to the selectable marker gene at their 5' end. Method (A) uses two standard primary PCR reactions (thin arrows) to produce the flanking regions U and D from chromosomal DNA. These fragments are then mixed with a plasmid carrying the selectable marker gene and in one fusion PCR reaction (thick arrows), are fused to the selectable marker. The second method (B) employs the same modified flanks and a PCR amplified selectable marker gene, but uses them in two separate fusion reactions increasing the probability of success. Using the product of the fusion of the upstream flank to the selectable marker as template, the downstream flank is introduced through a second fusion event. The final method described here (C), uses the same primary amplified products as in (B), and three fusion events. The first two are the fusion of each flank to the selectable marker separately. The products of these two reactions are then combined for a final fusion event again dependent on the homologous sequence, which here includes the entire selectable marker gene.

compared with other proof-reading DNA polymerases such as *PfuTurbo* (Stratagene, La Jolla, CA, USA). 1-3 × enhancer was often enough to achieve the success of difficult amplifications (Figure 3.2A). The high yield of PCR products was achieved with an optimized concentration of the enhancer. As a result, enriched templates after gel purification greatly improved the following fusion PCR. Individual amplification reactions contained 1 × *Pfx* amplification buffer, 0.2 mM each dNTP, 1mM MgSO<sub>4</sub>, 1 μM each primer, 500 ng template of chromosome DNA, 1-3 × Enhancer, and 2.5 units Plantinum *Pfx* DNA polymerase in a final volume of 100 μL. The cycling conditions started with a longer denaturation step at 94°C for 3 min, followed by 35 cycles of 94°C for 30 s, 55°C for 1 min, and 68°C for 1 min per kb. After completion of all 35 cycles, a final extension step at 68°C for 10 min was undertaken. Fewer cycles (25 versus 35) can also be used to minimize the error frequency, but often at some sacrifice in yield. The orange band of PCR products from 100 μL reaction was often visible on the gel containing 0.5 μg/ml ethidium bromide after electrophoresis. Therefore, the target fragment could be readily excised without the exposure of UV light.

For the step of fusion PCR, *Taq* DNA polymerase is generally employed because proofreading DNA polymerase is sensitive to template sources containing a garose and electrophoresis buffer (1). A compromise was adopted by using mixed DNA polymerases that keep 3'-5' proofreading activity and also improve the yield at the same time (Figure 3.2B). The optimized reaction of fusion PCR contained 1 × *Taq* amplification buffer (50 mM Tris-HCl, pH 8.0, 100 mM NaCl, 0.1 mM EDTA, 1 mM DTT, 50% glycerol and 1% Triton X-100), 0.2 mM each dNTP, 1.5 mM MgCl<sub>2</sub>, 1 μM



**Figure 3.2 Optimization of fusion PCR steps for *in vitro* construction of gene knockout fragments.** An equal volume of each 100  $\mu$ L PCR reaction was separated by size on an agarose gel and stained with ethidium bromide. (A) The amplification of the upstream flanking region of *slr1595* in *Synechocystis* with Plantium *Pfx* DNA polymerase and 2.5, 3.0, 3.5  $\times$  PCR enhancer supplied (Life Technologies). This PCR reaction did not work well without the addition of PCR enhancer. M, 100 bp DNA ladder (Life Technologies). (B) Final fusion PCR for the construction of *slr1595* knockout fragment with different combinations of templates. Mixed *Taq* (Promega) and *Pfx* DNA polymerases were used. M, 1 kb plus DNA ladder (Life Technology); U and D, up- and downstream flanking regions of *slr1595*; S, *Cm* resistance cassette; P, plasmid providing *Cm* cassette with the amount of plasmid used is indicated in parentheses; U-S and S-D, fused intermediate fragments.

each primer, 5  $\mu$ L each purified template, 1.25 units *Taq* DNA polymerase (Promega, Madison, WI, USA), and 1.25 units Platinum *Pfx* DNA polymerase in a final volume of 100  $\mu$ L. The cycling conditions started with a longer denaturation step at 94°C for 3 min, followed by 35 cycles of 94°C for 1 min, 55°C for 1 min, and 72°C for 1 min per kb. Again, fewer cycles (e.g. 25 versus 35) can also be used to minimize the error frequency. Again, after cycling, a final extension step at 72°C for 10 min was undertaken. The PCR fragments were collected by ethanol precipitation and were dissolved in sterile water for the use in transformation. It is worth while to mention that high-yield *Pfx* DNA polymerase alone could produce a reasonable amount of fusion fragments even in the presence of the template sources contaminating agarose and electrophoresis buffer according to these tests. Therefore, this proof-reading enzyme could be employed alone to complete all steps of fusion PCR for specific applications.

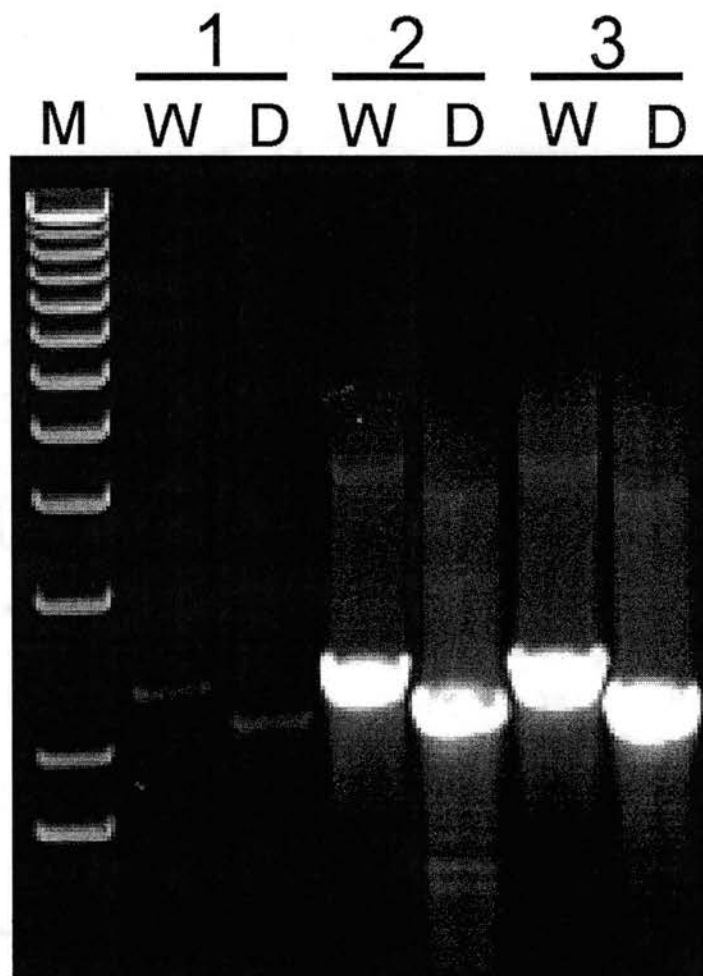
In the original strategy developed by Amberg, Botstein and Beasley, one flanking sequence is fused to a selectable marker first and then a second one is fused to the purified intermediate fragment subsequently (1). However, this is not the optimal solution because the yield of final fused fragment is still quite low often as a result of unstable match of two templates through only ~24 bases of primer sequence introduced (Figures 3.1B, 3.2B). The yield of the final fused fragment was much higher in the case where both intermediate fusion fragments were used as the templates for a final fusion PCR, i.e., the two flanking sequences were separately fused to a selectable marker and subsequently, both purified intermediate fragments served as templates for final fusion PCR (Figures 3.1C, 3.2B). The entire sequence of the antibiotic cassettes can be annealed when two intermediate fragments serve as template in the final fusion PCR.

Therefore, the match of the two intermediate fragments is much more stable than that of only ~24 bases of primer sequence introduced. Transformation with linear DNA generally demands a large amount of DNA fragments. Moreover, the fragments produced in high-yield PCR can be divided into aliquots for more than one usage. Therefore, it is necessary to improve the yield of desired fragments in the final fusion PCR.

Recently, another option has been developed to conduct fusion PCR (4, 6). This alternative utilizes two purified flanking sequences combined with a plasmid carrying the selectable marker that together serve as the templates for one-step fusion PCR (Figure 3.1A). It seems to be a simple strategy since only one round of fusion PCR is required in this case. This option was tested with three plasmids carrying *Cm*, *Km* or *Sm/Sp*. However, none of the desired fragments could be visible on the gel for two of the three plasmid templates. The yield of desired fragments was much lower, even when fusion PCR was successful for this combination of templates (Figure 3.2B). Moreover, there were more nonspecific products. This kind of fusion PCR could be partially improved by increasing the concentrations of plasmid templates. Apparently, the poor PCR performance results from the unstable matching of the templates through the use of only ~24 bases of primer sequence introduced. The other drawback to this method is that it requires two rare fusion events to occur in the same PCR reaction for success, which often is difficult to achieve. This strategy for fusion PCR may depend largely on the sequence of the gene flanking regions and the plasmid providing the selectable marker.

Currently, colony PCR has become popular in monitoring the segregation of gene disruption after transformation. Unfortunately, some eukaryotic and prokaryotic organisms such as *Saccharomyces cerevisiae* and *Synechocystis* possess cell walls, causing extra difficulty in releasing genomic DNA during colony PCR. It is necessary to optimize colony PCR in order to assure constant performance and also increase its sensitivity to confirm complete segregation. For this reason several conditions have been tested to improve colony PCR in *Synechocystis*. As shown in Figure 3.3, even when *Synechocystis* colonies were pretreated with Lyse-N-Go PCR reagent (Pierce, Rockford, IL, USA), the yields of PCR products were still low. In contrast, it was found that the colony PCR of *Synechocystis* was markedly improved with the use of Herculase DNA polymerase buffer (Stratagene) (Figure 3.3). The addition of DMSO could further increase the yield of PCR products (Figure 3.3). The use of Herculase amplification buffer during colony PCR enhances detection of segregation patterns by improving the yield of the products. The combination of Herculase buffer with other mixed enzymes such as *Taq* (Promega) and *Pfx* DNA Polymerase can also achieve the high yields of colony PCR products in *Synechocystis*, however no other suitable amplification buffer has been found to be as effective as Herculase buffer. It is not possible to define which substance in the buffer aids difficult colony PCR since the components of the buffer would not be released by the supplier. The YieldAce DNA Polymerase system (Stratagene), was also tested, but was not found to be helpful for this particular application (data not shown). Individual amplification reactions contained 1 × Herculase amplification buffer, 0.2 mM each dNTP, 1 μM each primer, 3-6 colonies of bacterium, 2.5 units Herculase or the same units of other mixed enzymes such as *Taq* (Promega) and Platinum *Pfx* DNA polymerases with the ratio of 1 : 1, and 0-3% DMSO in a final





**Figure 3.3 Colony PCRs of *Synechocystis* with *Taq* or Herculase DNA polymerases.** An equal volume of each 100  $\mu$ L PCR reaction was separated by size on an agarose gel and stained with ethidium bromide. (1) *Taq* DNA polymerase (Promega). Colonies were treated with Lyse-N-Go PCR reagent (Pierce) prior to PCR. (2) Herculase DNA polymerase (Stratagene). (3) Herculase DNA polymerase and 3% DMSO. M, 1 kb plus DNA Ladder (Life Technology); W, wild type; D, deletion mutant in which *slr1595* was substituted with a *Cm* resistance cassette.

volume of 50  $\mu$ L. The cycling conditions started with a longer denaturation step at 95°C for 5 min, followed by 30 cycles of 94°C for 1 min, 80°C for 15 s, 65°C for 15 s, 55°C for 1 min, 65°C for 15 s, 72°C for 1 min per kb, and 85°C 15 s. A final cycle at 94°C for 1 min, 55°C for 1min and 72°C for 10 min were undertaken.

In summary, mixed *Taq* and proofreading DNA polymerases can be employed to achieve the high yield and sequence fidelity in the application of fusion PCR. The match of templates is much more stable in the case where two intermediate products having long stretches of overlapping homology serve as the templates in the final fusion PCR, thereby specifically enhancing the synthesis of target fragments. For the difficult colony PCR of bacteria that possess thick cell walls, it is worthwhile to attempt the combination of Herculase amplification buffer and mixed DNA polymerases that greatly enhance colony PCR performance.

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## Chapter IV

# **Global gene expression profiling and physiological analyses of salt stress and acclimation in *Synechocystis* sp. PCC6803**

## Abstract

The time course of the salt stress response in the cyanobacterium *Synechocystis* sp. PCC6803 was analyzed by DNA microarray expression profiling in conjunction with physiological characterization. A multiphasic change in growth rate was observed, following an upshift from 36 to 650 mM NaCl, in exponentially growing cultures. These changes in growth rate during the adaptation to high salt were paralleled by characteristic changes in global gene expression. Superoxide accumulation showed a large increase associated with salt stress. The accumulation was dependent on light and was sensitive to DCMU indicating that it depends upon the photosynthetic light reactions. Parallel measurement of several photosynthetic parameters shows that the inhibition of the light reactions of PSII and PSI may be coupled to reduced  $C_i$  fixation. This is hypothesized to account for the production of  $O_2^-$ , presumably via the Mehler reaction at PSI, and rapid induction of superoxide dismutase. These results are consistent with the concept that the balance in the capacities and activities of the light reactions and the inorganic nutrient fixation reactions determines the light level that becomes damaging. This in turn, helps explain important commonalities of responses to a variety of stresses in plant, algae, and cyanobacteria.

## Introduction

*Synechocystis* PCC6803 (hereafter referred to as *Synechocystis*) is a robust microorganism. It is capable of oxygenic photosynthesis and photo-heterotrophic

growth, and has the capacity to respond to and survive a variety of environmental stresses (2). Because of these properties, *Synechocystis* has served as a model for understanding the function and regulation of the network of bioenergetic complexes in response to stress. It is hypothesized that mechanisms of resistance which are available to *Synechocystis* may be engineered into higher plants to improve their resistance to various types of stress. With this in mind, this work focuses on the responses of *Synechocystis* cells to treatments with high salt.

Naturally occurring salt stress can take many forms. Exposure may vary in severity, and may be sudden, drawn-out, or recurrent over time. The composition of the salt solution is typically mixed, but sodium is almost invariably the main cation. In addition, salt stress is typically coupled to other stresses such as high light or drought. To simplify analysis, this work looks at the effect of, and response to, hyperosmotic shock with NaCl without the influence of altered light or water availability. It is important to note that salt concentration can affect both the sensitivity to light and water availability and this relationship will be discussed in greater detail here.

#### *Effects of salt stress: osmotic potential and Na<sup>+</sup> toxicity*

The effects of salt stress on microbial organisms can be separated into two parts. At the cellular level, high salt shock imposes a hyperosmotic stress which targets the cytoplasmic and periplasmic membranes. At the molecular level, high salt shock is manifested as sodium toxicity. Sodium toxicity is more complex than osmotic stress. It is known to directly affect macromolecular structure and interactions as well as interfere with specific sites of catalytic activity (12, 27).

Hyperosmotic shock occurs when the solute concentration outside of the cell is suddenly and drastically increased to levels much greater than that to which the cell was previously exposed. Thus, an osmotic potential gradient is created across the membranes. Cellular membranes are less permeable to salts than to water. As a result, water rushes from the cell through water channels to balance the solute concentration between the cell and the environment (21, 24, 30). This effectively increases the solute concentration within the cell until it is equal to that outside. This high salt state is reached within one second (23). While this mechanism allows the cell to maintain its membranous structure by alleviating the osmotic stress, it does nothing to protect from the salts already present in the cell which are now concentrated. This condition is unfavorable, as microbes require internal turgor pressure to force cell expansion during growth.

In response to low osmotic potential, bacteria enhance production of compatible osmolytes or compatible solutes (7-10, 22). Osmolytes such as sugars, sugar alcohols, certain amino acids, or other soluble compounds accumulate within the cell and induce an osmotic potential to negate the effects of high salt shock. These osmolytes balance the cellular osmotic potential against the high external osmotic potential, but without introducing additional sodium toxicity. In this way, there is no net movement of water across the membranes and therefore no tendency for the cells contract or expand. Many of these osmolites, including betaine, glucosylglycerol, and proline also inhibit the damaging effect of sodium toxicity as discussed later. Another protective mechanism is to actively transport inward other positively charged ions, most commonly potassium,

into the cytoplasm. This requires energy as the potassium must be transferred against the natural gradient.

Sodium toxicity affects biological organisms at the molecular level in several ways. Hydrophobic and electrostatic interactions stabilize macromolecular structures. Both of these properties are altered under high salt conditions. Ions inherently associate within hydrophilic environments, and are excluded from hydrophobic environments. Therefore, when sodium accumulates in the cytoplasm, it causes the compression or collapse of the hydrophobic core of many proteins (19). The crowding of ions around a protein effectively shield electrostatic interactions, and slow or inhibit the electrostatic interaction between two molecules (31). At extremely high concentrations, the ions can prevent the normal ordering of water around macromolecular complexes (water shell) and can inhibit activity due to their inability to have a normal hydration layer (12).

One example of sodium toxicity involves RubisCO (Ribulose-1, 5-bisphosphate carboxylase/oxygenase, EC 4.1.1.39). RubisCO, the main carbon fixing enzyme of plants and cyanobacteria, is differentially inhibited by high salt (27). The RubisCO enzyme complex has two specific activities associated with it. In brief, the carboxylase activity builds carbon skeletons from  $\text{CO}_2$ , and the oxygenase activity initiates catabolism of the carbon skeletons, ultimately releasing  $\text{CO}_2$ . At 200 mM NaCl, the oxygenase activity of RubisCO is enhanced while the carboxylase activity is decreased. This reduces the production of carbohydrates and could, if left unchecked, become lethal.



A primary strategy for alleviating  $\text{Na}^+$  toxicity is the expulsion of this ion from the cytoplasm. There are several mechanisms known, including translocating pumps, which may depend on a proton gradient, may be coupled to the hydrolysis of ATP, or the oxidation of NADP(H) by NADP-dehydrogenase like complexes (15, 16, 25, 29, 35). These, however, require the expenditure of energy to drive the expulsion of sodium. Another common mechanism employed is to decrease the local concentration around macromolecular complexes. Sugars and sugar alcohols produced in response to osmotic stress crowd macromolecular complexes, protecting them from other dissolved ions without greatly affecting the water shell (18). Unfortunately, some osmolytes are known to inhibit specific protein activities (26, 28). However, under certain circumstances these effects may be beneficial as well. The amino acid proline is commonly accumulated in higher plants in response to osmotic stress. At concentrations as low as 50 mM, proline equally inhibits both the carboxylase and oxygenase activity of RubisCO. However, when it accumulates in combination with 200 mM NaCl it preferentially enhances the relative carboxylase activity. This reverses the effects that NaCl alone has upon RubisCO activity (27).

Due to its inherent similarities to higher plant chloroplasts, *Synechocystis* has served as a frequently used model for the analysis of salt stress. *Synechocystis* can tolerate up to 1.2 M NaCl and it can grow at lower rates in media containing 684 mM NaCl. More specifically, 650 mM NaCl shock stress is potent enough to temporarily inhibit protein synthesis and growth in *Synechocystis* (11). It enhances superoxide production, and is associated with considerable changes in energy metabolism (14, 32).

Other findings of importance which have been observed in related organisms include the disruption of carboxysomes, and the inhibition of carboxylase activity by RubisCO as mentioned above.

### *The response to salt stress by Synechocystis 6803*

Several of the mechanisms mentioned above are involved in the response by *Synechocystis* to salt stress. Most notably, it accumulates the osmolyte glucosylglycerol. Genetic analysis has identified three proteins, StpA, GgtA, and GgpS responsible for the production and transport of glucosylglycerol (6-8, 10). These proteins are constitutively expressed under normal conditions and are activated only after the onset of salt shock. Following exposure to 684 mM NaCl glucosylglycerol accumulates gradually until it reaches a maximum approximately 24 hours after the onset of salt stress. Interestingly, the increase in glucosylglycerol correlates with the gradual restoration in net protein synthesis, which is virtually abolished in the initial phase of salt stress and reaches a new stable rate at the same time glucosylglycerol accumulation reaches its plateau (20).

Several potential mechanisms for Na<sup>+</sup> efflux have been identified in the sequenced genome of *Synechocystis* (33). Six genes show homology to Na<sup>+</sup>/H<sup>+</sup> antiporters, none of which are essential for growth and only one is necessary for normal growth under high salt conditions. In addition, only one of seven putative Na<sup>+</sup>-ATPase deletion strains have shown high salt sensitivity. Conversely, it appears that the majority of these genes may be responsible for Na<sup>+</sup> import under low salt conditions. One other antiporter (sll0556, *nhaS6*) though not mentioned in the referenced report also has not shown a high salt sensitivity phenotype. (Hong Wang, personal communication)

Two potassium transport systems have been identified in the genome of *Synechocystis*. A Ktr-like system encoded by slr1509 (*ntpJ*) is reported to be the major potassium transporter used by *Synechocystis* under salt stress or low potassium conditions (1). NtpJ is a Na<sup>+</sup>/K<sup>+</sup> symporter requiring an inward Na<sup>+</sup> gradient. A second gene cluster also encodes proteins showing homology to the Kdp-ATPase potassium transporter of *Escherichia coli*. Mutants of *ntpJ* show some phenotypic differences from Wild-type including reduced growth under salt stress conditions whereas mutants of *kdpA* are generally indistinguishable from wild type strains. This indicates that the Ktr-like system in *Synechocystis* plays the predominant role in potassium influx during salt stress. Double mutants in the two loci could not be produced suggesting that at least one of the two is required for growth. Despite their apparent involvement in cell viability during salt stress, previous reports on transcriptional expression do not identify them as significantly induced at 3 or 12 hours after salt shock.

Many changes in cellular physiology have been associated with salt stress beyond that of simply producing compatible osmolytes. The response to salt stress includes many mechanisms which require energy in some form. To accommodate this, the bioenergetic complexes present in the thylakoid and cytoplasmic membranes alter their specific activities. Respiration and cyclic electron flow around Photosystem I (PSI) are increased (14). This enables H<sup>+</sup> translocation across the thylakoid membrane while becoming less dependent on PSII to contribute to electron transport. This is suggested to alleviate any additional damage to Photosystem II (PSII) due to over-reduction.

However, *Synechocystis* depends greatly on carbon fixation and therefore linear electron transport must have recovered during times of rapid growth. It is our argument that the changes in respiratory and photosynthetic activity are transient, and that acclimation to long term exposure includes the recovery of non-cyclic electron transport. Note that the salt acclimated growth, photosynthetic activity, and superoxide production in *Synechocystis* has not been reported yet in detail. Several questions remain concerning the long term response in both ionic homeostasis, and bio-energetic organization.

This study combines DNA microarray technology to monitor transcript abundance, and several non-invasive techniques to monitor corresponding physiological changes in photosynthetic activity during salt shock and after acclimation to high salt conditions. Observations made here support the hypothesis that many of the changes in photosynthetic physiology previously correlated with salt stress are transient solutions to the demand for a proton gradient, and that a time course of response to salt stress (650 mM NaCl) occurs over an 18 to 24 hour period. Furthermore, these results show that the photosynthetic activity of exponentially growing high salt acclimated cells is similar to cells exponentially growing under low salt conditions. In addition, the rate of superoxide production has diminished greatly after acclimation and remains only slightly higher than immediately prior to salt shock. This also corresponds to a reduced expression of superoxide dismutase (*sodB*) after acclimation relative to immediately after salt shock, as observed through DNA microarray analysis. Overall, the differences between gene expression profiles of salt acclimated cultures and low salt cultures are largely restricted

to genes involved in ion homeostasis, osmotic potential, and many unknown or hypothetical genes.

## **Materials and Methods**

### *Culture conditions and RNA isolation*

Cultures were grown in batch mode using BG-11 media as described by Williams (34) supplemented with two times iron and bubbled with air enriched with 3% CO<sub>2</sub>. One liter Roux culture flasks containing 700 ml cultures were maintained in a waterbath at 32°C under constant illumination with white fluorescent lights at 80  $\mu$ moles photons m<sup>-2</sup> s<sup>-1</sup>. All salt shock treatments were performed by the addition of crystalline NaCl (final concentration of 650 mM) to a logarithmically growing culture at an optical density within the range of 0.8 to 1 at 750 nm. Cultures for salt acclimated experiments were maintained in the same fashion by continuous sub-culturing of salt-shocked cultures. Once shocked cultures resumed growth and reached an optical density of 1.5, they were repeatedly transferred into fresh high salt media (650 mM NaCl) at an optical density no lower than 0.4 units.

Cells were harvested by brief centrifugation, flash frozen with liquid nitrogen and stored at -80°C. Control or time 0 hour cells were harvested during mid-log phase immediately prior to the addition of NaCl. Salt shocked cells were harvested at 1, 3, 6, 12, 18, and 24 hours after the addition of NaCl. Salt acclimated cells were harvested

after more than two successive subculturings of salt shocked cells in high salt media during mid-log phase. RNA was isolated by the hot phenol method described by Bhaya et al (3).

*Microarray analysis:*

*Preparation of Fluorescent-labeled Probes for DNA Microarray Analysis*

Fluorescently labeled cDNA was produced using a two-step procedure involving cDNA production from target RNA using a reverse transcriptase reaction incorporating aminoallyl-modified deoxynucleotide (aadUTP), followed by a second step involving chemical coupling of fluorescent dye (either Cy3 or Cy5) to the introduced amino moieties of the newly synthesized cDNA. The cDNA was synthesized from 16 µg total RNA using 8 µg random 8-base oligonucleotides (Sigma GenoSys) and Superscript II™ reverse transcriptase (Invitrogen). RNA samples were each mixed with random octamers in a total volume of 25 µl DEPC (diethylpyrocarbonate) treated water, heated to 65°C for 5 minutes and then transferred to 42°C. Subsequently, 25 µl of a premix containing 2 µl of 100 mM DTT (dithiothreitol), 10 µl 5X Superscript II First Strand buffer, 1 µl 50X aadNTP mix (25 mM dA, C, and GTP, 8.4 mM dTTP, and 16.6 mM aadUTP [Sigma Cat. No.A-5660]), 10 µl DEPC treated water, and 2 µl Superscript II was added to each tube. Following a two hour incubation at 42°C, 4 µl 50 mM EDTA and 2 µl 10 N NaOH was added to each tube and incubated at 65°C for 20 minutes to degrade RNA. The reaction was neutralized by the addition of 4 µl 5 M acetic acid. The cDNA was purified using Millipore Microcon 30 centrifugal filter devices by diluting the reaction mix with sterile deionized water to a volume of 500 µl according to the manufacturer's specifications.

Each of the two samples was washed five times using 500  $\mu\text{l}$  deionized water and the final retentate adjusted to approximately 50  $\mu\text{l}$  to facilitate handling. The resultant solutions were dried at room temperature in the Speed Vac, and the pellets were resuspended in 20  $\mu\text{l}$  0.1 M  $\text{Na}_2\text{CO}_3$  (pH 9.0) and mixed with 2  $\mu\text{l}$  of previously prepared Cy3 or Cy5 dye. Preparation of the dyes was performed in advance and involved dissolving one tube of powdered Cy3 or Cy5 dye (Amersham Pharmacia Biotech) respectively, in 55  $\mu\text{l}$  dimethyl sulfoxide and storing at  $-20^\circ\text{C}$  until use. The coupling reaction was carried out at room temperature in the dark for 1 hour. The reaction was quenched by the addition of 4.5  $\mu\text{l}$  4 M hydroxylamine, followed by incubation for an additional 5 min. The Cy3- or Cy5 dye-coupled cDNA samples were combined and purified using a Qiagen PCR product purification kit according to the manufacturer's specifications.

#### *Hybridization of DNA Microarray and Data analysis*

Labeled probes were adjusted to 14.75  $\mu\text{l}$  using a SpeedVac and mixed with the remainder of the hybridization components consisting of 2.5  $\mu\text{l}$  of 10  $\mu\text{g}/\mu\text{l}$  salmon sperm DNA, 8.75  $\mu\text{l}$  20X SSC, 0.25  $\mu\text{l}$  10% SDS, and 8.75  $\mu\text{l}$  formamide. The mixture was then heated for 2 minutes at  $99^\circ\text{C}$ , briefly centrifuged at high speed, and maintained at  $42^\circ\text{C}$  until use. DNA microarrays specific for *Synechocystis* 6803 were printed on Telechem slides as described in chapter two. Printed slides were baked at  $80^\circ\text{C}$  for 1 hour. The DNA on the microarray was subjected to UV-cross-linking at a dose of 150  $\text{mJ}/\text{cm}^2$ . The slides were washed twice for 2 minutes each at room temperature in 0.1% SDS and once in deionized water to remove unbound material. The slides were then

boiled in deionized water for 3 minutes to denature the printed DNA, dried using low speed centrifugation in a specialized microscope slide-accommodating rotor (Telechem). Prehybridization was performed by incubating the slide in a fresh 100 ml mixture of 25% formamide, 5X SSC, 0.1% SDS, and 1% BSA for 45 min. at 42°C in a Coplin jar. The slide was then rinsed under distilled water and dried using the same low speed centrifugation.

The slide was preheated at 42°C in a Telechem hybridization chamber by placing in a static 42°C incubator. The pre-warmed sample was pipetted and spread uniformly onto a pre-warmed 24 x 60 mm glass cover-slip (Fisher Scientific, Cat. No., 12-548-5P) and the pre-warmed slide was inverted and placed with the arrayed surface contacting the sample on the cover-slip surface. Deionized water (10 µl) was added to each of the reservoirs of a Telechem Hybridization Chamber, and the slide was transferred to and enclosed within the chamber. The slide was incubated in a static incubator at 42°C for 12-16 h. To complete the hybridization, the slides were washed by gently submerging in a 250 ml solution of 2X SSC and 0.1% SDS at 42°C for 5 minutes with gentle agitation provided by the slow rotation of a magnetic stir bar. The coverslips are allowed to slide off after submerging in the wash solution, prior to introducing the gentle agitation. The slide was transferred quickly to a solution of 0.1X SSC, and 0.1% SDS, incubated for 10 minutes at room temperature with gentle agitation. The slide was then washed five additional times in 0.1X SSC for one min. at room temperature. The slide was finally rinsed briefly with deionized water and dried by low speed centrifugation, and stored in the dark until scanned. Hybridization signals from the microarray were quantified using Axon GenePix Pro 4.1. The quality control procedures were conducted in the image



analysis software and then the data were saved and transferred to Acuity 3.1. For salt shock data, each microarray hybridization was normalized using the Lowess print-tip option available in the Acuity software. For salt acclimated conditions, two hybridizations were performed for each of three biological replicates and all data points were averaged together. The normalization procedures used on salt acclimated data are described in detail below. For the time course analysis of salt shock response, one hybridization from each of two biological replicates was performed. Unlike the salt acclimated condition, only technical replicates were averaged together, thus separating the two experiments into two independent time course analysis data sets. The results of individual  $t_3$  time points are comparable to previously reported data. All salt shock gene expression data is presented as  $\log_2(\text{experimental } (t_x) / \text{control } (t_0))$  where a two fold difference in expression correlates with values of  $\pm 1$ . Gene expression ratios for salt acclimated data are presented as ratios ( $\text{experimental } (t_x) / \text{control } (t_0)$ ) where a two fold difference in expression correlates with values of 2 (induced) or 0.5 (repressed).

#### *Salt acclimated array data analysis*

The analysis procedures for salt acclimated experiments are conducted in matlab software (Mathworks, MA). There are two steps in the analysis:

- 1) Normalization of array data. Normalization to correct for technical variation among individual microarray hybridizations was conducted using a two step procedure described in Dozmorov and Centola (4). In brief, the procedure is based on the fact that spot intensities from genes not expressed by the samples of interest constitute noise and are therefore normally distributed. The mean ( $S_0$ ) and standard deviation ( $SD_0$ ) of these

non-expressed genes were calculated using an iterative nonlinear curve fitting procedure and used as background parameters for normalization using the formula  $S'=(S- S_0)/ SD_0$ . After the first step, the normally distributed background signal for nonexpressed genes has a mean of 0 and standard deviation (SD) of 1.

A second normalization step is then performed using genes significantly expressed above background ( $>3SD$  above background). Gene expression values are log transformed, with negative values substituted by the lowest positive logarithmic value obtained. Expression profiles of genes statistically significantly expressed above background are then adjusted to each other using a robust regression procedure. This analysis is based on the observation that the expression levels of the majority of genes do not change in compared samples, and that expression values are normally distributed around a regression line with a small proportion of differentially expressed “outliers”. The outlier’s contribution in the regression analysis is down-weighted in an iterative manner until the residuals are normally distributed as measured by deviations from the regression line calculated against the averaged profile. Expression profiles of both control and experimental groups are then scaled to the averaged profile of the control group.

Variation in gene expression among samples is composed of technical variability and normal biological variation. A group of genes from the control sample, whose deviations fall within three SD from the average, is denoted as the “reference group” and is used to measure the technical variation between the samples. The parameters of variation defined by the reference group are used to confirm that the variation between samples is truly due to biological differences and not from instrumental variation.

2) Identification of genes differentially expressed in a paired sample analysis. Four parameters are introduced to categorize the gene expression profiles: a) Test the expression against background: variations among replicates were tested to differentiate genes from background using the Student's t-test. A threshold of  $T_h$  ( $1/(\text{number of genes})$ ) was used to determine if a gene is significantly expressed above background. b) Selection of statistically different levels of expression of the paired samples using the Student's t-test with the commonly accepted significance threshold of  $p < 0.05$ . Because of the large number of genes present on microarrays, a significant proportion of genes identified as differentially expressed in this manner will be false positive determinations at this threshold level. c) For genes expressed above background in both samples, an "Associative t-test" in which the replicated residuals for each gene in the experimental group are compared with the entire set of residuals from the "reference group" (defined above). The hypothesis that gene expression in the experimental group, presented as replicated residuals (deviations from the averaged control group profile), is distributed similarly to the several thousand members of the normally distributed set of residuals for gene expression in the reference group is tested. The significance threshold stringency was increased to  $T_h$  in order to abolish false positives due to analysis. Only genes with p-values below the threshold for both the Student's t-test and the "Associative t-test" and have a relative ratio of expression  $> 1.5$  or  $< 0.67$  are presented in tables as "differentially expressed genes". d) Genes expressed distinctively above background in only one group and not in another are defined as uniquely expressed genes.

### *Measurements of superoxide production rates*

Measurements of superoxide were performed using cultures treated identically to those used for RNA isolation. At each time point, cells were harvested by centrifugation as described above and resuspended in 1/50 volume of their supernatant medium. Aliquots of concentrated cells containing 100  $\mu\text{g}$  chlorophyll were mixed in micro-titre dish wells with the appropriate volumes of each reagent (5 mM glucose, 50  $\mu\text{M}$  DCMU [3-(3,4-dichlorophenyl)-1,1-dimethylurea], 650 mM NaCl, 500  $\mu\text{M}$  XTT [2,3-bis(2-methoxy-4-nitro-5-sulphophenyl)-2H-tetrazolium-5-carboxanilide]). Each well was filled to 1 ml with the remaining supernatant medium. The 24-well microtitre plate was incubated for 10 minutes under temperature and lighting conditions similar to previous culture conditions. The cells were centrifuged into a pellet in a microfuge tube. The supernatant medium was immediately transferred to a fresh tube and spectrophotometrically measured for the conversion of XTT to formazan. Measurements were based on the absorption of formazan at 470 nm (extinction coefficient of XTT =  $21,600 \text{ M}^{-1} \text{ cm}^{-1}$ , requiring two  $e^-$  per formazan formed).

### *Whole cell oxygen exchange*

Photosynthetic oxygen exchange in whole cells was measured using a Clark-type electrode. A known amount of chlorophyll, in the range of approximately 10  $\mu\text{g}$ , was added to the electrode and illuminated with  $\sim 1000 \mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$ . Carbon fixation-dependent rates were measured in the presence of 5 mM  $\text{NaHCO}_3$ . Rates independent of carbon fixation were measured using a red light filter ( $>620 \text{ nm}$ ) in the presence of the artificial electron acceptors  $\text{K}_2\text{Fe}_3(\text{CN})_6$  and DCBQ at 5 mM and 600  $\mu\text{M}$

respectively. Rates of oxygen consumption through respiration were taken in the dark under conditions identical to those coupled to carbon fixation. The electrode was calibrated based on the standard concentration of dissolved atmospheric oxygen. All rates are reported as the average of at least three replicates and are expressed in  $\mu\text{mol O}_2 \cdot \text{mg chl}^{-1} \cdot \text{hr}^{-1}$ .

### *Photosystem II Fluorescence*

The room temperature chlorophyll fluorescence in physiologically active whole cells gives information on the redox state of the PSII complex. Because the redox state of PSII depends upon a variety of factors including the availability of electron acceptors, chlorophyll fluorescence can be used to monitor the redox state of the cell. Measurements of chlorophyll fluorescence were made with a modified Pulse Amplitude Modulated (PAM 101) fluorometer (Heinz Walz GmbH, Effeltrich, Germany). Weak modulated measuring light stimulating chlorophyll fluorescence was given with red (660  $\pm$  10 nm) light-emitting diodes (Radio Shack). The resultant chlorophyll fluorescence was optically filtered using Schott long-pass ( $>700$  nm) prior to detection by the Walz detector circuitry. This measuring beam-detector arrangement tracks the relative quantum yield of fluorescence arising only from stimulation by the measuring beam and is unaffected by additional chlorophyll fluorescence in the same sample that results from the stronger actinic light sources also present intermittently during the experiment. In this way, changes in the quantum yield of fluorescence caused by actinic light-induced changes in the redox chemistry of the PSII reaction center can be followed accurately. The fluorescence signals described here are thus reporting changes in the redox state of

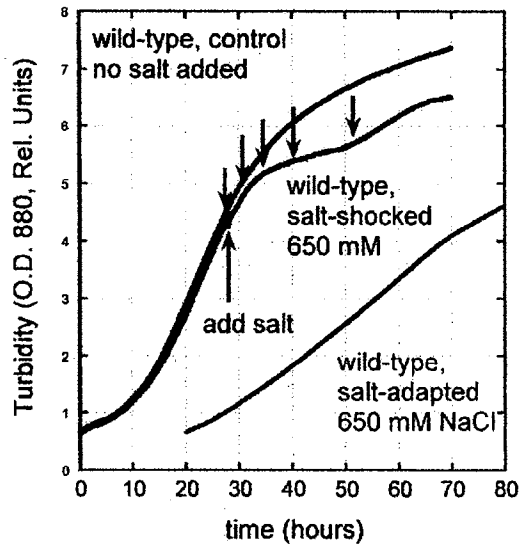
the PSII reaction center. The redox state of the PSII reaction center, in turn, is influenced by the state of cellular electron acceptors such as NADP<sup>+</sup>. Saturating actinic illumination ( $\sim 1500 \mu\text{moles m}^{-2} \text{s}^{-1}$ ) was given as 800 ms pulses via a computer-controlled electronic shutter. Background illumination at about  $80 \mu\text{moles m}^{-2} \text{s}^{-1}$ , simulating the intensity during cell culture, was given by a microscope stage illuminator. Cells were harvested from the growth vessels, adjusted to  $10 \mu\text{g Chl ml}^{-1}$  in media with NaCl present at the same salt concentration as the experimental growth medium.

#### *Photosystem I P700+ re-reduction kinetics*

It is possible to follow the redox state of the photosystem I reaction center by monitoring absorbance changes of PSI reaction center chlorophylls known as P700. The P700 chlorophylls lose absorbance upon photooxidation and the concomitant formation of P700<sup>+</sup>. The bleaching of P700 absorbance is reversed when the electrons from the photosynthetic electron transport chain are delivered by cytochrome  $c_6$  to PSI thereby reducing P700<sup>+</sup> and restoring its absorbance. By following the absorbance changes associated with the redox state of P700 it is possible to monitor rates of electron transfer through P700. The absorbance changes at  $\sim 820 \text{ nm}$  associated with changes in the redox state of P700 were determined using a Pulse Amplitude Modulated (PAM 101) fluorometer (Heinz Walz GmbH, Effeltrich, Germany) configured for monitoring absorbance changes using the Walz ED-800T emitter-detector unit also connected to the optical set-up described in the previous section.

## Results

Salt shock affects the growth of *Synechocystis* in several characteristic ways. The changes are reproducible after salt treatment until they resume exponential growth. Immediately following the onset of salt-shock, culture turbidity increases slightly and microscopic inspection of the culture cell revealed that many cells fail to separate following fission (“doublets”) and begin to accumulate immediately. The appearance of doublets increases in frequency through 18 hours after treatment, although this was not quantitated. Cells appear to aggregate and settle to the bottom or get trapped at the air/water interface. As a result, accurate growth curves for salt stress are difficult to obtain. Determinations of cell counts, optical density, and numbers of colony forming units yield conflicting data on growth rates. For example, optical density continues to increase for the first 3-4 hours after the addition of salt. It is known that cells collapse under osmotic stress, thus this brief increase is most likely due to differences in the light refracting properties of the individual cells rather than as a result of cell division and growth. Optical density is in part a function of light scattering off of the surface of the cell. As the surface changes by either expanding, or forming doublets, the light scattering properties change. Also, cells which collect at the air/water interface are, over time, bubbled out of the culture onto the inner walls of the container. This will affect optical density by essentially removing cells from the culture. Both effects prevent accurate measurements of optical density. Direct cell counts are difficult due to the size of the cells and like measures of optical density do not take into account cell viability. Measurements of colony forming units however, do not account for the doublets formed.



**Figure 4.1** The effect of an upshift in salt concentration (18 mM→650 mM NaCl) on the autotrophic growth of wild-type *Synechocystis* sp. PCC 6803. **Blue trace:** wild-type control culture without salt shock; **Red trace:** wild-type, salt shocked culture treated with 650 mM NaCl added as a powder (up arrow). Down arrows indicate sampling points. **Green trace:** growth of wild-type cell pre-adapted to 650 mM salt and transferred in media containing 650 mM NaCl, Note that the inoculation time is offset by approximately 25 hours in the plot to facilitate graphing. The basal medium was BG-11 (mineral salts) bubbled with sterile air enriched with 3% CO<sub>2</sub> under illumination intensity of ~100 μmoles photons m<sup>-2</sup>-sec<sup>-1</sup>. Optical density (O.D.) due to scattering was continuously followed using high-performance optical turbidity monitors. Optical measurements were validated in preliminary experiments using a standard spectrophotometer and the span ranges from an equivalent of 0 to ~3.0 O.D. at 750 nm .



Regardless, the observations described below are consistent with previous reports on *Synechocystis* and other cyanobacteria (5).

Because of its ease of use, its ability to produce real time measurements, and because no method is entirely accurate for this purpose it was decided that optical density would be used to measure growth. Figure 4.1 illustrates the effect of salt shock on culture growth and the relative rate of growth for a salt acclimated culture. To provide the physiological context for microarray experiments, growth rates were monitored and samples, taken at the appropriate time points (black arrows), were subject to analysis of photosynthetic parameters. In addition, samples were harvested during logarithmic growth of high salt acclimated cultures to compare with samples from low salt cultures (not shown in graph).

*Comparison of gene expression profiles for cultures acclimated to  
high and low salt conditions*

Gene expression profiles comparing high salt-acclimated and low salt-acclimated logarithmic growth identified 654 differentially expressed genes. This is a significant fraction of the 3167 genes present in the *Synechocystis* sp. PCC 6803 genome. Table 4.1 identifies 231 genes (not including 79 putative transposases also induced) whose expression is relatively higher in the salt acclimated culture as determined by the measures described in the Material and Methods. Many of the genes which are most strongly induced after salt acclimation (>two-fold) can be classified into three categories based on functional assignment. *A) Regulation of osmotic potential:* The *KdpA*, *B*,

**Table 4.1 Genes induced after acclimation to high salt conditions**

Expression ratio exp/control	Ts	Ta	Name	Symbol	Product
56.83	2.038E-09	0	sll1862		unknown protein
49.36	1.001E-08	0	sll1863		unknown protein
5.42	5.973E-06	0	ssl2923	vapC	similar to virulence-associated protein
5.34	3.389E-05	2.773E-13	slr1704		hypothetical protein
4.87	6.763E-07	0	sll1483		hypothetical protein
4.56	1.405E-06	0	sll1514	hspA	16.6 kDa small heat shock protein
4.01	0.0007088	1.212E-09	sll0428		unknown protein
3.75	1.028E-06	0	sll1411		hypothetical protein
3.44	2.357E-05	0	slr1728	kdpA	potassium-transporting ATPase A chain
3.31	2.719E-05	0	sll0939		hypothetical protein
3.15	1.715E-06	0	slr0732		hypothetical protein
3.12	7.398E-06	0	slr1516	sodB	superoxide dismutase
3.05	0.0004082	4.05E-13	slr0967		hypothetical protein
3.03	0.0002217	7.907E-09	ssr2912		unknown protein
2.98	2.144E-05	0	slr0590		hypothetical protein
2.95	0.0001974	1.132E-09	sll0800		hypothetical protein
2.92	0.0008034	3.465E-07	slr0915		putative endonuclease
2.82	8.232E-06	0	slr0530	ggtC	glucosylglycerol transport system permease
2.79	7.5E-05	3.809E-12	sll1549		hypothetical protein
2.78	5.383E-07	0	sll0762		unknown protein
2.73	1.925E-06	0	ssr2611		hypothetical protein
2.69	2.561E-05	0	slr1597		chromosome partitioning ATPase
2.62	0.0009312	6.127E-08	sll0664		unknown protein
2.62	4.438E-05	4.441E-16	slr1730	kdpC	potassium-transporting ATPase C chain
2.60	0.0005178	2.424E-07	sll1723		probable glycosyltransferase
2.59	0.005386	5.188E-05	slr0314		non-heme chloroperoxidase
2.55	6.961E-05	1.879E-11	sll1797	ycf21	hypothetical protein
2.54	0.0002049	8.754E-09	slr1729	kdpB	potassium-transporting ATPase B chain
2.51	8.091E-07	0	sll1035		uracil phosphoribosyltransferase
2.51	0.0001882	4.441E-16	sll0723		unknown protein
2.49	5.703E-05	1.332E-15	sll0936		putative oxidoreductase
2.47	0.0011275	0	sll1504		hypothetical protein
2.44	4.066E-06	0	sll1594	ndhR	ndhF3 operon transcriptional regulator
2.41	0.000448	8.722E-08	slr0510		hypothetical protein
2.39	4.589E-05	0	slr0554		hypothetical protein
2.37	2.184E-05	0	sll0817		tRNA delta-2-IPP transferase
2.37	0.0007956	0	sll0330		3-oxoacyl-[acyl-carrier protein] reductase
2.36	2.847E-05	0	slr0346	mc	ribonuclease III
2.35	0.0001215	0	slr0765		hypothetical protein
2.34	1.983E-07	0	sll1164		hypothetical protein
2.34	2.566E-07	0	sll1799	rpl3	50S ribosomal protein L3
2.32	0.0006089	3.196E-07	slr0303		hypothetical protein
2.31	0.0001501	2.052E-13	sll1912		hypothetical protein
2.28	2.67E-06	0	sll0595		unknown protein
2.28	0.0010782	6.97E-13	sll0322	hypF	hydrogenase maturation protein
2.26	0.0025373	1.176E-08	sll0727		hypothetical protein

Table 4.1 continued

Ratio	Ts	Ta	Orf	Symbol	Product
2.26	1.097E-06	0	slr1457		chromate transport protein
2.26	3.842E-05	5.507E-14	slr1879	cobI	precorrin-2 methyltransferase
2.24	0.0034906	1.324E-07	sll0659		hypothetical protein
2.23	0.0019289	3.875E-06	sll1598	mntC	Mn transporter
2.23	0.0002642	1.479E-09	sll0416	groEL-2	60kD chaperonin 2
2.22	2.888E-05	0	sll1204		similar to macrolide efflux protein
2.19	0.0003906	6.036E-09	slr0319		beta-lactamase
2.16	0.0003915	5.125E-13	slr0458		unknown protein
2.15	0.0002275	7.281E-13	sll1671		hypothetical protein
2.15	0.0002274	7.987E-11	slr0119		hypothetical protein
2.14	0.0008626	0	slr1368	cobL	precorrin decarboxylase
2.12	0.0001268	0	sll0984		hypothetical protein
2.12	0.0005466	6.649E-08	sll0630		unknown protein
2.10	3.711E-06	0	slr0589		hypothetical protein
2.10	0.0005843	7.952E-08	sll1070		transketolase
2.10	0.0014735	1.789E-06	sll1802	rpl2	50S ribosomal protein L2
2.09	3.043E-05	0	sll1170		unknown protein
2.09	2.352E-05	0	sll1544		two-component response regulator
2.08	0.0038315	7.364E-06	sll1801	rpl23	50S ribosomal protein L23
2.06	6.381E-05	1.374E-13	sll0785		unknown protein
2.06	6.09E-06	0	sll0553		hypothetical protein
2.06	0.0099256	5.403E-05	slr2076	groEL	60kD chaperonin
2.06	0.00127	4.521E-07	ssr2998		hypothetical protein
2.03	0.0037136	6.876E-06	sll0170	dnaK	DnaK protein
2.02	0.0001878	3.014E-11	slr1789		unknown protein
2.01	1.278E-06	0	slr0080	rnhA	ribonuclease H
1.98	5.992E-05	0	sll0430	htpG	heat shock protein
1.97	0.0011402	5.093E-07	sll0171		probable aminomethyltransferase
1.95	0.0105783	8.613E-07	sll0242		unknown protein
1.94	0.0003917	5.647E-12	sll0738		molybdate-binding periplasmic protein
1.94	9.905E-05	0	ssr2595	hliB	high light-inducible polypeptide
1.93	0.0011237	3.037E-07	sll0381		hypothetical protein
1.93	4.512E-05	0	slr1048		hypothetical protein
1.92	8.503E-05	0	slr0033		glutamyl-tRNA(Gln) amidotransferase
1.92	0.0066723	6.074E-05	sll0519	ndhA	NADH dehydrogenase subunit 1
1.91	0.0012077	4.238E-09	sll1653		menaquinone biosynthesis methyltransferase
1.91	7.709E-05	0	slr0093	dnaJ	DnaJ protein
1.91	0.0004455	1.532E-14	sll0776		serine/threonine kinase
1.90	1.031E-05	0	sll0657		
1.90	0.0002762	1.349E-10	slr1748		probable phosphoglycerate mutase
1.89	1.938E-07	0	sll2008		processing protease
1.89	0.0019258	9.004E-08	sll1169		hypothetical protein
1.87	6.251E-06	0	sll0064		binding protein of ABC transporter component
1.87	0.0022957	9.1E-06	ssl3177		hypothetical protein
1.87	2.167E-05	0	sll2009		processing protease
1.87	0.0001564	3.797E-14	sll0072		hypothetical protein
1.85	7.993E-07	0	slr1517	leuB	3-isopropylmalate dehydrogenase
1.84	0.0006387	5.84E-14	slr0701		transcriptional regulator

Table 4.1 continued

Ratio	Ts	Ta	Orf	Symbol	Product
1.83	0.0028517	7.429E-10	sl1127	menB	naphthoate synthase
1.83	0.0041595	8.602E-09	slr0394	pgk	phosphoglycerate kinase
1.83	0.0011672	1.014E-08	slr1963		water-soluble carotenoid protein
1.83	0.0006628	1.094E-07	slr0626		probable glycosyltransferase
1.82	0.0014342	2.04E-10	sl1022		hypothetical protein
1.82	0.0013748	4.782E-07	slr1673		probable tRNA/rRNA methyltransferase
1.82	0.0057377	2.101E-06	sl10282		unknown protein
1.81	0.0001334	1.351E-12	slr1536	recQ	ATP-dependent DNA helicase
1.81	0.0019588	4.004E-06	sl10815		unknown protein
1.81	0.0013303	0	slr1672	glpK	glycerol kinase
1.80	0.0003893	3.442E-14	slr0076		hypothetical protein
1.80	0.0029178	2.909E-11	sl11440	pdxH	pyridoxamine 5'-phosphate oxidase
1.80	5.788E-05	1.11E-15	sl10410		hypothetical protein
1.80	0.0003434	7.926E-12	sl1213		GDP-fucose synthetase
1.80	0.0085071	9.658E-05	sl11162		hypothetical protein
1.80	0.0031247	6.416E-06	sl11466		probable glycosyltransferase
1.80	0.0016538	5.017E-06	sl11409		ferrichrome-iron receptor
1.79	0.0008372	4.312E-11	sl1253		similar to polyA polymerase
1.79	0.0007294	9.255E-09	sl11023		succinyl-CoA synthetase beta chain
1.79	5.182E-05	0	sl10057	grpE	heat shock protein
1.78	6.662E-08	0	sl11566	ggpS	glucosylglycerolphosphate synthase
1.78	0.0020723	6.674E-06	sl11774		hypothetical protein
1.78	0.0038771	5.456E-07	sl11383		myo-inositol-1(or 4)-monophosphatase
1.77	0.0056577	3.557E-05	slr1135		unknown protein
1.77	0.0057721	1.467E-10	sl11703		protease IV
1.77	1.914E-05	0	slr1261		hypothetical protein
1.76	0.0010222	8.144E-11	sl11676		4-alpha-glucanotransferase
1.76	0.0029588	0	slr0529	ggfB	glucosylglycerol transport
1.76	0.000431	1.574E-10	slr0457		tRNA pseudouridine synthase B
1.75	0.0009635	0	sl10099	cobL	precorrin-6y c5,15-methyltransferase
1.75	6.196E-05	0	sl10529		hypothetical protein
1.74	3.162E-05	0	slr1365		hypothetical protein
1.74	0.0002469	0	sl11348		hypothetical protein
1.73	0.0153375	8.904E-05	slr1442		hypothetical protein
1.73	1.987E-05	0	slr0877		glutamyl-tRNA(Gln) amidotransferase
1.73	0.0062465	5.156E-05	sl10782		transcriptional regulator
1.72	0.0003347	3.617E-13	sl10679		phosphate-binding protein of ABC transporter
1.72	0.0046422	4.441E-16	slr1670		unknown protein
1.72	0.0028878	1.535E-05	slr1453	cysT	sulfate transport system permease protein
1.72	0.0006671	3.615E-13	sl11852		nucleoside diphosphate kinase
1.72	3.717E-05	2.22E-15	sl10711		isopentenyl monophosphate kinase
1.71	4.95E-05	1.046E-13	slr1229		sulfate permease
1.71	0.0009118	2.22E-14	slr1677		hypothetical protein
1.71	4.867E-05	0	sl10745		phosphofructokinase
1.71	0.0001291	2.22E-16	slr0642		hypothetical protein
1.70	5.935E-05	0	sl11321	atp1	ATP synthase protein I
1.70	0.0011521	3.296E-11	sl11883	argJ	arginine biosynthesis bifunctional protein ArgJ
1.70	0.0011758	1.397E-08	slr1120		leader peptide processing enzyme

Table 4.1 continued

Ratio	Ts	Ta	Orf	Symbol	Product
1.70	0.0011005	3.263E-10	slr0789		two-component response regulator
1.69	0.0030984	9.541E-08	slr0902	moaC	molybdenum cofactor biosynthesis protein C
1.68	0.0163811	1.351E-05	slr1250		phosphate transport ATP-binding protein
1.68	0.0010405	8.605E-11	slr1667		hypothetical protein
1.68	4.307E-05	0	slr1732		hypothetical protein
1.68	0.0018742	0	slr0918		methionine aminopeptidase
1.68	4.401E-06	0	slr0549	asd	aspartate beta-semialdehyde dehydrogenase
1.68	0.0004725	1.004E-09	slr0495	asnS	asparaginyl-tRNA synthetase
1.67	7.808E-06	0	slr1228		peptide-chain-release factor 3
1.67	0.0085469	1.467E-06	slr1481		ABC-transporter membrane fusion protein
1.67	0.0039628	0	slr0700		probable amino acid permease
1.66	0.0008014	9.659E-14	slr1959		unknown protein
1.66	0.0063151	4.217E-06	slr0470		hypothetical protein
1.66	0.0001062	7.749E-14	slr0959		hypothetical protein
1.65	3.486E-06	0	slr1197		SMF protein
1.65	7.538E-05	0	slr1737		hypothetical protein
1.65	0.0241012	8.218E-06	slr1099	ubiX	
1.65	1.722E-06	0	slr0421	purB	adenylosuccinate lyase
1.65	0.0003481	0	slr0577		hypothetical protein
1.65	0.0051119	7.143E-07	slr1670		heat-inducible transcription repressor
1.65	2.066E-07	0	slr0798	ziaA	Zinc exporter
1.65	0.0003806	6.077E-12	slr1662		probable prephenate dehydratase
1.64	0.0002474	4.39E-09	slr1094		hypothetical protein
1.64	0.0008197	1.898E-08	slr1648		hypothetical protein
1.64	0.0031388	1.079E-05	slr1882	ribF	riboflavin biosynthesis protein
1.64	0.0002675	5.758E-11	slr0230		hypothetical protein
1.64	0.0038805	5.474E-05	slr0160		hypothetical protein
1.62	4.053E-05	0	slr0044	cmpD	bicarbonate transport protein
1.62	0.0020506	1.096E-11	ssl3364	cp12	CP12 polypeptide
1.62	0.0006725	1.986E-08	slr1230		hypothetical protein
1.62	8.995E-05	2.473E-12	slr1282	ribH	riboflavin synthase beta subunit
1.62	0.0003899	4.265E-09	slr1979	trpE	anthranilate synthase component I
1.62	0.0001677	3.957E-13	slr1646	rnc	ribonuclease III
1.62	0.0056083	4.04E-05	slr0593		glucokinase
1.62	0.0170347	0.0003091	slr0916	cobH	precorrin isomerase
1.62	3.22E-05	0	slr0056	chlG	chlorophyll a synthase
1.62	0.0017296	0	slr0670		hypothetical protein
1.61	0.0006658	1.926E-08	slr1145	gltS	glutamate permease
1.61	0.0224939	3.642E-05	slr1281	ycf9	hypothetical protein
1.61	0.0008709	0	slr0254		hypothetical protein
1.61	0.0124409	7.258E-05	slr1176		glucose-1-phosphate adenylyltransferase
1.60	0.0004281	7.931E-08	slr1535		hypothetical protein
1.60	0.0045546	2.539E-06	slr1884		hypothetical protein
1.60	0.0141258	2.089E-06	slr1031	tyrS	tyrosyl tRNA synthetase
1.59	0.002247	1.735E-10	slr1415		hypothetical protein
1.59	0.0075231	0.0002564	slr1939		unknown protein
1.58	0.0017265	5.733E-06	slr1862		unknown protein
1.58	0.000184	1.643E-11	slr0520	purL	phosphoribosyl formylglycinamide synthase

Table 4.1 continued

Ratio	Ts	Ta	Orf	Symbol	Product
1.58	3.973E-06	0	sl11858		unknown protein
1.58	0.0013665	2.691E-07	sl10594		transcriptional regulator
1.58	0.0021166	3.233E-08	slr0841		unknown protein
1.58	0.0033007	4.678E-05	slr1924		D-alanyl-D-alanine carboxypeptidase
1.58	0.0005031	9.932E-11	slr0637		hypothetical protein
1.57	2.816E-05	0	slr0032		amino acid aminotransferase
1.57	0.0116988	1.371E-05	slr0833	dnaB	replicative DNA helicase
1.56	0.0054329	0.0002504	sl10851	psbC	photosystem II CP43 protein
1.56	0.0027687	3.943E-08	slr0624		UDP-N-acetylglucosamine 2-epimerase
1.56	0.0019915	4.607E-07	slr0306		unknown protein
1.56	0.0004463	2.251E-07	sl11633	ftsZ	cell division protein
1.56	0.0096658	3.081E-06	slr0835		MoxR protein homolog
1.55	0.00457	2.48E-11	slr1249		phosphate transport system permease protein
1.55	0.0033098	1.354E-05	slr1281	ndhJ	NADH dehydrogenase subunit I
1.55	0.0001733	1.554E-15	slr1751		carboxyl-terminal protease
1.55	0.0037441	1.114E-08	slr1330	atpE	ATP synthase epsilon subunit
1.55	0.0010762	5.195E-09	sl11600	mntB	manganese transport
1.55	0.0005569	1.811E-09	slr0958	cysS	cysteinyl-tRNA synthetase
1.55	0.0002562	2.22E-16	sl11663		phycocyanin alpha phycocyanobilin lyase
1.54	0.0008223	1.495E-07	slr1464		hypothetical protein
1.54	0.0004741	1.19E-08	sl10737		hypothetical protein
1.54	0.0026413	5.985E-08	slr0074	ycf24	ABC transporter subunit
1.53	0.0091237	4.118E-06	slr1047		hypothetical protein
1.53	0.0051153	4.485E-05	slr1498	hypD	hydrogenase isoenzymes formation protein
1.53	0.0001157	0	sl10271		N utilization substance protein B homolog
1.53	0.001183	6.687E-10	sl11172	thrC	threonine synthase
1.53	0.0031553	2.958E-06	slr1656	murG	
1.53	0.0018327	3.784E-07	sl10018	fbaA, fda	fructose-bisphosphate aldolase, class II
1.53	0.0162405	0.0002836	sl10517	rbpA	RNA binding protein
1.52	0.0023732	0	slr1202		permease protein of sugar ABC transporter
1.52	0.0005185	1.355E-08	sl11284		esterase
1.52	0.0001356	7.063E-13	sl11818	rpoA	RNA polymerase alpha subunit
1.52	0.0247227	2.849E-05	sl10060		hypothetical protein
1.52	0.0045008	0	sl11849		dioxygenase Rieske iron-sulfur component
1.51	0.0066838	0.0002549	slr0854	phrA	DNA photolyase
1.51	0.0053251	2.901E-05	sl10294		hypothetical protein
1.50	0.0006122	0	slr0750	chlN	protochlorophyllide reductase subunit
1.50	0.0007744	6.681E-13	slr1238	gshB	glutathione synthetase

**Table 4.1 Genes induced after acclimation to high salt conditions.** RNA samples purified from replicate *Synechocystis PCC6803* cultures grown under low (control) and high (experimental) salt conditions were fluorescently labeled and probed using full genome DNA microarrays. The genes included here provide signals statistically greater than background noise and pass both the student's T-test and the associative T-test for differential relative expression as described in materials and methods. Not included in this list are 79 putative transposases which pass the same criterion. Some product names have been abbreviated or omitted to simplify the table.

and *C* genes encoding a potassium transporter and the *ggtC* gene encoding the permease protein for the compatible osmolyte, glucosylglycerol, are all strongly induced. Two other genes important for glucosylglycerol accumulation (*ggpS*, *ggtB*) are also shown to be significantly induced using the statistical method described above. However they do not meet the commonly accepted requirement for a two-fold change in expression. The enhanced expression of these genes during high salt acclimated growth is consistent with the on-going homeostatic and osmotic stress challenge that must exist during continuous culture under conditions of high salt.

*B) Chaperonins and protein processing enzymes:* Several genes related to the maturation and folding of proteins are elevated in expression during salt acclimated conditions. These include: *hspA*, *hypF*, *groEL-2*, *groEL*, and *dnaK*. Other related genes which are significantly induced but do not meet the requirement of two fold induction include *dnaJ*, *hspG*, and *grpE*. The enhanced expression of such a large number of protein chaperonins suggests that protein fold stability may be a considerable issue under salt acclimated conditions. *C) Unknown or hypothetical genes:* Ninety-three open reading frames characterized only as hypothetical or unknown are also shown to be significantly induced. However, it is important to note that while these resemble genes in structure, they have yet to be fully explored and may not be expressed as predicted by the bioinformatics annotation assignments for these open reading frames. Regardless, the fact that expression is observed from the region of the chromosome defined by those particular open reading frames is significant, suggests that at least part of the identified

open reading frame is a real gene or at least part of a transcribed unit and therefore, warrants further investigation.

Two other important genes which do not fit into one of the above categories but are significantly expressed above two fold are *sodB* (slr1516) and slr0314 (a non-heme chloroperoxidase). The expression of these two genes suggests the production of oxidative radicals may be occurring under salt acclimated conditions. The source and rate of production of the radical superoxide is the subject of further investigation detailed below.

The repression of genes after salt acclimation is difficult to predict and as the results shown in table 4.2 demonstrate, very little is known about this subject. Of the 344 genes showing significant decreases in transcript abundance after high salt acclimation, 64% (219) are classified as having an unknown or hypothetical function. Seventeen regulatory genes, the second largest class of genes showing decreased expression, include several identified through sequence homology only. As a result, their actual regulatory pathway is not well detailed. A few of the repressed regulatory genes are characterized to some extent and might provide interesting insights into the biology of acclimation to high salt. The open reading frame slr1861 encodes a probable sigma regulatory factor. The protein product of slr1861 has been implicated in regulating carbon metabolism through the phosphorylation of the protein products of slr1856 and slr1859. Two other genes, *lrtA* (sl10947) and *kaiB2* (sl11596) are speculated to function in regulating the adaptation to dark conditions and circadian rhythms



Table 4.2 Genes repressed after acclimation to high salt conditions

Expression ratio (exp/control)		Ts	Ta	Orf	Symbol	Product
0.11	*	0.0034963	0.0001072	ssr2201		unknown protein
0.14		4.472E-08	4.607E-57	slr1957		hypothetical protein
0.14	*	0.0034434	0.0001349	ssr0336		hypothetical protein
0.14	*	0.009686	0.0013294	slr1613		hypothetical protein
0.15	*	0.0035556	0.0001468	ssl0312		hypothetical protein
0.15	*	0.012422	0.0023263	slr1853		carboxymuconolactone decarboxylase
0.16	*	0.0221876	0.006521	ssl3573		hypothetical protein
0.16	*	0.0168566	0.0041671	ssl1045		hypothetical protein
0.17	*	0.0016958	5.499E-06	slI0447		unknown protein
0.18	*	0.0237404	0.0076174	slr1168		unknown protein
0.18	*	0.0150749	0.0032352	slr0810		hypothetical protein
0.20	*	0.0069969	0.0005476	slr1614		hypothetical protein
0.20	*	0.0167225	0.0039539	ssr3571		hypothetical protein
0.20	*	0.0065318	0.0005925	ssl2384		unknown protein
0.20	*	0.0045274	0.0002515	ssr0759		unknown protein
0.20	*	0.0051466	0.0003387	slI0608	ycf49	hypothetical protein YCF49
0.20	*	0.0379535	0.0167747	slr0333		unknown protein
0.21	*	0.0247004	0.0080312	slI1510		unknown protein
0.21	*	0.0134667	0.0026068	ssr3570		unknown protein
0.21		0.0003232	1.485E-08	slr1854		unknown protein
0.22	*	0.0319871	0.0120524	slr0315		probable oxidoreductase
0.22	*	0.0012213	6.497E-06	slr0668		unknown protein
0.22	*	0.0244697	0.0073304	slr1037		two-component response regulator
0.22	*	0.0167006	0.0040212	slI0911		unknown protein
0.22	*	0.0087604	0.0011242	slr2128		hypothetical protein
0.23	*	0.0362245	0.0150937	slI1447		hypothetical protein
0.23	*	0.0076936	0.0008489	slI1834		hypothetical protein
0.24	*	0.0375292	0.0163172	slr0334		unknown protein
0.24	*	0.040288	0.018218	slI1897		hypothetical protein
0.25		2.366E-06	3.742E-33	slr0233	trxM1	thioredoxin M
0.25	*	0.0215644	0.0061641	slr1861		probable sigma regulatory factor
0.25		7.996E-08	6.85E-69	slI0543		hypothetical protein
0.25	*	0.0230845	0.007196	slr0518		similar to alpha-L-arabinofuranosidase B
0.25	*	0.0191324	0.0049023	slI1573		hypothetical protein
0.26	*	0.0090857	0.0011384	ssl1792		hypothetical protein
0.26	*	0.0233293	0.0074056	ssl3383		unknown protein
0.26		8.666E-07	4.52E-147	slI1528		unknown protein
0.27	*	0.0055641	0.0004246	slI0403		unknown protein
0.28	*	0.0261419	0.0088735	slI0205		hypothetical protein
0.28		5.697E-07	1.936E-40	ssl1046		hypothetical protein
0.28	*	0.0157948	0.0036104	slr0392		unknown protein
0.28	*	0.0095033	0.001314	slr0313		hypothetical protein
0.28	*	0.0101786	0.0014058	slI1630		unknown protein
0.28		2.197E-05	2.439E-58	slr1437		unknown protein
0.28		0.0002068	8.193E-09	ssr1375		hypothetical protein
0.29	*	0.0225233	0.006968	slI1678		similar to spore maturation protein A
0.29	*	0.0087157	0.001116	ssr3304		hypothetical protein
0.29		7.086E-07	5.05E-45	slr0888		hypothetical protein
0.29	*	0.0134701	0.0026779	slI1092		hypothetical protein
0.30		4.903E-06	5.858E-23	slI1009		unknown protein
0.30	*	0.0248157	0.0081626	slI1596	kaiB2	circadian clock protein KaiB homolog
0.31		1.133E-07	1.776E-71	slr1406		hypothetical protein

Table 4.2 continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.31	5.601E-08	7.72E-189	sll1783		hypothetical protein
0.32	*	0.0104361	0.0016392	ssl1300	hypothetical protein
0.32		0.0003261	1.825E-09	sll0809	hypothetical protein
0.32	*	0.0327489	0.012998	slr0573	unknown protein
0.33		9.016E-07	2.984E-50	sll0588	unknown protein
0.33		3.623E-06	1.887E-34	ssl1533	unknown protein
0.33	*	0.011089	0.0018175	ssr2009	hypothetical protein
0.33		3.714E-06	1.58E-49	slr1852	unknown protein
0.33		0.0001622	1.865E-13	ssr2554	hypothetical protein
0.34	*	0.0195064	0.0053782	slr1450	unknown protein
0.34		1.855E-05	1.286E-15	sll1735	hypothetical protein
0.34	*	0.0456054	0.0222917	slr1209	hypothetical protein
0.34		2.042E-05	3.474E-18	slr0514	unknown protein
0.34		0.0029832	8.112E-05	slr1327	hypothetical protein
0.35	*	0.0270746	0.0096397	ssr1951	hypothetical protein
0.35		2.972E-05	2.719E-98	sll0497	hypothetical protein
0.35	*	0.0353592	0.0141323	slr0238	hypothetical protein
0.35		1.466E-06	1.599E-58	sll1882	unknown protein
0.36		0.0015394	7.259E-06	ssr2062	hypothetical protein
0.36		0.0019623	1.719E-13	ssr0692	hypothetical protein
0.36	*	0.0125239	0.0023491	ssr2962	hypothetical protein
0.37		5.917E-05	1.113E-16	sll1138	hypothetical protein
0.37	*	0.0267156	0.0093282	ssr1041	hypothetical protein
0.37	*	0.0345407	0.0141623	slr1421	unknown protein
0.37	*	0.0380565	0.0165628	sll0783	unknown protein
0.37	*	0.014405	0.002923	slr2110	unknown protein
0.37		0.0007282	6.38E-07	slr1064	plobable glycosyltransferase
0.38	*	0.0125664	0.0023615	ssl2162	unknown protein
0.38		3.365E-06	1.98E-172	sll1286	transcriptional regulator
0.38		0.000609	3.793E-07	sll0218	hypothetical protein
0.38		0.0003008	6.019E-10	ssr0536	unknown protein
0.38	*	0.0112508	0.00188	slr0664	hypothetical protein
0.38		0.0060549	9.522E-07	sll0253	hypothetical protein
0.38	*	0.0294075	0.0110184	slr1340	unknown protein
0.38	*	0.0106235	0.0016308	ssl0350	unknown protein
0.39	*	0.0479401	0.0241392	sll1400	hypothetical protein
0.39		5.691E-06	4.811E-22	slr2057	water channel protein
0.39	*	0.0485548	0.024587	ssl3829	hypothetical protein
0.39		0.0009122	3.53E-15	slr1634	hypothetical protein
0.39	*	0.0373619	0.0163742	sll0082	hypothetical protein
0.40		0.0023798	3.005E-05	slr0487	hypothetical protein
0.40		3.682E-05	1.066E-27	ssl1911	hypothetical protein
0.40		0.0003164	9.392E-09	slr1218	hypothetical protein YCF39
0.40		2.518E-05	4.239E-17	slr1929	pilin
0.40		0.0003534	2.818E-13	sll1384	similar to DnaJ protein
0.41	*	0.0326997	0.0128176	ssr2060	unknown protein
0.41		0.0001185	3.421E-18	slr1591	hypothetical protein
0.41	*	0.029137	0.0106852	ssr2227	putative transposase
0.41		1.31E-05	1.653E-21	sll0829	probable methyltransferase
0.41	*	0.0390429	0.0174952	slr0022	hypothetical protein
0.41		0.0002391	2.214E-10	sll0426	unknown protein
0.41	*	0.0177207	0.003805	sml0007	psbY
0.41		6.191E-05	9.31E-22	sll1785	unknown protein
0.42	*	0.0104722	0.001591	slr0493	mannose-1-phosphate guanylyltransferase

Table 4.2 continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.42	0.0011889	2.911E-06	sll0478		unknown protein
0.42	0.0028685	2.032E-05	slr1851		hypothetical protein
0.42	* 0.0344668	0.0142963	sll0892	panD	aspartate 1-decarboxylase
0.42	0.0001851	3.702E-09	slr0447		substrate-binding protein of ABC transporter
0.42	* 0.0458617	0.0222772	ssr2317		unknown protein
0.42	* 0.0392036	0.017613	sll0101		unknown protein
0.42	* 0.0350807	0.014308	slr1070		unknown protein
0.42	2.244E-06	3.809E-41	slr0089		gamma-tocopherol methyltransferase
0.42	* 0.0320307	0.0122317	ssl1326		unknown protein
0.42	0.0009086	1.585E-09	sll1784		unknown protein
0.43	8.742E-06	2.286E-31	sll1001		ATP-binding protein of ABC transporter
0.43	0.0016264	3.054E-06	sll0283		hypothetical protein
0.43	9.975E-06	6.942E-45	slr1855		unknown protein
0.44	0.0009144	1.063E-06	ssr1398	rpl33	50S ribosomal protein L33
0.44	5.139E-06	3.147E-20	slr0983	rfbF	glucose-1-phosphate cytidyltransferase
0.44	0.0007244	3.071E-11	sll1892		unknown protein
0.44	5.199E-05	9.253E-21	sll0947	lrtA	light repressed protein A homolog
0.44	* 0.0170159	0.0041961	slr1772		probable hydrolase
0.44	* 0.0418856	0.0192835	ssl2138		unknown protein
0.44	* 0.0439815	0.0110401	ssr1766		hypothetical protein
0.44	* 0.0331172	0.0134194	ssl1707		hypothetical protein
0.45	0.0001308	1.316E-11	slr1444		hypothetical protein
0.45	1.411E-05	5.243E-21	sll1338		unknown protein
0.45	0.0043519	1.33E-05	sll0263		unknown protein
0.45	* 0.0362797	0.0153429	ssl0410		unknown protein
0.45	0.0007596	1.382E-10	sll0901	purE	phosphoribosylaminoimidazole carboxylase
0.45	0.0016849	7.019E-06	sll1739		unknown protein
0.45	0.0002854	2.245E-19	slr0820		probable glycosyltransferase
0.45	1.078E-05	7.863E-21	sll0921		two-component response regulator
0.46	* 0.0320867	0.0121705	slr1970		hypothetical protein
0.46	0.0019515	9.238E-13	sll1274		hypothetical protein
0.46	* 0.0180277	0.0045523	sll1062		unknown protein
0.46	0.0076543	3.135E-05	sll1150		hypothetical protein
0.46	0.0058335	9.551E-05	sll1609		hypothetical protein
0.46	4.194E-06	6.316E-47	sll1938		hypothetical protein
0.47	5.913E-05	2.161E-14	sll1893	hisF	cyclase
0.47	0.0001279	1.558E-15	smr0009	psbN	photosystem II PsbN protein
0.47	0.0036757	1.174E-05	sll1547		hypothetical protein
0.48	* 0.0162926	0.0038214	ssl0511		hypothetical protein
0.48	0.0001261	8.396E-12	ssr0693		unknown protein
0.48	* 0.0470581	0.0227861	sll1796	petJ	cytochrome c553
0.48	0.0001668	6.023E-10	slr2122		hypothetical protein
0.48	* 0.0455895	0.022277	slr1767		hypothetical protein
0.49	* 0.0246586	0.0070877	ssl0438		similar to 50S ribosomal protein L12
0.49	* 0.0401698	0.0171077	sll0624		unknown protein
0.49	0.0047454	1.688E-05	sll2013		hypothetical protein
0.49	9.804E-06	1.57E-26	slr1194		hypothetical protein
0.49	4.226E-05	1.336E-17	slr0737	psaD	photosystem I subunit II
0.49	0.0017139	1.039E-07	slr0146		hypothetical protein
0.49	0.0003966	1.39E-13	sml0008	psaJ	photosystem I subunit IX
0.49	* 0.0192653	0.0051074	slr1068		hypothetical protein
0.49	* 0.0464789	0.0230244	sll1956		hypothetical protein
0.49	3.922E-05	9.072E-20	slr1798		unknown protein
0.49	6.37E-06	3.984E-73	slr1169		unknown protein

Table 4.2 Continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.49	3.362E-05	3.53E-19	slr1623		hypothetical protein
0.49	5.433E-05	5.2E-21	slr0144		hypothetical protein
0.49	3.737E-05	6.69E-99	sll1358		hypothetical protein
0.49	3.894E-05	3.315E-18	sll1738		hypothetical protein
0.50	0.0004048	5.821E-10	slr1276		hypothetical protein
0.50	1.147E-06	6.732E-44	sll0022		unknown protein
0.50	0.0006091	1.929E-07	slr0489		unknown protein
0.50	0.0004073	5.876E-13	sll1926		hypothetical protein
0.50	0.0098544	0.0001156	sll1306		unknown protein
0.50	1.019E-06	5.642E-63	slr0708		unknown protein
0.50	5.119E-05	6.247E-16	sll1734	cupA	low CO2-inducible, high affinity CO2 uptake
0.50	* 0.0188901	0.0049194	slr1025		hypothetical protein
0.50	0.000117	3.712E-19	slr1521		GTP-binding protein
0.50	2.23E-05	1.573E-19	sll2002		hypothetical protein
0.50	0.003318	1.354E-05	sll0832		hypothetical protein
0.50	2.874E-06	1.968E-73	slr0272		unknown protein
0.51	0.0001038	7.166E-13	sll0819	psaF	photosystem I reaction center subunit III
0.51	0.0002842	2.883E-09	sll0686		cytochrome c-type biogenesis protein
0.51	1.091E-07	0	slr0698		hypothetical protein
0.51	1.434E-05	3.807E-52	sll0180		hypothetical protein
0.51	4.283E-05	4.148E-35	slr1977		hypothetical protein
0.52	0.0006706	5.299E-13	slr0780		hypothetical protein
0.52	5.76E-05	3.021E-36	ssr3341		hypothetical protein
0.52	0.003097	1.038E-05	sll0788		hypothetical protein
0.52	8.457E-05	7.629E-24	slr2073	ycf50	hypothetical protein YCF50
0.52	7.374E-05	4.817E-19	slr1420		probable sugar kinase
0.52	5.697E-05	5.816E-14	slr1636		unknown protein
0.52	2.554E-06	1.852E-30	sll0310		hypothetical protein
0.52	0.00703	0.0003011	slr0416		unknown protein
0.52	0.0001777	6.045E-15	ssr2142	ycf19	hypothetical protein YCF19
0.52	9.285E-05	1.079E-11	slr0794		cation efflux system protein
0.53	0.0017689	9.768E-08	slr0301		phosphoenolpyruvate synthase
0.53	9.76E-06	1.958E-46	slr0095		O-methyltransferase
0.53	0.0002421	9.42E-15	sll0876	ruvA	Holliday junction DNA helicase RuvA
0.53	0.0131223	3.926E-07	sll1500		hypothetical protein
0.53	0.0006727	1.34E-13	slr0658		unknown protein
0.53	6.048E-06	7.773E-70	sll1954		unknown protein
0.53	0.0011481	1.963E-10	slr1617		similar to UDP-glucose 4-epimerase
0.53	0.0002253	1.913E-10	slr0960		unknown protein
0.53	0.0002152	1.261E-42	slr1950	ctaA	copper-transporting CPx-type ATPase
0.53	0.0056519	0.0001226	slr2124		3-oxoacyl-[acyl-carrier protein] reductase
0.54	0.0011137	1.948E-18	slr0925	ssb	single-stranded DNA-binding protein
0.54	7.784E-05	8.138E-14	sll1534		probable glycosyltransferase
0.54	0.0001676	1.306E-24	slr0373		hypothetical protein
0.54	0.0003101	6.441E-12	sll1905		two-component hybrid sensor and regulator
0.54	0.0002016	4.58E-13	slr1619		hypothetical protein
0.54	1.578E-07	1.89E-67	slr0722		hypothetical protein
0.55	0.0024785	1.315E-07	sll0219		flavoprotein
0.55	3.875E-05	2.425E-19	sll0772		probable porin
0.55	0.0155916	0.0002606	sll1924	sycrp2	cAMP receptor protein sycrp1 homolog
0.55	0.002423	5.777E-15	slr1211	cobN	cobalamin biosynthetic protein CobN
0.55	0.001883	9.526E-08	slr1274	pilM	probable fimbrial assembly protein PilM
0.55	0.0001011	1.742E-13	slr1275		hypothetical protein
0.55	0.0145478	1.47E-08	slr0639		mechanosensitive ion channel homolog

Table 4.2 Continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.55	0.0004812	2.706E-14	ssr3307	secG	probable protein-export membrane protein
0.55	0.0001048	3.654E-24	sl11555		two-component hybrid sensor and regulator
0.55	0.0032274	2.195E-05	slr0216	cobP	bifunctional cobalamin biosynthesis protein
0.55	0.0053042	8.277E-06	sl10928	apcD	allophycocyanin-B
0.56	0.0002139	1.167E-09	slr0467	natA	ABC transporter for natural amino acids
0.56	0.0048184	2.861E-06	slr1964		hypothetical protein
0.56	0.0036661	1.931E-06	sl10626		putative neutral invertase
0.56	0.0025077	4.921E-07	sl10546		probable translation initiation factor
0.56	8.75E-06	4.141E-23	slr1087		hypothetical protein
0.56	0.0108508	4.492E-08	sl11694	pilA1	pilin polypeptide PilA1
0.56	0.0006315	2.822E-23	slr0477	purN	
0.56	0.0017152	4.15E-13	sl10728	accA	acetyl-CoA carboxylase alpha subunit
0.56	0.0029433	2.781E-09	slr0623	trxA	thioredoxin
0.56	0.0113398	5.869E-09	slr0897		probable endoglucanase
0.57	6.081E-05	5.749E-23	slr2017		unknown protein
0.57	0.0059472	4.289E-09	slr0108		unknown protein
0.57	0.0033359	9.983E-06	sl11969		hypothetical protein
0.58	1.012E-05	1.116E-19	sl10066		unknown protein
0.58	2.188E-05	4.773E-15	sl10250		pantothenate metabolism flavoprotein
0.58	0.000344	6.516E-13	ssl1690		hypothetical protein
0.58	0.0032991	5.941E-09	slr0591		ribonucleoside-diphosphate reductase
0.58	0.0017249	6.436E-13	slr0821		hypothetical protein
0.58	0.0006499	4.445E-12	slr0609		hypothetical protein
0.58	0.0024678	4.917E-06	slr1263		hypothetical protein
0.58	2.228E-06	1.545E-41	sl11184	ho1	heme oxygenase
0.58	2.493E-05	7.753E-22	sl11165		DNA mismatch repair protein
0.58	0.0001559	4.063E-42	ssr2799	rpl27	50S ribosomal protein L27
0.58	3.206E-05	6.799E-27	slr1312		arginine decarboxylase
0.58	0.0142516	2.21E-06	slr0653	sigA,rpoDI	principal RNA polymerase sigma factor
0.58	0.0044422	0.0001748	sl11142		hypothetical protein
0.59	0.0002421	1.04E-09	slr0950		hemolysin-like protein
0.59	0.0032875	3.89E-06	slr1909		two-component response regulator
0.59	5.42E-05	1.309E-29	sl10997		hypothetical protein
0.59	0.0040842	1.751E-05	slr1378		hypothetical protein
0.59	0.0029249	1.669E-08	slr0845		hypothetical protein
0.59	0.002395	4.032E-12	ssl3549		hypothetical protein
0.59	0.0136867	1.044E-07	sl11254		hypothetical protein
0.60	1.392E-05	1.306E-25	sl11333		unknown protein
0.60	1.425E-06	1.011E-37	slr0229		3-hydroxyisobutyrate dehydrogenase
0.60	0.0014319	1.769E-13	slr1869		unknown protein
0.60	3.449E-05	6.749E-21	sl11557		succinyl-CoA synthetase alpha chain
0.60	0.006343	0.0001874	slr2119		unknown protein
0.60	0.0012321	1.181E-78	slr1969		two-component sensor histidine kinase
0.60	0.010697	9.699E-05	slr0476		unknown protein
0.61	0.002582	5.339E-05	sl11297		dioxygenase, Rieske iron-sulfur component
0.61	0.0015499	1.66E-07	slr1898	argB	N-acetylglutamate kinase
0.61	0.0096551	2.04E-05	sl11612	folC	folylpolyglutamate synthase
0.61	1.666E-05	1.095E-26	slr0081		two-component response regulator
0.61	0.0003246	7.454E-14	sl10861		hypothetical protein
0.61	5.143E-05	1.298E-53	slr0109		unknown protein
0.61	1.128E-05	2.269E-21	sl11049		hypothetical protein
0.61	0.0089937	0.0002919	slr1530		hypothetical protein
0.61	0.000448	7.017E-12	slr0299		hypothetical protein
0.61	0.0016174	4.715E-07	slr2143		L-cysteine/cystine lyase

Table 4.2 Continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.61	0.0014167	1.696E-06	slr1841		probable porin
0.61	0.0010268	1.82E-10	slr0468		unknown protein
0.61	1.766E-07	9.87E-152	sll0828		putative amidase
0.62	0.0201946	5.038E-07	slr0527		transcription regulator ExsB homolog
0.62	0.0002979	5.736E-14	sll0767	rpl20	50S ribosomal protein L20
0.62	0.0035495	4.345E-08	sll1229		two-component hybrid sensor and regulator
0.62	0.0038235	2.506E-09	sll0023		hypothetical protein
0.62	0.0018395	9.453E-06	sll0750		two-component sensor histidine kinase
0.62	0.0009616	1.609E-08	slr1240		unknown protein
0.62	0.0015146	1.074E-07	slr1233		succinate dehydrogenase flavoprotein
0.62	0.0012695	3.672E-06	smi0001	psbl	photosystem II reaction center Psbl protein
0.62	0.000352	1.721E-12	slr1843	zwf	glucose 6-phosphate dehydrogenase
0.62	6.155E-06	5.755E-33	sll1369		putative peptidase
0.62	0.003774	1.774E-10	sll1222		hypothetical protein
0.62	0.000762	9.906E-08	slr0374		hypothetical protein
0.62	0.0026719	2.516E-05	slr1622	ppa	soluble inorganic pyrophosphatase
0.62	0.0005979	8.109E-08	slr0341		unknown protein
0.63	0.0128208	0.0001235	sll0204		glucose inhibited division protein
0.63	0.0052281	1.027E-05	sll1221	hoxF	NADH dehydrogenase I chain F
0.63	0.0099455	3.675E-06	slr0937		unknown protein
0.63	0.0132866	9.084E-05	slr0164	clpP	ATP-dependent Clp protease
0.63	0.0007729	3.4E-08	sll0397		hypothetical protein
0.63	8.071E-05	6.257E-23	sll1336		hypothetical protein
0.63	0.0010471	1.871E-11	slr0116		phycocyanobilin:ferredoxin oxidoreductase
0.63	0.0007415	3.581E-08	slr1710		penicillin-binding protein
0.63	0.00113	2.59E-06	slr1078		similar to UDP-glucose 4-epimerase
0.63	0.0261186	3.369E-07	sll1484	ndbC	type 2 NADH dehydrogenase
0.63	0.0002773	2.202E-16	slr1912		anti-sigma F factor antagonist
0.63	0.0021639	5.59E-14	slr1122		hypothetical protein
0.63	0.0025132	2.506E-09	slr1566		hypothetical protein
0.63	0.0068056	2.746E-05	sll0756		unknown protein
0.64	4.509E-05	3.771E-18	slr2099		two-component hybrid sensor and regulator
0.64	0.0024243	4.616E-11	sll1961		hypothetical protein
0.64	0.0004512	5.989E-10	slr0867		unknown protein
0.64	7.572E-05	9.95E-12	ssr2723		hypothetical protein
0.64	0.0180218	0.0001453	slr1395		hypothetical protein
0.64	0.0128688	9.76E-06	sll0144	pyrH	uridine monophosphate kinase
0.64	0.0005958	1.208E-09	sll1433		hypothetical protein
0.64	0.0002372	7.829E-12	slr1079		unknown protein
0.64	0.0153851	0.0001311	sll1214	ycf59	hypothetical protein YCF59
0.64	0.0138847	1.068E-07	sll1916		hypothetical protein
0.64	0.0001843	1.08E-11	sll1341		bacterioferritin
0.64	0.0007858	1.45E-10	slr1448		fructokinase
0.64	0.0007053	1.028E-14	slr1295	futA1	iron transport system protein
0.64	0.0007489	1.819E-10	sll0830	fus	elongation factor EF-G
0.64	4.377E-05	4.721E-33	sll0644		probable esterase
0.65	0.0022253	2.127E-11	sll0412		hypothetical protein
0.65	0.0075631	1.888E-06	sll1390		hypothetical protein
0.65	0.0004732	1.307E-09	sll0891		malate dehydrogenase
0.65	0.0007922	1.931E-14	slr1972	ycf81	hypothetical protein YCF81
0.65	0.0137054	4.154E-05	sll1765		unknown protein
0.65	0.0073192	2.234E-05	sll1511		unknown protein
0.65	0.0009511	1.315E-12	slr1262		hypothetical protein
0.65	0.0144463	9.084E-05	sll1468	crtR	beta-carotene hydroxylase

Table 4.2 Continued

Ratio	Ts	Ta	Orf	Symbol	Product
0.65	0.006274	2.092E-10	sll1459		stationary-phase survival protein
0.65	1.574E-05	1.174E-73	sll0270		primosomal protein N'
0.65	2.258E-05	1.441E-38	sll0194		sec-independent protein translocase
0.65	0.0015117	1.036E-07	slr0889		hypothetical protein
0.65	0.0002111	3.848E-12	slr1842	cysK	cysteine synthase
0.66	0.0036449	2.358E-06	sll0145	rrf	RNA-binding protein
0.66	0.0161622	6.785E-05	sll1939		unknown protein
0.66	2.163E-05	5.828E-62	slr0775	secF	protein-export membrane protein SecF
0.66	0.0013296	2.109E-11	sll1658		hypothetical protein
0.66	0.0194437	2.492E-16	slr0665		aconitate hydratase 2
0.66	0.0076297	2.07E-12	slr1509		V-type sodium ATP synthase subunit J
0.66	0.0177999	1.012E-09	ssr0390	psaK	photosystem I subunit X
0.66	0.0011696	7.492E-09	slr1198		antioxidant protein
0.66	3.593E-05	8.875E-14	slr1998		hypothetical protein
0.66	0.000162	7.949E-17	sll1489	cpmA	circadian phase modifier CpmA homolog
0.66	0.0040677	1.04E-13	slr1678	rpl21	50S ribosomal protein L21
0.66	1.247E-05	6.864E-29	sll1275		pyruvate kinase
0.66	0.0058579	2.39E-05	sll1680		hypothetical protein
0.66	0.005857	0.0002079	slr1173		hypothetical protein
0.66	0.0003074	4.371E-15	sll1365		unknown protein
0.67	0.0423245	0.0001413	sll0394		unknown protein
0.67	0.0009069	8.979E-24	sll1388		hypothetical protein

**Table 4.2 Genes repressed after acclimation to high salt conditions.** RNA samples, purified from replicate *Synechocystis PCC6803* cultures grown under low (control) and high (experimental) salt conditions, were fluorescently labeled and probed using full genome DNA microarrays. The genes included here provide signals statistically greater than background noise in at least one channel and pass both the student's T-test and the associative T-test for differential relative expression as described in materials and methods. Some product names have been abbreviated or omitted to simplify the table. Data points with an asterisk (\*) produced a signal above noise only in the control sample. Ts: Student t-test; Ta: Associative t-test; Thresholds: Ta<1/3176, Ts<0.05, P<1/3176. Shaded ratios show greater than two fold repression



respectively. One other regulatory factor repressed (1.7 fold) under these conditions is *sigA* (slr0653). SigA is known to be expressed coordinately with growth rate and as the principle RNA polymerase sigma factor it is responsible for regulating the expression of a large percentage of genes from the genome. Four photosynthesis genes, *psbY* (sml0007), *psbN* (smr0009), *psaD* (slr0737), and *psaJ* (sml0008) are all repressed greater than two fold under these conditions and are known to be coordinately expressed with *sigA*. Other genes, expressed under normal (non-stressed) conditions relating to photosynthetic physiology and growth, are also expected to be regulated by *sigA*. This would explain the slight repression of many other genes in figure 4.2. One other gene of interest relating directly to salt stress is the water channel protein (slr2057) shown in table 4.2 to be differentially expressed (-2.5 fold). A complete list of expression ratios for all genes is available as table A-1 in the appendix.

#### *Time course analysis of salt shock response by Synechocystis PCC6803*

Salt shock treatments on *Synechocystis* result in pronounced changes in photosynthetic physiology and respiration. In a report by Kanasaki et al. many genes associated with photosynthesis are differentially expressed at 30 minutes after treatment in accordance with the down-regulation of PSII capacity (17). However, from the observation that few genes related to photosynthesis and respiration are differentially regulated after salt acclimation, it is apparent that the previously reported profiles represent a single point along a transitional phase of recovery. To gain a better understanding of the process of adaptation to high salt conditions, a time course analysis of gene expression is presented here.



Figure 4.2 contains eight panels each depicting the results of hierarchical clustering of gene expression patterns for several genes belonging to a functional category of interest here. A complete list of expression values for all genes from each of the two replicate experiments is available in table A-2 of the appendix.

The 21 genes depicted in panel A are all related to transcription. Several are sigma factors or anti-sigma factor antagonists. Four encode for RNA polymerase itself. Two of the genes from this group, *sigB* (sll0306) and *sigD* (sll2012), are consistently induced to high levels. *sigB* (sll0306) is a known heat-shock responsive sigma factor. *sigD* (sll2012) is a known high light induced sigma factor responsible for regulating the expression of PsbA, the core protein of PSII. A third gene *crhR* (slr0083) is transiently induced from 3 to 12 hours reaching maximal expression at 6 hours. *crhR* is an RNA Helicase and is redox regulated. It is known to be induced under high light conditions when the electron transport chain is strongly reduced at *cyt b<sub>6</sub>f*. Induction of these three genes implies that salt shock is affecting protein folding, PSII activity, and the redox state of the electron transport chain. What specific genes these regulate in response has yet to be determined. Two other genes of significance are *sigA* (slr0653) and *sigG* (slr1545). Both are primary (group 1) sigma factors are repressed transiently and are responsible for regulating transcription during times of normal logarithmic growth. The down regulation of these would have strong effects on the transcription of many genes. The genes encoding RNA polymerase, *rpoA* (sll1818), *rpoB* (sll1787), *rpoC1* (slr1265), and *rpoC2* (sll1789) are all down regulated 24 hours after salt stress. This is indicative of a slower growth rate after acclimation to high salt.

**Figure 4.2 Hierarchical clustering of gene expression profiles**

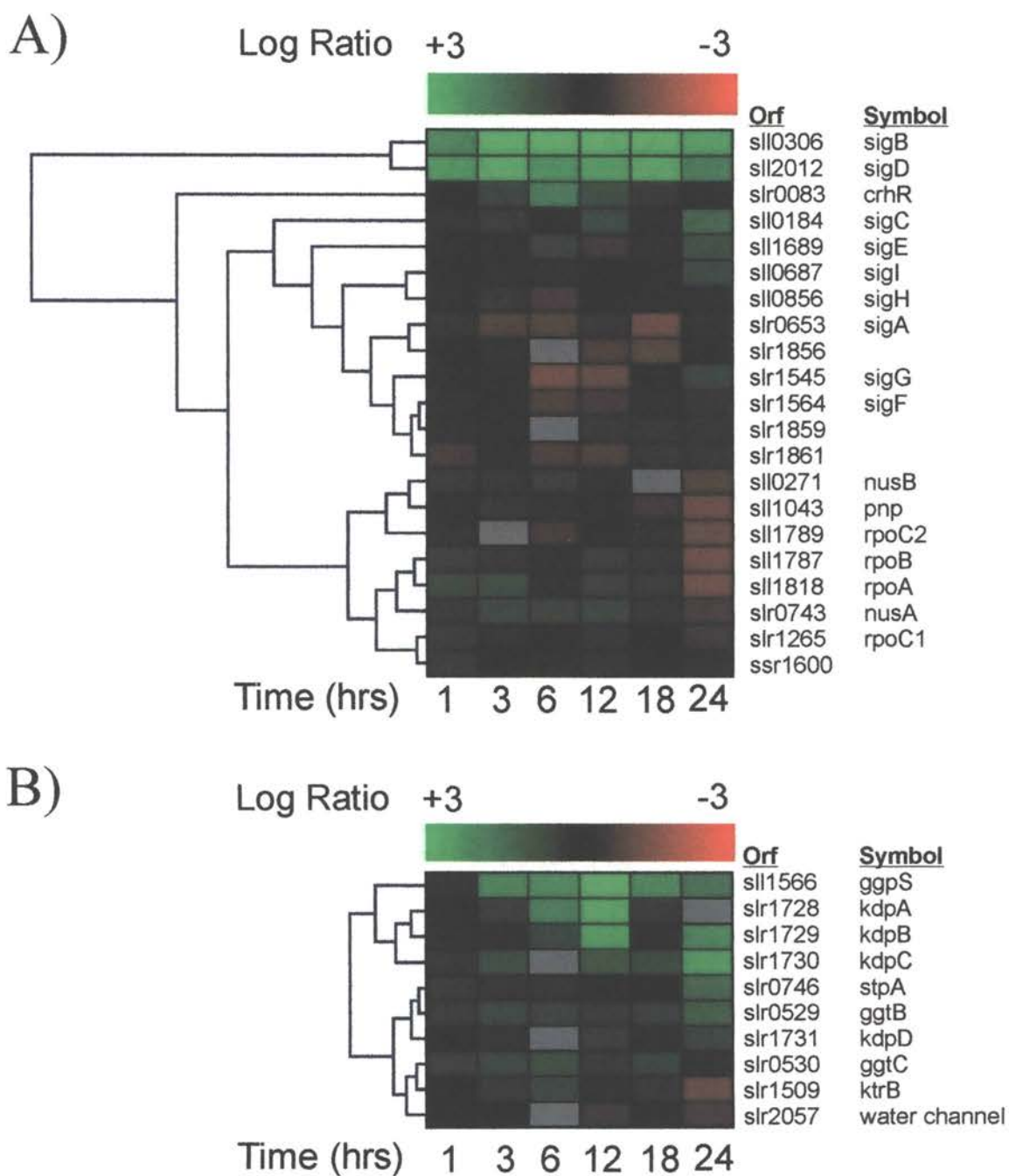


Figure 4.2 continued

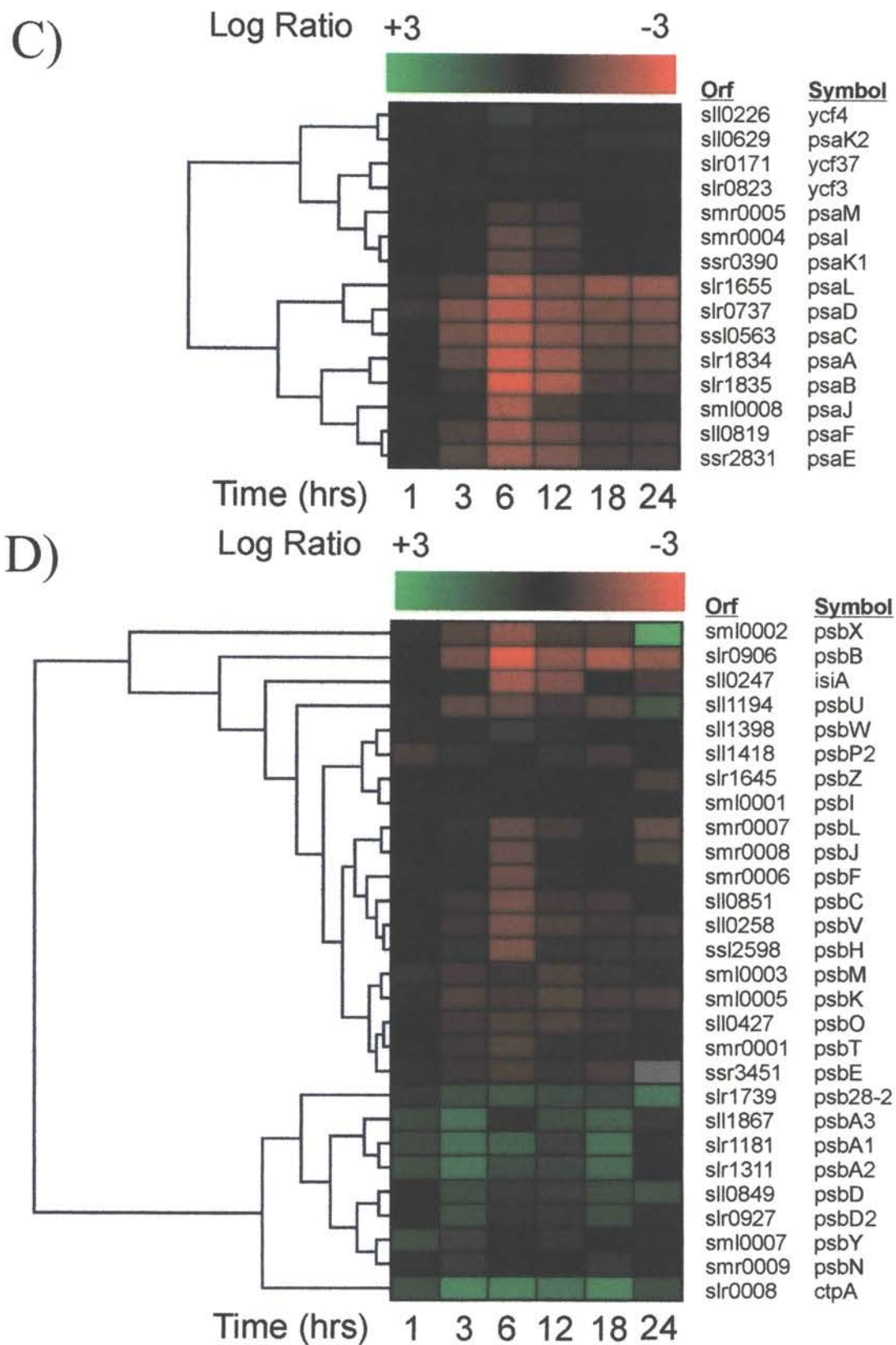


Figure 4.2 continued

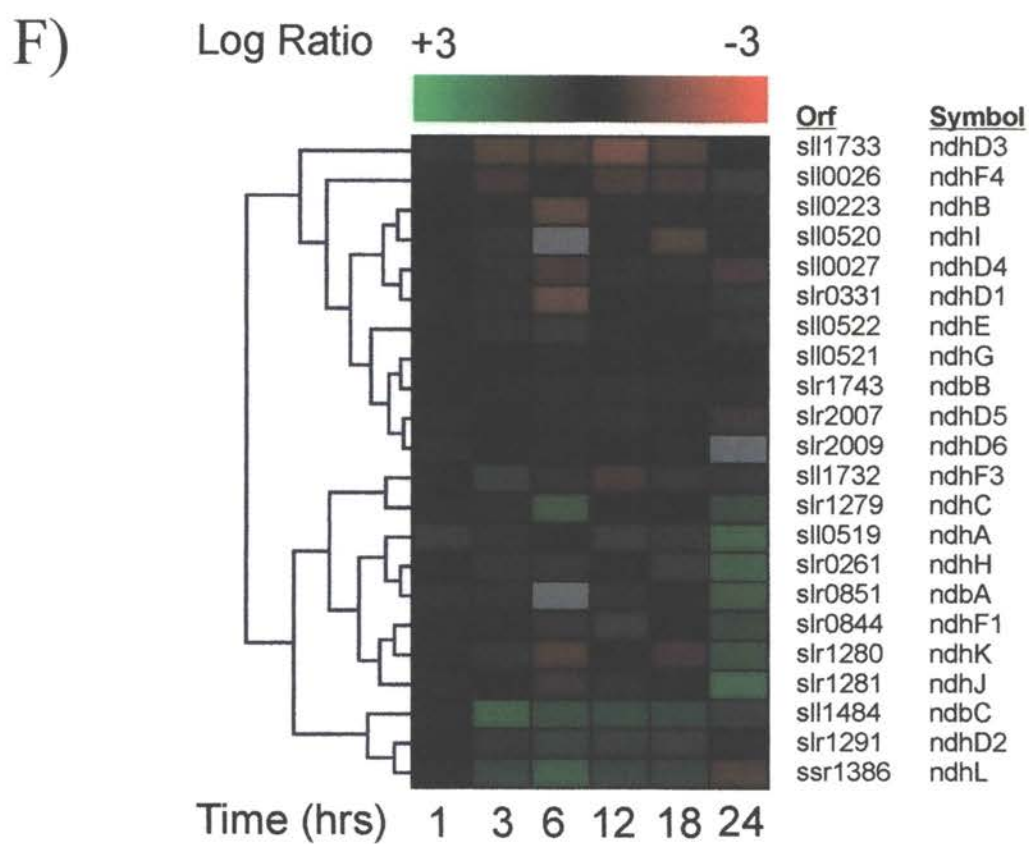
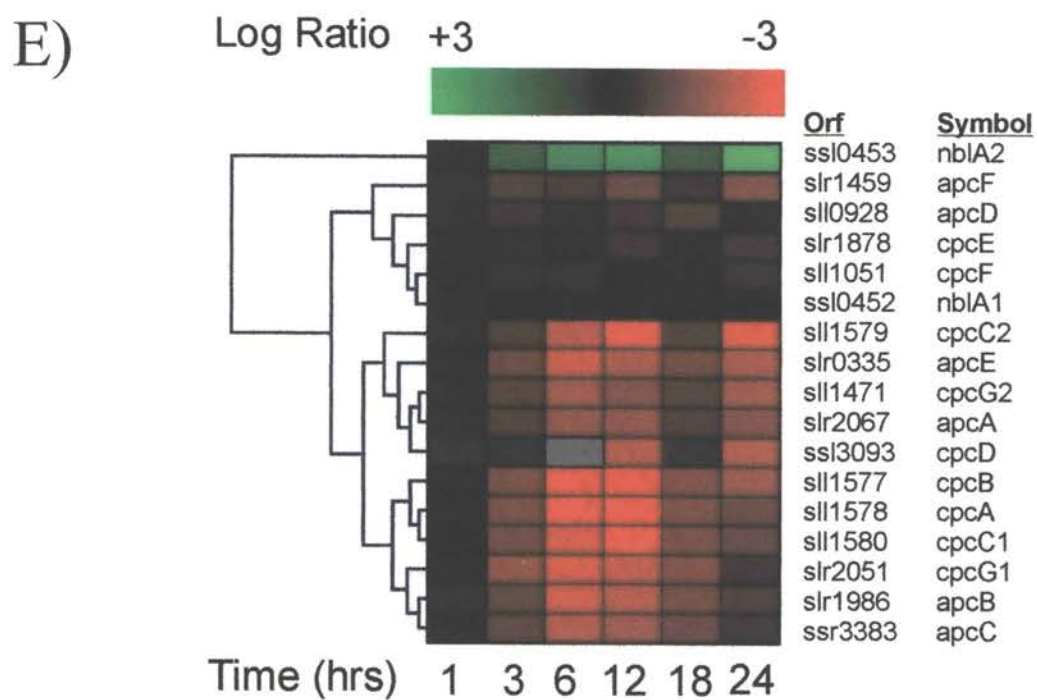
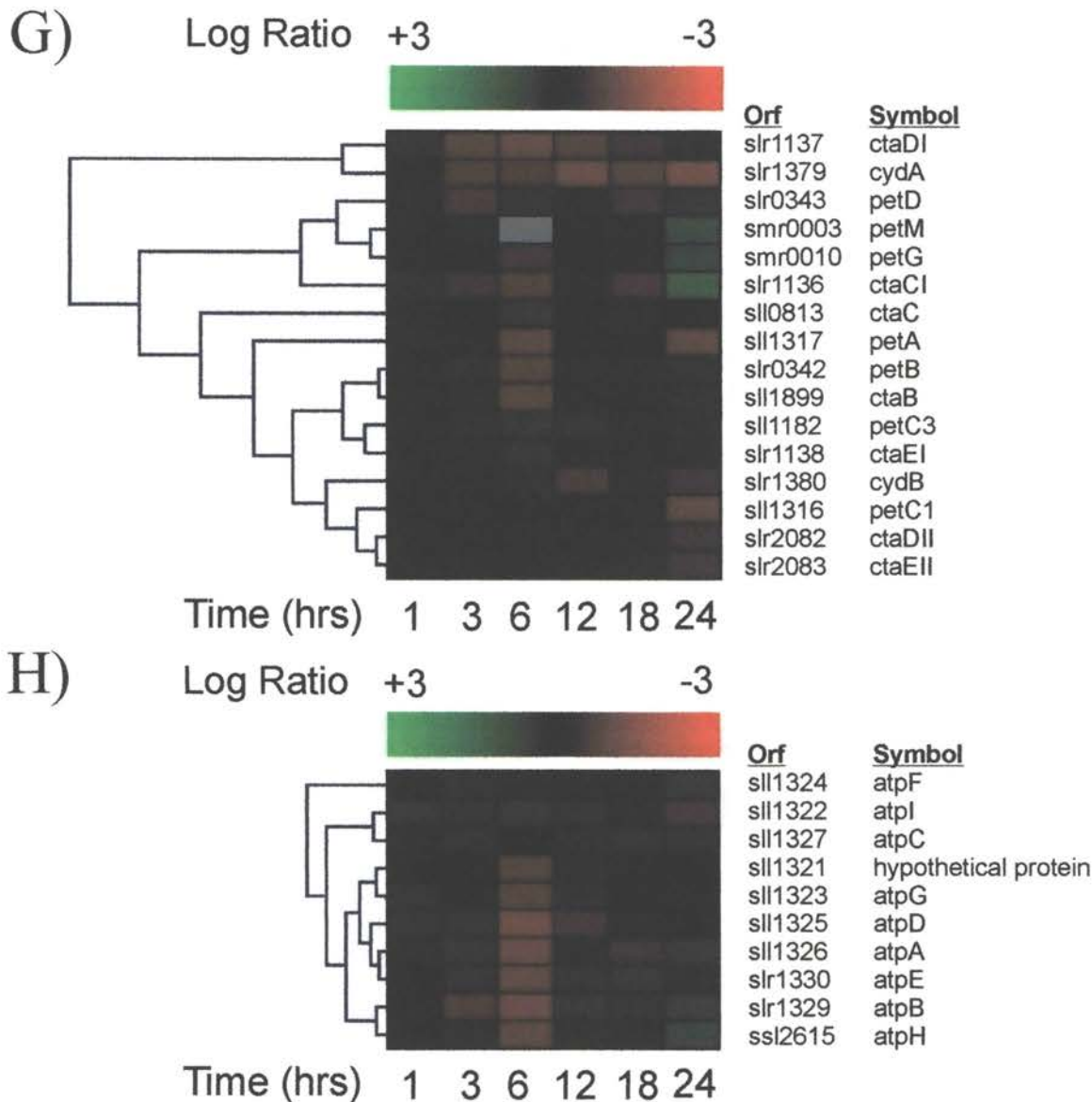


Fig. 4.2 continued



**Figure 4.2 Hierarchical clustering of gene expression patterns of various functional categories along a timcourse after salt shock** RNA samples were purified from *Synechocystis PCC6803* cultures grown in low salt medium (18 mM NaCl) and 1,3, 6, 12, 18, and 24 hours after exposure to high salt (650 mM NaCl). RNA samples were labeled with fluorescent dyes and probed with full genome DNA microarrays. Expression ratios were calculated from the average of replicate spots and transformed to  $\log_2$  ratios. The genes were divided into functional categories and their  $\log_2$  ratios were subjected to hierachial clustering using the Genesis software package (Average Linkage Clustering). Eight functional categories are shown: A) Transcription, B) various genes associated with osmotic regulation, C) Photosystem I, D) Photosystem II, E) Phycoblilisome, F) NADP(H) dehydrogenase, G) Cytochrome b6/f and Cytochrome Oxidase, H) ATP Synthase

The results shown in panel B are from a collection of genes known to play significant roles in osmoregulation. The genes *ggpS* (slr11566), *stpA* (slr0746), *ggtB* (slr0529), and *ggtC* (slr0530) are responsible for the synthesis or transport of glucosylglycerol. Mutant strains lacking any one of these genes show salt sensitivity phenotypes. The genes *kdpA* (slr1728), *kdpB* (slr1729), and *kdpC* (slr1730) are induced by the sensor protein encoded by *kdpD* (slr1731). Together they make up a K<sup>+</sup> transporter system. As shown above these genes are all induced in salt acclimated cultures as well as during salt shock. The *ktrB/ntpJ* (slr1509) gene, another K<sup>+</sup> transporter system, however, is not very strongly regulated under any of these conditions. Interestingly, the gene encoding the water channel protein does not appear to be significantly affected during the salt shock response despite its significant repression in salt acclimated cultures.

Figure 4.2 panel C depicts the relative expression patterns for 15 genes which encode one of the various protein components of the PSI complex or a protein associated with it. Hierarchical clustering of these expression patterns divides them into two main groups; those whose expression is only slightly changed and those whose expression is strongly repressed at six and 12 hours after salt shock. It appears as if the transcript abundance for these genes correlates with that of *sigA* and *sigG*.

Two features of panel D are striking. Most of the genes for the PSII reaction center core are induced with the exception of *psbB* which is just as strongly repressed. Induction of *sigD* (described earlier) is known to induce all three *psbA* transcripts (13). The protein product of *ctpA* is a protein processing enzyme responsible for the maturation of PsbA proteins, enabling them to form functional reaction centers. It is important to



note at this time, that the three genes encoding PsbA protein, *psbA1* (slr1181), *psbA2* (slr1311), and *psbA3* (sll1867) show greater than 97% sequence identity and as a result, the method used here cannot discriminate between them. The remaining genes in this group appear to also express coordinately with *sigA* and *sigG* showing maximal repression at six hours after salt shock. It is important to note however that relative expression for most of these genes has returned to pre-stress levels after 24 hours. This implies that PSII activity has been restored.

Panel E includes all the major subunits for phycobilisome synthesis. Phycobilisomes are structures attached to the cytoplasmic side of the thylakoid membrane and are capable of funneling energy from light to the reaction center of PSII. The gene *nblA2* (ssl0453) encodes a small peptide responsible for the degradation of phycobilisomes during times of high light stress, or nutrient deficiency. The exact mechanism by which this occurs has yet to be deciphered. Nonetheless it is appealing to see the inverse relationship between its expression and the rest of the phycobilisome genes.

Of all of the functional categories shown here, panel F is the most difficult to explain. The genes encoding the various components of the NADH dehydrogenase complex show the least amount of coordinated expression. The function of the NADH dehydrogenase core can be modulated by the incorporation of different *ndhD* and *ndhF* subunits. In one configuration, it is responsible for low CO<sub>2</sub> inducible CO<sub>2</sub> transport,

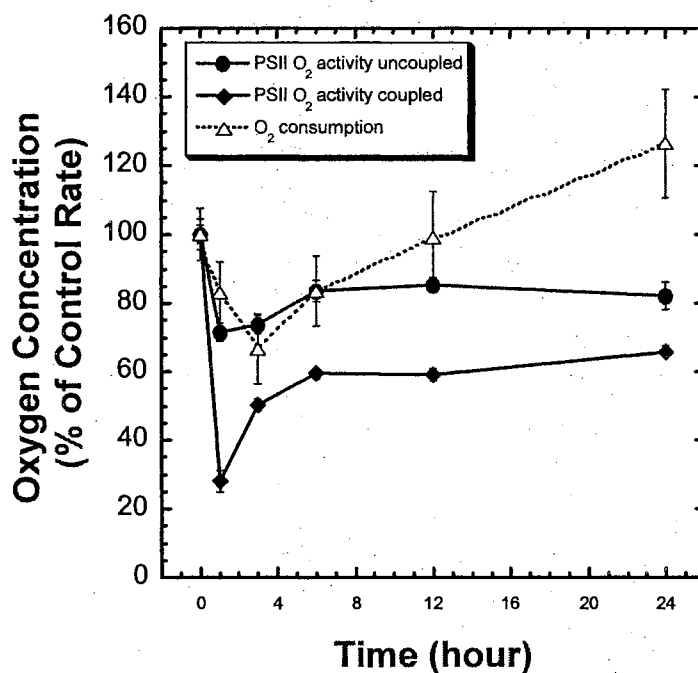
and in another it is considered a  $\text{Na}^+$  transporter. However, due to the lack of obvious signal correlation, it is difficult to predict their involvement in the salt shock response.

Panel G and H illustrate the results of clustering the genes for the respiratory complexes Cytochrome Oxidase and Cytochrome *b<sub>6</sub>f*, and ATP synthase respectively. Most of these genes show little differential regulation except at six hours after high salt shock. Like PSI, the genes associated with these three complexes show coordinate expression with that of *sigG*.

*Photosystem II activity is reduced immediately and transiently after salt shock*

The products of photosystem II activity are a proton gradient, molecular oxygen ( $\text{O}_2$ ) and a reduced plastoquinone pool. Measuring the rates of  $\text{O}_2$  evolution is one method to measure the activity of PSII. Under low light conditions however, rates of  $\text{O}_2$  consumption are also a measure for dark respiration. Figure 4.3 illustrates the effect salt shock has on PSII activity and respiration over a 24 hour period. The oxygen evolving activity of PSII decreases along with dark respiratory activity immediately following the up-shift to high salt conditions. Within six hours after treatment nearly 60% of the oxygen evolving activity of PSII is recovered, a level which is maintained through the entirety of this experiment. By 24 hours, oxygen consumption through respiration has increased to 120%, possibly to compensate for the loss of PSII activity. The addition of the artificial electron acceptors  $\text{K}_3\text{Fe}(\text{CN})_6$  and 2,6-dichlorobenzoquinone (DCBQ) reduce the loss of activity. This implies that the loss of photosynthetic activity is coupled to electron transfer and is not entirely the result of damage to PSII.





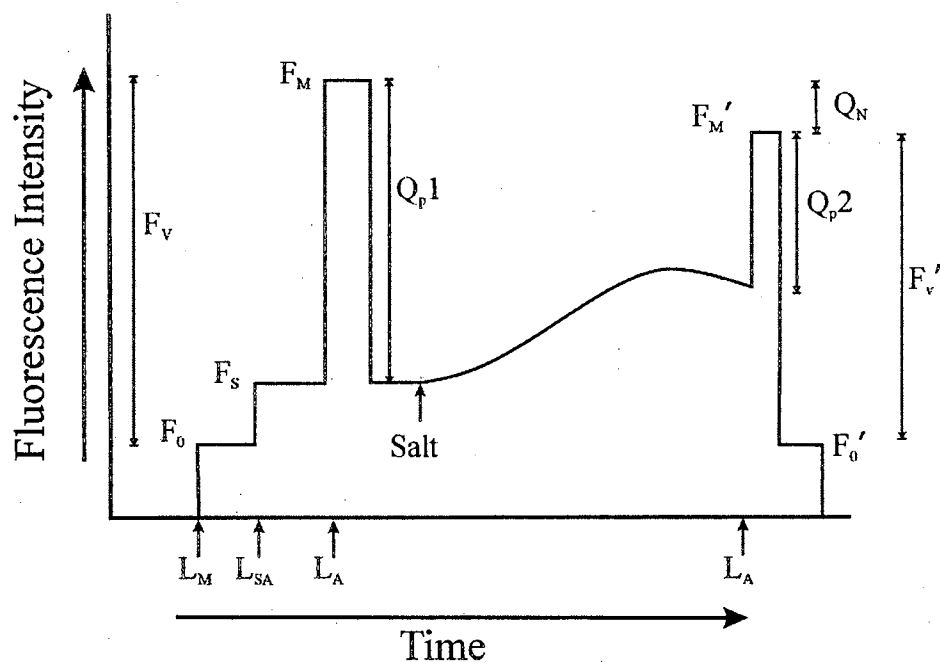
**Figure 4.3** Polarographically measured rates of photosynthesis and respiration following salt shock of *Synechocystis* sp. PCC6803 cells. Oxygen evolution was measured under saturating illumination where PSII activity is coupled to C<sub>i</sub>-fixation (added as bicarbonate) and uncoupled (DCBQ + KFeCN as artificial acceptor system). Rates of respiration were measured as oxygen consumption following transfer of cells to the dark. Control rates of oxygen evolution prior to salt addition were 550 and 220  $\mu\text{moles/mg Chl/hr}$  for DCBQ + KFeCN supported rates and NaHCO<sub>3</sub> supported rates, respectively. Rates of respiration prior to salt addition were 40  $\mu\text{moles/mg Chl/hr}$ .

To determine the extent of PSII damage, variable fluorescence was measured using a Pulse Amplitude Modulated (PAM) Fluorometer. Fluorescence occurs after a photon of light excites chlorophyll molecules of the photosynthetic apparatus. In plants, algae, and cyanobacteria, most fluorescence is associated with the PSII reaction center and the level of fluorescence is a function of its redox state. If photons absorbed by PSII cannot be used to oxidize water and reduce the primary electron acceptor of PSII (a quinone molecule called Qa), then it is dissipated as heat or as light. This most frequently happens when Qa is already reduced by a previous excitation of the reaction center. High fluorescence occurs, for example, when the electron acceptors for the electron on Qa are not available. This can occur by the addition of an inhibitor blocking electron flow from Qa or by physiological conditions making the pool of acceptors reduced and therefore unavailable to accept additional electrons from PSII. For a graphical depiction of fluorescence measurements and the different phases of the fluorescence yield, see figure 4.4. Three parameters of PSII fluorescence are reported in figure 4.5. Quantum efficiency ( $\Phi_{\text{PSII}}$ ) is a measure of the fraction of PSII reaction centers which are capable of being excited and is calculated from the formula:

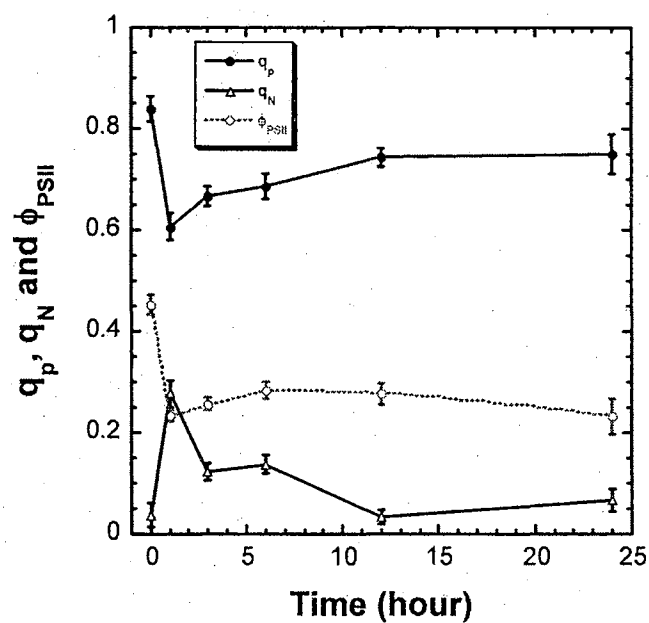
$$\Phi_{\text{PSII}} = (F_M' - F_S) / F_M'$$

After salt shock the fraction of oxidized centers decreases immediately to a level which is maintained throughout the course of this experiment. Photochemical quenching ( $q_p$ ) occurs when the plastoquinone pool oxidizes Qa allowing the oxidation of water thus reducing fluorescence. Photochemical quenching is calculated using the equation:

$$q_p = (F_M' - F_S) / (F_M' - F_O')$$



**Figure 4.4 PAM Fluorometer measurements of PSII activity** Fluorescence as measured by a PAM fluorometer can be used to characterize the quantum efficiency and relative amount of active PSII reaction centers.  $L_M$ , measuring light;  $L_{SA}$ , sub-actinic light (to establish growth-like conditions);  $L_A$ , actinic light;  $F_S$ , steady state of fluorescence;  $F_0$ , basal level of fluorescence;  $F_M$ , maximal fluorescence;  $F_V$ , variable fluorescence is a measure of total active PSII reaction centers;  $Q_P$  (1&2), photochemical quenching.



**Figure 4.5 Salt shock reduces PSII efficiency** Changes in quantum yield of PSII electron transport ( $\Phi_{PSII}$ ), photochemical quenching coefficient ( $q_p$ ), and the non-photochemical quenching coefficient ( $q_N$ ) following salt upshift.

Because the rate of photochemical quenching decreases after salt shock and photochemical quenching is dependent on the oxidative state of the plastoquinone pool, then the plastoquinone pool must also be relatively reduced.

Non-photochemical quenching ( $q_N$ ) is defined as the result of fluorescence quenching arising from some means other than through the oxidation of the  $Q_A$  site of PSII by electron transport.  $q_N$  is calculated by the equation:

$$q_N = 1 - (F_V'/F_V)$$

One common means of non-photochemical quenching is the dissipation of energy as heat. Non-photochemical quenching is immediately induced after the onset of salt stress, decreases to moderate levels after three and six hours and is near basal levels after 12 hours.

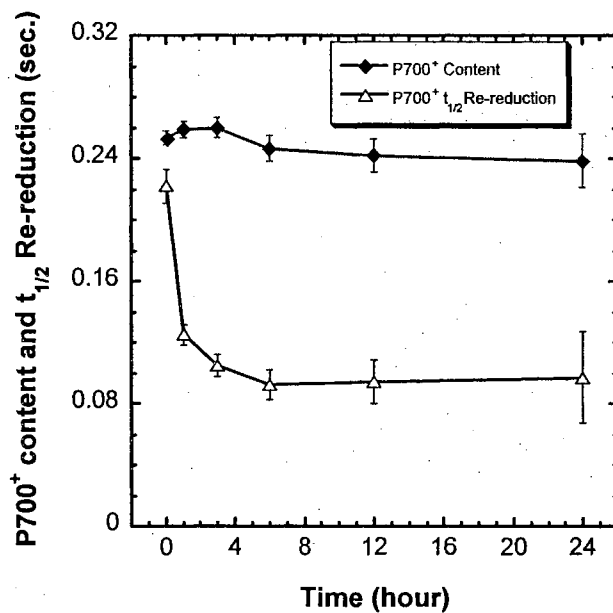
#### *Salt shock induces cyclic electron transport*

Electron transport downstream of Photosystem I (PSI) is capable of operating in two modes; linear and cyclic. More specifically, linear electron transport is the preferred mode under normal conditions where electrons are shunted towards carbon fixation. However under conditions of stress or when carbon fixation is inhibited, an alternate route for electrons is required. Cyclic electron transport is an alternate path by which electrons are cycled through PSI multiple times. This occurs by the transfer of electrons

from PSI, via ferredoxin:NADP<sup>+</sup> reductase, to the plastoquinone pool. The plastoquinone pool then transfers electrons to the cytochrome b<sub>6</sub>/f complex and eventually back to PSI. Induction of this cyclic electron transfer has one very significant benefit in that it permits the generation of a H<sup>+</sup> gradient across the thylakoid membrane by PSI and decreases the dependency for PSII to contribute to electron transport. To explore whether or not cyclic electron transport is indeed enhanced under these conditions, measurements of P700 content and P700<sup>+</sup> re-reduction rates were collected. From figure 4.6 it is apparent that while the P700 content is relatively stable, the rate of P700<sup>+</sup> re-reduction is increased dramatically after salt shock. The increased re-reduction rate is indicative of cyclic electron transport and supports the observations made previously regarding the rate of PSII oxidation by the plastoquinone pool. This is consistent with that previously reported by Joset et al (14). Additionally, salt acclimated cultures maintain re-reduction rates similar to that of pre-stressed levels (data not shown).

#### *Cyclic electron transport enhances superoxide production*

Superoxide production in *Synechocystis* closely correlates with the induction of cyclic electron transport. As mentioned above, many stress conditions can induce cyclic electron transport. These same conditions also induce oxidative stress. To gain further insight into the production of superoxide, a photometric assay for the conversion of XTT to formazan was developed using whole cells directly from experimental cultures. Salt shock enhances superoxide production ~ three fold, and drops to ~1.5x pre-stress conditions after 24 hours exposure as shown in figure 4.7. Under the salt acclimated



**Figure 4.6 Impact of salt shock on P700 content and P700<sup>+</sup> re-reduction kinetics.** The kinetics of P700<sup>+</sup> re-reduction were obtained from samples treated with DCMU to eliminate the contribution of PSII generated electrons to the intersystem electron transport chain and were determined assuming a single exponential decay component. Experiments were repeated from three to seven times.

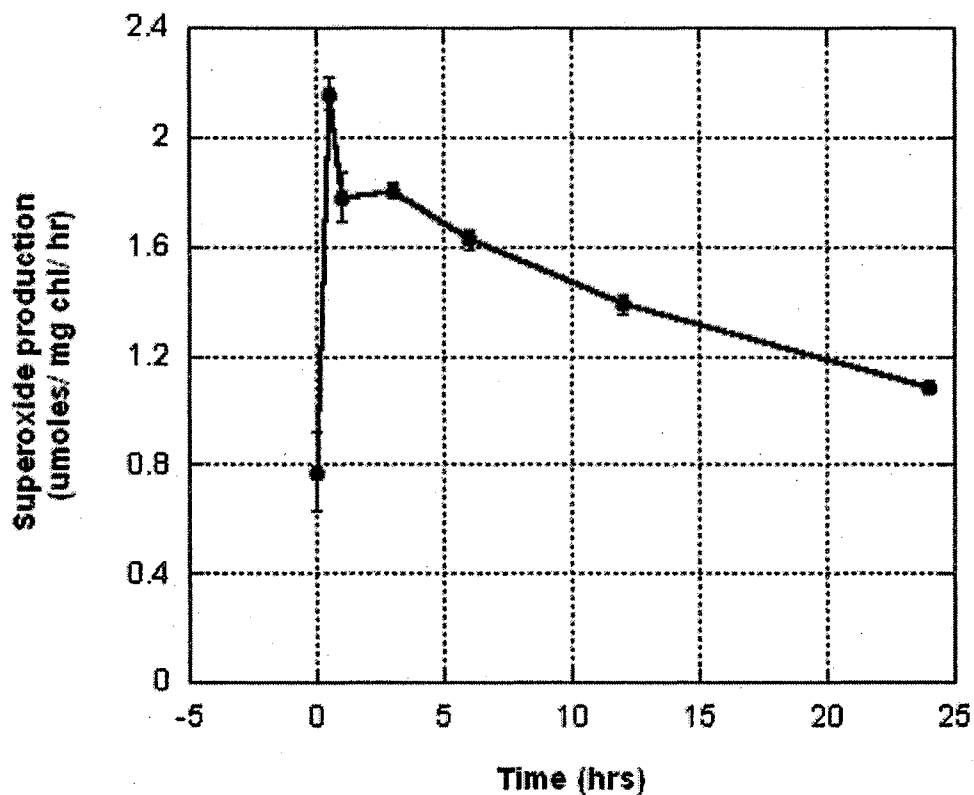
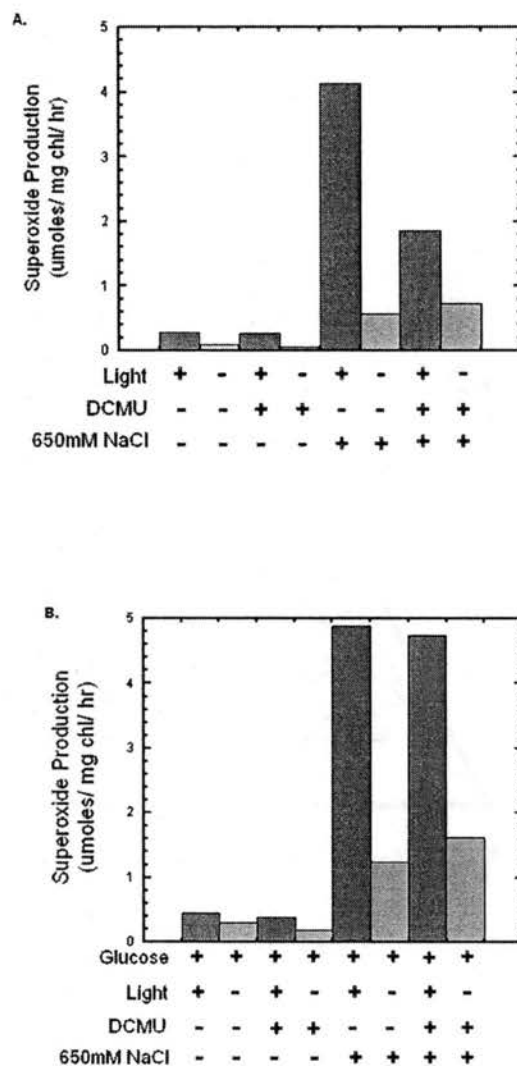


Fig 4.7 **Salt shock induced superoxide production.** Addition of crystalline NaCl (650 mM final) to logarithmically growing cultures of *Synechocystis PCC6803* induces the production of superoxide radicals. At each time point, concentrated samples were assayed for superoxide production by a 10 minute exposure to XTT and subsequent spectro-photometric measurement at 470nm on the cell cleared medium. Under salt acclimated conditions, cells produced superoxide at rates similar to that of stationary phase cells (~1.2 umoles/mg chl/hr).



conditions, *Synechocystis* produces superoxide at a rate of 1.2  $\mu\text{moles/mg chl/hr}$ , similar to the rate after 24 hours exposure to salt shock conditions. To demonstrate that the production of superoxide is linked to electron transport and PSII activity, samples were treated with salt for 10 minutes in the presence (+) or absence (-) of PSII inhibitors, glucose, and altering light conditions. The results shown in figure 4.8 are the average of three replicate samples. In the absence of glucose (panel A) maximal superoxide production is obtained after salt shock when PSII is active. When PSII activity is inhibited by DCMU, production is decreased to about 20%. After the addition of glucose (panel B), superoxide production is enhanced even when PSII activity is low (+DCMU and in dark), though not at maximal levels. This suggests that as long as a source of reductant is available and cyclic electron transport is active, then superoxide production will result.



**Fig 4.8 Superoxide production requires some source of reductant** A.) Photosynthetic activity heightens superoxide production during salt stress. B.) Reductant may also be available through the addition of glucose. Logarithmically growing cultures were treated with or without 650 mM NaCl for 40 minutes. Subsequently, each combination of reagents (80 uE light/m<sup>2</sup>/s, mM glucose, mM DCMU) were added to replicate samples and incubated for 10 minutes. Each sample was assayed for superoxide production by measuring the accumulation of formazan evident through spectro-photometric measurement of absorbance at 470 nm of the cell cleared media.

## Discussion

Ionic homeostasis is a complex phenomenon that all active cells must deal with at every moment. The process requires the regulation of internal ionic composition through the energy consuming import or export of various components across the cytoplasmic and periplasmic membranes. The proper maintenance of cytoplasmic ionic composition is required for optimal performance of the various macromolecular complexes. Under conditions where the ionic composition of the external milieu is changing, then changes in transport activity occur and counter flows must be activated. If those changes are drastic or sudden, such as the sudden exposure to a hypersaline solution, then the impacts may be too great to overcome. The result is a loss of ionic homeostasis and if not corrected quickly then cell death ensues. This process of maintaining ion homeostasis and survival during times when it is disturbed is of interest to plant physiologists hoping to improve plant survival strategies. To this end, the effects of salt stress and the subsequent response by cyanobacteria have been the focus of many studies. Specifically, topics of interest include the accumulation of the compatible osmolyte glucosylglycerol,  $K^+$  transport, and the various effects of salt stress on key components of the electron transport chain and alterations in the bioenergetics associated with adaptation. There are three objectives to the work presented here; 1) to characterize the gene expression profile of salt acclimated cultures of *Synechocystis*, 2) to correlate changes in photosynthetic physiology in response to high salt shock with a time course analysis of gene expression profiles of *Synechocystis*, and 3) to identify the source of superoxide production and its relationship to salt shock.

From the results of gene expression profiles for salt acclimated cultures of *Synechocystis*, several features are immediately obvious. For one, the list of genes differentially regulated is longer than one would achieve through the currently accepted criteria that a gene assigned as significantly induced must have a two fold or greater change in expression. The 2-fold criterion limits the analysis to genes which are expressed at moderate to high levels, however there is no a priori reason to assign functionally significant changes to 2-fold or greater. For example, relatively small changes in expression by regulatory genes may result in large changes in the genes they regulate and these genes may never be expressed at levels to obtain such changes. In fact, small changes in regulatory gene expression can have significant effects on physiology. The method used here for statistical analysis of gene expression and the subsequent assignment of significance based on the common Student's and associative t-tests presents a more appealing option than the arbitrary 2-fold criterion. This however does not address the issue that the lack of change in expression can be perceived as significant in a biological sense. For instance, many of the genes encoding subunits of the two photosystems are noticeably absent from either list of differentially regulated genes after salt acclimation. This implies that their expression is not significantly different from pre-stress levels and assuming they are translated, this in turn implies that their assigned function has been recovered. This conclusion leads to the implication that the photosynthetic activity of cultures acclimated to high salt are similar to those acclimated to low salt. This is consistent with observations of PSII quantum efficiency and P700 content, both of which return to near pre-stress levels.

Another important feature of the gene expression analysis is the continued induction of salt stress related genes. Many genes associated with regulating ion homeostasis and osmotic potential are induced. These include those responsible for accumulation of glucosylglycerol, and transport of  $K^+$ . The energetic requirements for their activity may contribute significantly to the decreased growth rate as the energy consumed by these mechanisms would have otherwise been invested in growth and reproduction.

Based upon the persistent up-regulation of chaperonins, it is obvious that maintaining properly folded proteins continues to be an important function even after acclimation to high salt. This observation is also manifested in the increased expression of the *psbA* genes of PSII known for their high turnover rates and relative ease at which they are damaged.

An important contribution of the present work is the information obtained by the analysis of superoxide production. Superoxide production is one result of cyclic electron transport. During salt shock, superoxide production is increased 2.7 fold after 30 minutes and decreases to only 1.4 fold after 24 hours. Gene expression for *sodB* (*slr1516*) is induced very strongly after salt shock (maximum of 20 fold at 3 hours) and decreases to three fold induction after acclimation. It has been proposed that the production of superoxide radicals may actually be a benefit to the cell, despite its damaging potential. When RubisCO (the key  $CO_2$ -fixing enzyme of the Calvin cycle

which is effectively the terminal electron acceptor of the electron transfer chain) activity is reduced, it oxidizes the electron transport chain at a slower rate. This effect provides the potential for increased damage to PSII since electrons will be less efficiently removed from  $Q_A$ , which is a condition that directly correlates to damage at the acceptor-side domain of PSII. This potentially damaging condition can occur with any stress that causes the electron transport chain 'downstream' of the PSII complex to become over-reduced. Thus, any mechanism that would prevent the over-reduction of the electron transport chain would, in principal, help alleviate this kind of damage to PSII. In this context, the production of superoxide could be considered an alternative electron acceptor. SodB protein catalyzes the conversion of superoxide to peroxide which is then disproportionated to water and  $O_2$ . The cycle of PSII splitting water to produce electrons which are eventually transferred back to water is called the "water-water" cycle.

On the other hand, the increased level of superoxide production could simply be an incidental by-product of the increased level of cyclic electron transport. As mentioned, cyclic electron transport activity is increased following salt shock and this appears to be a mechanism to increase the level of ATP production even under conditions where linear electron transport is decreased due to PSII damage. In this context, it is interesting to note that flavoproteins have been recently identified in *Synechocystis* that have the activity of catalyzing the direct reduction of  $O_2$  by NADPH without having the potentially dangerous production of superoxide as the intermediate. These proteins are postulated to act as an 'escape valve' for excess reductant generated by the light reactions. These proteins, however, are not induced under salt stress conditions.

Therefore, evaluation of these alternative proposals will need further investigation. Nevertheless, the present studies do provide resolution to the long-standing question as to the source of superoxide in photosynthetic organisms exposed to salt stress.

Probably the most intriguing observations from salt acclimated expression analysis is the regulation of a very large number of genes with no assigned function, particularly in the list of repressed genes. This provides many opportunities for future investigation and potential for reward. It is at the very least amusing that the most differentially expressed genes (both induced and repressed) are of unknown function. Despite a decade of effort to characterize the salt shock response of cyanobacteria, these genes have never been characterized beyond their expression and sequence homology. In fact many of these unknown or hypothetical genes are conserved evolutionarily, which points to their significance and our lack of understanding.

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## Summary

Cyanobacteria occupy a very interesting niche in scientific research. The currently accepted endosymbiotic theory suggests that higher plant chloroplasts and cyanobacteria have common progenitors. This postulate can be contributed to their common structure, physiological activity, and gene conservation. As a result, cyanobacteria have been used extensively as a model system for photosynthetic physiology and protein structure function relationships. Some of the landmark achievements made through the use of cyanobacteria include the characterization of crystal structures for PSI, PSII and the cytochrome *b<sub>6</sub>/f* complex as well as the biosynthetic pathway for carotenoids (9, 10, 13). With these interests in mind, the genome of *Synechocystis PCC6803* was fully sequenced (11, 12). Further information about the genome is available at: <http://www.kazusa.or.jp/cyano/cyano.html>.

The literature review in Chapter I introduces many of the concepts and practices involved in a functional genomics program. These include techniques for the further characterization of genes based on sequence homology, gene order (and its conservation between various organisms), mutational analysis, and condition specific patterns of expression. Chapters II and III detail two techniques: production of directed gene replacement mutants and gene expression profiling using DNA microarrays. These two technologies are key components of a functional genomics strategy developed to begin the process of assigning function of each of the genes on the genome of *Synechocystis PCC6803*.

Mutational analysis allows the determination of function through monitoring the effects on growth or physiology after introduction of a mutation. Mutations can be introduced as single point mutations, as gene insertions or gene replacements (knockouts). Point mutations can be used to determine protein interactions with itself, or with other molecules without the total loss of protein activity. Insertional and gene replacement mutations provide the opportunity to completely eliminate all protein expression and activity. Gene replacement also provides a background strain for the reintroduction of that gene with point mutations. A method developed for the purpose of introducing gene replacements is the subject of chapter III. An earlier version of this method was first introduced into *Saccharomyces cerevisiae* (1). The current slightly improved method introduced here permits the efficient production and detection of gene knockouts in *Synechocystis PCC6803* through the use of fusion PCR (Polymerase Chain Reaction). This technique produces DNA fragments consisting of a selectable marker gene (antibiotic cassette) flanked by two regions of chromosomal DNA as depicted in figure 3.1 on page 82. All components are amplified by PCR and fused together in subsequent PCR reactions through overlapping identical sequence. These fragments are mutagenic when introduced into *Synechocystis PCC6803*, as the flanking regions undergo homologous recombination and carry with them the selectable marker between their loci. This effectively replaces any sequence between the two loci (homologous to the fragment flanks) on the genome with a selectable marker. These mutagenic fragments can be produced without cloning of any sequence. This significantly reduces the amount of time and work that it takes to produce a directed mutation.

*Synechocystis PCC6803* maintains approximately eight copies of its genome at any given time. The presence of any one functional copy of a specific gene is dominant, and as a result, the effect of incomplete mutagenesis is usually not apparent until all eight copies of the genome contain the mutation. Isolation of complete segregants is promoted by the application of increasing amounts of antibiotics to the media and selection of bacterial colonies which survive the strongest dosage. The complete segregation of the mutation throughout all eight copies may be detected through the use of colony PCR as depicted in Figure 3.3 on page 89 of Chapter III. While this method does not necessarily eliminate the need for Southern analysis, it is useful as a screen prior to isolation of chromosomal DNA.

Chapter two introduces one of many methods (2-6) used for the efficient production and reproduction of DNA microarrays for *Synechocystis PCC6803*. These DNA microarrays are produced from a DNA fragment library. This library is produced using PCR and oligonucleotides designed to amplify every open reading frame from the genome of *Synechocystis PCC6803*. The oligonucleotides are modified at the 5' end so that the resulting fragments can be reamplified using universal primers. This permits the storage of fragments in 384 well microtiter plates, and the transfer of the fragment library between collaborating laboratories allowing the proliferation of the technology. In addition, multiple variations can be produced by changing the glass substrate, printing buffer, the percent of fragments printed (sub-genomic arrays) or can be improved if the genomic sequence has been re-annotated. This technique can also be applied to any

prokaryote whose genome has been sequenced or even to all known sequences of organisms whose genome has not been completely sequenced. In fact, only introns limit the application to eukaryotes. PCR from genomic DNA of a eukaryote would need to be limited to only coding regions and thus more fragments would need to be produced for each gene.

Chapter IV introduces the implementation of DNA microarray technology towards an analysis of the salt stress response by *Synechocystis PCC6803*. This chapter correlates gene expression profiles of salt shocked and salt acclimated cultures with several measures of physiological activity, specifically photosynthetic parameters. In addition the relationship between salt stress, cyclic electron flow around photosystem I and superoxide production is explored. Previous studies on photosynthetic and respiratory activity suggest considerable changes in the specific activity of many proteins and the expression of their transcripts (8). However, it is demonstrated here, that after acclimation to high salt conditions, much of the photosynthetic activity of *Synechocystis PCC6803* has been recovered (figures 4.3-6 on pages 136, 138, 139, and 142 respectively). Following acclimation, most of the changes in gene expression profiles of known genes are limited to those related to maintenance of osmotic potential and ionic homeostasis (Table 4.1 and 4.2 on pages 114 and 120 respectively). It was decided then that a time course analysis of gene expression profiles could be used to identify regulatory mechanisms which control the modulation of photosynthetic activity at the transcriptional level. The data presented here suggests that many of the genes associated with photosynthesis are regulated by the primary sigma factors *sigA* and *sigG* (figure 4.2

on pages 129-132). This correlation is drawn from the observation of their coordinated transient decrease in transcript abundance. However, a few genes from the reaction center of PSII appear to be regulated coordinately with *psbA* which is known to be regulated by SigD expression (7). This suggests the hypothesis that they also are regulated by SigD expression. Other notable changes in transcript abundance can be associated with protein denaturing. The sigma factor *sigB* is strongly induced along with *sigD*. SigB has been characterized previously as a heat shock response sigma factor and has been implicated in regulating a number of chaperonins.

Many genes of unknown function are differentially regulated by salt stress, some of which show homology to well characterized protein motifs. However, their biological role in salt stress or normal growth has not yet been explored. These differentially expressed unknown genes represent new opportunities for exploration. They have the potential of being the next innovation in crop plant genetic engineering.

A further conclusion from this work includes the finding; that the increased production of superoxide radicals is dependent on activity from photosystem II or respiration, and are most likely a byproduct of increased cyclic electron transport around photosystem I. This helps to understand synergistic effects of salt shock with high light stress and heat, all of which induce cyclic electron transport around photosystem I and induce superoxide production.

Overall, this work defines several strategies implemented in a functional genomics analysis of *Synechocystis PCC6803*. These include the development of technologies designed to introduce mutations within the genome and to monitor global changes in transcript abundance. In addition, the latter has been used to gain insight into the response of *Synechocystis PCC6803* to salt stress. Observations made here improve the functional assignment of many genes through their implicated role in salt stress response.

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Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sgl0001		hypothetical protein	1.70	2.68	0.120553	8.03	13.85	0.16	0.85	0.79	4.74	2.24
sgl0002		hypothetical protein	82.25	13.53	0	64.52	7.95	0.00	0.02	0.00	0.78	-0.35
sil0002		penicillin-binding prote	187.74	13.12	0	215.82	26.05	0.00	0.04	0.01	1.15	0.20
sil0005		hypothetical protein	280.61	37.37	0	241.80	45.77	0.00	0.13	0.04	0.86	-0.21
sil0006		putative aminotransfer	176.18	31.14	0	158.46	24.21	0.00	0.30	0.09	0.90	-0.15
sil0007		hypothetical protein	50.98	9.79	0	55.09	16.18	0.00	0.66	0.58	1.08	0.11
sil0008		unknown protein	23.66	14.16	4.25E-05	8.75	7.59	0.00	0.08	0.05	0.37	-1.44
sil0010		unknown protein	46.85	9.81	0	20.35	14.18	0.00	0.13	0.10	0.43	-1.20
sil0012		putative transposase [	98.21	11.28	0	467.99	171.66	0.00	0.00	0.00	4.77	2.25
sil0016		probable membrane-b	102.26	27.59	0	66.02	27.60	0.00	0.06	0.01	0.65	-0.63
sil0017	hemL	glutamate-1-semialdel	132.49	21.22	0	177.58	16.24	0.00	0.00	0.00	1.34	0.42
sil0018	fbxA	fructose-bisphosphate	2299.31	311.56	0	3516.28	730.19	0.00	0.00	0.00	1.53	0.61
sil0019		1-deoxy-d-xylulose 5-p	172.27	39.32	0	186.20	44.50	0.00	0.64	0.50	1.08	0.11
sil0020	clpC	ATP-dependent Clp pr	728.79	44.86	0	887.87	224.46	0.00	0.14	0.10	1.22	0.28
sil0021		probable exonuclease	202.87	19.16	0	215.51	31.83	0.00	0.47	0.37	1.06	0.09
sil0022		unknown protein	244.10	25.51	0	121.06	15.13	0.00	0.00	0.00	0.50	-1.01
sil0023		hypothetical protein	151.54	34.65	0	93.35	19.15	0.00	0.00	0.00	0.62	-0.70
sil0024		unknown protein	55.87	13.10	0	71.16	19.43	0.00	0.13	0.02	1.27	0.35
sil0026	ndhF4	NADH dehydrogenase	192.53	23.59	0	283.56	49.16	0.00	0.00	0.00	1.47	0.56
sil0027	ndhD4	NADH dehydrogenase	179.48	28.35	0	249.20	32.71	0.00	0.00	0.00	1.39	0.47
sil0030	cmpR	cmp operon transcripti	26.62	5.80	0	15.89	21.16	0.07	0.08	0.05	0.60	-0.74
sil0031		hypothetical protein	115.26	27.69	0	172.99	53.15	0.00	0.05	0.00	1.50	0.59
sil0033	crhH	carotene isomerase	230.85	71.01	1.78E-15	280.07	59.54	0.00	0.24	0.03	1.21	0.28
sil0034		putative carboxypeptic	109.75	22.89	0	96.51	16.61	0.00	0.29	0.07	0.88	-0.19
sil0036		hypothetical protein	90.15	28.94	2.35E-14	87.26	25.04	0.00	0.94	0.90	0.97	-0.05
sil0037		hypothetical protein	180.03	29.82	0	230.08	47.20	0.00	0.05	0.00	1.28	0.35
sil0038		two-component respon	204.97	37.27	0	193.59	32.61	0.00	0.58	0.42	0.94	-0.08
sil0039		two-component respon	116.43	21.00	0	89.84	43.04	0.00	0.18	0.13	0.77	-0.37
sil0040		similar to chemotaxis p	112.75	18.71	0	105.15	33.31	0.00	0.50	0.43	0.93	-0.10
sil0041		probable methyl-accep	503.03	34.25	0	557.64	49.26	0.00	0.05	0.00	1.11	0.15
sil0042		probable methyl-accep	75.23	8.87	0	82.73	28.45	0.00	0.83	0.82	1.10	0.14
sil0043		two-component hybrid	323.15	31.24	0	291.68	21.21	0.00	0.06	0.00	0.90	-0.15
sil0044		unknown protein	30.46	4.02	0	30.21	10.78	0.00	0.73	0.70	0.99	-0.01
sil0045	sps	sucrose phosphate sy	235.31	14.92	0	210.73	8.29	0.00	0.01	0.00	0.90	-0.16
sil0047	ycf12	hypothetical protein YC	470.31	158.08	3.15E-13	547.36	322.10	0.00	0.86	0.82	1.16	0.22
sil0048		unknown protein	234.75	49.03	0	259.89	59.32	0.00	0.45	0.25	1.11	0.15
sil0051		hypothetical protein	220.36	39.08	0	148.95	19.06	0.00	0.00	0.00	0.68	-0.57
sil0053	accC	biotin carboxylase	181.62	38.54	0	153.59	43.30	0.00	0.26	0.14	0.85	-0.24
sil0055		processing protease	397.86	78.18	0	388.19	62.30	0.00	0.86	0.78	0.98	-0.04
sil0057	grpE	heat shock protein Gr	124.27	22.20	0	222.38	31.66	0.00	0.00	0.00	1.79	0.84
sil0058	dnaK	DnaK protein	622.04	76.17	0	929.00	118.53	0.00	0.00	0.00	1.49	0.58
sil0060		hypothetical protein	42.14	13.56	2.66E-14	63.86	16.56	0.00	0.02	0.00	1.52	0.60
sil0062		hypothetical protein	78.55	10.41	0	60.01	11.84	0.00	0.02	0.00	0.76	-0.39
sil0063		hypothetical protein	220.61	16.87	0	191.81	32.11	0.00	0.08	0.03	0.87	-0.20
sil0064		binding protein of ABC	69.07	8.87	0	129.24	15.83	0.00	0.00	0.00	1.87	0.90
sil0065	ilvN	acetolactate synthase	207.80	42.28	0	143.50	33.81	0.00	0.02	0.00	0.69	-0.53
sil0066		unknown protein	257.92	18.94	0	148.65	21.48	0.00	0.00	0.00	0.58	-0.80
sil0067		glutathione S-transfer	65.92	7.85	0	64.56	11.34	0.00	0.75	0.70	0.98	-0.03
sil0068		unknown protein	176.59	28.08	0	196.36	19.53	0.00	0.19	0.01	1.11	0.15
sil0069		hypothetical protein	63.56	17.27	0	67.82	31.12	0.00	0.93	0.92	1.07	0.09
sil0070	purU	phosphoribosylglycina	66.23	10.07	0	58.10	7.61	0.00	0.13	0.02	0.88	-0.19
sil0071		hypothetical protein	32.91	11.11	3.89E-13	45.42	9.69	0.00	0.06	0.00	1.38	0.46
sil0072		hypothetical protein	33.70	5.45	0	63.00	12.39	0.00	0.00	0.00	1.87	0.90
sil0078	thrS	threonyl-tRNA synthet	198.23	19.47	0	197.69	51.35	0.00	0.82	0.80	1.00	0.00
sil0080	argC	N-acetyl-gamma-gluta	425.92	111.08	0	545.93	185.02	0.00	0.15	0.05	1.28	0.36
sil0082		hypothetical protein	31.14	3.67	0	12.28	14.03	0.03	0.04	0.02	0.39	-1.34
sil0083		phosphoheptose isom	115.95	18.01	0	92.52	12.11	0.00	0.02	0.00	0.80	-0.33
sil0084		putative phosphatase	288.97	124.92	1.46E-08	388.84	193.58	0.00	0.33	0.18	1.35	0.43
sil0085		unknown protein	136.42	20.19	0	121.87	13.02	0.00	0.18	0.01	0.89	-0.16
sil0086		putative arsenical purr	134.19	13.09	0	145.18	33.06	0.00	0.54	0.48	1.08	0.11
sil0088		hypothetical protein	95.73	26.40	0	85.96	23.89	0.00	0.54	0.34	0.90	-0.16
sil0092		putative transposase [	88.30	17.32	0	175.37	47.72	0.00	0.00	0.00	1.99	0.99
sil0094		two-component senso	95.16	22.70	0	67.74	14.94	0.00	0.03	0.00	0.71	-0.49
sil0095		hypothetical protein	127.50	27.01	0	175.31	59.79	0.00	0.14	0.06	1.38	0.46
sil0096		hypothetical protein	108.40	32.58	4.44E-16	119.15	22.68	0.00	0.44	0.09	1.10	0.14
sil0098		hypothetical protein	108.96	17.41	0	138.97	40.41	0.00	0.12	0.05	1.28	0.35
sil0099	cobL	preco-m-ty c5,15-mel	32.16	8.04	0	56.31	7.58	0.00	0.00	0.00	1.75	0.81
sil0100		N-acyl-L-amino acid ar	120.58	20.10	0	145.62	54.59	0.00	0.41	0.34	1.21	0.27
sil0101		unknown protein	11.78	1.96	0	4.96	5.67	0.03	0.04	0.02	0.42	-1.25
sil0102		hypothetical protein	78.84	13.45	0	93.75	24.11	0.00	0.23	0.12	1.19	0.25
sil0103		hypothetical protein	178.63	40.53	0	206.03	24.18	0.00	0.13	0.00	1.15	0.21
sil0107		KHG/KDPG aldolase	39.10	13.47	1.15E-12	29.05	14.29	0.00	0.22	0.14	0.74	-0.43
sil0108	amt1	ammonium/methylam	810.39	143.87	0	1110.73	196.43	0.00	0.01	0.00	1.37	0.45
sil0109	aroH	chorismate mutase	44.89	7.22	0	57.37	30.19	0.00	0.86	0.85	1.28	0.35
sil0135		5-methylthioadenosine	134.01	10.47	0	120.18	12.02	0.00	0.06	0.01	0.90	-0.16
sil0136		aminopeptidase P	919.85	227.54	0	861.98	253.51	0.00	0.61	0.49	0.94	-0.09
sil0141		hypothetical protein	304.71	25.70	0	334.67	26.96	0.00	0.08	0.00	1.10	0.14
sil0142		probable cation efflux	487.17	63.24	0	442.25	107.78	0.00	0.33	0.25	0.91	-0.14

Table A-1 Gene expression profiles for *Synechocytis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slf0144	pyrH	uridine monophosphat	134.17	34.58	0	85.58	21.95	0.00	0.01	0.00	0.64	-0.65
slf0145	rf	RNA-binding protein	230.60	38.96	0	151.25	33.95	0.00	0.00	0.00	0.66	-0.61
slf0146	natC	Integral membrane pr	141.94	9.81	0	128.42	18.05	0.00	0.15	0.08	0.90	-0.14
slf0147		hypothetical protein	359.45	216.18	4.64E-05	547.08	321.28	0.00	0.27	0.14	1.52	0.61
slf0148		hypothetical protein	213.95	64.03	2.22E-16	220.06	34.56	0.00	0.71	0.39	1.03	0.04
slf0149		hypothetical protein	305.38	102.47	2.88E-13	359.16	122.69	0.00	0.44	0.26	1.18	0.23
slf0154		hypothetical protein	299.39	54.94	0	203.60	71.80	0.00	0.02	0.00	0.68	-0.56
slf0156		unknown protein	105.53	11.19	0	102.28	20.93	0.00	0.65	0.59	0.97	-0.05
slf0157		hypothetical protein	75.28	10.92	0	86.34	16.96	0.00	0.24	0.13	1.15	0.20
slf0158	glgB	1,4-alpha-glucan bran	121.93	38.84	1.47E-14	121.17	49.62	0.00	0.87	0.84	0.99	-0.01
slf0160		hypothetical protein	52.51	6.13	0	85.92	22.93	0.00	0.00	0.00	1.64	0.71
slf0161		putative transposase [	792.36	118.37	0	988.38	144.74	0.00	0.03	0.00	1.25	0.32
slf0162		hypothetical protein	68.28	7.06	0	62.25	24.66	0.00	0.38	0.34	0.91	-0.13
slf0163		WD-repeat protein	917.56	125.49	0	915.60	108.54	0.00	1.00	1.00	1.00	0.00
slf0166	hemD	porphyrin biosynthesis	130.24	16.68	0	132.71	23.15	0.00	0.88	0.85	1.02	0.03
slf0167		unknown protein	61.66	11.29	0	51.77	9.92	0.00	0.16	0.04	0.84	-0.25
slf0168		hypothetical protein	72.86	17.58	0	52.06	16.62	0.00	0.05	0.01	0.71	-0.48
slf0169		cell division protein Ftr	1265.01	96.10	0	1304.02	193.32	0.00	0.74	0.71	1.03	0.04
slf0170	dnaK	DnaK protein	634.73	149.08	0	1289.84	524.36	0.00	0.00	0.00	2.03	1.02
slf0171		probable aminomethyl	68.95	9.95	0	135.79	40.32	0.00	0.00	0.00	1.97	0.98
slf0172		unknown protein	57.06	8.74	0	55.72	8.26	0.00	0.80	0.69	0.98	-0.03
slf0173		hypothetical protein	82.40	7.41	0	97.64	21.70	0.00	0.15	0.09	1.19	0.24
slf0174		hypothetical protein	59.58	6.05	0	84.74	11.33	0.00	0.00	0.00	1.42	0.51
slf0175		hypothetical protein	159.14	20.33	0	120.74	15.30	0.00	0.00	0.00	0.76	-0.40
slf0176		hypothetical protein	78.56	6.04	0	79.68	16.25	0.00	1.00	0.99	1.01	0.02
slf0177		hypothetical protein	151.00	40.02	0	184.16	54.70	0.00	0.28	0.12	1.22	0.29
slf0178		hypothetical protein	70.02	99.79	0.085694	83.46	94.02	0.03	0.54	0.34	1.19	0.25
slf0179	glx	glutamyl-tRNA synthet	229.33	21.49	0	281.45	37.12	0.00	0.01	0.00	1.23	0.30
slf0180		hypothetical protein	265.44	49.19	0	135.88	14.26	0.00	0.00	0.00	0.51	-0.97
slf0181		unknown protein	42.66	6.05	0	38.02	22.95	0.00	0.33	0.29	0.89	-0.17
slf0182		ABC transporter ATP-	178.39	34.71	0	161.81	38.76	0.00	0.45	0.32	0.91	-0.14
slf0183		hypothetical protein	285.52	51.38	0	227.03	46.30	0.00	0.06	0.00	0.80	-0.33
slf0184	sigC	group2 RNA polymera	162.17	33.05	0	163.46	27.50	0.00	0.91	0.85	1.01	0.01
slf0185		hypothetical protein	380.59	49.90	0	405.60	74.76	0.00	0.54	0.43	1.07	0.09
slf0188		unknown protein	404.46	25.59	0	353.57	38.92	0.00	0.02	0.00	0.87	-0.19
slf0189		hypothetical protein	30.34	8.33	0	28.19	12.04	0.00	0.62	0.54	0.93	-0.11
slf0191		unknown protein	63.66	17.17	0	37.42	29.08	0.00	0.09	0.05	0.59	-0.77
slf0192		hypothetical protein	99.39	8.97	0	72.48	6.77	0.00	0.00	0.00	0.73	-0.46
slf0194		putative sec-independ	184.37	20.55	0	120.58	10.03	0.00	0.00	0.00	0.65	-0.61
slf0195		probable ATP-depend	228.68	80.41	3.26E-12	253.75	53.20	0.00	0.41	0.09	1.11	0.15
slf0198		hypothetical protein	59.41	14.22	0	43.94	12.71	0.00	0.08	0.02	0.74	-0.44
slf0199	petE	plastocyanin	1537.59	436.74	0	1693.17	297.29	0.00	0.40	0.10	1.10	0.14
slf0200		putative transposase [	56.96	7.35	0	401.20	159.73	0.00	0.00	0.00	7.04	2.82
slf0201		putative transposase [	188.90	29.67	0	636.17	214.23	0.00	0.00	0.00	3.37	1.75
slf0202		glucose inhibited divisi	292.25	73.25	0	433.17	79.34	0.00	0.01	0.00	1.48	0.57
slf0204		glucose inhibited divisi	218.11	51.59	0	136.53	43.88	0.00	0.01	0.00	0.63	-0.68
slf0205		hypothetical protein	35.47	10.95	2.22E-15	9.89	11.23	0.03	0.03	0.01	0.28	-1.84
slf0207	rfbA	glucose-1-phosphate t	110.31	13.77	0	97.64	14.28	0.00	0.13	0.03	0.89	-0.18
slf0208		hypothetical protein	454.28	89.39	0	578.89	137.81	0.00	0.12	0.03	1.27	0.35
slf0209		hypothetical protein	159.68	26.61	0	169.36	24.73	0.00	0.51	0.32	1.06	0.08
slf0210		bacitracin resistance p	54.21	12.46	0	94.41	49.28	0.00	0.08	0.03	1.74	0.80
slf0216		hypothetical protein	54.06	12.01	0	57.12	18.44	0.00	0.89	0.87	1.06	0.08
slf0217		flavoprotein	370.20	64.62	0	456.91	141.51	0.00	0.22	0.13	1.23	0.30
slf0218		hypothetical protein	66.32	8.72	0	25.06	10.96	0.00	0.00	0.00	0.38	-1.40
slf0219		flavoprotein	151.00	38.98	0	82.48	23.66	0.00	0.00	0.00	0.55	-0.87
slf0220	glmS	L-glutamine:D-fructose	184.70	45.64	0	132.29	15.31	0.00	0.03	0.00	0.72	-0.48
slf0221		bacterioferritin comigr	50.64	9.68	0	83.91	31.37	0.00	0.02	0.00	1.66	0.73
slf0222		putative purple acid ph	220.85	10.46	0	222.65	48.97	0.00	0.91	0.91	1.01	0.01
slf0223	ndhB	NADH dehydrogenase	512.61	243.85	2.62E-07	594.51	226.17	0.00	0.45	0.24	1.16	0.21
slf0224		amino-acid ABC transp	209.74	79.09	8.26E-11	205.94	80.74	0.00	0.88	0.83	0.98	-0.03
slf0225		unknown protein	77.75	11.99	0	99.41	22.85	0.00	0.06	0.01	1.28	0.35
slf0226	ycf4	photosystem I assembl	271.29	59.67	0	206.93	27.56	0.00	0.04	0.00	0.76	-0.39
slf0227		peptidyl-prolyl cis-tran	121.84	17.26	0	106.84	10.16	0.00	0.10	0.00	0.88	-0.19
slf0228	speB1	arginase	145.66	23.53	0	181.18	51.78	0.00	0.18	0.10	1.24	0.31
slf0230		hypothetical protein	117.13	14.65	0	191.90	34.63	0.00	0.00	0.00	1.64	0.71
slf0236		unknown protein	160.97	22.15	0	116.97	15.80	0.00	0.00	0.00	0.73	-0.46
slf0237		unknown protein	100.48	13.05	0	104.70	16.18	0.00	0.67	0.56	1.04	0.06
slf0238		unknown protein	206.27	72.94	4.3E-12	242.98	84.60	0.00	0.41	0.22	1.18	0.24
slf0240		ABC transporter ATP-	78.41	17.86	0	32.85	26.01	0.00	0.09	0.06	0.42	-1.26
slf0241		unknown protein	149.20	22.02	0	108.86	34.89	0.00	0.03	0.00	0.73	-0.45
slf0242		unknown protein	178.59	90.44	1.32E-06	347.98	138.23	0.00	0.01	0.00	1.95	0.96
slf0243		unknown protein	62.14	15.29	0	79.06	11.59	0.00	0.05	0.00	1.27	0.35
slf0244		UDP-glucose 4-epimer	105.03	10.34	0	119.71	20.37	0.00	0.17	0.09	1.14	0.19
slf0245		probable GTP binding	134.87	26.35	0	127.13	11.47	0.00	0.64	0.23	0.94	-0.09
slf0247	isiA	iron-stress chlorophyll	407.94	112.22	0	237.70	149.79	0.00	0.04	0.01	0.58	-0.78
slf0248	isiB	flavodoxin	30.85	22.53	0.000797	15.21	23.54	0.11	0.02	0.01	0.49	-1.02
slf0249		hypothetical protein	38.21	9.58	0	26.87	12.31	0.00	0.11	0.06	0.70	-0.51
slf0250		pantothenate metaboli	302.26	17.28	0	174.77	30.95	0.00	0.00	0.00	0.58	-0.79

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slf0252		unknown protein	248.89	60.75	0	270.62	73.10	0.00	0.64	0.51	1.09	0.12
slf0253		hypothetical protein	160.58	63.17	4.76E-10	61.54	25.28	0.00	0.01	0.00	0.38	-1.38
slf0254		probable phytoene del	236.79	25.15	0	252.60	37.35	0.00	0.44	0.32	1.07	0.09
slf0257		hypothetical protein	226.07	38.89	0	181.93	40.90	0.00	0.09	0.02	0.80	-0.31
slf0258	psbV	cytochrome c550	728.55	152.20	0	515.92	104.93	0.00	0.02	0.00	0.71	-0.50
slf0260		hypothetical protein	211.25	44.93	0	178.11	23.75	0.00	0.15	0.00	0.84	-0.25
slf0261		hypothetical protein	219.37	50.84	0	164.19	60.07	0.00	0.09	0.02	0.75	-0.42
slf0262	desD	delta-6 desaturase	161.10	8.13	0	114.92	32.90	0.00	0.01	0.00	0.71	-0.49
slf0263		unknown protein	114.00	31.24	0	51.04	21.76	0.00	0.00	0.00	0.45	-1.16
slf0264		probable dioxygenase	73.14	24.23	1.43E-13	90.14	53.37	0.00	0.65	0.58	1.23	0.30
slf0265		unknown protein	46.00	15.85	1.17E-12	48.35	20.90	0.00	0.88	0.84	1.05	0.07
slf0266		unknown protein	49.84	6.30	0	48.08	16.00	0.00	0.61	0.57	0.96	-0.05
slf0267		unknown protein	379.23	45.11	0	396.37	29.03	0.00	0.42	0.10	1.05	0.06
slf0268		hypothetical protein	63.53	4.51	0	70.43	8.75	0.00	0.11	0.04	1.11	0.15
slf0269		hypothetical protein	27.36	3.50	0	19.36	11.54	0.00	0.27	0.24	0.71	-0.50
slf0270		prinosomal protein N'	239.49	28.74	0	156.57	8.87	0.00	0.00	0.00	0.65	-0.61
slf0271		N utilization substance	70.24	10.37	0	107.63	8.96	0.00	0.00	0.00	1.53	0.62
slf0272		hypothetical protein	94.48	12.76	0	100.65	20.23	0.00	0.60	0.52	1.07	0.09
slf0273	nhaS2	Na+/H+ antiporter	301.69	58.54	0	318.49	50.55	0.00	0.54	0.33	1.06	0.08
slf0274		hypothetical protein	55.84	14.98	0	55.83	20.74	0.00	0.87	0.84	1.00	0.00
slf0280		unknown protein	35.81	4.30	0	49.22	7.69	0.00	0.01	0.00	1.37	0.46
slf0281		unknown protein	34.31	7.82	0	33.29	4.40	0.00	0.88	0.76	0.97	-0.04
slf0282		unknown protein	49.60	13.66	0	90.14	28.07	0.00	0.01	0.00	1.82	0.86
slf0283		hypothetical protein	86.73	17.74	0	37.18	15.24	0.00	0.00	0.00	0.43	-1.22
slf0284		hypothetical protein	137.65	32.35	0	186.71	40.25	0.00	0.03	0.00	1.36	0.44
slf0286	ycf52	hypothetical protein YC	31.01	3.80	0	39.72	7.22	0.00	0.02	0.00	1.28	0.36
slf0288	minC	septum site-determinir	93.34	24.73	0	102.54	25.12	0.00	0.54	0.36	1.10	0.14
slf0289	minD	septum site-determinir	113.79	21.94	0	89.39	15.26	0.00	0.04	0.00	0.79	-0.35
slf0290	ppk	polyphosphate kinase	236.49	13.99	0	204.31	65.87	0.00	0.20	0.17	0.86	-0.21
slf0293		unknown protein	118.86	11.66	0	113.26	36.34	0.00	0.55	0.52	0.95	-0.07
slf0294		hypothetical protein	94.85	13.74	0	142.86	33.45	0.00	0.01	0.00	1.51	0.59
slf0295		hypothetical protein	65.66	12.58	0	55.17	12.27	0.00	0.19	0.07	0.84	-0.25
slf0296		hypothetical protein	372.56	87.83	0	349.16	111.42	0.00	0.61	0.52	0.94	-0.09
slf0297		hypothetical protein	119.23	15.22	0	95.66	18.99	0.00	0.04	0.00	0.80	-0.32
slf0298		hypothetical protein	115.61	21.69	0	95.06	27.99	0.00	0.19	0.09	0.82	-0.28
slf0300	ribC	riboflavin synthase alp	99.49	26.33	0	95.55	31.18	0.00	0.79	0.70	0.96	-0.06
slf0301		hypothetical protein	71.21	11.77	0	58.33	27.81	0.00	0.24	0.19	0.82	-0.29
slf0306	sigB	group2 RNA polymera	388.45	95.28	0	428.00	111.51	0.00	0.51	0.33	1.10	0.14
slf0309		unknown protein	33.64	15.06	4.45E-08	31.99	17.57	0.00	0.74	0.67	0.95	-0.07
slf0310		hypothetical protein	198.21	18.75	0	103.12	15.18	0.00	0.00	0.00	0.52	-0.94
slf0312		probable oligopeptides	60.05	19.97	1.75E-13	27.96	24.33	0.00	0.10	0.07	0.47	-1.10
slf0314		hypothetical protein	172.23	24.49	0	213.36	43.42	0.00	0.07	0.01	1.24	0.31
slf0315		putative transposase [	389.75	40.73	0	620.39	83.58	0.00	0.00	0.00	1.59	0.67
slf0317		putative transposase [	15.64	3.66	0	127.64	30.14	0.00	0.00	0.00	8.16	3.03
slf0318		hypothetical protein	63.07	20.56	5.75E-14	52.48	34.43	0.00	0.35	0.28	0.83	-0.27
slf0319		hypothetical protein	260.56	54.17	0	265.97	91.51	0.00	0.97	0.96	1.02	0.03
slf0320		probable ribonuclease	86.85	15.98	0	87.36	16.64	0.00	0.96	0.94	1.01	0.01
slf0321		unknown protein	80.86	3.14	0	118.74	9.50	0.00	0.00	0.00	1.47	0.55
slf0322	hypF	hydrogenase maturatik	76.23	31.11	1.95E-09	173.92	53.17	0.00	0.00	0.00	2.28	1.19
slf0325		hypothetical protein	111.86	9.53	0	115.18	13.10	0.00	0.66	0.57	1.03	0.04
slf0327		unknown protein	30.26	8.23	0	34.20	15.74	0.00	0.87	0.85	1.13	0.18
slf0328		unknown protein	17.11	4.86	0	8.65	9.56	0.03	0.05	0.03	0.51	-0.98
slf0329		6-phosphogluconate d	406.67	46.42	0	362.53	54.07	0.00	0.14	0.04	0.89	-0.17
slf0330		3-oxoacyl-acyl-carrier	36.91	15.72	8.85E-09	87.56	23.28	0.00	0.00	0.00	2.37	1.25
slf0335		hypothetical protein	129.48	26.24	0	151.48	36.94	0.00	0.30	0.17	1.17	0.23
slf0336	accD	acetyl-CoA carboxylas	178.30	40.98	0	255.59	132.86	0.00	0.22	0.16	1.43	0.52
slf0337		two-component senso	107.84	18.04	0	90.08	24.15	0.00	0.15	0.07	0.84	-0.26
slf0350		hypothetical protein	453.03	146.82	4.09E-14	770.10	373.13	0.00	0.12	0.03	1.70	0.77
slf0354		hypothetical protein	89.31	8.63	0	67.48	13.76	0.00	0.01	0.00	0.76	-0.40
slf0355		hypothetical protein	52.78	17.80	3.78E-13	74.99	13.49	0.00	0.03	0.00	1.42	0.51
slf0356	trpF	N-(5'-phosphoribosyl)z	56.30	6.71	0	67.23	14.37	0.00	0.12	0.05	1.19	0.26
slf0359		hypothetical protein	1108.33	111.89	0	870.99	395.00	0.00	0.13	0.09	0.79	-0.35
slf0360		hypothetical protein	91.88	28.23	1.55E-15	75.55	12.28	0.00	0.25	0.01	0.82	-0.28
slf0361		hypothetical protein	38.78	4.64	0	11.15	9.95	0.01	0.05	0.03	0.29	-1.80
slf0362	alaS	alanyl-tRNA synthetas	229.98	16.76	0	239.55	23.71	0.00	0.46	0.35	1.04	0.06
slf0364		hypothetical protein	107.48	5.51	0	105.96	15.40	0.00	0.74	0.71	0.99	-0.02
slf0368		uracil phosphoribosyltr	70.29	2.94	0	70.88	12.32	0.00	0.96	0.96	1.01	0.01
slf0369		unknown protein	128.29	48.70	1.1E-10	111.53	41.81	0.00	0.57	0.40	0.87	-0.20
slf0370	pyrA	carbamoyl-phosphate	214.30	38.91	0	210.32	65.38	0.00	0.77	0.73	0.98	-0.03
slf0371		unknown protein	70.39	127.19	0.175232	101.37	162.76	0.13	0.43	0.23	1.44	0.53
slf0372		hypothetical protein	71.69	6.58	0	73.41	14.79	0.00	0.93	0.92	1.02	0.03
slf0373	proA	gamma-glutamyl phos	199.23	19.15	0	166.08	49.49	0.00	0.10	0.06	0.83	-0.26
slf0374		probable branched ch	134.78	22.63	0	174.28	22.56	0.00	0.01	0.00	1.29	0.37
slf0376		unknown protein	54.23	2.73	0	29.10	22.13	0.00	0.08	0.05	0.54	-0.90
slf0377		transcription-repair coi	172.63	17.44	0	156.05	22.07	0.00	0.16	0.07	0.90	-0.15
slf0378	cobA	uroporphyrin-III C-metl	150.67	52.50	2.06E-12	117.89	15.40	0.00	0.16	0.00	0.78	-0.35
slf0379		acyl-acyl-carrier-prote	114.35	18.87	0	86.70	14.18	0.00	0.02	0.00	0.76	-0.40
slf0380		probable glycosyltrans	48.30	8.11	0	52.99	9.77	0.00	0.42	0.27	1.10	0.13

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slf0381		hypothetical protein	312.04	50.46	0	602.36	174.37	0.00	0.00	0.00	1.93	0.95
slf0382		hypothetical protein	239.18	15.86	0	264.90	45.75	0.00	0.26	0.20	1.11	0.15
slf0383		cobalamin biosynthesi	57.73	13.42	0	79.46	14.21	0.00	0.02	0.00	1.38	0.46
slf0384		unknown protein	58.06	12.17	0	71.61	14.32	0.00	0.10	0.01	1.23	0.30
slf0385		ATP-binding protein of	89.93	13.26	0	74.62	18.54	0.00	0.12	0.05	0.83	-0.27
slf0394		unknown protein	87.86	23.79	0	58.45	13.04	0.00	0.04	0.00	0.67	-0.59
slf0395		phosphoglycerate mut	64.28	6.86	0	56.72	7.89	0.00	0.11	0.03	0.88	-0.18
slf0396		two-component respor	67.77	10.76	0	69.21	12.72	0.00	0.86	0.81	1.02	0.03
slf0397		hypothetical protein	98.90	12.29	0	62.05	13.37	0.00	0.00	0.00	0.63	-0.67
slf0398		deoxyguanosinetripho	84.22	15.07	0	122.43	19.42	0.00	0.00	0.00	1.45	0.54
slf0400		hypothetical protein	84.41	11.72	0	56.67	10.88	0.00	0.00	0.00	0.67	-0.57
slf0401		citrate synthase	585.10	59.30	0	582.54	63.06	0.00	0.94	0.91	1.00	-0.01
slf0402	aspC	aspartate aminotransf	158.00	37.66	0	207.42	30.25	0.00	0.04	0.00	1.31	0.39
slf0403		unknown protein	8.98	1.72	0	2.41	5.00	0.24	0.01	0.00	0.27	-1.90
slf0404	glcD	glycolate oxidase sub	228.74	5.49	0	167.36	14.85	0.00	0.00	0.00	0.73	-0.45
slf0405		unknown protein	116.89	16.52	0	127.22	37.15	0.00	0.67	0.62	1.09	0.12
slf0406		unknown protein	52.67	4.29	0	39.78	13.31	0.00	0.10	0.06	0.76	-0.40
slf0408		peptidyl-prolyl cis-trans	136.87	37.62	0	200.14	54.36	0.00	0.07	0.01	1.46	0.55
slf0409		similar to O-succinylbe	51.45	17.62	8.66E-13	62.01	21.96	0.00	0.45	0.27	1.21	0.27
slf0410		hypothetical protein	38.08	4.68	0	68.58	12.44	0.00	0.00	0.00	1.80	0.85
slf0412		hypothetical protein	193.85	39.24	0	125.39	18.36	0.00	0.00	0.00	0.65	-0.63
slf0413		hypothetical protein	73.96	14.27	0	81.36	20.75	0.00	0.55	0.43	1.10	0.14
slf0414		hypothetical protein	148.76	43.69	0	106.03	45.14	0.00	0.09	0.02	0.71	-0.49
slf0415		ATP-binding protein of	373.00	50.06	0	459.91	57.00	0.00	0.01	0.00	1.23	0.30
slf0416	groEL-2	60kD chaperonin 2	320.64	46.79	0	714.68	227.46	0.00	0.00	0.00	2.23	1.16
slf0418		delta(24)-sterol C-mett	305.97	85.29	0	253.24	83.59	0.00	0.35	0.21	0.83	-0.27
slf0419		unknown protein	48.63	6.29	0	30.70	12.28	0.00	0.02	0.00	0.63	-0.66
slf0420	ureB	urease beta subunit	37.82	8.30	0	30.20	17.50	0.00	0.26	0.21	0.80	-0.32
slf0421	purB	adenylosuccinate lyas	145.24	12.09	0	239.71	21.20	0.00	0.00	0.00	1.65	0.72
slf0422		asparaginase	79.40	10.83	0	94.16	9.18	0.00	0.02	0.00	1.19	0.25
slf0423		hypothetical protein	146.40	30.83	0	106.21	21.50	0.00	0.03	0.00	0.73	-0.46
slf0424		hypothetical protein	289.22	26.48	0	348.81	34.46	0.00	0.01	0.00	1.21	0.27
slf0426		unknown protein	136.44	24.38	0	56.27	19.15	0.00	0.00	0.00	0.41	-1.28
slf0427	psbO	photosystem II manga	3151.63	285.97	0	3463.54	518.85	0.00	0.22	0.12	1.10	0.14
slf0428		unknown protein	14.07	7.00	8.65E-07	56.39	25.40	0.00	0.00	0.00	4.01	2.00
slf0430	htpG	heat shock protein Htp	153.75	28.38	0	303.77	48.40	0.00	0.00	0.00	1.98	0.98
slf0431		putative transposase [	154.98	43.87	0	1149.08	287.18	0.00	0.00	0.00	7.41	2.89
slf0436		hypothetical protein	24.16	4.47	0	17.02	12.04	0.00	0.13	0.09	0.70	-0.50
slf0441		unknown protein	63.16	12.52	0	72.85	31.15	0.00	0.67	0.62	1.15	0.21
slf0442		hypothetical protein	6.85	1.75	0	7.06	7.50	0.02	0.29	0.26	1.03	0.04
slf0443		unknown protein	118.94	14.03	0	131.95	15.75	0.00	0.16	0.03	1.11	0.15
slf0444		unknown protein	35.77	3.13	0	26.71	15.17	0.00	0.11	0.08	0.75	-0.42
slf0445		unknown protein	200.53	43.97	0	166.80	28.29	0.00	0.20	0.02	0.83	-0.27
slf0446		unknown protein	69.51	7.76	0	81.26	10.65	0.00	0.05	0.00	1.17	0.23
slf0447		unknown protein	5.28	3.37	0.000123	0.91	2.17	0.31	0.00	0.00	0.17	-2.54
slf0448		unknown protein	10.57	4.58	1.6E-08	22.96	12.26	0.00	0.06	0.01	2.17	1.12
slf0449		unknown protein	22.89	6.96	8.88E-16	30.01	17.81	0.00	0.98	0.98	1.31	0.39
slf0450		probable nitric oxide re	157.09	13.58	0	202.11	17.92	0.00	0.00	0.00	1.29	0.36
slf0451		hypothetical protein	35.82	7.87	0	47.15	10.04	0.00	0.05	0.00	1.32	0.40
slf0454	pheS	phenylalanyl-tRNA syr	1094.78	46.15	0	1550.27	164.65	0.00	0.00	0.00	1.42	0.50
slf0455	thrA	homoserine dehydrogt	227.95	25.43	0	193.64	14.77	0.00	0.02	0.00	0.85	-0.24
slf0456		hypothetical protein	124.28	11.46	0	165.69	39.60	0.00	0.02	0.00	1.33	0.41
slf0459		excinuclease ABC sut	105.46	16.25	0	118.15	8.29	0.00	0.11	0.00	1.12	0.16
slf0461	proA	gamma-glutamyl phos	142.03	19.13	0	181.49	39.33	0.00	0.05	0.01	1.28	0.35
slf0462		hypothetical protein	102.85	39.19	1.29E-10	114.29	49.00	0.00	0.69	0.57	1.11	0.15
slf0467		S-adenosylmethionine	544.72	84.51	0	479.28	99.15	0.00	0.19	0.07	0.88	-0.18
slf0469		ribose-phosphate pyro	396.56	56.87	0	361.00	43.91	0.00	0.25	0.06	0.91	-0.14
slf0470		hypothetical protein	245.83	59.67	0	408.52	115.15	0.00	0.01	0.00	1.66	0.73
slf0471		hypothetical protein	207.72	36.12	0	219.76	16.11	0.00	0.42	0.02	1.06	0.08
slf0473		unknown protein	36.27	5.11	0	36.94	17.24	0.00	0.74	0.72	1.02	0.03
slf0474		two-component hybrid	1213.97	77.53	0	1328.52	195.30	0.00	0.25	0.19	1.09	0.13
slf0477		putative biopolymer tr	175.87	16.97	0	137.87	38.91	0.00	0.07	0.03	0.78	-0.35
slf0478		unknown protein	71.73	10.41	0	29.88	11.69	0.00	0.00	0.00	0.42	-1.26
slf0479		unknown protein	22.85	3.53	0	14.77	9.65	0.00	0.22	0.19	0.65	-0.63
slf0480		probable aminotransfe	484.25	427.39	0.005514	472.88	322.92	0.00	0.88	0.80	0.98	-0.03
slf0481		unknown protein	65.97	6.50	0	56.52	7.66	0.00	0.05	0.00	0.86	-0.22
slf0482		unknown protein	221.44	49.50	0	187.53	41.16	0.00	0.26	0.08	0.85	-0.24
slf0484		ATP-binding protein of	67.95	14.12	0	62.27	10.66	0.00	0.47	0.24	0.92	-0.13
slf0485		two-component respor	67.42	17.86	0	34.09	15.50	0.00	0.01	0.00	0.51	-0.98
slf0486	kaiB3	circadian clock protein	32.97	3.76	0	19.33	7.25	0.00	0.01	0.00	0.59	-0.77
slf0487		hypothetical protein	127.62	23.46	0	128.45	18.86	0.00	0.90	0.82	1.01	0.01
slf0488		hypothetical protein	58.23	11.90	0	55.73	11.44	0.00	0.69	0.59	0.96	-0.06
slf0489		ATP-binding protein of	88.65	12.95	0	130.72	31.02	0.00	0.01	0.00	1.47	0.56
slf0493		hypothetical protein	55.27	25.28	8.51E-08	34.59	31.08	0.01	0.15	0.11	0.63	-0.68
slf0494		unknown protein	23.21	7.11	1.33E-15	28.93	16.45	0.00	0.64	0.59	1.25	0.32
slf0495	asnS	asparaginy-tRNA synt	157.32	19.38	0	263.58	53.34	0.00	0.00	0.00	1.68	0.74
slf0496		hypothetical protein	58.31	17.71	6.66E-16	58.97	20.30	0.00	1.00	1.00	1.01	0.02
slf0497		hypothetical protein	181.35	64.21	4.55E-12	62.95	7.35	0.00	0.00	0.00	0.35	-1.53

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slI0498		hypothetical protein	96.93	20.65	0	74.18	37.17	0.00	0.24	0.19	0.77	-0.39
slI0499		hypothetical protein	163.85	15.04	0	136.38	16.30	0.00	0.01	0.00	0.83	-0.26
slI0501		probable glycosyltrans	58.41	10.02	0	30.23	19.52	0.00	0.05	0.02	0.52	-0.95
slI0502	argS	arginyl-tRNA-synthetase	221.11	24.71	0	185.39	21.15	0.00	0.02	0.00	0.84	-0.25
slI0503		hypothetical protein	184.83	23.61	0	230.61	54.26	0.00	0.09	0.03	1.25	0.32
slI0504	lysA	diaminopimelate decarboxylase	342.40	49.50	0	244.06	47.77	0.00	0.01	0.00	0.71	-0.49
slI0505		hypothetical protein	117.40	14.76	0	131.14	20.27	0.00	0.19	0.06	1.12	0.16
slI0506		undecaprenyl pyrophosphatase	45.73	20.97	9.13E-08	26.51	30.61	0.03	0.06	0.04	0.58	-0.79
slI0507		probable cation transporter	71.12	14.58	0	85.62	35.74	0.00	0.53	0.47	1.20	0.27
slI0508		unknown protein	12.69	3.12	0	15.36	9.64	0.00	0.50	0.49	1.21	0.27
slI0509		similar to 5',5''-P-1, P-2	67.15	6.09	0	97.14	14.27	0.00	0.00	0.00	1.45	0.53
slI0513		hypothetical protein	123.18	21.97	0	128.41	28.41	0.00	0.79	0.73	1.04	0.06
slI0514		hypothetical protein	222.36	32.67	0	180.98	29.71	0.00	0.05	0.00	0.81	-0.30
slI0517	rbpA	RNA binding protein	133.60	28.55	0	204.22	56.98	0.00	0.02	0.00	1.53	0.61
slI0518		unknown protein	239.58	40.96	0	314.73	58.43	0.00	0.02	0.00	1.31	0.39
slI0519	ndhA	NADH dehydrogenase	353.22	91.96	0	676.60	245.19	0.00	0.01	0.00	1.92	0.94
slI0520	ndhI	NADH dehydrogenase	172.85	49.69	0	174.06	33.30	0.00	0.84	0.70	1.01	0.01
slI0521	ndhG	NADH dehydrogenase	141.77	26.18	0	190.54	22.46	0.00	0.01	0.00	1.34	0.43
slI0522	ndhE	NADH dehydrogenase	75.38	18.31	0	66.16	40.75	0.00	0.35	0.31	0.88	-0.19
slI0524		hypothetical protein	126.35	19.25	0	149.61	31.97	0.00	0.17	0.06	1.18	0.24
slI0525		hypothetical protein	14.59	1.81	0	17.46	10.83	0.00	0.50	0.48	1.20	0.26
slI0528		hypothetical protein	174.63	59.40	5.98E-13	253.00	79.43	0.00	0.13	0.02	1.45	0.53
slI0529		hypothetical protein	205.47	30.89	0	358.91	59.63	0.00	0.00	0.00	1.75	0.80
slI0533		trigger factor	168.14	36.84	0	177.49	31.49	0.00	0.64	0.43	1.06	0.08
slI0534	clpP	ATP-dependent Clp protease	157.02	21.68	0	144.41	37.54	0.00	0.42	0.34	0.92	-0.12
slI0535	clpX	ATP-dependent protease	201.31	26.54	0	176.04	16.14	0.00	0.07	0.00	0.87	-0.19
slI0536		probable potassium channel	85.10	6.82	0	76.47	11.21	0.00	0.12	0.05	0.90	-0.15
slI0537	amt3	ammonium/methylammonium transporter	195.82	36.42	0	149.58	45.17	0.00	0.11	0.05	0.76	-0.39
slI0539		unknown protein	34.99	5.17	0	47.26	4.87	0.00	0.00	0.00	1.35	0.43
slI0540		phosphate-binding protein	83.25	14.06	0	115.48	18.49	0.00	0.01	0.00	1.39	0.47
slI0541	desC	acyl-CoA desaturase	1489.37	231.04	0	1840.61	441.75	0.00	0.10	0.03	1.24	0.31
slI0542		acetyl-coenzyme A synthetase	290.53	29.39	0	261.83	24.61	0.00	0.10	0.01	0.90	-0.15
slI0543		hypothetical protein	306.58	44.60	0	77.35	14.86	0.00	0.00	0.00	0.25	-1.99
slI0544		hypothetical protein	59.57	8.24	0	87.80	25.18	0.00	0.02	0.00	1.47	0.56
slI0545		hypothetical protein	41.66	7.13	0	53.32	25.51	0.00	0.46	0.41	1.28	0.36
slI0546		probable translation initiation factor	88.72	20.26	0	49.47	13.72	0.00	0.00	0.00	0.56	-0.84
slI0547		unknown protein	66.52	12.84	0	81.61	15.17	0.00	0.09	0.01	1.23	0.29
slI0549		hypothetical protein	122.40	11.70	0	124.52	9.68	0.00	0.72	0.55	1.02	0.02
slI0550		flavoprotein	491.41	77.86	0	398.65	34.68	0.00	0.02	0.00	0.81	-0.30
slI0552		unknown protein	83.36	26.53	1.4E-14	100.07	30.65	0.00	0.31	0.14	1.20	0.26
slI0553		hypothetical protein	82.74	13.70	0	170.32	19.08	0.00	0.00	0.00	2.06	1.04
slI0554		ferredoxin-thioredoxin reductase	79.33	11.79	0	78.80	21.88	0.00	0.80	0.78	0.99	-0.01
slI0555		methionine aminopeptidase	1107.90	102.47	0	1242.31	194.54	0.00	0.15	0.07	1.12	0.17
slI0556		Na <sup>+</sup> /H <sup>+</sup> antiporter	210.16	22.37	0	247.73	27.62	0.00	0.03	0.00	1.18	0.24
slI0558	ycf53	hypothetical protein YC	116.84	26.45	0	143.48	25.66	0.00	0.11	0.01	1.23	0.30
slI0563		unknown protein	60.32	22.50	5.16E-11	42.36	34.63	0.00	0.23	0.20	0.70	-0.51
slI0564		hypothetical protein	157.38	28.11	0	152.52	27.15	0.00	0.77	0.67	0.97	-0.05
slI0565		hypothetical protein	21.12	7.35	1.98E-12	22.53	16.62	0.00	0.46	0.43	1.07	0.09
slI0567	fur	ferric uptake regulator	157.04	12.12	0	165.22	17.47	0.00	0.39	0.26	1.05	0.07
slI0569	recA	RecA gene product	111.81	19.05	0	119.29	53.82	0.00	0.90	0.89	1.07	0.09
slI0572		hypothetical protein	130.26	40.69	4.44E-15	97.05	31.18	0.00	0.14	0.02	0.75	-0.42
slI0573		carbamate kinase	98.70	11.20	0	77.06	10.12	0.00	0.01	0.00	0.78	-0.36
slI0574		probable permease protein	53.34	10.48	0	77.65	32.14	0.00	0.11	0.05	1.46	0.54
slI0575		probable lipopolysaccharide transferase	1133.76	209.47	0	1289.93	246.52	0.00	0.23	0.08	1.14	0.19
slI0576		putative sugar-nucleotidyltransferase	131.12	18.37	0	109.05	11.20	0.00	0.03	0.00	0.83	-0.27
slI0577		hypothetical protein	152.98	29.26	0	252.15	28.69	0.00	0.00	0.00	1.65	0.72
slI0578	purK	phosphonobosyl aminotransferase	166.31	24.24	0	217.00	40.23	0.00	0.01	0.00	1.30	0.38
slI0584	ycf36	hypothetical protein YC	41.32	5.79	0	43.32	12.44	0.00	0.91	0.90	1.05	0.07
slI0585		hypothetical protein	104.86	15.02	0	128.77	40.58	0.00	0.23	0.16	1.23	0.30
slI0586		hypothetical protein	180.99	24.53	0	192.27	55.05	0.00	0.78	0.76	1.06	0.09
slI0587		pyruvate kinase	136.86	8.60	0	148.36	23.75	0.00	0.31	0.25	1.08	0.12
slI0588		unknown protein	214.49	36.58	0	71.29	12.71	0.00	0.00	0.00	0.33	-1.59
slI0590		unknown protein	64.67	9.23	0	96.35	22.24	0.00	0.01	0.00	1.49	0.58
slI0593		glucokinase	50.23	8.60	0	81.46	23.58	0.00	0.01	0.00	1.62	0.70
slI0594		transcriptional regulator	111.38	14.91	0	175.91	40.82	0.00	0.00	0.00	1.58	0.66
slI0595		unknown protein	23.52	3.71	0	53.69	8.55	0.00	0.00	0.00	2.28	1.19
slI0596		hypothetical protein	63.83	3.76	0	84.82	17.59	0.00	0.01	0.00	1.33	0.41
slI0597		hypothetical protein	58.58	15.45	0	87.45	30.08	0.00	0.06	0.00	1.49	0.58
slI0601		nitrilase homolog	132.76	13.20	0	158.00	24.74	0.00	0.06	0.01	1.19	0.25
slI0602		hypothetical protein	515.82	44.91	0	380.73	61.67	0.00	0.00	0.00	0.74	-0.44
slI0603	menD	menaquinone biosynthesis protein	109.47	13.23	0	135.44	13.80	0.00	0.01	0.00	1.24	0.31
slI0606		hypothetical protein	270.55	77.95	0	182.96	42.31	0.00	0.03	0.00	0.68	-0.56
slI0608	ycf49	hypothetical protein YC	18.07	5.51	1.11E-15	3.67	6.98	0.20	0.01	0.00	0.20	-2.30
slI0609		hypothetical protein	19.87	3.70	0	19.91	19.60	0.01	0.22	0.19	1.00	0.00
slI0611		hypothetical protein	25.54	4.07	0	11.12	8.89	0.00	0.10	0.07	0.44	-1.20
slI0613	ruvB	Holliday junction DNA endonuclease	78.81	17.60	0	97.14	38.16	0.00	0.44	0.36	1.23	0.30
slI0614		unknown protein	10.36	3.85	4.13E-11	19.66	17.44	0.01	0.75	0.74	1.90	0.92
slI0615		hypothetical protein	98.85	12.93	0	134.35	7.44	0.00	0.00	0.00	1.36	0.44

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sl0616	secA	preprotein translocase	532.53	157.50	2.22E-16	347.28	95.87	0.00	0.05	0.00	0.65	-0.62
sl0617		hypothetical protein	401.52	55.96	0	422.50	46.97	0.00	0.48	0.24	1.05	0.07
sl0621	ccdA	putative c-type cytochrome	95.37	24.70	0	74.01	29.83	0.00	0.19	0.08	0.78	-0.37
sl0622	nadA	quinolinate synthetase	161.63	38.65	0	195.88	39.95	0.00	0.17	0.02	1.21	0.28
sl0623		unknown protein	203.29	31.82	0	261.88	52.07	0.00	0.04	0.00	1.29	0.37
sl0624		unknown protein	10.96	6.35	2.36E-05	5.33	8.75	0.14	0.04	0.02	0.49	-1.04
sl0625		unknown protein	65.25	23.94	2.46E-11	31.21	26.07	0.00	0.12	0.09	0.48	-1.06
sl0626		putative neutral invertase	165.77	36.53	0	92.26	27.78	0.00	0.00	0.00	0.56	-0.85
sl0629	psaK	photosystem I reaction center protein	164.60	35.48	0	205.54	38.04	0.00	0.07	0.01	1.25	0.32
sl0630		unknown protein	52.54	7.25	0	111.19	37.68	0.00	0.00	0.00	2.12	1.08
sl0631	nadB	L-aspartate oxidase	101.57	29.06	0	53.56	28.13	0.00	0.01	0.00	0.53	-0.92
sl0634	btpA	photosystem I biogenesis protein	100.18	28.12	0	109.79	39.46	0.00	0.71	0.62	1.10	0.13
sl0635	thiE	probable thiamine-phosphate synthase	93.92	13.78	0	121.70	25.79	0.00	0.04	0.00	1.30	0.37
sl0638		hypothetical protein	108.40	29.47	0	92.83	46.00	0.00	0.39	0.34	0.86	-0.22
sl0639		hypothetical protein	218.52	25.27	0	202.23	15.07	0.00	0.24	0.02	0.93	-0.11
sl0640		probable sodium/sulfate symporter	203.22	34.60	0	184.58	49.56	0.00	0.40	0.30	0.91	-0.14
sl0641		unknown protein	113.57	35.88	8.88E-15	156.13	50.85	0.00	0.16	0.03	1.37	0.46
sl0643	ureG	urease accessory protein	82.90	26.31	1.18E-14	40.19	36.02	0.01	0.11	0.08	0.48	-1.04
sl0644		probable esterase	120.57	15.43	0	77.55	6.69	0.00	0.00	0.00	0.64	-0.64
sl0645		unknown protein	154.28	21.56	0	125.25	27.98	0.00	0.07	0.02	0.81	-0.30
sl0646	cya2	guanylyl cyclase	217.54	35.53	0	203.06	30.26	0.00	0.46	0.26	0.93	-0.10
sl0647		unknown protein	104.62	15.34	0	86.14	11.30	0.00	0.03	0.00	0.82	-0.28
sl0648		probable glycosyltransferase	946.55	152.92	0	879.50	137.84	0.00	0.46	0.27	0.93	-0.11
sl0649		two-component response regulator	284.14	45.73	0	303.22	37.05	0.00	0.39	0.13	1.07	0.09
sl0650		putative transposase [	33.82	6.64	0	253.00	107.30	0.00	0.00	0.00	7.48	2.90
sl0651		putative transposase [	306.15	69.98	0	570.49	187.01	0.00	0.00	0.00	1.86	0.90
sl0654		alkaline phosphatase	140.19	18.92	0	186.94	31.32	0.00	0.01	0.00	1.33	0.42
sl0656		unknown protein	227.13	23.50	0	247.88	26.17	0.00	0.17	0.04	1.09	0.13
sl0657		phospho-N-acetylmuramoyl transferase	67.99	6.19	0	129.28	22.99	0.00	0.00	0.00	1.90	0.93
sl0658		hypothetical protein	20.75	9.29	4.52E-08	12.87	17.14	0.07	0.06	0.03	0.62	-0.69
sl0659		hypothetical protein	33.89	10.66	7.11E-15	75.85	22.83	0.00	0.00	0.00	2.24	1.16
sl0660	pdxA	pyridoxal phosphate biosynthesis protein	142.64	6.90	0	143.75	15.65	0.00	0.94	0.93	1.01	0.01
sl0661	ycf35	hypothetical protein Ynf35	188.24	49.11	0	145.93	17.66	0.00	0.07	0.00	0.78	-0.37
sl0662		hypothetical protein	55.71	9.68	0	48.19	23.67	0.00	0.32	0.27	0.87	-0.21
sl0664		unknown protein	11.90	3.17	0	31.24	13.20	0.00	0.00	0.00	2.62	1.39
sl0665		putative transposase [	62.67	5.35	0	350.33	123.10	0.00	0.00	0.00	5.59	2.48
sl0666		putative transposase [	54.98	7.39	0	228.76	114.15	0.00	0.00	0.00	4.16	2.06
sl0667		putative transposase [	68.85	18.87	0	303.41	101.08	0.00	0.00	0.00	4.41	2.14
sl0668		putative transposase [	76.52	22.94	2.22E-16	122.51	56.44	0.00	0.11	0.04	1.60	0.68
sl0669		unknown protein	9.61	3.49	1.52E-11	4.96	7.76	0.12	0.02	0.01	0.52	-0.95
sl0670		hypothetical protein	5.68	2.43	9.96E-09	6.28	6.92	0.03	0.14	0.11	1.11	0.15
sl0671		probable cation transporter	25.31	8.08	1.69E-14	29.89	12.90	0.00	0.64	0.58	1.18	0.24
sl0672		cation-transporting ATPase	215.36	38.88	0	198.45	50.12	0.00	0.49	0.36	0.92	-0.12
sl0676		hypothetical protein	20.55	6.31	1.55E-15	12.97	6.51	0.00	0.08	0.03	0.63	-0.66
sl0677		putative transposase [	99.97	15.88	0	520.39	263.37	0.00	0.00	0.00	5.21	2.38
sl0678		hypothetical protein	1.65	1.25	0.001215	4.27	4.08	0.01	0.74	0.62	2.58	1.37
sl0679		periplasmic phosphate-binding protein	547.51	93.28	0	944.00	183.13	0.00	0.00	0.00	1.72	0.79
sl0680		phosphate-binding protein	142.90	27.99	0	1031.23	1099.56	0.02	0.01	0.00	7.22	2.85
sl0681		phosphate transport system	199.91	47.32	0	510.20	448.49	0.01	0.11	0.07	2.55	1.35
sl0682		phosphate transport system	342.94	87.13	0	423.59	120.62	0.00	0.22	0.08	1.24	0.30
sl0683		phosphate transport system	73.55	10.04	0	209.80	171.66	0.00	0.03	0.01	2.85	1.51
sl0684		phosphate transport system	53.28	9.13	0	93.49	52.28	0.00	0.07	0.03	1.75	0.81
sl0685		hypothetical protein	21.38	4.01	0	36.11	21.18	0.00	0.46	0.44	1.69	0.76
sl0686		probable cytochrome c	88.20	11.51	0	44.98	12.18	0.00	0.00	0.00	0.51	-0.97
sl0687	sigI	group3 RNA polymerase	91.95	28.30	1.78E-15	98.05	29.44	0.00	0.75	0.65	1.07	0.09
sl0688		unknown protein	25.58	7.39	0	39.04	6.21	0.00	0.01	0.00	1.53	0.61
sl0689	nhaS3	Na <sup>+</sup> /H <sup>+</sup> antiporter	249.44	25.41	0	235.02	39.76	0.00	0.43	0.34	0.94	-0.09
sl0690		probable transcription factor	540.32	74.98	0	398.55	64.92	0.00	0.01	0.00	0.74	-0.44
sl0691		hypothetical protein	67.32	13.65	0	79.26	7.07	0.00	0.06	0.00	1.18	0.24
sl0696		hypothetical protein	258.19	49.02	0	223.09	80.73	0.00	0.31	0.24	0.86	-0.21
sl0698	dfp	drug sensory protein A	251.89	57.50	0	314.68	62.08	0.00	0.09	0.01	1.25	0.32
sl0699		putative transposase [	59.15	9.80	0	484.09	241.59	0.00	0.00	0.00	8.18	3.03
sl0700		putative transposase [	70.53	6.99	0	643.98	273.25	0.00	0.00	0.00	9.13	3.19
sl0702		unknown protein	48.42	10.34	0	30.53	17.79	0.00	0.06	0.02	0.63	-0.67
sl0703		unknown protein	72.53	13.87	0	88.73	13.55	0.00	0.06	0.00	1.22	0.29
sl0704	nifS	cysteine desulfurase	152.21	31.19	0	165.41	45.54	0.00	0.67	0.58	1.09	0.12
sl0708		dimethyladenosine triphosphatase	1041.31	269.05	0	987.34	253.43	0.00	0.73	0.62	0.95	-0.08
sl0709		putative endonuclease	29.60	4.75	0	21.65	12.06	0.00	0.12	0.07	0.73	-0.45
sl0710		unknown protein	38.16	9.23	0	18.14	16.26	0.01	0.10	0.07	0.48	-1.07
sl0711		isopenicillin N synthase	120.35	10.26	0	206.54	33.07	0.00	0.00	0.00	1.72	0.78
sl0712	cysM	cysteine synthase	66.40	22.09	1.81E-13	42.73	40.73	0.01	0.21	0.18	0.64	-0.64
sl0716		signal peptidase I	71.79	9.38	0	60.04	17.95	0.00	0.16	0.10	0.84	-0.26
sl0720		RTX toxin activating protein	1.04	1.83	0.162147	0.67	1.01	0.11	0.52	0.36	0.64	-0.64
sl0721		unknown protein	425.58	74.32	0	437.73	117.21	0.00	0.92	0.91	1.03	0.04
sl0722		unknown protein	19.85	4.57	0	37.64	25.83	0.00	0.16	0.11	1.90	0.92
sl0723		unknown protein	158.64	42.77	0	398.17	116.49	0.00	0.00	0.00	2.51	1.33
sl0726		phosphoglucosyltransferase	231.37	29.07	0	273.61	79.94	0.00	0.24	0.17	1.18	0.24
sl0727		hypothetical protein	34.40	12.63	2.55E-11	77.86	27.55	0.00	0.00	0.00	2.26	1.18

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slf0728	accA	acetyl-CoA carboxylas	156.07	36.63	0	87.64	15.76	0.00	0.00	0.00	0.56	-0.83
slf0729		probable DNA methylt	56.19	15.77	0	42.22	20.88	0.00	0.15	0.08	0.75	-0.41
slf0732		hypothetical protein	40.62	3.30	0	40.49	10.55	0.00	0.80	0.79	1.00	0.00
slf0733		unknown protein	26.91	9.47	3.31E-12	14.42	14.12	0.01	0.11	0.08	0.54	-0.90
slf0735		hypothetical protein	178.42	37.78	0	179.48	35.30	0.00	0.94	0.91	1.01	0.01
slf0736		hypothetical protein	40.31	13.34	1.38E-13	51.47	25.26	0.00	0.50	0.41	1.28	0.35
slf0737		hypothetical protein	157.05	14.86	0	241.35	44.15	0.00	0.00	0.00	1.54	0.62
slf0738		molybdate-binding per	50.90	10.00	0	98.98	21.96	0.00	0.00	0.00	1.94	0.96
slf0739		ATP-binding protein of	128.42	22.95	0	150.21	31.02	0.00	0.22	0.09	1.17	0.23
slf0740		hypothetical protein	398.79	62.51	0	383.14	57.83	0.00	0.65	0.51	0.96	-0.06
slf0741		pyruvate flavodoxin ox	110.18	19.72	0	93.06	10.70	0.00	0.08	0.00	0.84	-0.24
slf0742		hypothetical protein	14.23	2.92	0	11.23	8.33	0.00	0.27	0.24	0.79	-0.34
slf0743		hypothetical protein	6.72	4.09	5.75E-05	10.43	15.06	0.09	0.17	0.14	1.55	0.63
slf0744		hypothetical protein	42.40	15.63	3.03E-11	37.83	32.99	0.00	0.20	0.17	0.89	-0.16
slf0745		phosphofructokinase	70.02	11.88	0	119.63	10.00	0.00	0.00	0.00	1.71	0.77
slf0749		hypothetical protein	134.64	34.68	0	215.79	100.97	0.00	0.07	0.02	1.60	0.68
slf0750		two-component senso	118.36	11.43	0	72.96	20.49	0.00	0.00	0.00	0.62	-0.70
slf0751	ycf22	hypothetical protein Yc	42.81	6.69	0	27.80	19.95	0.00	0.19	0.16	0.65	-0.62
slf0752		hypothetical protein	62.92	9.87	0	76.54	26.29	0.00	0.30	0.22	1.22	0.28
slf0753	folD	FolD bifunctional prote	125.45	39.31	5.33E-15	123.90	31.89	0.00	0.98	0.97	0.99	-0.02
slf0754		ribosome binding factc	70.78	11.84	0	70.08	14.96	0.00	0.87	0.84	0.99	-0.01
slf0755	tpx	thioredoxin peroxidase	93.52	10.91	0	70.40	16.15	0.00	0.02	0.00	0.75	-0.41
slf0756		unknown protein	55.31	11.84	0	35.08	8.84	0.00	0.01	0.00	0.63	-0.66
slf0757	purF	amidophosphoribosylt	335.23	85.66	0	338.76	86.63	0.00	0.93	0.89	1.01	0.02
slf0759		ABC transporter ATP-	248.12	50.08	0	364.00	152.94	0.00	0.12	0.06	1.47	0.55
slf0760	ycf38	hypothetical protein Yc	135.33	27.27	0	178.69	46.85	0.00	0.06	0.01	1.32	0.40
slf0761		unknown protein	153.93	34.19	0	227.34	37.24	0.00	0.00	0.00	1.48	0.56
slf0762		unknown protein	50.37	3.98	0	139.82	25.43	0.00	0.00	0.00	2.78	1.47
slf0763		hypothetical protein	18.05	4.83	0	28.45	15.80	0.00	0.25	0.19	1.58	0.66
slf0764		probable branched-chi	512.77	95.63	0	409.83	132.35	0.00	0.15	0.07	0.80	-0.32
slf0765		hypothetical protein	70.50	15.32	0	72.62	27.00	0.00	0.99	0.99	1.03	0.04
slf0766	radC	DNA repair protein Ra	586.96	36.60	0	515.94	112.13	0.00	0.16	0.12	0.88	-0.19
slf0767	rpl20	50S ribosomal protein	885.26	136.50	0	545.00	88.62	0.00	0.00	0.00	0.62	-0.70
slf0771	glcP	glucose transport proti	269.43	48.30	0	197.68	31.70	0.00	0.01	0.00	0.73	-0.45
slf0772		probable porin; major	706.58	96.97	0	386.31	60.57	0.00	0.00	0.00	0.55	-0.87
slf0775		unknown protein	12.30	2.82	0	10.58	12.74	0.04	0.09	0.06	0.86	-0.22
slf0776		serine/threonine kinas	37.13	9.13	0	70.76	13.78	0.00	0.00	0.00	1.91	0.93
slf0777		putative carboxypeptic	1937.41	487.24	0	1722.74	314.65	0.00	0.39	0.13	0.89	-0.17
slf0778		ABC transporter, ATP-	1000.85	269.67	0	997.63	222.63	0.00	0.96	0.94	1.00	0.00
slf0779		unknown protein	969.40	225.67	0	1116.25	287.17	0.00	0.46	0.30	1.15	0.20
slf0780		unknown protein	29.81	8.52	0	23.87	16.41	0.00	0.24	0.18	0.80	-0.32
slf0781		hypothetical protein	48.54	9.48	0	39.74	16.80	0.00	0.23	0.17	0.82	-0.29
slf0782		transcriptional regulatc	34.41	6.58	0	59.41	16.64	0.00	0.01	0.00	1.73	0.79
slf0783		unknown protein	19.49	4.72	0	7.27	9.93	0.07	0.04	0.02	0.37	-1.42
slf0784	merR	nitrilase	49.91	5.22	0	49.18	14.58	0.00	0.72	0.70	0.99	-0.02
slf0785		unknown protein	35.65	4.27	0	73.57	17.37	0.00	0.00	0.00	2.06	1.05
slf0786		unknown protein	11.26	5.06	4.86E-08	17.42	9.40	0.00	0.74	0.73	1.55	0.63
slf0787		hypothetical protein	41.43	10.72	0	50.60	19.61	0.00	0.38	0.24	1.22	0.29
slf0788		hypothetical protein	149.25	32.14	0	77.12	33.23	0.00	0.00	0.00	0.52	-0.95
slf0789		two-component respor	88.53	17.51	0	150.23	30.77	0.00	0.00	0.00	1.70	0.76
slf0790		two-component senso	272.52	296.05	0.024147	290.93	195.96	0.00	0.58	0.35	1.07	0.09
slf0792	ziaR	Zinc-responsive repre	95.77	32.10	2.71E-13	70.64	15.30	0.00	0.11	0.00	0.74	-0.44
slf0793		hypothetical protein	20.78	6.86	1.16E-13	18.70	12.14	0.00	0.37	0.34	0.90	-0.15
slf0794	coaR	cobalt-responsive regl	47.54	7.87	0	40.05	5.96	0.00	0.10	0.01	0.84	-0.25
slf0797	nrsR	two-component respor	304.02	98.13	3.24E-14	292.84	90.24	0.00	0.83	0.75	0.96	-0.05
slf0798	nrsS	two-component senso	826.15	78.66	0	710.78	93.89	0.00	0.05	0.01	0.86	-0.22
slf0800		hypothetical protein	46.47	7.30	0	136.93	56.72	0.00	0.00	0.00	2.95	1.56
slf0802		hypothetical protein	48.15	8.47	0	38.66	12.10	0.00	0.13	0.07	0.80	-0.32
slf0803		hypothetical protein	224.03	56.69	0	201.96	43.28	0.00	0.51	0.30	0.90	-0.15
slf0804		hypothetical protein	154.77	5.36	0	155.29	13.65	0.00	0.99	0.99	1.00	0.00
slf0807	rpe	pentose-5-phosphate-	399.11	112.56	0	587.92	115.99	0.00	0.02	0.00	1.47	0.56
slf0808		putative transposase [	37.52	7.98	0	69.83	13.04	0.00	0.00	0.00	1.86	0.90
slf0809		hypothetical protein	89.86	20.94	0	28.44	11.44	0.00	0.00	0.00	0.32	-1.66
slf0810		unknown protein	39.40	5.75	0	36.89	10.10	0.00	0.50	0.42	0.94	-0.10
slf0811		unknown protein	35.63	8.50	0	31.73	23.87	0.00	0.35	0.31	0.89	-0.17
slf0812		hypothetical protein	27.87	4.91	0	41.17	6.67	0.00	0.00	0.00	1.48	0.56
slf0813	ctaC	cytochrome c oxidase	71.32	15.46	0	104.59	16.06	0.00	0.01	0.00	1.47	0.55
slf0814		hypothetical protein	125.73	17.01	0	163.10	18.51	0.00	0.01	0.00	1.30	0.38
slf0815		unknown protein	29.33	3.92	0	53.02	14.70	0.00	0.00	0.00	1.81	0.85
slf0816		probable oxidoreducta	66.44	24.52	3.19E-11	80.74	22.63	0.00	0.30	0.07	1.22	0.28
slf0817		tRNA delta-2-isopente	31.82	4.64	0	75.51	18.98	0.00	0.00	0.00	2.37	1.25
slf0818		tetrapyrrole methylase	50.52	14.65	0	70.15	10.34	0.00	0.02	0.00	1.39	0.47
slf0819	psaF	photosystem I reactor	4850.52	661.96	0	2453.58	615.39	0.00	0.00	0.00	0.51	-0.98
slf0821		hypothetical protein	201.73	30.88	0	237.74	32.04	0.00	0.08	0.00	1.18	0.24
slf0822		hypothetical protein	251.64	61.49	0	264.62	32.21	0.00	0.56	0.17	1.05	0.07
slf0823		probable succinate de	79.13	9.02	0	59.57	28.87	0.00	0.12	0.08	0.75	-0.41
slf0825		polyA polymerase	104.90	8.31	0	75.67	11.49	0.00	0.00	0.00	0.72	-0.47
slf0827		hypothetical protein	83.57	16.42	0	92.51	22.56	0.00	0.51	0.40	1.11	0.15



Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sl0828		putative amidase	277.91	22.93	0	170.73	7.68	0.00	0.00	0.00	0.61	-0.70
sl0829		probable methyltransf	97.46	14.83	0	40.16	9.50	0.00	0.00	0.00	0.41	-1.28
sl0830	fus	elongation factor EF-G	313.54	49.36	0	201.64	33.78	0.00	0.00	0.00	0.64	-0.64
sl0832		hypothetical protein	153.09	32.43	0	76.92	30.52	0.00	0.00	0.00	0.50	-0.99
sl0833		probable oligopeptides	186.88	48.02	0	139.45	32.17	0.00	0.08	0.00	0.75	-0.42
sl0834		low affinity sulfate tran	606.25	57.14	0	584.41	85.66	0.00	0.56	0.47	0.96	-0.05
sl0837		hypothetical protein	178.65	30.62	0	198.92	45.98	0.00	0.44	0.32	1.11	0.16
sl0838	pyrF	orotidine 5' monophos	75.73	21.43	0	57.79	13.12	0.00	0.14	0.01	0.76	-0.39
sl0839		hypothetical protein	56.04	4.06	0	64.96	10.80	0.00	0.09	0.04	1.16	0.21
sl0842		neopullulanase	174.39	38.83	0	113.50	39.30	0.00	0.03	0.00	0.65	-0.62
sl0843		unknown protein	84.34	14.43	0	69.23	12.63	0.00	0.07	0.01	0.82	-0.28
sl0844		tRNA (5-methylaminor	100.17	30.25	4.44E-16	68.01	59.16	0.00	0.15	0.12	0.68	-0.56
sl0846		hypothetical protein	132.58	118.78	0.006256	198.84	143.19	0.00	0.29	0.12	1.50	0.58
sl0847		unknown protein	183.47	48.48	0	175.53	45.22	0.00	0.75	0.64	0.96	-0.06
sl0848	dnaA	chromosomal replicati	76.93	18.04	0	97.64	23.69	0.00	0.12	0.01	1.27	0.34
sl0849	psbD	photosystem II reactio	3840.36	579.47	0	5838.89	2327.08	0.00	0.05	0.02	1.52	0.60
sl0851	psbC	photosystem II CP43 p	2867.01	219.12	0	4483.67	1264.35	0.00	0.01	0.00	1.56	0.65
sl0853		hypothetical protein	106.92	23.37	0	116.59	55.52	0.00	0.95	0.94	1.09	0.12
sl0854		hypothetical protein	177.53	13.72	0	142.22	7.33	0.00	0.00	0.00	0.80	-0.32
sl0855		putative channel trans	156.31	34.47	0	210.37	34.45	0.00	0.03	0.00	1.35	0.43
sl0856	sigH	group3 RNA polymera	40.91	9.51	0	72.60	27.04	0.00	0.02	0.00	1.77	0.83
sl0857		unknown protein	261.18	84.31	3.24E-14	563.49	330.41	0.00	0.05	0.02	2.16	1.11
sl0858		hypothetical protein	54.47	10.56	0	48.23	33.60	0.00	0.31	0.27	0.89	-0.18
sl0860		hypothetical protein	140.06	10.01	0	99.84	16.09	0.00	0.00	0.00	0.71	-0.49
sl0861		hypothetical protein	172.56	25.58	0	105.29	17.47	0.00	0.00	0.00	0.61	-0.71
sl0862		hypothetical protein	165.19	15.91	0	203.13	35.57	0.00	0.03	0.00	1.23	0.30
sl0863		hypothetical protein	15.43	4.01	0	14.94	17.12	0.03	0.18	0.15	0.97	-0.05
sl0864		hypothetical protein	88.59	133.14	0.103129	63.90	76.50	0.04	0.73	0.66	0.72	-0.47
sl0865	uvrC	excinuclease ABC sut	63.23	9.16	0	60.09	11.35	0.00	0.56	0.42	0.95	-0.07
sl0867		hypothetical protein	90.20	10.09	0	90.21	18.16	0.00	0.90	0.89	1.00	0.00
sl0868		lipic acid synthetase	120.33	12.99	0	120.84	29.19	0.00	0.90	0.88	1.00	0.01
sl0869	aat	Leu/Phe-tRNA-protein	26.11	8.46	4E-14	32.49	7.15	0.00	0.16	0.01	1.24	0.32
sl0871		hypothetical protein	45.09	4.78	0	26.65	14.30	0.00	0.02	0.00	0.59	-0.76
sl0872		unknown protein	79.85	28.27	4.55E-12	27.68	24.20	0.01	0.07	0.05	0.35	-1.53
sl0873		carboxymorspermidine	79.85	26.23	8.84E-14	58.51	11.04	0.00	0.19	0.00	0.73	-0.45
sl0875		hypothetical protein	68.46	17.16	0	69.66	14.07	0.00	0.84	0.75	1.02	0.03
sl0876	ruvA	Holliday junction DNA	189.73	41.71	0	100.34	22.90	0.00	0.00	0.00	0.53	-0.92
sl0877		hypothetical protein	166.24	25.04	0	173.72	27.49	0.00	0.63	0.48	1.04	0.06
sl0886		hypothetical protein	58.47	5.55	0	82.95	16.31	0.00	0.00	0.00	1.42	0.50
sl0887		putative modulator of f	201.29	17.01	0	248.18	32.06	0.00	0.01	0.00	1.23	0.30
sl0888		hypothetical protein	28.38	6.90	0	24.45	8.72	0.00	0.35	0.25	0.86	-0.22
sl0891		malate dehydrogenase	222.74	26.18	0	144.43	25.61	0.00	0.00	0.00	0.65	-0.63
sl0892	panD	aspartate 1-decarboxy	27.78	4.97	0	11.59	15.36	0.06	0.03	0.01	0.42	-1.26
sl0895		CysQ protein homolog	177.94	50.72	0	164.71	77.57	0.00	0.54	0.48	0.93	-0.11
sl0896	ruvC	Holliday junction resolv	30.61	9.19	4.44E-16	20.98	17.24	0.00	0.15	0.12	0.69	-0.54
sl0897	dnaJ	DnaJ protein	127.38	24.74	0	159.33	43.69	0.00	0.15	0.05	1.25	0.32
sl0898		hypothetical protein	214.52	29.48	0	259.25	83.63	0.00	0.31	0.24	1.21	0.27
sl0899		UDP-N-acetylglucosar	199.43	33.28	0	198.64	28.49	0.00	1.00	0.99	1.00	-0.01
sl0900	hisG	ATP phosphoribosyltra	73.20	8.74	0	61.40	20.70	0.00	0.17	0.12	0.84	-0.25
sl0901	purE	phosphoribosylaminoir	101.39	27.51	0	45.67	14.19	0.00	0.00	0.00	0.45	-1.15
sl0902	argF	ornithine carbamoyltra	107.70	11.14	0	105.37	13.17	0.00	0.73	0.64	0.98	-0.03
sl0905		hypothetical protein	216.56	55.44	0	163.82	34.84	0.00	0.09	0.00	0.76	-0.40
sl0909		unknown protein	40.14	14.54	1.37E-11	46.48	28.07	0.00	0.84	0.81	1.16	0.21
sl0910		unknown protein	46.32	17.46	8.14E-11	26.19	29.69	0.03	0.11	0.08	0.57	-0.82
sl0911		unknown protein	16.23	3.18	0	3.62	4.18	0.03	0.02	0.00	0.22	-2.16
sl0912		ABC transporter ATP I	639.93	129.53	0	704.56	163.44	0.00	0.49	0.33	1.10	0.14
sl0913		hypothetical protein	52.23	10.65	0	29.75	21.74	0.00	0.18	0.15	0.57	-0.81
sl0914		unknown protein	39.93	10.35	0	27.79	16.54	0.00	0.16	0.11	0.70	-0.52
sl0915		putative zinc protease	167.82	40.39	0	120.03	26.75	0.00	0.07	0.00	0.72	-0.48
sl0916	cobH	precoir isomerase	85.82	19.40	0	138.95	42.41	0.00	0.02	0.00	1.62	0.70
sl0920	ppc	phosphoenolpyruvate	167.04	15.84	0	185.67	23.36	0.00	0.13	0.04	1.11	0.15
sl0921		two-component respor	145.86	18.04	0	66.33	15.39	0.00	0.00	0.00	0.45	-1.14
sl0922		unknown protein	57.87	12.48	0	20.44	17.16	0.00	0.07	0.04	0.35	-1.50
sl0923		unknown protein	525.24	95.18	0	549.48	133.69	0.00	0.81	0.76	1.05	0.07
sl0924		hypothetical protein	32.15	7.31	0	39.52	18.15	0.00	0.60	0.56	1.23	0.30
sl0925		hypothetical protein	92.78	29.34	9.55E-15	125.75	15.51	0.00	0.03	0.00	1.36	0.44
sl0926		hypothetical protein	54.08	3.75	0	80.37	13.32	0.00	0.00	0.00	1.49	0.57
sl0927		S-adenosylmethionine	383.16	40.61	0	389.75	40.32	0.00	0.78	0.69	1.02	0.02
sl0928	apcD	allophycocyanin-B	1838.60	474.27	0	1020.08	335.16	0.00	0.01	0.00	0.55	-0.85
sl0930		unknown protein	52.84	14.87	0	50.98	29.43	0.00	0.57	0.53	0.96	-0.05
sl0931		hypothetical protein	62.40	6.67	0	50.80	12.85	0.00	0.09	0.05	0.81	-0.30
sl0932		hypothetical protein	80.91	22.24	0	92.99	16.96	0.00	0.27	0.04	1.15	0.20
sl0933		hypothetical protein	85.44	18.63	0	107.55	14.19	0.00	0.05	0.00	1.26	0.33
sl0934	ccmA	carboxysome formatio	447.84	79.70	0	423.64	106.02	0.00	0.59	0.49	0.95	-0.08
sl0936		putative oxidoreductas	224.23	40.56	0	558.77	152.06	0.00	0.00	0.00	2.49	1.32
sl0938		aspartate transaminas	128.12	36.43	0	112.02	19.50	0.00	0.48	0.12	0.87	-0.19
sl0939		hypothetical protein	57.56	11.50	0	190.61	57.06	0.00	0.00	0.00	3.31	1.73
sl0943		unknown protein	55.37	26.68	3.69E-07	29.87	24.98	0.00	0.13	0.09	0.54	-0.89

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sil0944		hypothetical protein	86.56	19.81	0	66.63	7.07	0.00	0.05	0.00	0.77	-0.38
sil0945	glgA	glycogen synthase	171.80	41.88	0	175.01	37.59	0.00	0.85	0.78	1.02	0.03
sil0947	lraA	light repressed protein	1210.31	247.76	0	533.56	102.16	0.00	0.00	0.00	0.44	-1.18
sil0980		unknown protein	136.88	8.61	0	118.88	7.01	0.00	0.00	0.00	0.87	-0.20
sil0981		unknown protein	67.26	23.59	2.87E-12	45.48	36.96	0.00	0.16	0.12	0.68	-0.56
sil0982		unknown protein	57.35	10.32	0	61.76	11.30	0.00	0.50	0.32	1.08	0.11
sil0983		hypothetical protein	58.19	15.45	0	69.93	29.89	0.00	0.48	0.36	1.20	0.27
sil0984		hypothetical protein	11.68	3.14	0	24.72	4.37	0.00	0.00	0.00	2.12	1.08
sil0985		unknown protein	93.63	10.98	0	126.94	43.17	0.00	0.12	0.07	1.36	0.44
sil0986		putative transposase [	77.31	7.58	0	136.30	38.40	0.00	0.00	0.00	1.76	0.82
sil0990		glutathione-dependent	131.56	11.44	0	124.39	22.17	0.00	0.43	0.36	0.95	-0.08
sil0992		putative esterase	125.86	22.58	0	166.22	75.76	0.00	0.27	0.20	1.32	0.40
sil0993		potassium channel	84.16	12.72	0	67.12	15.69	0.00	0.07	0.02	0.80	-0.33
sil0994		hypothetical protein	82.29	8.52	0	87.98	23.59	0.00	0.71	0.68	1.07	0.10
sil0995		hypothetical protein	105.31	26.70	0	122.22	26.29	0.00	0.28	0.08	1.16	0.21
sil0996		hypothetical protein	303.14	35.98	0	207.90	34.03	0.00	0.00	0.00	0.69	-0.54
sil0997		hypothetical protein	215.86	31.68	0	126.92	15.12	0.00	0.00	0.00	0.59	-0.77
sil0998	ycf30	LysR family transcripti	236.45	40.83	0	215.43	33.51	0.00	0.37	0.16	0.91	-0.13
sil1001		ATP-binding protein of	154.78	28.13	0	66.00	11.93	0.00	0.00	0.00	0.43	-1.23
sil1002	ycf22	hypothetical protein YC	101.48	28.03	0	84.09	21.54	0.00	0.29	0.08	0.83	-0.27
sil1003		two-component senso	62.63	11.00	0	81.18	37.41	0.00	0.35	0.29	1.30	0.37
sil1004		hypothetical protein	88.58	8.61	0	131.65	15.25	0.00	0.00	0.00	1.49	0.57
sil1005		MazG protein homolog	88.03	20.15	0	88.38	30.60	0.00	0.92	0.89	1.00	0.01
sil1006		unknown protein	126.16	47.64	8.74E-11	129.22	47.23	0.00	0.85	0.75	1.02	0.03
sil1009		unknown protein	661.50	99.37	0	200.35	50.32	0.00	0.00	0.00	0.30	-1.72
sil1011		hypothetical protein	85.92	14.23	0	81.81	6.46	0.00	0.58	0.21	0.95	-0.07
sil1017	amt2	ammonium/methylamni	137.20	22.71	0	183.64	52.76	0.00	0.06	0.02	1.34	0.42
sil1018	pyrC	dihydroorotase	108.65	11.13	0	141.39	21.56	0.00	0.01	0.00	1.30	0.38
sil1019		hydroxyacylglutathione	54.48	8.63	0	77.37	23.20	0.00	0.05	0.01	1.42	0.51
sil1020		probable glycosyltrans	82.03	13.32	0	114.18	22.16	0.00	0.01	0.00	1.39	0.48
sil1021		hypothetical protein	296.47	81.59	0	284.34	73.44	0.00	0.82	0.73	0.96	-0.06
sil1022		hypothetical protein	127.45	30.96	0	232.25	53.62	0.00	0.00	0.00	1.82	0.87
sil1023		succinyl-CoA syntheta	946.79	153.03	0	1697.71	416.32	0.00	0.00	0.00	1.79	0.84
sil1024		hypothetical protein	60.84	14.74	0	72.97	15.70	0.00	0.18	0.04	1.20	0.26
sil1025		hypothetical protein	215.05	20.16	0	244.27	35.33	0.00	0.10	0.03	1.14	0.18
sil1027	gltd	NADH-dependent glut	451.53	83.73	0	549.82	89.84	0.00	0.08	0.01	1.22	0.28
sil1028	ccmK	carbon dioxide concer	437.95	114.02	0	550.83	250.70	0.00	0.43	0.35	1.26	0.33
sil1029	ccmK	carbon dioxide concer	397.93	57.59	0	434.96	153.09	0.00	0.75	0.72	1.09	0.13
sil1030	ccmL	carbon dioxide concer	146.50	32.74	0	142.99	58.83	0.00	0.69	0.65	0.98	-0.04
sil1031	ccmM	carbon dioxide concer	357.24	101.26	0	242.51	64.14	0.00	0.05	0.00	0.68	-0.56
sil1032	ccmN	similar to carbon dioxit	157.84	18.63	0	188.06	48.69	0.00	0.22	0.15	1.19	0.25
sil1033		probable protein phosj	247.19	26.57	0	289.65	32.98	0.00	0.03	0.00	1.17	0.23
sil1035		uracil phosphoribosyltr	72.21	5.53	0	181.43	33.10	0.00	0.00	0.00	2.51	1.33
sil1036		hypothetical protein	27.84	13.27	2.77E-07	14.00	16.70	0.04	0.09	0.05	0.50	-0.99
sil1037		unknown protein	133.43	46.79	2.85E-12	155.47	38.93	0.00	0.40	0.14	1.17	0.22
sil1039		hypothetical protein	226.21	16.82	0	195.74	24.80	0.00	0.03	0.00	0.87	-0.21
sil1040		unknown protein	58.00	33.27	1.95E-05	34.08	36.66	0.02	0.13	0.10	0.59	-0.77
sil1041	cysA	similar to sulfate transj	71.63	4.10	0	61.39	17.11	0.00	0.20	0.16	0.86	-0.22
sil1043		polynucleotide nuc	521.27	23.51	0	534.08	40.56	0.00	0.55	0.48	1.02	0.04
sil1045		mutator MutT protein	63.68	23.38	2.53E-11	44.58	23.66	0.00	0.17	0.06	0.70	-0.51
sil1049		hypothetical protein	438.98	34.66	0	268.14	34.83	0.00	0.00	0.00	0.61	-0.71
sil1051	cpcF	phycocyanin alpha-sul	73.20	11.96	0	41.03	34.92	0.00	0.13	0.09	0.56	-0.84
sil1052		hypothetical protein	39.62	15.07	1.2E-10	12.33	11.51	0.01	0.06	0.03	0.31	-1.68
sil1053		hypothetical protein	518.30	163.55	8.44E-15	528.39	162.51	0.00	0.92	0.88	1.02	0.03
sil1054		hypothetical protein	97.51	8.68	0	104.33	12.81	0.00	0.35	0.22	1.07	0.10
sil1056	purL	phosphoribosylformyl	438.26	76.78	0	297.94	52.54	0.00	0.00	0.00	0.68	-0.56
sil1057	trxM2	thioredoxin M	70.58	13.28	0	85.23	26.48	0.00	0.32	0.21	1.21	0.27
sil1058	dapB	dihydrodipicolinate red	91.83	10.09	0	128.88	22.96	0.00	0.00	0.00	1.40	0.49
sil1059		adenylate kinase	31.51	5.32	0	45.34	7.37	0.00	0.00	0.00	1.44	0.52
sil1060		hypothetical protein	110.43	10.54	0	125.38	11.75	0.00	0.04	0.00	1.14	0.18
sil1061		unknown protein	10.28	2.61	0	16.54	19.55	0.04	0.28	0.25	1.61	0.69
sil1062		unknown protein	5.51	1.49	0	2.52	3.88	0.11	0.02	0.00	0.46	-1.13
sil1063		hypothetical protein	87.76	13.63	0	76.90	6.51	0.00	0.13	0.00	0.88	-0.19
sil1064		hypothetical protein	99.45	28.61	0	64.95	42.45	0.00	0.09	0.04	0.65	-0.61
sil1068		unknown protein	31.67	5.23	0	37.41	11.96	0.00	0.43	0.36	1.18	0.24
sil1069		3-oxoacyl-acyl-carrier	206.68	39.13	0	294.73	56.64	0.00	0.01	0.00	1.43	0.51
sil1070		transketolase	900.39	127.64	0	1889.05	706.81	0.00	0.00	0.00	2.10	1.07
sil1071		hypothetical protein	89.17	17.64	0	109.01	31.20	0.00	0.22	0.10	1.22	0.29
sil1072		hypothetical protein	81.83	9.51	0	88.13	14.55	0.00	0.43	0.32	1.08	0.11
sil1074	leuS	leucyl-tRNA synthetas	245.48	59.13	0	236.28	32.51	0.00	0.82	0.66	0.96	-0.06
sil1076		cation-transporting AT	967.98	230.25	0	1052.49	306.41	0.00	0.65	0.55	1.09	0.12
sil1077	speB2	agmatinase	75.34	13.10	0	88.61	12.43	0.00	0.10	0.01	1.18	0.23
sil1078	hypA	hydrogenase expressi	30.92	3.45	0	12.11	12.24	0.02	0.08	0.05	0.39	-1.35
sil1079	hypB	hydrogenase expressi	46.41	10.12	0	40.28	12.25	0.00	0.34	0.19	0.87	-0.20
sil1080		ABC transport system	112.49	23.59	0	86.30	19.85	0.00	0.08	0.01	0.77	-0.38
sil1081		ABC transport system	38.32	6.50	0	30.90	10.76	0.00	0.15	0.08	0.81	-0.31
sil1082		ABC transport system	60.64	13.24	0	45.26	17.33	0.00	0.12	0.06	0.75	-0.42
sil1084		hypothetical protein	214.32	10.64	0	216.13	16.64	0.00	0.86	0.83	1.01	0.01

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sil1085	glpD	glycerol-3-phosphate c	229.51	25.10	0	290.16	47.92	0.00	0.01	0.00	1.26	0.34
sil1086		unknown protein	71.76	19.64	0	104.85	16.08	0.00	0.01	0.00	1.46	0.55
sil1087		similar to sodium/gluc	226.59	20.08	0	207.17	32.57	0.00	0.22	0.13	0.91	-0.13
sil1089		unknown protein	111.30	22.75	0	102.17	15.57	0.00	0.49	0.23	0.92	-0.12
sil1091	chpP	geranylgeranyl hydrog	900.98	200.39	0	683.20	105.21	0.00	0.03	0.00	0.76	-0.40
sil1092		hypothetical protein	16.04	3.33	0	4.72	7.87	0.14	0.01	0.00	0.29	-1.76
sil1094		putative transposase	9.13	2.77	6.66E-16	8.55	11.90	0.08	0.09	0.06	0.94	-0.09
sil1095		hypothetical protein	36.55	11.00	4.44E-16	27.98	17.56	0.00	0.23	0.18	0.77	-0.39
sil1096	rps12	30S ribosomal protein	227.43	61.03	0	212.99	58.77	0.00	0.67	0.56	0.94	-0.09
sil1097	rps7	30S ribosomal protein	87.41	21.69	0	79.48	35.96	0.00	0.49	0.43	0.91	-0.14
sil1098	fus	elongation factor EF-G	792.89	189.16	0	957.89	250.84	0.00	0.30	0.14	1.21	0.27
sil1099	tufA	elongation factor Tu	2237.20	464.62	0	2726.54	718.03	0.00	0.17	0.06	1.22	0.29
sil1101	rps10	30S ribosomal protein	142.05	20.17	0	116.42	37.00	0.00	0.16	0.10	0.82	-0.29
sil1102	gtrA	integral membrane prc	48.97	7.24	0	33.13	15.85	0.00	0.07	0.04	0.68	-0.56
sil1103	gtrB	integral membrane prc	117.12	9.61	0	138.61	18.60	0.00	0.04	0.00	1.18	0.24
sil1104	gtrC	periplasmic substrate-	440.42	51.65	0	409.79	54.97	0.00	0.31	0.16	0.93	-0.10
sil1106		hypothetical protein	181.35	40.71	0	215.71	51.73	0.00	0.29	0.15	1.19	0.25
sil1107		type IV pilus biogenes	51.25	6.98	0	52.62	12.16	0.00	0.94	0.93	1.03	0.04
sil1108		stationary-phase survi	170.39	13.67	0	166.55	24.45	0.00	0.68	0.63	0.98	-0.03
sil1109		hypothetical protein	152.25	23.94	0	145.37	23.38	0.00	0.62	0.49	0.95	-0.07
sil1110	prfA	peptide chain release	163.06	17.85	0	114.73	14.62	0.00	0.00	0.00	0.70	-0.51
sil1112	aroQ	3-dehydroquinate dehy	58.98	9.02	0	84.12	38.29	0.00	0.31	0.26	1.43	0.51
sil1118		hypothetical protein	32.45	5.02	0	29.01	22.33	0.00	0.25	0.22	0.89	-0.16
sil1119		hypothetical protein	164.20	7.07	0	132.17	32.91	0.00	0.04	0.02	0.80	-0.31
sil1120		chromosome segregal	171.32	22.15	0	174.24	35.50	0.00	0.95	0.94	1.02	0.02
sil1121		hypothetical protein	122.45	47.82	3.56E-10	73.74	59.89	0.00	0.14	0.11	0.60	-0.73
sil1123		hypothetical protein	177.14	23.60	0	216.49	58.65	0.00	0.14	0.07	1.22	0.29
sil1124	plpA	phytochrome like prote	82.65	13.83	0	38.93	29.28	0.00	0.05	0.03	0.47	-1.09
sil1127	menB	naphthoate synthase	119.09	30.79	0	217.88	46.65	0.00	0.00	0.00	1.83	0.87
sil1129		2-hydroxy-6-oxohepta-	91.43	8.18	0	89.32	15.28	0.00	0.70	0.65	0.98	-0.03
sil1130		unknown protein	279.95	49.97	0	291.73	48.71	0.00	0.69	0.56	1.04	0.06
sil1131		unknown protein	46.60	6.63	0	40.73	11.87	0.00	0.29	0.23	0.87	-0.19
sil1132		unknown protein	81.53	13.11	0	84.55	24.89	0.00	0.94	0.93	1.04	0.05
sil1135		unknown protein	69.10	13.32	0	59.76	6.90	0.00	0.18	0.00	0.86	-0.21
sil1138		hypothetical protein	217.45	44.11	0	79.42	19.69	0.00	0.00	0.00	0.37	-1.45
sil1142		hypothetical protein	80.73	7.20	0	47.22	15.25	0.00	0.00	0.00	0.58	-0.77
sil1143	pcrA	ATP-dependent helica	141.38	15.54	0	103.36	11.93	0.00	0.00	0.00	0.73	-0.45
sil1144		hypothetical protein	47.65	5.58	0	49.32	21.82	0.00	0.81	0.80	1.04	0.05
sil1147		glutathione S-transfere	79.59	18.32	0	74.05	22.80	0.00	0.59	0.49	0.93	-0.10
sil1150		hypothetical protein	368.22	130.81	5.37E-12	168.92	69.04	0.00	0.01	0.00	0.46	-1.12
sil1151		unknown protein	287.79	112.59	3.82E-10	422.65	186.12	0.00	0.16	0.05	1.47	0.55
sil1154		putative antibiotic efflu	614.64	127.99	0	642.11	198.23	0.00	0.93	0.92	1.04	0.06
sil1155		hypothetical protein	278.47	53.67	0	238.31	66.65	0.00	0.24	0.11	0.86	-0.22
sil1156		putative transposase [	68.09	7.69	0	114.31	27.00	0.00	0.00	0.00	1.68	0.75
sil1157		putative transposase [	115.22	25.83	0	192.53	44.52	0.00	0.00	0.00	1.67	0.74
sil1158		hypothetical protein	29.08	5.12	0	18.83	10.93	0.00	0.09	0.05	0.65	-0.63
sil1159		probable bacterioferriti	23.04	3.09	0	13.26	14.35	0.02	0.07	0.05	0.58	-0.80
sil1160		hypothetical protein	23.06	6.79	0	14.45	12.78	0.01	0.13	0.10	0.63	-0.67
sil1161		probable adenylate cy	20.58	5.57	0	25.27	9.18	0.00	0.45	0.37	1.23	0.30
sil1162		hypothetical protein	17.21	3.82	0	30.97	9.79	0.00	0.01	0.00	1.80	0.85
sil1163		unknown protein	9.60	1.98	0	13.10	7.21	0.00	0.60	0.59	1.36	0.45
sil1164		hypothetical protein	15.57	2.64	0	36.44	2.02	0.00	0.00	0.00	2.34	1.23
sil1165		DNA mismatch repair	218.95	23.94	0	127.75	17.94	0.00	0.00	0.00	0.58	-0.78
sil1166		hypothetical protein	187.03	34.84	0	135.93	21.87	0.00	0.01	0.00	0.73	-0.46
sil1167		unknown protein	184.43	36.51	0	125.70	49.30	0.00	0.07	0.03	0.68	-0.55
sil1169		hypothetical protein	21.18	4.90	0	40.12	9.82	0.00	0.00	0.00	1.89	0.92
sil1170		unknown protein	23.65	3.94	0	49.53	9.54	0.00	0.00	0.00	2.09	1.07
sil1172	thrC	threonine synthase	162.72	25.55	0	249.16	42.20	0.00	0.00	0.00	1.53	0.61
sil1173		hypothetical protein	21.59	3.59	0	29.89	10.48	0.00	0.17	0.11	1.38	0.47
sil1174		unknown protein	40.33	5.28	0	41.14	11.04	0.00	0.96	0.96	1.02	0.03
sil1178		probable carbamoyl tr	283.80	37.57	0	203.10	62.88	0.00	0.03	0.00	0.72	-0.48
sil1180		toxin secretion ABC tr	465.52	56.41	0	551.93	60.64	0.00	0.02	0.00	1.19	0.25
sil1181		similar to hemolysin se	526.15	100.97	0	521.13	165.13	0.00	0.83	0.79	0.99	-0.01
sil1182		Rieske iron-sulfur prot	69.39	6.13	0	56.67	22.47	0.00	0.16	0.13	0.82	-0.29
sil1184	ho1	heme oxygenase	2733.92	259.01	0	1590.53	156.89	0.00	0.00	0.00	0.58	-0.78
sil1185	hemF	coproporphyrinogen III	136.75	12.77	0	185.69	16.89	0.00	0.00	0.00	1.36	0.44
sil1186		hypothetical protein	66.29	18.73	0	42.88	34.81	0.00	0.18	0.15	0.65	-0.63
sil1187		prolipoprotein diacylgl	147.80	23.18	0	149.08	32.70	0.00	0.99	0.99	1.01	0.01
sil1188		hypothetical protein	47.18	8.03	0	28.97	19.84	0.00	0.10	0.07	0.61	-0.70
sil1189	glcE	glycolate oxidase subt	123.53	18.39	0	179.01	48.39	0.00	0.02	0.00	1.45	0.54
sil1191		hypothetical protein	88.64	26.21	2.22E-16	86.79	27.69	0.00	0.90	0.85	0.98	-0.03
sil1192		hypothetical protein	133.59	34.78	0	96.36	51.45	0.00	0.16	0.10	0.72	-0.47
sil1193		hypothetical protein	160.48	25.31	0	120.41	15.50	0.00	0.01	0.00	0.75	-0.41
sil1194	psbU	photosystem II 12 kDa	1285.70	186.45	0	912.77	201.16	0.00	0.01	0.00	0.71	-0.49
sil1196		phosphofruktokinase	113.52	4.52	0	121.56	39.50	0.00	0.90	0.89	1.07	0.10
sil1198		tRNA (guanine-N1)-mt	272.29	51.67	0	218.21	28.26	0.00	0.05	0.00	0.80	-0.32
sil1200		hypothetical protein	136.64	30.39	0	115.75	13.67	0.00	0.16	0.00	0.85	-0.24
sil1201		hypothetical protein	215.99	34.39	0	335.43	104.39	0.00	0.02	0.00	1.55	0.64

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slf1202		iron(III) dicitrate-bindin	117.81	21.82	0	84.49	58.18	0.00	0.26	0.23	0.72	-0.48
slf1203		hypothetical protein	9.39	4.12	2.36E-08	9.40	11.49	0.05	0.14	0.11	1.00	0.00
slf1204		similar to macrolide eff	201.69	42.58	0	447.16	85.51	0.00	0.00	0.00	2.22	1.15
slf1205		transcriptional regulatc	37.63	6.89	0	47.02	26.11	0.00	0.63	0.60	1.25	0.32
slf1206		probable ferric aeroba-	555.28	78.23	0	645.06	48.83	0.00	0.04	0.00	1.16	0.22
slf1209	lig	DNA ligase	1336.08	152.65	0	1183.75	84.55	0.00	0.05	0.00	0.89	-0.17
slf1212		GDP-mannose 4,6-del	159.88	31.30	0	234.43	55.23	0.00	0.01	0.00	1.47	0.55
slf1213		GDP-fucose synthetas	304.13	51.28	0	547.67	114.16	0.00	0.00	0.00	1.80	0.85
slf1214	ycf59	hypothetical protein Yf	1921.48	479.48	0	1229.17	402.53	0.00	0.02	0.00	0.64	-0.64
slf1217		unknown protein	160.88	22.63	0	155.13	29.00	0.00	0.68	0.59	0.96	-0.05
slf1218	ycf39	hypothetical protein Yf	293.31	25.51	0	262.69	23.75	0.00	0.06	0.00	0.90	-0.16
slf1219		hypothetical protein	114.64	9.25	0	119.80	11.60	0.00	0.43	0.28	1.05	0.06
slf1220		NADH dehydrogenase	226.45	28.78	0	199.51	42.00	0.00	0.21	0.12	0.88	-0.18
slf1221	hoxF	NADH dehydrogenase	402.93	73.57	0	252.33	64.53	0.00	0.01	0.00	0.63	-0.68
slf1222		hypothetical protein	60.45	15.79	0	37.47	6.62	0.00	0.00	0.00	0.62	-0.69
slf1223	hoxU	NAD-reducing hydroge	50.18	2.96	0	35.42	8.40	0.00	0.01	0.00	0.71	-0.50
slf1224	hoxY	NAD-reducing hydroge	78.27	30.83	5.02E-10	99.55	24.04	0.00	0.15	0.01	1.27	0.35
slf1225		unknown protein	13.13	3.78	0	8.89	8.11	0.01	0.15	0.11	0.68	-0.56
slf1226	hoxH	NAD-reducing hydroge	90.94	10.96	0	96.08	14.63	0.00	0.55	0.43	1.06	0.08
slf1228		two-component hybrid	152.66	18.51	0	164.64	18.37	0.00	0.30	0.10	1.08	0.11
slf1229		two-component hybrid	146.74	31.17	0	90.35	20.40	0.00	0.00	0.00	0.62	-0.70
slf1231		mannosyltransferase	31.01	4.37	0	50.33	23.67	0.00	0.07	0.03	1.62	0.70
slf1232		hypothetical protein	19.80	5.33	0	17.92	13.86	0.00	0.21	0.18	0.91	-0.14
slf1233		hypothetical protein	123.79	32.69	0	79.05	33.97	0.00	0.03	0.00	0.64	-0.65
slf1234		adenosylhomocysteine	620.64	124.78	0	926.41	202.67	0.00	0.01	0.00	1.49	0.58
slf1236		unknown protein	17.69	4.00	0	23.97	22.86	0.01	0.60	0.58	1.35	0.44
slf1237	hemG	protoporphyrinogen IX	82.16	27.75	4.15E-13	79.16	15.90	0.00	0.96	0.92	0.96	-0.05
slf1239		unknown protein	15.44	4.72	1.11E-15	10.80	12.97	0.04	0.11	0.08	0.70	-0.52
slf1240		unknown protein	8.26	6.01	0.00075	3.14	5.37	0.15	0.02	0.00	0.38	-1.39
slf1241		unknown protein	11.34	3.80	2.61E-13	9.18	10.09	0.03	0.09	0.06	0.81	-0.31
slf1242		hypothetical protein	284.77	57.92	0	329.51	86.56	0.00	0.36	0.22	1.16	0.21
slf1244	rpl9	50S ribosomal protein	259.21	66.46	0	271.03	61.58	0.00	0.73	0.60	1.05	0.06
slf1245	cytM	cytochrome CytM	184.90	102.64	1.02E-05	251.91	112.42	0.00	0.18	0.03	1.36	0.45
slf1247		hypothetical protein	137.00	17.71	0	112.33	26.03	0.00	0.09	0.04	0.82	-0.29
slf1249	panC	pantothenate syntheta	132.20	29.26	0	114.83	29.54	0.00	0.39	0.24	0.87	-0.20
slf1250		hypothetical protein	14.61	7.92	6.34E-06	8.53	10.51	0.05	0.07	0.04	0.58	-0.78
slf1251		hypothetical protein	32.35	6.29	0	37.29	12.88	0.00	0.67	0.64	1.15	0.20
slf1252		hypothetical protein	51.04	15.64	1.33E-15	67.61	17.67	0.00	0.15	0.01	1.32	0.41
slf1253		similar to polyA polym	77.56	15.32	0	139.10	31.40	0.00	0.00	0.00	1.79	0.84
slf1254		hypothetical protein	143.38	49.26	1.01E-12	85.31	18.63	0.00	0.01	0.00	0.59	-0.75
slf1255		putative transposase [	384.34	74.47	0	609.37	145.30	0.00	0.00	0.00	1.59	0.66
slf1256		putative transposase [	63.90	10.77	0	434.45	129.01	0.00	0.00	0.00	6.80	2.77
slf1257		putative transposase [	118.59	12.62	0	391.03	57.10	0.00	0.00	0.00	3.30	1.72
slf1258		dCTP deaminase	21.23	2.58	0	12.00	10.43	0.00	0.04	0.01	0.57	-0.82
slf1260	rps2	30S ribosomal protein	353.69	84.48	0	371.45	110.00	0.00	0.84	0.79	1.05	0.07
slf1261	tsf	elongation factor TS	287.77	38.66	0	309.10	74.74	0.00	0.65	0.60	1.07	0.10
slf1262		hypothetical protein	160.19	22.04	0	142.57	26.85	0.00	0.22	0.10	0.89	-0.17
slf1263		cation efflux system pr	111.81	19.24	0	88.40	14.59	0.00	0.04	0.00	0.79	-0.34
slf1265		unknown protein	473.07	330.59	0.000456	1244.11	1058.15	0.00	0.04	0.00	2.63	1.39
slf1267		unknown protein	454.79	123.58	0	474.87	110.35	0.00	0.74	0.59	1.04	0.06
slf1268		unknown protein	150.41	58.95	4.11E-10	202.51	73.42	0.00	0.24	0.07	1.35	0.43
slf1270	BgtB	Periplasmic substrate-	204.58	41.08	0	211.83	12.20	0.00	0.56	0.04	1.04	0.05
slf1271		probable porin, major	624.05	106.00	0	506.33	129.07	0.00	0.09	0.02	0.81	-0.30
slf1272		unknown protein	5.21	7.51	0.089571	8.70	14.63	0.15	0.47	0.34	1.67	0.74
slf1273		unknown protein	75.85	16.17	0	77.28	16.61	0.00	0.89	0.84	1.02	0.03
slf1274		hypothetical protein	81.63	28.65	2.96E-12	37.28	10.58	0.00	0.00	0.00	0.46	-1.13
slf1275		pyruvate kinase	300.83	26.74	0	199.35	18.53	0.00	0.00	0.00	0.66	-0.59
slf1276		ATP-binding protein of	177.08	28.10	0	176.34	37.12	0.00	0.92	0.90	1.00	-0.01
slf1277	recF	RecF protein	61.75	18.79	8.88E-16	66.36	23.37	0.00	0.71	0.58	1.07	0.10
slf1280		hypothetical protein	151.89	26.02	0	160.30	40.44	0.00	0.76	0.70	1.06	0.08
slf1281	ycf9	hypothetical protein Yf	112.04	39.59	4.16E-12	180.45	52.01	0.00	0.02	0.00	1.61	0.69
slf1282	nbH	riboflavin synthase bet	96.28	8.05	0	156.28	24.91	0.00	0.00	0.00	1.62	0.70
slf1283		similar to stage II spor	405.57	45.79	0	450.42	52.11	0.00	0.14	0.02	1.11	0.15
slf1284		esterase	56.14	5.31	0	85.18	14.78	0.00	0.00	0.00	1.52	0.60
slf1285		hypothetical protein	72.71	8.01	0	73.55	22.08	0.00	0.88	0.87	1.01	0.02
slf1286		transcriptional regulatc	241.03	53.82	0	90.66	7.51	0.00	0.00	0.00	0.38	-1.41
slf1289		hypothetical protein	77.55	10.17	0	89.38	15.40	0.00	0.16	0.06	1.15	0.20
slf1290		probable ribonuclease	291.16	39.46	0	211.63	27.59	0.00	0.00	0.00	0.73	-0.46
slf1291		two-component respor	165.89	15.38	0	124.26	29.46	0.00	0.01	0.00	0.75	-0.42
slf1292		two-component respor	67.20	16.48	0	39.74	35.42	0.01	0.19	0.16	0.59	-0.76
slf1293		unknown protein	25.75	2.55	0	43.85	21.27	0.00	0.05	0.02	1.70	0.77
slf1294		methyl-accepting chen	445.77	50.47	0	365.04	68.36	0.00	0.03	0.00	0.82	-0.29
slf1296		two-component hybrid	622.01	145.82	0	551.59	152.50	0.00	0.43	0.28	0.89	-0.17
slf1297		probable dioxygenase,	70.05	3.76	0	42.56	12.41	0.00	0.00	0.00	0.61	-0.72
slf1298		putative carboxymethy	77.28	12.90	0	92.62	17.64	0.00	0.11	0.02	1.20	0.26
slf1299		acetate kinase	106.74	18.05	0	135.87	38.94	0.00	0.17	0.09	1.27	0.35
slf1300		putative methyltransfe	48.45	13.56	0	70.15	8.55	0.00	0.01	0.00	1.45	0.53
slf1304		unknown protein	102.31	22.92	0	48.27	22.91	0.00	0.01	0.00	0.47	-1.08

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sil1305		probable hydrolase	91.99	17.98	0	66.47	14.71	0.00	0.02	0.00	0.72	-0.47
sil1306		unknown protein	173.00	48.79	0	86.10	41.80	0.00	0.01	0.00	0.50	-1.01
sil1307		hypothetical protein	56.18	10.88	0	47.52	7.21	0.00	0.14	0.01	0.85	-0.24
sil1308		probable oxidoreducta	47.82	5.61	0	49.08	13.37	0.00	0.98	0.98	1.03	0.04
sil1314		hypothetical protein	159.41	25.64	0	119.61	15.49	0.00	0.01	0.00	0.75	-0.41
sil1315		unknown protein	76.38	12.82	0	65.73	9.27	0.00	0.14	0.01	0.86	-0.22
sil1316	petC	cytochrome b6-f comp	903.04	217.47	0	1013.64	202.00	0.00	0.33	0.11	1.12	0.17
sil1317	petA	apocytochrome f, con	542.01	56.14	0	610.04	162.63	0.00	0.40	0.35	1.13	0.17
sil1318		hypothetical protein	37.12	13.95	7.18E-11	58.05	25.80	0.00	0.12	0.02	1.56	0.65
sil1319		hypothetical protein	86.53	16.90	0	75.91	36.37	0.00	0.37	0.31	0.88	-0.19
sil1321	atp1	ATP synthase protein	776.01	92.33	0	1321.65	196.97	0.00	0.00	0.00	1.70	0.77
sil1322	atpI	ATP synthase subunit	1432.29	99.99	0	1882.52	409.48	0.00	0.02	0.00	1.31	0.39
sil1323	atpG	ATP synthase subunit	281.92	62.51	0	428.33	148.20	0.00	0.03	0.00	1.52	0.60
sil1324	atpF	ATP synthase subunit	241.57	59.53	0	411.95	211.18	0.00	0.08	0.03	1.71	0.77
sil1325	atpD	ATP synthase d subur	402.65	114.70	0	640.38	346.79	0.00	0.15	0.08	1.59	0.67
sil1326	atpA	ATP synthase a subur	893.32	145.43	0	955.61	358.62	0.00	0.85	0.83	1.07	0.10
sil1327	atpC	ATP synthase g subur	605.91	106.02	0	701.96	132.27	0.00	0.19	0.06	1.16	0.21
sil1329		inositol monophosphat	151.19	31.14	0	200.46	23.33	0.00	0.01	0.00	1.33	0.41
sil1330		two-component syster	376.89	65.71	0	455.54	51.59	0.00	0.04	0.00	1.21	0.27
sil1333		unknown protein	124.94	12.99	0	74.54	9.03	0.00	0.00	0.00	0.60	-0.75
sil1334		two-component senso	167.24	14.96	0	137.96	24.83	0.00	0.03	0.00	0.82	-0.28
sil1336		hypothetical protein	498.10	63.39	0	312.56	37.64	0.00	0.00	0.00	0.63	-0.67
sil1338		unknown protein	2347.81	320.60	0	1050.23	237.58	0.00	0.00	0.00	0.45	-1.16
sil1340		hypothetical protein	54.24	5.21	0	19.75	13.31	0.00	0.10	0.07	0.36	-1.46
sil1341		bacterioferritin	148.61	14.26	0	95.20	16.30	0.00	0.00	0.00	0.64	-0.64
sil1342	gap2	NAD(P)-dependent gly	1313.23	290.49	0	1057.06	205.72	0.00	0.09	0.01	0.80	-0.31
sil1343		aminopeptidase	169.20	11.76	0	191.97	31.30	0.00	0.15	0.09	1.13	0.18
sil1344		unknown protein	94.65	16.19	0	80.42	36.31	0.00	0.31	0.27	0.85	-0.24
sil1348		hypothetical protein	44.05	8.89	0	76.48	11.68	0.00	0.00	0.00	1.74	0.80
sil1349		phosphoglycolate pho:	36.98	7.62	0	42.45	28.31	0.00	0.91	0.91	1.15	0.20
sil1350		hypothetical protein	77.96	5.24	0	104.14	12.37	0.00	0.00	0.00	1.34	0.42
sil1352		unknown protein	114.53	13.82	0	130.96	27.85	0.00	0.26	0.17	1.14	0.19
sil1353		two-component senso	231.17	10.74	0	236.98	29.12	0.00	0.71	0.69	1.03	0.04
sil1354	recJ	single-strand-DNA-spe	147.24	29.47	0	199.41	51.83	0.00	0.07	0.01	1.35	0.44
sil1355		hypothetical protein	88.88	8.46	0	67.04	15.22	0.00	0.02	0.00	0.75	-0.41
sil1356		glycogen phosphoryla:	130.37	18.60	0	138.52	29.83	0.00	0.62	0.55	1.06	0.09
sil1358		hypothetical protein	173.59	42.43	0	85.75	6.97	0.00	0.00	0.00	0.49	-1.02
sil1359		unknown protein	151.54	27.63	0	132.94	26.10	0.00	0.28	0.11	0.88	-0.19
sil1360		DNA polymerase III su	182.84	20.63	0	184.66	40.41	0.00	0.96	0.95	1.01	0.01
sil1362	ileS	isoleucyl-tRNA synthet	227.08	56.04	0	291.39	66.86	0.00	0.10	0.01	1.28	0.36
sil1363	ilvC	ketol-acid reductosorr	597.59	68.34	0	515.10	67.46	0.00	0.06	0.00	0.86	-0.21
sil1365		unknown protein	207.47	26.72	0	137.83	17.76	0.00	0.00	0.00	0.66	-0.59
sil1366		putative SNF2 helicase	187.63	26.58	0	163.06	35.16	0.00	0.19	0.09	0.87	-0.20
sil1367		hypothetical protein	84.65	24.78	0	61.35	36.27	0.00	0.20	0.14	0.72	-0.46
sil1369		putative peptidase	168.15	15.72	0	103.92	10.00	0.00	0.00	0.00	0.62	-0.69
sil1370	rfbM	mannose-1-phosphate	87.67	25.75	0	78.69	18.88	0.00	0.63	0.39	0.90	-0.16
sil1371	sycr1	cAMP receptor protei	49.38	6.63	0	37.91	21.63	0.00	0.16	0.12	0.77	-0.38
sil1372		hypothetical protein	175.12	25.36	0	132.90	52.01	0.00	0.07	0.03	0.76	-0.40
sil1373		unknown protein	19.99	3.82	0	16.03	12.70	0.00	0.25	0.22	0.80	-0.32
sil1374		probable sugar transp	189.56	24.63	0	283.22	56.00	0.00	0.00	0.00	1.49	0.58
sil1376		hypothetical protein	127.53	24.51	0	163.31	29.52	0.00	0.04	0.00	1.28	0.36
sil1377		probable glycosyltrans	390.03	83.58	0	462.18	137.56	0.00	0.31	0.19	1.18	0.24
sil1378		hypothetical protein	43.61	15.52	5.85E-12	32.32	9.05	0.00	0.18	0.02	0.74	-0.43
sil1380		hypothetical protein	103.94	20.46	0	76.73	13.16	0.00	0.02	0.00	0.74	-0.44
sil1381		hypothetical protein	22.03	3.40	0	7.59	7.94	0.02	0.05	0.03	0.34	-1.54
sil1382		ferredoxin, petF-like pr	93.87	23.70	0	102.41	38.40	0.00	0.74	0.67	1.09	0.13
sil1383		probable myo-inositol-	87.32	22.56	0	155.42	44.50	0.00	0.00	0.00	1.78	0.83
sil1384		similar to DnaJ protein	672.22	189.57	0	272.22	75.47	0.00	0.00	0.00	0.40	-1.30
sil1386		hypothetical protein	218.04	33.45	0	247.27	62.12	0.00	0.36	0.25	1.13	0.18
sil1387	pppA	serine/threonine protei	88.00	10.64	0	114.11	11.84	0.00	0.00	0.00	1.30	0.37
sil1388		hypothetical protein	54.53	10.66	0	36.33	3.52	0.00	0.00	0.00	0.67	-0.59
sil1389		hypothetical protein	335.91	36.77	0	253.90	42.06	0.00	0.00	0.00	0.76	-0.40
sil1390		hypothetical protein	394.24	90.72	0	255.19	59.59	0.00	0.01	0.00	0.65	-0.63
sil1392		transcriptional regulat	37.22	8.83	0	46.31	11.44	0.00	0.19	0.06	1.24	0.32
sil1393	glgA	glycogen (starch) synt	268.48	43.22	0	269.12	53.25	0.00	0.97	0.96	1.00	0.00
sil1394		peptide methionine sul	68.53	13.84	0	80.20	27.56	0.00	0.48	0.41	1.17	0.23
sil1395	rfbD	dTDP-6-deoxy-L-manr	56.65	4.28	0	68.82	15.01	0.00	0.09	0.04	1.21	0.28
sil1396		unknown protein	77.06	20.22	0	64.36	51.46	0.00	0.18	0.15	0.84	-0.26
sil1397		putative transposase [	109.91	23.94	0	722.50	318.58	0.00	0.00	0.00	6.57	2.72
sil1398	psbW	photosystem II reactio	163.87	31.68	0	145.42	19.53	0.00	0.28	0.04	0.89	-0.17
sil1399		hypothetical protein	200.39	32.72	0	188.41	44.94	0.00	0.55	0.46	0.94	-0.09
sil1400		hypothetical protein	13.78	1.74	0	5.34	5.99	0.03	0.05	0.02	0.39	-1.37
sil1401		unknown protein	22.81	5.51	0	19.60	16.86	0.00	0.19	0.16	0.86	-0.22
sil1404		biopolymer transport E	306.71	90.88	2.22E-16	309.13	99.70	0.00	0.98	0.98	1.01	0.01
sil1405		biopolymer transport E	66.75	15.09	0	50.42	6.94	0.00	0.03	0.00	0.76	-0.40
sil1406		ferrichrome-iron recep	275.87	31.15	0	280.77	87.75	0.00	0.88	0.87	1.02	0.03
sil1407		probable methyltransfe	113.91	41.03	1.04E-11	82.24	60.77	0.00	0.20	0.15	0.72	-0.47
sil1408		transcriptional regulat	38.90	11.04	0	50.25	19.57	0.00	0.30	0.18	1.29	0.37

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sll1409		ferrichrome-iron recep	32.48	3.52	0	58.39	17.43	0.00	0.00	0.00	1.80	0.85
sll1411		hypothetical protein	27.11	4.98	0	101.61	22.92	0.00	0.00	0.00	3.75	1.91
sll1414		hypothetical protein	253.76	68.54	0	215.83	43.65	0.00	0.34	0.07	0.85	-0.23
sll1415		hypothetical protein	89.93	33.83	7.46E-11	67.72	24.93	0.00	0.26	0.08	0.75	-0.41
sll1418	psbP	similar to photosystem	80.02	11.97	0	92.95	30.61	0.00	0.42	0.36	1.16	0.22
sll1423	ntcA	global nitrogen regulat	236.99	21.89	0	286.70	39.62	0.00	0.02	0.00	1.21	0.27
sll1424		hypothetical protein	155.43	14.31	0	201.36	23.93	0.00	0.00	0.00	1.30	0.37
sll1425	proS	proline-tRNA ligase	475.65	54.55	0	520.63	96.04	0.00	0.42	0.33	1.09	0.13
sll1426		unknown protein	127.80	28.36	0	153.91	35.44	0.00	0.19	0.05	1.20	0.27
sll1427		protease	230.65	24.83	0	239.89	25.60	0.00	0.55	0.38	1.04	0.06
sll1428		probable sodium-depe	856.78	111.71	0	1039.95	130.98	0.00	0.03	0.00	1.21	0.28
sll1429		unknown protein	22.23	6.54	0	16.60	9.99	0.00	0.30	0.27	0.75	-0.42
sll1430		adenine phosphoribos	21.50	3.35	0	25.87	14.62	0.00	0.98	0.98	1.20	0.27
sll1432	hypB	hydrogenase isoenzyn	134.74	24.49	0	116.92	18.10	0.00	0.19	0.03	0.87	-0.20
sll1433		hypothetical protein	216.36	27.49	0	138.02	25.26	0.00	0.00	0.00	0.64	-0.65
sll1434		penicillin-binding prote	231.31	37.63	0	227.38	35.77	0.00	0.88	0.82	0.98	-0.02
sll1435		glutanyl-tRNA(Gin) an	356.02	34.86	0	321.88	55.30	0.00	0.21	0.13	0.90	-0.15
sll1436		putative transposase [	47.60	6.71	0	372.40	155.66	0.00	0.00	0.00	7.82	2.97
sll1437		putative transposase [	229.33	51.28	0	577.67	191.50	0.00	0.00	0.00	2.52	1.33
sll1439		unknown protein	12.97	3.63	0	9.47	10.84	0.03	0.08	0.05	0.73	-0.45
sll1440	pdxH	pyridoxamine 5'-phosp	88.31	25.68	0	159.23	35.13	0.00	0.00	0.00	1.80	0.85
sll1441	desB	delta 15 desaturase	61.44	6.07	0	74.00	14.61	0.00	0.09	0.03	1.20	0.27
sll1442		hypothetical protein	27.42	3.72	0	11.13	10.01	0.01	0.08	0.05	0.41	-1.30
sll1443	pyrG	CTP synthetase	343.34	52.59	0	335.38	77.80	0.00	0.75	0.70	0.98	-0.03
sll1444		3-isopropylmalate deh	149.67	11.42	0	105.05	28.52	0.00	0.01	0.00	0.70	-0.51
sll1446		hypothetical protein	135.87	44.21	5.17E-14	171.71	74.94	0.00	0.41	0.29	1.26	0.34
sll1447		hypothetical protein	45.57	11.07	0	10.36	9.39	0.01	0.04	0.02	0.23	-2.14
sll1450	nitA	nitrate/nitrite transport	480.23	75.40	0	491.09	177.37	0.00	0.86	0.85	1.02	0.03
sll1451	nitB	nitrate/nitrite transport	273.40	27.81	0	286.44	27.91	0.00	0.45	0.24	1.05	0.07
sll1452	nitC	nitrate/nitrite transport	535.13	57.95	0	661.50	130.06	0.00	0.05	0.01	1.24	0.31
sll1453	nitD	nitrate/nitrite transport	226.43	25.33	0	214.22	32.39	0.00	0.44	0.31	0.95	-0.08
sll1454	narB	nitrate reductase	210.45	22.06	0	235.12	45.31	0.00	0.31	0.22	1.12	0.16
sll1455		hypothetical protein	29.02	8.24	0	12.22	9.36	0.00	0.12	0.08	0.42	-1.25
sll1456		unknown protein	65.70	7.24	0	59.04	6.60	0.00	0.12	0.02	0.90	-0.15
sll1457		probable glycosyltrans	65.38	5.89	0	80.11	15.10	0.00	0.06	0.02	1.23	0.29
sll1459		stationary-phase survi	168.57	41.83	0	110.10	17.64	0.00	0.01	0.00	0.65	-0.61
sll1461		hypothetical protein	123.64	21.31	0	139.14	17.20	0.00	0.16	0.01	1.13	0.17
sll1462	hypE	hydrogenase expressi	153.76	49.29	2.13E-14	96.31	40.84	0.00	0.05	0.00	0.63	-0.67
sll1463	ftsH	cell division protein Fts	411.41	51.71	0	362.05	75.24	0.00	0.19	0.10	0.88	-0.18
sll1464		hypothetical protein	211.62	39.74	0	280.98	53.72	0.00	0.02	0.00	1.33	0.41
sll1466		probable glycosyltrans	111.03	21.04	0	199.69	59.83	0.00	0.00	0.00	1.80	0.85
sll1468	ctrR	beta-carotene hydroxy	223.91	51.45	0	146.11	40.05	0.00	0.01	0.00	0.65	-0.62
sll1469		hypothetical protein	122.26	5.15	0	94.71	12.12	0.00	0.00	0.00	0.77	-0.37
sll1470	leuC	3-isopropylmalate deh	246.27	39.77	0	264.50	45.96	0.00	0.51	0.37	1.07	0.10
sll1471	cpcG2	phycobilisome rod-con	268.06	23.69	0	255.97	78.48	0.00	0.55	0.52	0.95	-0.07
sll1472		unknown protein	34.73	15.06	1.6E-08	25.04	24.37	0.01	0.20	0.17	0.72	-0.47
sll1473		hypothetical protein	81.70	25.23	2.22E-15	51.52	41.41	0.00	0.17	0.14	0.63	-0.67
sll1474		putative transposase [	324.22	82.61	0	562.03	193.53	0.00	0.01	0.00	1.73	0.79
sll1475		two-component senso	222.29	31.25	0	274.54	41.84	0.00	0.02	0.00	1.24	0.30
sll1476		unknown protein	78.23	17.81	0	49.27	39.95	0.00	0.17	0.14	0.63	-0.67
sll1477		hypothetical protein	115.07	24.50	0	132.33	17.42	0.00	0.18	0.00	1.15	0.20
sll1479		6-phosphogluconolact	101.28	10.44	0	71.31	12.31	0.00	0.00	0.00	0.70	-0.51
sll1481		ABC-transporter mem1	129.65	30.76	0	216.42	49.43	0.00	0.01	0.00	1.67	0.74
sll1482		ABC transporter perm	100.99	7.27	0	119.48	14.89	0.00	0.02	0.00	1.18	0.24
sll1483		hypothetical protein	83.66	19.56	0	407.14	107.41	0.00	0.00	0.00	4.87	2.28
sll1484	ndbC	type 2 NADH dehydro	183.80	54.07	0	116.15	25.29	0.00	0.03	0.00	0.63	-0.66
sll1485		hypothetical protein	74.78	18.90	0	73.11	23.48	0.00	0.84	0.79	0.98	-0.03
sll1486		hypothetical protein	140.54	30.45	0	106.28	28.69	0.00	0.08	0.01	0.76	-0.40
sll1488		hypothetical protein	170.01	11.56	0	129.09	37.08	0.00	0.04	0.02	0.76	-0.40
sll1489	cpmA	circadian phase modifi	192.78	23.67	0	127.57	15.28	0.00	0.00	0.00	0.66	-0.60
sll1491		WD-repeat protein	644.20	183.02	0	550.67	223.62	0.00	0.41	0.30	0.85	-0.23
sll1495		hypothetical protein	86.73	11.24	0	97.45	11.75	0.00	0.14	0.02	1.12	0.17
sll1496		mannose-1-phosphate	207.60	22.37	0	165.12	26.13	0.00	0.01	0.00	0.80	-0.33
sll1498		carbamoyl-phosphate	153.62	27.65	0	203.41	46.68	0.00	0.05	0.00	1.32	0.40
sll1499	glxF	ferredoxin-dependent	3473.76	531.75	0	3060.45	582.91	0.00	0.21	0.08	0.88	-0.18
sll1500		hypothetical protein	157.32	52.68	2.59E-13	83.23	21.53	0.00	0.01	0.00	0.53	-0.92
sll1501	cobB	cobyrinic acid a,c-dian	244.43	63.69	0	342.13	71.49	0.00	0.03	0.00	1.40	0.49
sll1502	glxB	NADH-dependent glut	2666.09	681.43	0	2461.88	430.00	0.00	0.66	0.42	0.92	-0.11
sll1503		unknown protein	101.88	30.54	2.22E-16	91.02	25.29	0.00	0.53	0.34	0.89	-0.16
sll1504		hypothetical protein	17.16	10.16	3.55E-05	42.32	8.98	0.00	0.00	0.00	2.47	1.30
sll1505		hypothetical protein	2.80	2.74	0.012315	20.11	14.24	0.00	0.22	0.04	7.18	2.84
sll1507		hypothetical protein	78.45	18.67	0	89.45	22.89	0.00	0.43	0.28	1.14	0.19
sll1508		UDP-3-O-acetyl N-acetyl	88.65	16.95	0	79.17	17.78	0.00	0.37	0.20	0.89	-0.16
sll1509	ycf20	hypothetical protein Yc	34.41	7.58	0	39.85	8.25	0.00	0.28	0.07	1.16	0.21
sll1510		unknown protein	39.19	9.49	0	8.34	9.78	0.04	0.02	0.01	0.21	-2.23
sll1511		unknown protein	72.99	14.04	0	47.57	12.56	0.00	0.01	0.00	0.65	-0.62
sll1512		hypothetical protein	71.00	13.51	0	65.06	5.47	0.00	0.40	0.03	0.92	-0.13
sll1513	ccsA	c-type cytochrome syr	167.10	26.28	0	160.03	22.55	0.00	0.67	0.48	0.96	-0.06

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sl1514	hspA	16.6 kDa small heat st	54.59	8.63	0	249.09	81.61	0.00	0.00	0.00	4.56	2.19
sl1515		unknown protein	225.22	39.18	0	201.84	47.69	0.00	0.34	0.21	0.90	-0.16
sl1516		hypothetical protein	294.80	39.65	0	297.23	74.31	0.00	0.94	0.93	1.01	0.01
sl1520	recN	DNA repair protein Re	123.13	20.00	0	138.32	24.25	0.00	0.28	0.13	1.12	0.17
sl1521		flavoprotein	354.94	69.93	0	282.33	52.29	0.00	0.07	0.00	0.80	-0.33
sl1522		CDP-diacylglycerol-gl	33.23	4.85	0	37.52	25.27	0.00	0.58	0.56	1.13	0.18
sl1524		hypothetical protein	266.17	27.36	0	241.32	33.29	0.00	0.21	0.10	0.91	-0.14
sl1525	prk	phosphoribulokinase	1156.85	227.64	0	1483.63	265.96	0.00	0.03	0.00	1.28	0.36
sl1526		hypothetical protein	196.11	23.20	0	166.41	21.35	0.00	0.05	0.00	0.85	-0.24
sl1527		unknown protein	70.95	9.04	0	57.67	10.10	0.00	0.04	0.01	0.81	-0.30
sl1528		unknown protein	367.23	91.06	0	97.19	12.08	0.00	0.00	0.00	0.26	-1.92
sl1530		unknown protein	105.95	20.36	0	115.13	21.61	0.00	0.47	0.26	1.09	0.12
sl1531		unknown protein	210.90	24.64	0	165.81	20.20	0.00	0.01	0.00	0.79	-0.35
sl1532		hypothetical protein	91.64	9.42	0	88.07	26.02	0.00	0.59	0.56	0.96	-0.06
sl1533	pilT	twitching mobility prote	243.27	40.39	0	190.13	51.85	0.00	0.06	0.01	0.78	-0.36
sl1534		probable glycosyltrans	169.98	19.57	0	91.36	20.65	0.00	0.00	0.00	0.54	-0.90
sl1535		putative sugar transfer	593.72	102.07	0	591.19	104.83	0.00	0.96	0.94	1.00	-0.01
sl1536	moeB	molybdopterin biosynt	239.14	39.98	0	232.92	43.83	0.00	0.77	0.69	0.97	-0.04
sl1537		similar to mutator Mut	26.62	3.39	0	10.90	12.14	0.03	0.06	0.04	0.41	-1.29
sl1538		similar to beta-hexosa	128.79	47.22	2.37E-11	90.34	23.17	0.00	0.14	0.00	0.70	-0.51
sl1540		alpha, alpha-trehalose-	151.23	15.31	0	110.89	18.31	0.00	0.00	0.00	0.73	-0.45
sl1541		hypothetical protein	119.68	9.73	0	146.55	20.97	0.00	0.01	0.00	1.22	0.29
sl1542		hypothetical protein	98.93	11.83	0	111.35	15.78	0.00	0.15	0.04	1.13	0.17
sl1543		hypothetical protein	23.62	6.81	0	29.40	11.44	0.00	0.44	0.36	1.24	0.32
sl1544		two-component respon	44.91	9.04	0	94.05	12.81	0.00	0.00	0.00	2.09	1.07
sl1545		glutathione S-transfere	114.33	18.45	0	125.73	24.08	0.00	0.41	0.25	1.10	0.14
sl1546	ppx	exopolyphosphatase	165.86	37.99	0	225.65	65.07	0.00	0.09	0.02	1.36	0.44
sl1547		hypothetical protein	82.68	19.08	0	39.01	16.20	0.00	0.00	0.00	0.47	-1.08
sl1549		hypothetical protein	38.54	5.41	0	107.48	32.66	0.00	0.00	0.00	2.79	1.48
sl1550		probable porin; major r	797.43	251.62	8.22E-15	801.89	338.51	0.00	0.90	0.87	1.01	0.01
sl1552		unknown protein	70.39	19.21	0	100.04	37.54	0.00	0.16	0.07	1.42	0.51
sl1553	pheT	phenylalanyl-tRNA syr	283.49	23.00	0	219.07	34.49	0.00	0.00	0.00	0.77	-0.37
sl1555		two-component hybrid	144.42	25.24	0	79.60	12.11	0.00	0.00	0.00	0.55	-0.86
sl1556		isopentenyl-dephosph-	262.85	75.66	0	224.01	83.19	0.00	0.39	0.24	0.85	-0.23
sl1557		succinyl-CoA syntheta	181.38	20.58	0	109.08	15.08	0.00	0.00	0.00	0.60	-0.73
sl1558		mannose-1-phosphate	137.96	25.88	0	156.15	47.91	0.00	0.49	0.39	1.13	0.18
sl1559		soluble hydrogenase 4	990.09	156.61	0	1242.09	285.32	0.00	0.11	0.03	1.25	0.33
sl1560		putative transposase [	290.27	24.33	0	522.95	116.58	0.00	0.00	0.00	1.80	0.85
sl1561	putA	proline oxidase	233.23	22.70	0	293.83	51.61	0.00	0.02	0.00	1.26	0.33
sl1562		unknown protein	15.81	2.96	0	11.57	12.97	0.03	0.08	0.05	0.73	-0.45
sl1563		unknown protein	34.30	4.75	0	51.27	14.47	0.00	0.02	0.00	1.49	0.58
sl1564		putative lyase	214.67	31.36	0	166.22	33.84	0.00	0.02	0.00	0.77	-0.37
sl1566	ggpS	glucosylglycerolphospl	243.02	15.05	0	433.30	33.64	0.00	0.00	0.00	1.78	0.83
sl1568		fibrillin	127.17	15.44	0	144.54	41.24	0.00	0.50	0.45	1.14	0.18
sl1570		unknown protein	31.08	4.12	0	29.41	11.98	0.00	0.52	0.48	0.95	-0.08
sl1571		hypothetical protein	265.75	24.59	0	295.45	24.51	0.00	0.06	0.00	1.11	0.15
sl1572	dnaE	DNA polymerase III al	128.26	21.44	0	187.35	66.90	0.00	0.06	0.02	1.46	0.55
sl1573		hypothetical protein	21.99	7.42	3.73E-13	5.58	8.39	0.10	0.02	0.00	0.25	-1.98
sl1574		similar to serine/threor	27.70	3.52	0	33.49	17.90	0.00	0.73	0.71	1.21	0.27
sl1575		similar to serine/threor	54.54	4.97	0	73.00	17.66	0.00	0.02	0.00	1.34	0.42
sl1577	cpcB	phycocyanin beta subu	8791.09	916.12	0	6389.74	1324.57	0.00	0.01	0.00	0.73	-0.46
sl1578	cpcA	phycocyanin alpha sut	9567.18	2076.70	0	9199.99	2227.24	0.00	0.76	0.66	0.96	-0.06
sl1579	cpcC2	phycobilisome rod link	4528.13	606.60	0	4190.81	1234.72	0.00	0.43	0.36	0.93	-0.11
sl1580	cpcC1	phycobilisome rod link	5922.02	578.14	0	6232.00	1171.92	0.00	0.65	0.59	1.05	0.07
sl1581		hypothetical protein	314.23	64.99	0	243.35	66.92	0.00	0.09	0.02	0.77	-0.37
sl1582		unknown protein	182.68	35.40	0	141.64	68.68	0.00	0.16	0.11	0.78	-0.37
sl1583		unknown protein	707.31	171.38	0	472.74	103.19	0.00	0.01	0.00	0.67	-0.58
sl1584		ferredoxin like protein	44.17	3.86	0	43.87	9.95	0.00	0.81	0.79	0.99	-0.01
sl1586		unknown protein	255.75	59.22	0	259.62	48.84	0.00	0.87	0.80	1.02	0.02
sl1590		two-component senso	186.81	34.24	0	152.15	20.03	0.00	0.07	0.00	0.81	-0.30
sl1592		two-component respon	116.55	5.59	0	89.16	24.63	0.00	0.04	0.02	0.76	-0.39
sl1594	ndhR	ndhF3 operon transcri	48.21	8.25	0	117.48	20.90	0.00	0.00	0.00	2.44	1.29
sl1595	kaiC2	circadian clock protein	125.32	13.82	0	104.80	29.43	0.00	0.11	0.06	0.84	-0.26
sl1596	kaiB2	circadian clock protein	11.24	2.43	0	3.41	3.93	0.03	0.02	0.01	0.30	-1.72
sl1598	mntC	Mn transporter MntC	33.80	6.58	0	75.43	31.52	0.00	0.00	0.00	2.23	1.16
sl1599	mntA	manganese transport	42.24	13.30	7.33E-15	57.08	15.89	0.00	0.11	0.00	1.35	0.43
sl1600	mntB	manganese transport	43.63	6.25	0	67.52	11.11	0.00	0.00	0.00	1.55	0.63
sl1601		hypothetical protein	112.80	30.00	0	84.39	18.30	0.00	0.10	0.00	0.75	-0.42
sl1605		(3R)-hydroxymyristol a	77.23	23.10	2.22E-16	82.22	27.70	0.00	0.82	0.77	1.06	0.09
sl1606		hypothetical protein	146.95	21.97	0	166.34	26.89	0.00	0.22	0.06	1.13	0.18
sl1608		hypothetical protein	168.25	30.74	0	169.97	26.07	0.00	0.90	0.85	1.01	0.01
sl1609		hypothetical protein	40.16	10.13	0	18.54	8.59	0.00	0.01	0.00	0.46	-1.11
sl1611		unknown protein	39.00	9.74	0	37.59	24.38	0.00	0.47	0.43	0.96	-0.05
sl1612	folC	folypolyglutamate syn	130.87	30.23	0	79.60	20.96	0.00	0.01	0.00	0.61	-0.72
sl1613		unknown protein	29.93	8.14	0	15.89	15.42	0.01	0.11	0.08	0.53	-0.91
sl1614	pma1	cation-transporting AT	518.54	129.71	0	316.49	111.70	0.00	0.02	0.00	0.61	-0.71
sl1615		thiophen and furan oxi	134.51	17.23	0	184.80	19.65	0.00	0.00	0.00	1.37	0.46
sl1618		hypothetical protein	247.01	46.98	0	206.15	50.83	0.00	0.16	0.06	0.83	-0.26

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sl11620		hypothetical protein	38.68	8.21	0	68.73	31.89	0.00	0.04	0.01	1.78	0.83
sl11621		AhpC/TSA family prot	664.31	236.33	5.76E-12	873.50	353.60	0.00	0.33	0.20	1.31	0.39
sl11623		ABC transporter ATP-	54.34	3.32	0	47.13	7.07	0.00	0.05	0.01	0.87	-0.21
sl11624		two-component respor	213.08	35.46	0	232.41	29.71	0.00	0.31	0.10	1.09	0.13
sl11625		succinate dehydrogen	88.48	12.15	0	93.25	17.99	0.00	0.66	0.57	1.05	0.08
sl11626		LexA repressor	1236.15	185.81	0	1069.17	122.73	0.00	0.09	0.00	0.86	-0.21
sl11628		hypothetical protein	104.21	5.60	0	119.61	15.17	0.00	0.04	0.01	1.15	0.20
sl11629	phr	DNA photolyase	71.88	17.14	0	58.59	17.63	0.00	0.21	0.08	0.82	-0.29
sl11630		unknown protein	8.82	3.96	5.09E-08	2.48	3.96	0.13	0.01	0.00	0.28	-1.83
sl11631		putative cytidine and d	78.57	27.38	2.07E-12	52.04	40.87	0.00	0.15	0.12	0.66	-0.59
sl11632		hypothetical protein	129.31	28.22	0	93.46	22.31	0.00	0.03	0.00	0.72	-0.47
sl11633	ftsZ	cell division protein Fts	338.20	9.61	0	526.18	110.68	0.00	0.00	0.00	1.56	0.64
sl11634		hypothetical protein	87.80	14.78	0	69.13	11.53	0.00	0.03	0.00	0.79	-0.34
sl11635		Thy1 protein homolog	117.27	33.44	0	137.03	35.74	0.00	0.28	0.09	1.17	0.22
sl11636		ferricytochrome binding p	200.53	51.13	0	143.42	24.44	0.00	0.04	0.00	0.72	-0.48
sl11638		hypothetical protein	732.16	144.86	0	1082.84	185.75	0.00	0.00	0.00	1.48	0.56
sl11639	ureD	urease accessory prot	60.32	14.18	0	54.76	31.32	0.00	0.42	0.37	0.91	-0.14
sl11640		hypothetical protein	99.64	9.89	0	72.87	18.34	0.00	0.01	0.00	0.73	-0.45
sl11641		glutamate decarboxylase	156.42	20.20	0	180.17	48.49	0.00	0.31	0.23	1.15	0.20
sl11642		hypothetical protein	6.66	1.64	0	4.64	5.60	0.04	0.07	0.05	0.70	-0.52
sl11643		hypothetical protein	48.73	9.60	0	80.92	26.65	0.00	0.02	0.00	1.66	0.73
sl11647		probable phosphinotransferase	69.79	15.55	0	55.34	9.48	0.00	0.08	0.00	0.79	-0.33
sl11652		hypothetical protein	65.22	13.66	0	77.55	30.38	0.00	0.45	0.36	1.19	0.25
sl11653		similar to menaquinone	46.39	10.53	0	88.74	25.23	0.00	0.00	0.00	1.91	0.94
sl11654		hypothetical protein	142.81	41.51	0	154.55	52.73	0.00	0.75	0.67	1.08	0.11
sl11655		similar to biotin [acetyl	109.92	23.69	0	155.62	24.64	0.00	0.01	0.00	1.42	0.50
sl11656		hypothetical protein	143.98	25.32	0	146.33	16.22	0.00	0.78	0.57	1.02	0.02
sl11658		hypothetical protein	70.21	11.02	0	46.22	6.70	0.00	0.00	0.00	0.66	-0.60
sl11659		hypothetical protein	82.42	11.93	0	111.38	23.89	0.00	0.02	0.00	1.35	0.43
sl11660		hypothetical protein	110.29	16.02	0	112.63	13.13	0.00	0.75	0.58	1.02	0.03
sl11662		probable prephenate carboxylase	97.14	14.11	0	159.81	26.38	0.00	0.00	0.00	1.65	0.72
sl11663		phycocyanin alpha phy	82.99	12.26	0	128.29	16.39	0.00	0.00	0.00	1.55	0.63
sl11664		probable glycosyl transferase	101.36	18.82	0	157.59	48.65	0.00	0.02	0.00	1.55	0.64
sl11665		unknown protein	707.41	169.96	0	585.05	135.55	0.00	0.24	0.06	0.83	-0.27
sl11666	dnaJ	DnaJ protein	85.53	7.12	0	67.74	9.11	0.00	0.01	0.00	0.79	-0.34
sl11667		hypothetical protein	60.50	12.07	0	101.67	20.77	0.00	0.00	0.00	1.68	0.75
sl11669	aroK	shikimate kinase	33.23	3.59	0	39.86	12.75	0.00	0.33	0.28	1.20	0.26
sl11670		heat-inducible transcription factor	80.46	19.92	0	132.46	34.20	0.00	0.01	0.00	1.65	0.72
sl11671		hypothetical protein	18.07	3.99	0	38.91	9.75	0.00	0.00	0.00	2.15	1.11
sl11672		two-component hybrid	113.90	17.49	0	102.60	22.83	0.00	0.33	0.22	0.90	-0.15
sl11673		two-component response regulator	306.19	34.97	0	306.88	36.98	0.00	0.98	0.98	1.00	0.00
sl11675		hypothetical protein	56.19	13.81	0	42.07	9.03	0.00	0.06	0.00	0.75	-0.42
sl11676		4-alpha-glucanotransferase	102.41	22.92	0	180.49	41.01	0.00	0.00	0.00	1.76	0.82
sl11677		similar to spore maturation protein	117.39	33.72	0	82.44	12.89	0.00	0.04	0.00	0.70	-0.51
sl11678		similar to spore maturation protein	21.31	4.15	0	6.10	7.66	0.05	0.02	0.01	0.29	-1.81
sl11679		protease	182.02	48.76	0	208.81	48.72	0.00	0.40	0.15	1.15	0.20
sl11680		hypothetical protein	128.51	21.28	0	85.22	20.12	0.00	0.01	0.00	0.66	-0.59
sl11681		unknown protein	208.41	27.77	0	265.51	27.66	0.00	0.01	0.00	1.27	0.35
sl11682		alanine dehydrogenase	113.86	34.27	4.44E-16	78.73	16.64	0.00	0.06	0.00	0.69	-0.53
sl11683		lysine decarboxylase	81.40	26.23	2.91E-14	72.37	21.98	0.00	0.62	0.41	0.89	-0.17
sl11685	pxcA	protein involved in light response	51.71	3.23	0	42.24	11.71	0.00	0.07	0.03	0.82	-0.29
sl11686		hypothetical protein	132.17	33.52	0	116.25	22.94	0.00	0.43	0.15	0.88	-0.19
sl11687		unknown protein	151.43	19.92	0	111.91	13.89	0.00	0.00	0.00	0.74	-0.44
sl11688	thrC	threonine synthase	448.38	57.95	0	334.09	60.41	0.00	0.01	0.00	0.75	-0.42
sl11689	sigE	group 2 RNA polymerase	262.29	45.63	0	257.23	36.37	0.00	0.86	0.78	0.98	-0.03
sl11691		hypothetical protein	121.93	28.16	0	95.29	8.53	0.00	0.05	0.00	0.78	-0.36
sl11692		hypothetical protein	55.83	9.12	0	21.34	18.17	0.00	0.09	0.06	0.38	-1.39
sl11693		hypothetical protein	144.35	49.21	6.69E-13	174.79	62.67	0.00	0.32	0.16	1.21	0.28
sl11694	pilA1	pilin polypeptide PilA1	4963.86	1405.17	0	2779.51	657.47	0.00	0.01	0.00	0.56	-0.84
sl11695	pilA2	pilin polypeptide PilA2	166.50	24.80	0	220.94	22.22	0.00	0.00	0.00	1.33	0.41
sl11696		hypothetical protein	66.12	23.57	6.39E-12	49.15	15.18	0.00	0.16	0.04	0.74	-0.43
sl11697		hypothetical protein	100.13	28.63	0	126.51	45.92	0.00	0.32	0.18	1.26	0.34
sl11698		hypothetical protein	31.14	4.77	0	22.26	15.72	0.00	0.20	0.17	0.71	-0.48
sl11699		oligopeptide-binding protein	138.69	18.82	0	181.85	30.31	0.00	0.01	0.00	1.31	0.39
sl11702	ycf51	hypothetical protein Ycf51	75.22	13.46	0	97.29	16.82	0.00	0.03	0.00	1.29	0.37
sl11703		protease IV	79.11	24.87	6.66E-15	140.28	28.28	0.00	0.01	0.00	1.77	0.83
sl11704		probable short chain dehydrogenase	44.87	10.73	0	27.61	9.79	0.00	0.03	0.01	0.62	-0.70
sl11708		two-component response regulator	96.59	7.49	0	115.33	14.51	0.00	0.02	0.00	1.19	0.26
sl11709		3-ketoacyl-acyl carrier protein	75.50	5.18	0	85.40	24.54	0.00	0.40	0.37	1.13	0.18
sl11710		putative transposase	110.57	18.54	0	629.76	339.84	0.00	0.00	0.00	5.70	2.51
sl11712		DNA binding protein H	932.17	168.19	0	674.97	89.70	0.00	0.01	0.00	0.72	-0.47
sl11713	hisC	histidinol-phosphate aminotransferase	218.08	27.40	0	178.73	31.86	0.00	0.05	0.01	0.82	-0.29
sl11714		unknown protein	8.56	2.07	0	9.36	6.73	0.00	0.44	0.42	1.09	0.13
sl11715		hypothetical protein	14.69	4.10	0	8.26	9.40	0.03	0.06	0.03	0.56	-0.83
sl11716		putative transposase	108.21	15.17	0	608.24	249.29	0.00	0.00	0.00	5.62	2.49
sl11717		unknown protein	37.27	7.06	0	40.30	17.98	0.00	0.98	0.97	1.08	0.11
sl11721		pyruvate dehydrogenase	227.97	23.34	0	169.31	28.48	0.00	0.00	0.00	0.74	-0.43
sl11722		hypothetical protein	166.20	55.22	1.67E-13	239.42	34.36	0.00	0.03	0.00	1.44	0.53



Table A-1 Gene expression profiles for *Synechocytis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sil1723		probable glycosyltrans	59.51	5.69	0	154.91	73.76	0.00	0.00	0.00	2.60	1.38
sil1724		probable glycosyltrans	90.88	20.57	0	72.21	28.81	0.00	0.17	0.09	0.79	-0.33
sil1725		ATP-binding protein of	122.29	31.43	0	147.67	55.77	0.00	0.35	0.20	1.21	0.27
sil1726		hypothetical protein	53.24	12.45	0	65.63	19.73	0.00	0.21	0.10	1.23	0.30
sil1730		unknown protein	96.04	33.95	4.25E-12	69.92	25.93	0.00	0.19	0.04	0.73	-0.46
sil1732	ndhF3	NADH dehydrogenase	97.66	5.04	0	118.73	11.24	0.00	0.00	0.00	1.22	0.28
sil1733	ndhD3	NADH dehydrogenase	106.49	17.43	0	107.94	25.58	0.00	0.98	0.97	1.01	0.02
sil1734	cupA	protein involved in low	182.09	27.63	0	90.80	19.51	0.00	0.00	0.00	0.50	-1.00
sil1735		hypothetical protein	122.12	13.87	0	41.18	15.59	0.00	0.00	0.00	0.34	-1.57
sil1736		hypothetical protein	40.59	5.42	0	39.26	10.42	0.00	0.66	0.60	0.97	-0.05
sil1737	ycf60	hypothetical protein Yf	54.84	9.16	0	41.35	22.17	0.00	0.17	0.13	0.75	-0.41
sil1738		hypothetical protein	127.76	18.79	0	63.19	11.81	0.00	0.00	0.00	0.49	-1.02
sil1739		unknown protein	266.66	42.02	0	120.49	57.36	0.00	0.00	0.00	0.45	-1.15
sil1740	rpl19	50S ribosomal protein	153.21	28.21	0	144.99	52.87	0.00	0.58	0.52	0.95	-0.08
sil1742	nusG	transcription antitermir	160.89	32.41	0	187.35	41.93	0.00	0.27	0.12	1.16	0.22
sil1743	rpl11	50S ribosomal protein	178.95	30.85	0	198.65	65.23	0.00	0.71	0.68	1.11	0.15
sil1744	rpl1	50S ribosomal protein	986.74	432.53	2.3E-08	950.69	440.44	0.00	0.88	0.84	0.96	-0.05
sil1745	rpl10	50S ribosomal protein	901.90	233.82	0	768.71	121.94	0.00	0.27	0.03	0.85	-0.23
sil1746	rpl12	50S ribosomal protein	901.43	209.52	0	710.59	126.58	0.00	0.08	0.00	0.79	-0.34
sil1747	arcC	chorismate synthase	231.87	35.15	0	194.38	29.54	0.00	0.08	0.01	0.84	-0.25
sil1749		hypothetical protein	35.85	6.51	0	34.15	19.92	0.00	0.46	0.43	0.95	-0.07
sil1750	ureC	urease alpha subunit	294.11	25.45	0	291.55	30.31	0.00	0.86	0.81	0.99	-0.01
sil1751		hypothetical protein	26.64	5.10	0	13.52	11.58	0.00	0.12	0.09	0.51	-0.98
sil1752		hypothetical protein	519.75	154.75	2.22E-16	608.13	218.50	0.00	0.42	0.27	1.17	0.23
sil1755		unknown protein	91.81	18.24	0	113.86	17.94	0.00	0.07	0.00	1.24	0.31
sil1757		hypothetical protein	69.92	25.72	2.74E-11	40.33	35.50	0.01	0.08	0.04	0.58	-0.79
sil1758		MrsA protein homolog	228.51	30.54	0	326.12	56.35	0.00	0.00	0.00	1.43	0.51
sil1760	thrB	homoserine kinase	112.96	9.58	0	157.14	21.30	0.00	0.00	0.00	1.39	0.48
sil1761		unknown protein	44.67	8.86	0	16.87	12.96	0.00	0.09	0.06	0.38	-1.40
sil1762		binding protein of ABC	309.72	46.84	0	219.42	33.10	0.00	0.00	0.00	0.71	-0.50
sil1763		unknown protein	59.11	10.45	0	48.63	14.51	0.00	0.20	0.12	0.82	-0.28
sil1764		unknown protein	62.02	5.20	0	39.06	18.61	0.00	0.06	0.03	0.63	-0.67
sil1765		unknown protein	56.34	14.48	0	36.61	9.08	0.00	0.01	0.00	0.65	-0.62
sil1766		hypothetical protein	135.93	28.50	0	134.72	27.47	0.00	0.94	0.91	0.99	-0.01
sil1767	rps6	30S ribosomal protein	676.03	156.24	0	678.47	162.79	0.00	0.99	0.98	1.00	0.01
sil1768		probable oligopeptides	375.66	75.90	0	340.39	141.61	0.00	0.44	0.38	0.91	-0.14
sil1769		hypothetical protein	36.97	7.74	0	22.44	16.32	0.00	0.19	0.16	0.61	-0.72
sil1770		hypothetical protein	200.02	35.06	0	175.15	49.16	0.00	0.28	0.17	0.88	-0.19
sil1771	pphA	protein serin-threonin	177.64	28.92	0	171.05	54.80	0.00	0.65	0.59	0.96	-0.05
sil1772	mutS	DNA mismatch repair	154.34	31.25	0	159.25	26.48	0.00	0.75	0.60	1.03	0.05
sil1773		hypothetical protein	171.68	41.47	0	191.46	39.62	0.00	0.37	0.14	1.12	0.16
sil1774		hypothetical protein	244.57	32.77	0	435.83	127.03	0.00	0.00	0.00	1.78	0.83
sil1775		hypothetical protein	192.99	62.30	3.24E-14	257.65	86.70	0.00	0.18	0.05	1.34	0.42
sil1776		deoxyribose-phosphat	55.64	9.36	0	43.80	21.46	0.00	0.22	0.17	0.79	-0.35
sil1780		putative transposase [	405.13	37.10	0	643.60	106.63	0.00	0.00	0.00	1.59	0.67
sil1783		hypothetical protein	231.40	38.80	0	72.06	6.98	0.00	0.00	0.00	0.31	-1.68
sil1784		unknown protein	269.55	76.47	0	114.07	39.71	0.00	0.00	0.00	0.42	-1.24
sil1785		unknown protein	309.04	77.79	0	127.81	29.76	0.00	0.00	0.00	0.41	-1.27
sil1786	tatD	similar to Sec-indepen	377.48	77.10	0	530.13	120.83	0.00	0.02	0.00	1.40	0.49
sil1787	rpoB	RNA polymerase beta	439.60	74.81	0	566.27	210.51	0.00	0.19	0.13	1.29	0.37
sil1789	rpoC2	RNA polymerase beta	306.33	49.58	0	279.75	23.63	0.00	0.28	0.02	0.91	-0.13
sil1791		putative transposase [	29.55	5.47	0	51.55	21.12	0.00	0.08	0.04	1.74	0.80
sil1792		putative transposase [	70.95	15.31	0	102.44	26.33	0.00	0.03	0.00	1.44	0.53
sil1796	petJ	cytochrome c553	23.20	7.50	3.62E-14	11.07	13.78	0.05	0.05	0.02	0.48	-1.07
sil1797	ycf21	hypothetical protein Yf	36.97	3.19	0	94.25	30.50	0.00	0.00	0.00	2.55	1.35
sil1799	rpl3	50S ribosomal protein	282.01	35.68	0	658.68	78.81	0.00	0.00	0.00	2.34	1.22
sil1800	rpl4	50S ribosomal protein	158.39	32.99	0	287.56	127.94	0.00	0.03	0.01	1.82	0.86
sil1801	rpl23	50S ribosomal protein	109.07	27.52	0	226.87	80.84	0.00	0.00	0.00	2.08	1.06
sil1802	rpl2	50S ribosomal protein	227.73	38.21	0	477.34	167.38	0.00	0.00	0.00	2.10	1.07
sil1803	rpl22	50S ribosomal protein	114.91	13.66	0	177.40	93.07	0.00	0.44	0.41	1.54	0.63
sil1804	rps3	30S ribosomal protein	216.83	59.40	0	367.97	206.85	0.00	0.09	0.03	1.70	0.76
sil1805	rpl16	50S ribosomal protein	106.46	36.21	5.98E-13	171.56	126.46	0.00	0.61	0.58	1.61	0.69
sil1806	rpl14	50S ribosomal protein	132.49	27.31	0	169.83	82.14	0.00	0.48	0.43	1.28	0.36
sil1807	rpl24	50S ribosomal protein	128.76	29.56	0	243.31	100.91	0.00	0.03	0.01	1.89	0.92
sil1808	rpl5	50S ribosomal protein	196.46	46.86	0	297.25	107.33	0.00	0.07	0.02	1.51	0.60
sil1809	rps8	30S ribosomal protein	1456.39	119.97	0	1411.57	310.59	0.00	0.62	0.58	0.97	-0.05
sil1810	rpl6	50S ribosomal protein	180.42	30.48	0	276.83	103.33	0.00	0.08	0.04	1.53	0.62
sil1811	rpl18	50S ribosomal protein	93.75	31.90	6.04E-13	107.07	70.13	0.00	0.79	0.78	1.14	0.19
sil1812	rps5	30S ribosomal protein	184.11	27.92	0	274.08	70.93	0.00	0.02	0.00	1.49	0.57
sil1813	rpl15	50S ribosomal protein	135.09	19.51	0	154.42	77.15	0.00	0.95	0.95	1.14	0.19
sil1814	secY	preprotein translocase	668.22	93.95	0	742.98	145.75	0.00	0.39	0.28	1.11	0.15
sil1815		adenylate kinase	77.86	11.82	0	68.09	14.90	0.00	0.23	0.10	0.87	-0.19
sil1816	rps13	30S ribosomal protein	185.64	45.25	0	258.85	62.82	0.00	0.05	0.00	1.39	0.48
sil1817	rps11	30S ribosomal protein	105.13	16.37	0	130.13	48.22	0.00	0.44	0.39	1.24	0.31
sil1818	rpoA	RNA polymerase alpha	325.23	29.58	0	493.08	68.54	0.00	0.00	0.00	1.52	0.60
sil1819	rpl17	50S ribosomal protein	83.99	12.07	0	110.39	63.60	0.00	0.91	0.91	1.31	0.39
sil1820		tRNA pseudouridine s	251.43	38.97	0	326.64	88.88	0.00	0.11	0.05	1.30	0.38
sil1821	rpl13	50S ribosomal protein	228.39	45.19	0	294.51	77.43	0.00	0.13	0.04	1.29	0.37

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sl11822	rps9	30S ribosomal protein	224.42	41.90	0	237.83	67.07	0.00	0.84	0.81	1.06	0.08
sl11823	purA	adenylosuccinate synt	267.27	23.87	0	293.45	37.17	0.00	0.21	0.10	1.10	0.13
sl11824	rpl25	50S ribosomal protein	423.23	93.16	0	323.22	18.47	0.00	0.02	0.00	0.76	-0.39
sl11825		hypothetical protein	146.34	16.67	0	118.16	12.00	0.00	0.01	0.00	0.81	-0.31
sl11830		unknown protein	137.83	20.57	0	126.73	25.48	0.00	0.40	0.27	0.92	-0.12
sl11831		glycolate oxidase sub	178.60	13.87	0	135.18	19.11	0.00	0.00	0.00	0.76	-0.40
sl11832		hypothetical protein	271.85	76.27	0	181.56	52.43	0.00	0.03	0.00	0.67	-0.58
sl11833		penicillin-binding prote	281.27	57.04	0	272.57	91.63	0.00	0.71	0.65	0.97	-0.05
sl11834		hypothetical protein	31.04	8.89	0	7.21	11.15	0.11	0.01	0.00	0.23	-2.11
sl11835		hypothetical protein	194.53	33.10	0	223.72	19.09	0.00	0.08	0.00	1.15	0.20
sl11837		unknown protein	111.91	21.99	0	96.91	30.67	0.00	0.32	0.22	0.87	-0.21
sl11841		pyruvate dehydrogena	575.18	90.71	0	587.90	113.25	0.00	0.86	0.81	1.02	0.03
sl11845		hypothetical protein	45.37	9.76	0	46.43	21.08	0.00	0.75	0.73	1.02	0.03
sl11848		putative acyltransferas	71.74	20.36	0	48.25	26.46	0.00	0.13	0.08	0.67	-0.57
sl11849		probable dioxygenase	30.94	8.74	0	46.88	5.17	0.00	0.00	0.00	1.52	0.60
sl11851		unknown protein	21.97	3.38	0	37.54	14.73	0.00	0.04	0.02	1.71	0.77
sl11852		nucleoside diphosphat	44.57	9.01	0	76.65	12.84	0.00	0.00	0.00	1.72	0.78
sl11853		unknown protein	83.73	17.12	0	78.98	9.21	0.00	0.60	0.29	0.94	-0.08
sl11854		exodeoxyribonuclease	39.22	7.58	0	48.60	12.74	0.00	0.15	0.05	1.24	0.31
sl11858		unknown protein	240.73	22.69	0	380.80	33.85	0.00	0.00	0.00	1.58	0.66
sl11860		putative transposase [	89.33	11.18	0	419.88	141.46	0.00	0.00	0.00	4.70	2.23
sl11861		putative transposase [	43.31	6.97	0	194.12	34.46	0.00	0.00	0.00	4.48	2.16
sl11862		unknown protein	34.46	7.36	0	1958.29	862.43	0.00	0.00	0.00	56.83	5.83
sl11863		unknown protein	29.33	4.38	0	1447.70	640.07	0.00	0.00	0.00	49.36	5.63
sl11864		probable chloride char	628.49	131.36	0	609.86	148.92	0.00	0.80	0.73	0.97	-0.04
sl11865	prfB	peptide chain release	126.76	9.73	0	122.96	32.92	0.00	0.63	0.60	0.97	-0.04
sl11866		hypothetical protein	82.98	5.89	0	66.62	18.79	0.00	0.08	0.04	0.80	-0.32
sl11867	psbA3	photosystem II D1 pro	11014.33	1474.90	0	10863.76	2593.62	0.00	0.79	0.76	0.99	-0.02
sl11868	dnaG	DNA primase	102.31	21.18	0	147.58	46.83	0.00	0.06	0.01	1.44	0.53
sl11869		probable dioxygenase,	71.71	15.10	0	67.06	18.25	0.00	0.63	0.51	0.94	-0.10
sl11870		ATP-binding protein of	104.86	27.09	0	67.75	43.72	0.00	0.09	0.04	0.65	-0.63
sl11871		two-component syst	57.23	6.05	0	51.70	14.76	0.00	0.32	0.27	0.90	-0.15
sl11872		transcriptional regulat	231.35	70.00	6.66E-16	165.58	24.36	0.00	0.05	0.00	0.72	-0.48
sl11873		unknown protein	287.25	66.94	0	242.60	50.19	0.00	0.22	0.07	0.84	-0.24
sl11874		hypothetical protein	503.45	50.28	0	484.89	79.64	0.00	0.58	0.50	0.96	-0.05
sl11875	ho2	heme oxygenase	49.68	5.35	0	73.20	16.27	0.00	0.00	0.00	1.47	0.56
sl11876	hemN	oxygen independent c	98.87	11.44	0	66.29	13.08	0.00	0.00	0.00	0.67	-0.58
sl11878		iron(III)-transport ATP-	341.87	63.76	0	278.32	52.03	0.00	0.08	0.01	0.81	-0.30
sl11879	ycf55	two-component respon	314.00	57.35	0	263.05	34.07	0.00	0.11	0.00	0.84	-0.26
sl11880		hypothetical protein	44.10	6.56	0	22.31	17.39	0.00	0.11	0.08	0.51	-0.98
sl11882		unknown protein	305.18	57.73	0	108.08	17.09	0.00	0.00	0.00	0.35	-1.50
sl11883	argJ	arginine biosynthesis t	126.32	26.81	0	214.70	43.24	0.00	0.00	0.00	1.70	0.77
sl11884		hypothetical protein	108.86	22.31	0	174.39	45.62	0.00	0.00	0.00	1.60	0.68
sl11885		unknown protein	281.37	40.85	0	245.31	10.78	0.00	0.06	0.00	0.87	-0.20
sl11886		hypothetical protein	90.78	8.81	0	102.43	20.19	0.00	0.27	0.19	1.13	0.17
sl11888		two-component senso	128.69	24.05	0	135.83	40.79	0.00	0.80	0.76	1.06	0.08
sl11890	cobN	similar to cobalamin bi	230.31	17.16	0	248.35	15.88	0.00	0.08	0.00	1.08	0.11
sl11891		unknown protein	208.19	41.89	0	164.95	34.63	0.00	0.08	0.01	0.79	-0.34
sl11892		unknown protein	138.09	35.64	0	60.51	19.54	0.00	0.00	0.00	0.44	-1.19
sl11893	hisF	cyclase	182.35	25.31	0	84.94	17.89	0.00	0.00	0.00	0.47	-1.10
sl11894	ribA	riboflavin biosynthesis	204.84	45.23	0	244.96	11.22	0.00	0.05	0.00	1.20	0.26
sl11895		hypothetical protein	159.03	42.40	0	213.68	47.18	0.00	0.07	0.00	1.34	0.43
sl11897		hypothetical protein	45.45	10.28	0	10.92	10.36	0.01	0.04	0.02	0.24	-2.06
sl11898		hypothetical protein	96.95	11.46	0	142.55	34.05	0.00	0.01	0.00	1.47	0.56
sl11899	ctaB	cytochrome c oxidase	185.59	51.39	0	226.05	97.98	0.00	0.44	0.31	1.22	0.28
sl11900	act	acetyltransferase	24.24	4.95	0	25.10	4.87	0.00	0.75	0.64	1.04	0.05
sl11902		hypothetical protein	63.60	21.41	3.41E-13	80.29	16.53	0.00	0.14	0.00	1.26	0.34
sl11905		two-component hybrid	2479.07	384.25	0	1338.95	268.73	0.00	0.00	0.00	0.54	-0.89
sl11906		hypothetical protein	158.85	21.54	0	166.86	17.25	0.00	0.47	0.23	1.05	0.07
sl11908	serA	D-3-phosphoglycerate	227.26	36.77	0	224.17	33.98	0.00	0.89	0.84	0.99	-0.02
sl11909		probable methyltransfe	95.42	15.45	0	136.60	23.17	0.00	0.00	0.00	1.43	0.52
sl11910	zam	protein conferring resit	673.83	70.47	0	595.35	35.03	0.00	0.03	0.00	0.88	-0.18
sl11911		hypothetical protein	28.27	3.40	0	45.86	17.51	0.00	0.02	0.00	1.62	0.70
sl11912		hypothetical protein	27.36	5.32	0	63.18	15.93	0.00	0.00	0.00	2.31	1.21
sl11913		hypothetical protein	146.76	7.70	0	135.62	13.71	0.00	0.12	0.05	0.92	-0.11
sl11915		hypothetical protein	122.75	17.65	0	95.46	6.61	0.00	0.00	0.00	0.78	-0.36
sl11916		hypothetical protein	72.28	18.94	0	46.29	9.33	0.00	0.01	0.00	0.64	-0.64
sl11917	hemN	oxygen independent c	83.57	31.88	1.34E-10	81.50	29.26	0.00	0.92	0.89	0.98	-0.04
sl11920	pacS	copper transporting Ci	249.94	49.31	0	263.76	62.77	0.00	0.70	0.60	1.06	0.08
sl11921		hypothetical protein	109.97	19.27	0	77.94	14.19	0.00	0.01	0.00	0.71	-0.50
sl11924	syacr2	cAMP receptor proteir	74.57	26.85	1.03E-11	40.77	16.97	0.00	0.02	0.00	0.55	-0.87
sl11925		hypothetical protein	103.31	19.98	0	105.06	17.72	0.00	0.84	0.74	1.02	0.02
sl11926		hypothetical protein	204.30	46.40	0	101.45	27.68	0.00	0.00	0.00	0.50	-1.01
sl11927		ABC transporter ATP-	488.37	103.40	0	386.26	122.38	0.00	0.16	0.07	0.79	-0.34
sl11929	comE	competence protein C	178.21	20.51	0	192.17	25.30	0.00	0.33	0.18	1.08	0.11
sl11930		putative transposase [	408.30	59.39	0	842.80	180.09	0.00	0.00	0.00	2.06	1.05
sl11931	gylA	serine hydroxymethyltr	494.80	113.92	0	407.42	122.04	0.00	0.21	0.08	0.82	-0.28
sl11932	dnaK	DnaK protein	1232.39	126.08	0	1594.47	280.36	0.00	0.01	0.00	1.29	0.37

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sil1933	dnaJ	DnaJ protein	277.54	53.27	0	190.20	44.05	0.00	0.01	0.00	0.69	-0.55
sil1934		hypothetical protein	165.52	39.30	0	122.38	70.79	0.00	0.14	0.09	0.74	-0.44
sil1937		ferric uptake regulator	338.64	36.42	0	360.38	62.06	0.00	0.55	0.47	1.06	0.09
sil1938		hypothetical protein	145.25	23.47	0	67.39	9.55	0.00	0.00	0.00	0.46	-1.11
sil1939		unknown protein	220.76	54.86	0	144.85	38.42	0.00	0.02	0.00	0.66	-0.61
sil1940		hypothetical protein	111.83	18.40	0	114.09	23.70	0.00	0.90	0.87	1.02	0.03
sil1941	gyrA	DNA gyrase A subunit	124.56	18.35	0	146.36	14.72	0.00	0.05	0.00	1.17	0.23
sil1942		unknown protein	258.91	36.58	0	187.77	47.70	0.00	0.02	0.00	0.73	-0.46
sil1945		1-deoxyxylulose-5-pho	576.94	113.06	0	585.63	142.87	0.00	0.96	0.95	1.02	0.02
sil1946		hypothetical protein	120.67	27.28	0	183.16	68.07	0.00	0.05	0.01	1.52	0.60
sil1949		unknown protein	226.67	45.23	0	164.10	24.68	0.00	0.01	0.00	0.72	-0.47
sil1950		unknown protein	140.61	22.87	0	174.54	33.62	0.00	0.08	0.01	1.24	0.31
sil1951		unknown protein	2210.24	309.94	0	2478.82	347.41	0.00	0.19	0.04	1.12	0.17
sil1954		unknown protein	179.26	28.16	0	94.92	8.25	0.00	0.00	0.00	0.53	-0.92
sil1956		hypothetical protein	25.83	3.94	0	12.70	15.27	0.04	0.05	0.02	0.49	-1.02
sil1957		transcriptional regulat	116.22	21.43	0	128.08	26.78	0.00	0.44	0.28	1.10	0.14
sil1958	hisC	histidinol phosphate ar	198.56	25.88	0	266.34	35.33	0.00	0.00	0.00	1.34	0.42
sil1959		probable inositol monc	446.48	77.64	0	334.75	61.39	0.00	0.02	0.00	0.75	-0.42
sil1960		hypothetical protein	346.78	61.91	0	337.24	93.55	0.00	0.73	0.67	0.97	-0.04
sil1961		hypothetical protein	229.18	44.16	0	145.66	23.23	0.00	0.00	0.00	0.64	-0.65
sil1965		hypothetical protein	19.26	2.98	0	19.74	9.03	0.00	0.77	0.76	1.02	0.04
sil1967		probable RNA methyl	156.16	59.51	1.3E-10	148.25	54.42	0.00	0.85	0.77	0.95	-0.08
sil1968	pmgA	photomixotrophic grow	117.90	20.14	0	123.48	16.93	0.00	0.59	0.37	1.05	0.07
sil1969		hypothetical protein	133.11	24.07	0	76.48	25.89	0.00	0.00	0.00	0.57	-0.80
sil1971		probable hexosyltransi	108.72	9.65	0	93.20	12.68	0.00	0.03	0.00	0.86	-0.22
sil1973		hypothetical protein	174.04	42.84	0	175.17	29.03	0.00	0.87	0.75	1.01	0.01
sil1979		hypothetical protein	85.02	28.41	2.27E-13	62.70	40.35	0.00	0.22	0.15	0.74	-0.44
sil1980	trxA	thiol:disulfide interchar	160.08	27.61	0	174.23	40.11	0.00	0.51	0.38	1.09	0.12
sil1981	ilvB	acetolactate synthase	301.16	52.18	0	321.11	47.19	0.00	0.50	0.27	1.07	0.09
sil1982		putative transposase [	113.50	23.94	0	256.61	73.31	0.00	0.00	0.00	2.26	1.18
sil1983		putative transposase [	63.94	10.07	0	404.61	153.67	0.00	0.00	0.00	6.33	2.66
sil1984		putative transposase [	64.81	8.60	0	539.77	148.41	0.00	0.00	0.00	8.33	3.06
sil1985		putative transposase [	61.94	11.07	0	141.66	62.48	0.00	0.01	0.00	2.29	1.19
sil1987	cpx	catalase peroxidase	278.26	74.13	0	360.83	82.55	0.00	0.11	0.01	1.30	0.37
sil1988	hsp33	33 kDa chaperonin	164.13	71.72	2.07E-08	128.24	43.60	0.00	0.26	0.08	0.78	-0.36
sil1994	hemB	porphobilinogen synthe	176.53	18.71	0	229.47	33.41	0.00	0.00	0.00	1.30	0.38
sil1995		hypothetical protein	104.18	22.55	0	98.48	19.08	0.00	0.69	0.51	0.95	-0.08
sil1997		putative transposase [	316.04	54.50	0	521.79	145.23	0.00	0.00	0.00	1.65	0.72
sil1998		putative transposase [	126.57	27.13	0	888.25	272.80	0.00	0.00	0.00	7.02	2.81
sil1999		putative transposase [	21.49	2.47	0	223.09	102.84	0.00	0.00	0.00	10.38	3.38
sil2001		leucine aminopeptidas	160.78	23.97	0	176.21	17.23	0.00	0.20	0.01	1.10	0.13
sil2002		hypothetical protein	190.87	26.20	0	95.84	18.13	0.00	0.00	0.00	0.50	-0.99
sil2003		hypothetical protein	113.99	10.30	0	166.93	24.71	0.00	0.00	0.00	1.46	0.55
sil2005	gyrB	DNA gyrase B subunit	191.14	12.70	0	138.32	29.89	0.00	0.01	0.00	0.72	-0.47
sil2006		hypothetical protein	49.57	14.87	2.22E-16	16.43	14.88	0.01	0.07	0.04	0.33	-1.59
sil2007		hypothetical protein	21.46	4.00	0	14.36	15.42	0.02	0.09	0.06	0.67	-0.58
sil2008		processing protease	206.50	7.10	0	391.22	44.90	0.00	0.00	0.00	1.89	0.92
sil2009		processing protease	119.53	15.48	0	223.55	35.43	0.00	0.00	0.00	1.87	0.90
sil2010	murD	UDP-N-acetylmuramo	164.31	25.36	0	114.29	7.76	0.00	0.00	0.00	0.70	-0.52
sil2011		hypothetical protein	37.11	14.42	2.94E-10	20.41	16.46	0.00	0.13	0.09	0.55	-0.86
sil2012	sigD	group2 RNA polymera	144.86	17.87	0	118.86	24.42	0.00	0.05	0.01	0.82	-0.29
sil2013		hypothetical protein	146.40	40.80	0	71.29	30.84	0.00	0.00	0.00	0.49	-1.04
sil2014		sugar fermentation stii	71.90	11.57	0	60.06	34.12	0.00	0.29	0.26	0.84	-0.26
sil2015		hypothetical protein	84.27	10.14	0	62.39	21.85	0.00	0.07	0.03	0.74	-0.43
slr0001		hypothetical protein	312.18	58.71	0	374.29	71.51	0.00	0.10	0.01	1.20	0.26
slr0006		unknown protein	182.55	22.66	0	191.04	53.49	0.00	0.87	0.86	1.05	0.07
slr0007		probable sugar-phospl	135.51	11.23	0	113.44	11.40	0.00	0.01	0.00	0.84	-0.26
slr0008	ctpA	carboxyl-terminal proc	247.07	63.06	0	213.13	66.06	0.00	0.31	0.17	0.86	-0.21
slr0009	rbcl	ribulose bisphosphate	4094.37	724.27	0	3381.48	614.83	0.00	0.09	0.01	0.83	-0.28
slr0011	rbcX	hypothetical protein	528.98	147.28	0	476.52	123.10	0.00	0.62	0.46	0.90	-0.15
slr0012	rbcs	ribulose bisphosphate	1698.21	238.23	0	1280.82	140.41	0.00	0.00	0.00	0.75	-0.41
slr0013		hypothetical protein	79.53	13.50	0	71.42	27.82	0.00	0.38	0.32	0.90	-0.16
slr0014		Mg2+ transport ATPase	153.94	17.55	0	121.75	11.41	0.00	0.00	0.00	0.79	-0.34
slr0015		lipid A disaccharide sy	105.59	24.63	0	128.69	34.09	0.00	0.21	0.09	1.22	0.29
slr0016		hypothetical protein	42.52	2.87	0	43.69	9.13	0.00	0.90	0.89	1.03	0.04
slr0017	murZ	UDP-N-acetylglucosar	287.24	84.23	0	244.40	88.73	0.00	0.34	0.19	0.85	-0.23
slr0018		fumarase	132.88	11.43	0	107.03	10.38	0.00	0.00	0.00	0.81	-0.31
slr0019		unknown protein	154.22	25.25	0	111.40	30.36	0.00	0.02	0.00	0.72	-0.47
slr0020	recG	DNA recombinase	83.05	15.86	0	92.48	15.76	0.00	0.33	0.13	1.11	0.16
slr0021		protease	55.16	6.89	0	67.03	10.57	0.00	0.04	0.00	1.22	0.28
slr0022		hypothetical protein	24.18	4.30	0	9.97	11.50	0.03	0.04	0.02	0.41	-1.28
slr0023		unknown protein	37.51	9.23	0	38.41	19.04	0.00	0.70	0.68	1.02	0.03
slr0031		hypothetical protein	106.69	16.74	0	144.30	11.45	0.00	0.00	0.00	1.35	0.44
slr0032		probable branched-chi	144.66	20.37	0	227.25	17.38	0.00	0.00	0.00	1.57	0.65
slr0033		glutamyl-tRNA(Gln) an	42.70	6.74	0	81.82	16.10	0.00	0.00	0.00	1.92	0.94
slr0036	aspC	aspartate aminotransf	112.69	18.68	0	116.02	22.30	0.00	0.80	0.71	1.03	0.04
slr0038		hypothetical protein	40.42	6.63	0	51.07	24.88	0.00	0.57	0.54	1.26	0.34
slr0039		hypothetical protein	83.75	13.77	0	92.96	17.08	0.00	0.36	0.19	1.11	0.15

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

## Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0040	cmpA	bicarbonate transport	76.54	12.31	0	78.27	16.19	0.00	0.91	0.89	1.02	0.03
slr0041	cmpB	bicarbonate transport	80.43	19.09	0	49.89	26.75	0.00	0.03	0.01	0.62	-0.69
slr0042		probable porin; major c	346.00	62.31	0	246.87	63.72	0.00	0.02	0.00	0.71	-0.49
slr0043	cmpC	bicarbonate transport	822.22	208.78	0	845.26	254.83	0.00	0.89	0.86	1.03	0.04
slr0044	cmpD	bicarbonate transport	44.71	5.05	0	72.64	8.70	0.00	0.00	0.00	1.62	0.70
slr0049		hypothetical protein	177.84	17.44	0	233.86	15.43	0.00	0.00	0.00	1.31	0.40
slr0050	ycf56	hypothetical protein Yc	80.36	9.79	0	109.85	8.49	0.00	0.00	0.00	1.37	0.45
slr0051	ictA	carbonic anhydrase	95.05	19.22	0	121.13	28.28	0.00	0.09	0.01	1.27	0.35
slr0053		hypothetical protein	141.05	25.66	0	137.54	39.36	0.00	0.76	0.71	0.98	-0.04
slr0054		diacylglycerol kinase	58.43	8.13	0	37.83	21.55	0.00	0.05	0.02	0.65	-0.63
slr0055	trpG	anthranilate synthase	55.41	11.51	0	61.58	15.39	0.00	0.50	0.39	1.11	0.15
slr0056	chlG	chlorophyll a synthase	148.93	22.55	0	240.97	16.82	0.00	0.00	0.00	1.62	0.69
slr0058		hypothetical protein	98.20	21.10	0	70.01	4.43	0.00	0.01	0.00	0.71	-0.49
slr0059		unknown protein	65.52	9.34	0	43.38	13.70	0.00	0.02	0.00	0.66	-0.59
slr0060		unknown protein	51.47	5.52	0	55.48	7.58	0.00	0.35	0.21	1.08	0.11
slr0061		unknown protein	33.28	9.78	0	59.54	26.16	0.00	0.03	0.00	1.79	0.84
slr0063		general secretion path	325.55	49.32	0	343.04	54.12	0.00	0.58	0.43	1.05	0.08
slr0064		hypothetical protein	105.97	11.49	0	141.12	14.20	0.00	0.00	0.00	1.33	0.41
slr0065		hypothetical protein	97.71	9.61	0	86.26	18.41	0.00	0.16	0.10	0.88	-0.18
slr0066	ribD	riboflavin biosynthesis	82.91	16.18	0	86.33	17.91	0.00	0.77	0.68	1.04	0.06
slr0067		MRP protein homolog	387.67	35.09	0	311.17	16.23	0.00	0.00	0.00	0.80	-0.32
slr0069		unknown protein	38.97	5.89	0	27.84	18.95	0.00	0.13	0.09	0.71	-0.49
slr0070	fnt	methionyl-tRNA formyl	132.29	46.72	4.05E-12	106.76	21.25	0.00	0.39	0.06	0.81	-0.31
slr0072	gidB	glucose inhibited divisi	58.53	13.98	0	60.68	11.42	0.00	0.72	0.53	1.04	0.05
slr0073		two-component senso	339.71	30.58	0	303.15	21.73	0.00	0.04	0.00	0.89	-0.16
slr0074	ycf24	ABC transporter subu	229.48	44.73	0	352.53	74.34	0.00	0.00	0.00	1.54	0.62
slr0075	ycf16	ABC transporter ATP-	59.75	6.97	0	74.62	8.61	0.00	0.01	0.00	1.25	0.32
slr0076		hypothetical protein	100.63	21.59	0	181.47	37.44	0.00	0.00	0.00	1.80	0.85
slr0077	nifS	cysteine desulfurase	83.40	9.58	0	86.14	13.27	0.00	0.74	0.66	1.03	0.05
slr0078		putative G-pyruvoyl tet	56.05	8.85	0	26.04	16.48	0.00	0.01	0.00	0.46	-1.11
slr0079		probable general secr	308.49	27.43	0	292.48	38.40	0.00	0.39	0.28	0.95	-0.08
slr0080	mha	ribonuclease H	33.27	2.05	0	66.83	9.80	0.00	0.00	0.00	2.01	1.01
slr0081		two-component respon	366.98	39.41	0	223.22	25.50	0.00	0.00	0.00	0.61	-0.72
slr0082		hypothetical protein	183.35	27.11	0	306.02	122.54	0.00	0.02	0.00	1.67	0.74
slr0083	crhR	RNA helicase Light	881.59	181.56	0	1111.95	236.39	0.00	0.08	0.01	1.26	0.33
slr0084	hisH	amidotransferase His	66.53	20.87	5.77E-15	70.54	31.53	0.00	0.98	0.97	1.06	0.08
slr0086		similar to DnaK protei	207.40	50.55	0	161.33	35.46	0.00	0.11	0.01	0.78	-0.36
slr0088	crfO	beta-carotene ketolase	226.78	31.13	0	219.74	21.77	0.00	0.70	0.49	0.97	-0.05
slr0089		gamma-tocopherol me	144.29	22.45	0	60.89	9.41	0.00	0.00	0.00	0.42	-1.24
slr0090		probable 4-hydroxyph	63.98	14.86	0	43.74	16.25	0.00	0.05	0.01	0.68	-0.55
slr0091		aldehyde dehydrogen	152.02	34.84	0	152.21	58.48	0.00	0.83	0.80	1.00	0.00
slr0092		hypothetical protein	63.11	16.07	0	70.84	24.06	0.00	0.59	0.46	1.12	0.17
slr0093	dnaJ	DnaJ protein	106.88	17.11	0	203.79	38.03	0.00	0.00	0.00	1.91	0.93
slr0095		O-methyltransferase	143.21	23.05	0	75.54	7.88	0.00	0.00	0.00	0.53	-0.92
slr0096		low affinity sulfate tran	205.47	42.34	0	293.00	73.10	0.00	0.02	0.00	1.43	0.51
slr0099		putative transposase [	149.15	40.63	0	376.08	121.98	0.00	0.00	0.00	2.52	1.33
slr0103		unknown protein	83.93	16.03	0	67.46	20.05	0.00	0.12	0.05	0.80	-0.32
slr0104		hypothetical protein	197.57	26.18	0	134.02	15.88	0.00	0.00	0.00	0.68	-0.56
slr0105		hypothetical protein	60.41	8.27	0	84.62	33.49	0.00	0.18	0.13	1.40	0.49
slr0106		unknown protein	24.45	4.90	0	23.42	20.00	0.00	0.31	0.29	0.96	-0.06
slr0108		unknown protein	85.88	23.30	0	49.15	12.12	0.00	0.01	0.00	0.57	-0.81
slr0109		unknown protein	85.08	13.38	0	51.93	4.15	0.00	0.00	0.00	0.61	-0.71
slr0110		hypothetical protein	106.98	14.73	0	114.88	13.77	0.00	0.36	0.15	1.07	0.10
slr0111		unknown protein	31.09	5.67	0	20.84	14.12	0.00	0.13	0.09	0.66	-0.59
slr0112		unknown protein	61.51	12.94	0	86.90	14.83	0.00	0.01	0.00	1.41	0.50
slr0114		unknown protein	109.50	27.07	0	168.27	50.99	0.00	0.02	0.00	1.54	0.62
slr0115	rpaA	response regulator for	86.70	12.30	0	120.03	15.18	0.00	0.00	0.00	1.38	0.47
slr0116		phycocyanobilin:ferred	73.56	12.49	0	46.17	7.94	0.00	0.00	0.00	0.63	-0.67
slr0118	thiC	thiamine biosynthesis	418.13	52.24	0	392.55	58.60	0.00	0.42	0.27	0.94	-0.09
slr0119		hypothetical protein	25.05	4.29	0	53.91	15.25	0.00	0.00	0.00	2.15	1.11
slr0120		probable tRNA/rRNA t	112.68	30.60	0	138.49	26.06	0.00	0.12	0.00	1.23	0.30
slr0121		hypothetical protein	304.62	43.71	0	280.27	38.36	0.00	0.31	0.14	0.92	-0.12
slr0142		hypothetical protein	22.72	9.38	2.95E-09	27.34	10.16	0.00	0.43	0.24	1.20	0.27
slr0143		WD-repeat protein	169.39	53.34	7.33E-15	131.62	32.43	0.00	0.26	0.05	0.78	-0.36
slr0144		hypothetical protein	683.81	123.27	0	336.67	66.45	0.00	0.00	0.00	0.49	-1.02
slr0145		unknown protein	128.36	16.18	0	107.84	40.64	0.00	0.22	0.17	0.84	-0.25
slr0146		hypothetical protein	165.24	40.16	0	80.61	30.35	0.00	0.00	0.00	0.49	-1.04
slr0147		hypothetical protein	230.51	67.34	0	127.06	54.14	0.00	0.01	0.00	0.55	-0.86
slr0148		hypothetical protein	204.23	53.66	0	141.50	43.32	0.00	0.05	0.00	0.69	-0.53
slr0149		hypothetical protein	137.64	26.94	0	93.32	25.69	0.00	0.01	0.00	0.68	-0.56
slr0150		ferredoxin, petF-like pr	102.27	15.33	0	77.97	29.68	0.00	0.11	0.07	0.76	-0.39
slr0151		unknown protein	293.16	51.13	0	213.72	34.56	0.00	0.01	0.00	0.73	-0.46
slr0152		serine/threonine protei	143.88	26.01	0	126.43	27.69	0.00	0.27	0.11	0.88	-0.19
slr0156	clpB	ClpB protein	141.70	33.25	0	170.47	38.58	0.00	0.16	0.03	1.20	0.27
slr0157		unknown protein	11.00	2.63	0	17.95	10.84	0.00	0.68	0.67	1.63	0.71
slr0161	pilT	twitching motility prote	310.24	48.15	0	214.19	36.76	0.00	0.00	0.00	0.69	-0.53
slr0162	pilC	similar to fimbrial asse	85.86	22.22	0	74.68	26.42	0.00	0.40	0.27	0.87	-0.20
slr0163	pilC	similar to fimbrial asse	208.17	38.09	0	154.03	39.36	0.00	0.03	0.00	0.74	-0.43

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0164	clpP	ATP-dependent Clp pr	689.49	169.37	0	432.41	141.23	0.00	0.01	0.00	0.63	-0.67
slr0165	clpP	ATP-dependent Clp pr	347.53	37.56	0	290.61	27.24	0.00	0.01	0.00	0.84	-0.26
slr0166		putative transposase [	19.08	1.57	0	100.53	40.40	0.00	0.00	0.00	5.27	2.40
slr0168		unknown protein	218.00	28.20	0	206.82	27.44	0.00	0.50	0.33	0.95	-0.08
slr0169		hypothetical protein	169.58	21.58	0	145.67	10.45	0.00	0.04	0.00	0.86	-0.22
slr0171	ycf37	photosystem I assem	116.11	12.56	0	86.26	17.46	0.00	0.01	0.00	0.74	-0.43
slr0172		hypothetical protein	455.41	33.24	0	437.79	38.21	0.00	0.40	0.26	0.96	-0.06
slr0179		hypothetical protein	63.06	14.62	0	64.03	22.47	0.00	0.95	0.94	1.02	0.02
slr0180		putative transposase [	385.68	32.67	0	567.98	58.19	0.00	0.00	0.00	1.47	0.56
slr0181		hypothetical protein	151.56	35.06	0	116.47	34.01	0.00	0.10	0.02	0.77	-0.38
slr0184		unknown protein	42.22	8.12	0	23.99	14.96	0.00	0.06	0.03	0.57	-0.82
slr0185		orotate phosphoribosy	40.34	7.99	0	57.63	7.94	0.00	0.00	0.00	1.43	0.51
slr0186	leuA	2-isopropylmalate synt	948.18	97.23	0	643.09	119.62	0.00	0.00	0.00	0.68	-0.56
slr0191		similar to amidase enh	195.03	21.57	0	161.17	32.94	0.00	0.05	0.01	0.83	-0.28
slr0192		hypothetical protein	50.86	10.23	0	39.41	16.38	0.00	0.16	0.10	0.77	-0.37
slr0193		RNA-binding protein	273.60	71.53	0	275.00	67.84	0.00	0.96	0.94	1.01	0.01
slr0194	rpiA	ribose 5-phosphate isc	89.81	15.31	0	110.65	20.50	0.00	0.08	0.01	1.23	0.30
slr0195		hypothetical protein	44.55	9.76	0	42.46	17.67	0.00	0.63	0.56	0.95	-0.07
slr0196		unknown protein	17.51	4.75	0	12.98	4.66	0.00	0.12	0.04	0.74	-0.43
slr0197		hypothetical protein	202.39	40.27	0	167.12	22.78	0.00	0.11	0.00	0.83	-0.28
slr0199		hypothetical protein	103.08	12.82	0	88.10	28.80	0.00	0.26	0.21	0.85	-0.23
slr0201		heterodisulfide reduct	98.53	9.60	0	86.46	20.57	0.00	0.19	0.13	0.88	-0.19
slr0204	ycf83	hypothetical protein Yc	24.96	5.91	0	21.80	16.64	0.00	0.31	0.29	0.87	-0.19
slr0207		hypothetical protein	65.63	17.64	0	68.64	32.94	0.00	0.93	0.91	1.05	0.06
slr0208		hypothetical protein	71.80	11.25	0	104.26	9.72	0.00	0.00	0.00	1.45	0.54
slr0209		unknown protein	45.16	7.31	0	42.15	9.38	0.00	0.54	0.45	0.93	-0.10
slr0210		two-component senso	89.24	12.78	0	55.63	21.21	0.00	0.02	0.00	0.62	-0.68
slr0211		hypothetical protein	265.63	47.34	0	294.47	59.96	0.00	0.38	0.21	1.11	0.15
slr0212	metH	5-methyltetrahydrofola	261.90	48.49	0	229.67	75.29	0.00	0.34	0.27	0.88	-0.19
slr0213	guaA	GMP synthetase	409.96	78.16	0	347.65	74.85	0.00	0.15	0.04	0.85	-0.24
slr0214		cytosine-specific meth	36.64	3.14	0	52.90	13.76	0.00	0.01	0.00	1.44	0.53
slr0216	cobP	bifunctional cobalamin	63.39	11.80	0	34.95	12.45	0.00	0.00	0.00	0.55	-0.86
slr0217		hypothetical protein	113.07	23.44	0	100.01	19.68	0.00	0.32	0.14	0.88	-0.18
slr0220	glyS	glycyl-tRNA synthetasi	170.50	15.13	0	201.87	40.71	0.00	0.11	0.05	1.18	0.24
slr0222		two-component hybrid	214.10	44.43	0	180.28	58.40	0.00	0.25	0.15	0.84	-0.25
slr0224		similar to sterol C5-de	67.11	24.81	3.46E-11	26.47	17.26	0.00	0.02	0.00	0.39	-1.34
slr0226		unknown protein	329.75	61.33	0	253.14	25.95	0.00	0.02	0.00	0.77	-0.38
slr0228	ftsH	cell division protein Fts	685.80	174.39	0	979.29	353.02	0.00	0.08	0.02	1.43	0.51
slr0229		3-hydroxyisobutyrate c	119.67	9.14	0	71.42	7.30	0.00	0.00	0.00	0.60	-0.74
slr0230		putative transposase [	126.04	37.33	2.22E-16	884.84	183.00	0.00	0.00	0.00	7.02	2.81
slr0231		probable DNA-3-methy	10.25	3.35	6.17E-14	11.70	12.02	0.02	0.23	0.19	1.14	0.19
slr0232		hypothetical protein	55.53	8.84	0	61.15	10.34	0.00	0.33	0.16	1.10	0.14
slr0233	trxM1	thioredoxin M	107.35	23.93	0	26.68	8.45	0.00	0.00	0.00	0.25	-2.01
slr0236		similar to glutathione S	100.19	12.33	0	123.08	25.62	0.00	0.07	0.02	1.23	0.30
slr0237		glycogen operon prote	99.48	11.26	0	89.06	14.14	0.00	0.17	0.06	0.90	-0.16
slr0238		hypothetical protein	74.61	18.35	0	26.30	21.10	0.00	0.04	0.01	0.35	-1.50
slr0239	cobM	precormin-4 C11-methy	133.83	43.19	3.18E-14	120.60	42.21	0.00	0.53	0.37	0.90	-0.15
slr0240		transcriptional regulat	104.46	13.07	0	70.29	11.88	0.00	0.00	0.00	0.67	-0.57
slr0241		hypothetical protein	239.38	39.04	0	173.48	30.04	0.00	0.01	0.00	0.72	-0.46
slr0242		bacterioferritin comigr	81.32	10.55	0	91.11	23.36	0.00	0.44	0.37	1.12	0.16
slr0243		hypothetical protein	71.83	8.63	0	51.93	9.35	0.00	0.00	0.00	0.72	-0.47
slr0244		hypothetical protein	372.06	61.06	0	253.01	32.37	0.00	0.00	0.00	0.68	-0.56
slr0245		Histone deacetylase fe	103.17	17.73	0	108.35	26.84	0.00	0.80	0.76	1.05	0.07
slr0249		hypothetical protein	29.47	6.97	0	42.94	7.58	0.00	0.01	0.00	1.46	0.54
slr0250		hypothetical protein	388.91	63.63	0	428.51	74.81	0.00	0.36	0.19	1.10	0.14
slr0251	ycf85	ATP-binding protein of	1089.41	124.09	0	1036.12	171.79	0.00	0.49	0.37	0.95	-0.07
slr0252		probable precormin-6x i	67.10	20.66	1.78E-15	34.36	27.32	0.00	0.12	0.08	0.51	-0.97
slr0254		hypothetical protein	53.01	12.59	0	85.37	9.04	0.00	0.00	0.00	1.61	0.69
slr0257	clpB	carboxyl-terminal prote	250.95	31.27	0	235.03	27.72	0.00	0.38	0.18	0.94	-0.09
slr0260	cobO	cob(I)alamin adenosyl	97.72	8.71	0	115.41	17.21	0.00	0.05	0.01	1.18	0.24
slr0261	ndhH	NADH dehydrogenase	462.33	90.04	0	577.62	88.59	0.00	0.04	0.00	1.25	0.32
slr0262		unknown protein	61.48	5.31	0	54.14	16.65	0.00	0.24	0.19	0.88	-0.18
slr0263		hypothetical protein	105.35	26.16	0	73.92	44.78	0.00	0.14	0.10	0.70	-0.51
slr0264		hypothetical protein	163.65	13.20	0	149.34	20.62	0.00	0.18	0.10	0.91	-0.13
slr0265		putative transposase [	112.28	12.45	0	654.21	216.89	0.00	0.00	0.00	5.83	2.54
slr0267		hypothetical protein	67.90	11.27	0	68.45	24.76	0.00	0.85	0.83	1.01	0.01
slr0269		hypothetical protein	56.88	17.35	8.88E-16	70.64	13.87	0.00	0.14	0.00	1.24	0.31
slr0270		hypothetical protein	45.21	9.19	0	29.79	15.63	0.00	0.12	0.08	0.66	-0.60
slr0271		unknown protein	22.81	8.26	1.35E-11	8.49	8.11	0.01	0.07	0.04	0.37	-1.43
slr0272		unknown protein	160.14	25.67	0	80.66	7.17	0.00	0.00	0.00	0.50	-0.99
slr0273		unknown protein	84.78	25.84	8.88E-16	67.51	24.40	0.00	0.28	0.15	0.80	-0.33
slr0280		hypothetical protein	323.87	69.93	0	364.97	19.78	0.00	0.16	0.00	1.13	0.17
slr0284		hypothetical protein	115.64	16.35	0	74.82	38.41	0.00	0.07	0.04	0.65	-0.63
slr0285		hypothetical protein	14.24	4.51	9.77E-15	22.62	12.46	0.00	0.35	0.27	1.59	0.67
slr0286		unknown protein	21.87	6.47	2.22E-16	11.60	12.36	0.02	0.09	0.06	0.53	-0.92
slr0287		hypothetical protein	157.24	15.23	0	142.59	24.55	0.00	0.23	0.14	0.91	-0.14
slr0288	glnN	glutamate-ammonia li	158.15	25.43	0	133.97	30.43	0.00	0.21	0.10	0.85	-0.24
slr0291		hypothetical protein	25.37	5.25	0	24.70	4.77	0.00	0.81	0.74	0.97	-0.04

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0292		hypothetical protein	94.05	18.48	0	103.59	26.13	0.00	0.19	0.06	1.23	0.30
slr0293		glycine dehydrogenas	254.04	39.95	0	222.69	38.99	0.00	0.21	0.07	0.88	-0.19
slr0294		unknown protein	28.06	10.30	2.52E-11	14.57	9.72	0.00	0.06	0.03	0.52	-0.95
slr0298		FraH protein homolog	131.14	13.17	0	91.35	9.61	0.00	0.00	0.00	0.70	-0.52
slr0299		hypothetical protein	41.94	6.79	0	25.63	4.56	0.00	0.00	0.00	0.61	-0.71
slr0300		hypothetical protein	48.50	12.03	0	27.18	15.31	0.00	0.06	0.03	0.56	-0.84
slr0301		phosphoenolpyruvate	104.41	23.06	0	54.83	13.93	0.00	0.00	0.00	0.53	-0.93
slr0302		unknown protein	117.31	10.62	0	175.64	29.35	0.00	0.00	0.00	1.50	0.58
slr0303		hypothetical protein	46.54	4.99	0	107.89	36.77	0.00	0.00	0.00	2.32	1.21
slr0304		hypothetical protein	42.08	7.63	0	37.17	13.14	0.00	0.41	0.36	0.88	-0.18
slr0305		hypothetical protein	18.83	6.39	5.37E-13	23.13	16.38	0.00	0.50	0.48	1.23	0.30
slr0306		unknown protein	98.12	14.28	0	153.30	32.47	0.00	0.00	0.00	1.56	0.64
slr0309		probable methyltransf	204.75	30.03	0	143.96	31.17	0.00	0.01	0.00	0.70	-0.51
slr0311		two-component senso	392.37	46.29	0	359.58	52.17	0.00	0.26	0.12	0.92	-0.13
slr0312		two-component respor	305.28	80.44	0	263.29	72.84	0.00	0.30	0.13	0.86	-0.21
slr0313		hypothetical protein	11.93	3.56	2.22E-16	3.35	5.15	0.11	0.01	0.00	0.28	-1.83
slr0314		non-heme chloroperox	14.39	3.41	0	37.32	16.63	0.00	0.01	0.00	2.59	1.38
slr0315		probable oxidoreducta	145.09	42.02	0	31.21	23.26	0.00	0.03	0.01	0.22	-2.22
slr0316		hypothetical protein	31.87	6.58	0	26.77	10.46	0.00	0.27	0.20	0.84	-0.25
slr0317		hypothetical protein	16.50	1.80	0	24.52	15.14	0.00	0.67	0.66	1.49	0.57
slr0318		unknown protein	37.21	6.63	0	34.15	11.27	0.00	0.48	0.41	0.92	-0.12
slr0319		beta-lactamase	59.77	9.23	0	131.18	41.36	0.00	0.00	0.00	2.19	1.13
slr0320		hypothetical protein	182.70	51.07	0	152.75	36.28	0.00	0.32	0.12	0.84	-0.26
slr0321		GTP-binding protein E	191.95	82.23	1.08E-08	288.72	121.93	0.00	0.16	0.04	1.50	0.59
slr0322		two-component hybrid	450.37	45.13	0	369.22	38.98	0.00	0.01	0.00	0.82	-0.29
slr0323		putative alpha-manno	110.96	22.51	0	77.90	19.46	0.00	0.02	0.00	0.70	-0.51
slr0324		probable oligopeptid	102.34	14.49	0	109.82	28.56	0.00	0.72	0.68	1.07	0.10
slr0325		hypothetical protein	19.55	3.00	0	26.38	13.56	0.00	0.80	0.79	1.35	0.43
slr0326		hypothetical protein	69.45	6.23	0	64.08	10.97	0.00	0.29	0.20	0.92	-0.12
slr0327		iron(III) ABC transport	179.71	25.62	0	264.88	42.22	0.00	0.00	0.00	1.47	0.56
slr0328		low molecular weight p	1915.36	367.63	0	2170.46	309.44	0.00	0.20	0.02	1.13	0.18
slr0329		glucokinase	353.98	40.23	0	250.23	30.35	0.00	0.00	0.00	0.71	-0.50
slr0331	ndhD1	NADH dehydrogenase	550.99	87.20	0	424.60	63.90	0.00	0.02	0.00	0.77	-0.38
slr0333		unknown protein	90.82	12.02	0	18.56	14.68	0.00	0.04	0.02	0.20	-2.29
slr0334		unknown protein	49.10	10.86	0	11.61	10.66	0.01	0.04	0.02	0.24	-2.08
slr0335	apcE	phycobilisome core-me	1510.16	146.13	0	1644.89	374.89	0.00	0.49	0.43	1.09	0.12
slr0337		hypothetical protein	144.81	11.53	0	145.89	15.45	0.00	0.92	0.90	1.01	0.01
slr0338		probable oxidoreducta	278.11	48.56	0	299.11	41.37	0.00	0.43	0.18	1.08	0.11
slr0341		unknown protein	155.67	14.53	0	97.24	20.86	0.00	0.00	0.00	0.62	-0.68
slr0342	petB	cytochrome b6	918.07	121.32	0	1030.25	293.68	0.00	0.48	0.40	1.12	0.17
slr0343	petD	cytochrome b6-f comp	1309.73	355.42	0	1212.94	209.78	0.00	0.65	0.41	0.93	-0.11
slr0344		probable glycosyltrans	56.34	8.85	0	29.05	16.64	0.00	0.05	0.02	0.52	-0.96
slr0345		unknown protein	74.80	8.34	0	77.81	18.07	0.00	0.84	0.82	1.04	0.06
slr0346	rc	ribonuclease III	46.77	11.57	0	110.25	19.52	0.00	0.00	0.00	2.36	1.24
slr0347		probable permease pn	49.78	18.02	1.3E-11	80.21	42.69	0.00	0.26	0.18	1.61	0.69
slr0348		hypothetical protein	163.79	15.27	0	175.48	9.64	0.00	0.14	0.00	1.07	0.10
slr0350		putative transposase [	102.37	16.00	0	485.16	210.97	0.00	0.00	0.00	4.74	2.24
slr0351		hypothetical protein	198.92	26.78	0	179.42	38.93	0.00	0.31	0.21	0.90	-0.15
slr0352		putative transposase [	98.45	15.23	0	614.92	207.62	0.00	0.00	0.00	6.25	2.64
slr0353		unknown protein	59.15	11.77	0	52.62	21.54	0.00	0.41	0.35	0.89	-0.17
slr0354		ATP-binding protein of	63.48	11.22	0	59.97	18.85	0.00	0.56	0.51	0.94	-0.08
slr0355		hypothetical protein	224.25	16.47	0	158.10	13.03	0.00	0.00	0.00	0.71	-0.50
slr0356		hypothetical protein	66.53	15.88	0	60.36	19.60	0.00	0.48	0.38	0.91	-0.14
slr0357	hisS	histidyl-tRNA syntheta	119.37	36.55	1.33E-15	147.47	18.13	0.00	0.10	0.00	1.24	0.30
slr0358		unknown protein	230.06	38.73	0	251.57	60.21	0.00	0.57	0.48	1.09	0.13
slr0359		hypothetical protein	170.29	16.92	0	175.44	44.28	0.00	0.96	0.96	1.03	0.04
slr0360		hypothetical protein	179.90	29.89	0	168.84	18.82	0.00	0.50	0.21	0.94	-0.09
slr0361		probable ribosomal lar	26.82	7.59	0	12.70	12.09	0.01	0.05	0.02	0.47	-1.08
slr0362		hypothetical protein	90.91	9.89	0	111.21	30.93	0.00	0.16	0.10	1.22	0.29
slr0363		hypothetical protein	97.81	3.51	0	69.52	13.35	0.00	0.00	0.00	0.71	-0.49
slr0364		hypothetical protein	156.39	52.35	2.53E-13	105.97	25.25	0.00	0.07	0.00	0.68	-0.56
slr0366		unknown protein	84.96	16.77	0	104.42	11.23	0.00	0.03	0.00	1.23	0.30
slr0369		RND multidrug efflux ti	878.31	217.50	0	766.97	259.58	0.00	0.34	0.21	0.87	-0.20
slr0370		succinate-semialdehyc	211.03	28.17	0	266.01	56.21	0.00	0.05	0.01	1.26	0.33
slr0373		hypothetical protein	870.87	190.27	0	470.21	68.68	0.00	0.00	0.00	0.54	-0.89
slr0374		hypothetical protein	1138.01	129.62	0	706.64	152.74	0.00	0.00	0.00	0.62	-0.69
slr0376		hypothetical protein	500.97	232.23	1.26E-07	239.54	128.38	0.00	0.02	0.00	0.48	-1.06
slr0377		unknown protein	158.69	22.00	0	132.44	21.92	0.00	0.07	0.01	0.83	-0.26
slr0378		similar to 7-beta-(4-cal	296.25	36.82	0	311.28	22.81	0.00	0.38	0.06	1.05	0.07
slr0379		thymidylate kinase	82.25	12.66	0	111.32	45.66	0.00	0.11	0.05	1.35	0.44
slr0380		hypothetical protein	148.01	42.76	0	191.64	31.64	0.00	0.08	0.00	1.29	0.37
slr0381		lactoylglutathione lyas	145.63	30.80	0	154.47	52.65	0.00	0.88	0.85	1.06	0.08
slr0383		hypothetical protein	48.21	4.51	0	58.99	16.42	0.00	0.19	0.14	1.22	0.29
slr0384		sulfolipid sulfoquinov	137.66	23.57	0	183.71	23.75	0.00	0.01	0.00	1.33	0.42
slr0386		unknown protein	60.32	3.58	0	71.69	17.33	0.00	0.14	0.09	1.19	0.25
slr0387	nifS	cysteine desulfurase N	97.83	14.31	0	102.53	18.34	0.00	0.68	0.59	1.05	0.07
slr0388		hypothetical protein	68.92	29.61	1.18E-08	65.06	29.45	0.00	0.79	0.71	0.94	-0.08
slr0392		unknown protein	7.58	1.44	0	2.13	2.93	0.08	0.02	0.00	0.28	-1.83

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0393		unknown protein	1.76	1.60	0.00707	4.83	3.67	0.00	0.41	0.20	2.75	1.46
slr0394	pgk	phosphoglycerate kina	429.81	135.86	9.33E-15	786.00	228.10	0.00	0.00	0.00	1.83	0.87
slr0395	ntcB	nitrate assimilation tra	38.92	6.48	0	38.66	9.20	0.00	0.86	0.83	0.99	-0.01
slr0397		hypothetical protein	36.65	8.36	0	28.34	15.12	0.00	0.32	0.29	0.77	-0.37
slr0398		unknown protein	67.65	12.86	0	89.58	7.96	0.00	0.01	0.00	1.32	0.41
slr0399	ycf39	chaperon-like protein f	130.96	11.90	0	149.66	20.76	0.00	0.09	0.03	1.14	0.19
slr0400		hypothetical protein	122.65	17.60	0	124.86	26.56	0.00	0.93	0.92	1.02	0.03
slr0401		periplasmic polyamine	98.29	22.00	0	90.18	21.56	0.00	0.55	0.39	0.92	-0.12
slr0402		hypothetical protein	24.27	2.94	0	14.61	16.02	0.03	0.14	0.11	0.60	-0.73
slr0404		hypothetical protein	259.25	74.47	0	398.17	114.66	0.00	0.05	0.00	1.54	0.62
slr0406	pyrC	dihydroorotase	68.77	12.48	0	62.24	22.29	0.00	0.41	0.32	0.90	-0.14
slr0407		hypothetical protein	58.90	11.49	0	64.91	9.08	0.00	0.29	0.07	1.10	0.14
slr0408		unknown protein	181.97	23.98	0	155.08	24.21	0.00	0.08	0.01	0.85	-0.23
slr0415	nhaS5	Na <sup>+</sup> /H <sup>+</sup> antiporter	244.40	21.90	0	299.60	17.43	0.00	0.00	0.00	1.23	0.29
slr0416		unknown protein	35.43	6.76	0	18.45	6.28	0.00	0.01	0.00	0.52	-0.94
slr0417	gyrA	DNA gyrase A subunit	290.73	45.41	0	247.01	39.34	0.00	0.11	0.02	0.85	-0.24
slr0418		putative transcripton f	105.89	36.93	2.15E-12	87.84	35.85	0.00	0.42	0.22	0.83	-0.27
slr0420		hypothetical protein	129.57	24.73	0	125.42	21.92	0.00	0.80	0.69	0.97	-0.05
slr0421		unknown protein	33.52	3.31	0	20.10	14.08	0.00	0.21	0.18	0.60	-0.74
slr0423		hypothetical protein	127.38	19.10	0	166.57	34.90	0.00	0.03	0.00	1.31	0.39
slr0426	folE	GTP cyclohydrolase I	125.47	27.15	0	111.94	16.04	0.00	0.35	0.08	0.89	-0.16
slr0427		putative competence-c	103.62	13.99	0	82.56	7.40	0.00	0.01	0.00	0.80	-0.33
slr0431		hypothetical protein	166.16	26.69	0	135.78	19.27	0.00	0.04	0.00	0.82	-0.29
slr0434	efp	elongation factor P	493.89	31.55	0	422.75	53.81	0.00	0.02	0.00	0.86	-0.22
slr0435	accB	biotin carboxyl carrier	103.62	6.49	0	75.55	17.80	0.00	0.01	0.00	0.73	-0.46
slr0436	ccmK	carbon dioxide concen	144.34	22.64	0	135.14	13.48	0.00	0.49	0.15	0.94	-0.09
slr0438		hypothetical protein	58.35	10.86	0	54.61	15.09	0.00	0.54	0.46	0.94	-0.10
slr0439		unknown protein	197.13	27.26	0	155.65	39.91	0.00	0.07	0.02	0.79	-0.34
slr0440		hypothetical protein	85.38	13.05	0	52.86	22.73	0.00	0.01	0.00	0.62	-0.69
slr0442		unknown protein	494.54	151.57	1.33E-15	840.66	411.80	0.00	0.07	0.02	1.70	0.77
slr0443		hypothetical protein	402.19	125.65	4.44E-15	500.98	123.55	0.00	0.18	0.03	1.25	0.32
slr0444	aroA	3-phosphoshikimate 1-	107.96	37.33	1.4E-12	117.91	21.30	0.00	0.48	0.08	1.09	0.13
slr0445		hypothetical protein	99.59	13.73	0	83.92	13.90	0.00	0.07	0.01	0.84	-0.25
slr0446	dnaX	DNA polymerase III de	100.58	9.05	0	85.82	27.51	0.00	0.16	0.11	0.85	-0.23
slr0447		substrate-binding prot	1440.43	124.95	0	601.17	202.48	0.00	0.00	0.00	0.42	-1.26
slr0448	radA	DNA repair protein Ra	904.30	159.80	0	1006.88	105.05	0.00	0.19	0.01	1.11	0.16
slr0449		probable transcription	54.87	6.77	0	59.34	9.23	0.00	0.39	0.23	1.08	0.11
slr0451		putative helicase	312.70	78.10	0	395.79	138.91	0.00	0.24	0.13	1.27	0.34
slr0452	ilvD	dihydroxyacid dehydra	547.80	56.10	0	541.10	42.43	0.00	0.84	0.74	0.99	-0.02
slr0453		hypothetical protein	306.79	38.86	0	209.21	24.96	0.00	0.00	0.00	0.68	-0.55
slr0454		RND multidrug efflux t	290.14	81.36	0	240.36	74.18	0.00	0.34	0.16	0.83	-0.27
slr0455		hypothetical protein	50.56	12.63	0	63.30	27.93	0.00	0.56	0.49	1.25	0.32
slr0456		unknown protein	78.99	16.09	0	105.11	31.81	0.00	0.12	0.04	1.33	0.41
slr0457		tRNA pseudouridine s	47.68	7.13	0	83.78	18.40	0.00	0.00	0.00	1.76	0.81
slr0458		unknown protein	34.75	9.01	0	75.17	18.52	0.00	0.00	0.00	2.16	1.11
slr0459		hypothetical protein	91.32	11.86	0	109.65	15.48	0.00	0.05	0.00	1.20	0.26
slr0460		putative transposase [	903.99	196.80	0	1049.59	213.92	0.00	0.21	0.05	1.16	0.22
slr0462		putative transposase [	73.90	21.20	0	305.18	99.37	0.00	0.00	0.00	4.13	2.05
slr0467	nata	conserved component	209.06	19.61	0	116.18	26.88	0.00	0.00	0.00	0.56	-0.85
slr0468		unknown protein	81.69	14.54	0	50.14	9.25	0.00	0.00	0.00	0.61	-0.70
slr0469	rps4	30S ribosomal protein	284.23	75.01	0	323.73	140.17	0.00	0.74	0.70	1.14	0.19
slr0473	phy	phytochrome	363.62	36.49	0	417.28	69.28	0.00	0.12	0.05	1.15	0.20
slr0474		two-component respor	77.66	15.36	0	54.01	14.28	0.00	0.02	0.00	0.70	-0.52
slr0476		unknown protein	470.46	120.94	0	284.20	90.88	0.00	0.01	0.00	0.60	-0.73
slr0477	purN	phosphoribosylglycina	162.04	45.05	0	90.74	12.94	0.00	0.00	0.00	0.56	-0.84
slr0479		hypothetical protein	93.17	11.48	0	69.94	14.15	0.00	0.01	0.00	0.75	-0.41
slr0480	ycf46	hypothetical protein Yf	148.52	22.72	0	109.22	8.75	0.00	0.00	0.00	0.74	-0.44
slr0482		unknown protein	90.73	11.22	0	107.17	21.58	0.00	0.13	0.05	1.18	0.24
slr0483		hypothetical protein	489.95	161.83	1.21E-13	730.75	319.56	0.00	0.15	0.06	1.49	0.58
slr0484		two-component senso	319.33	46.94	0	242.27	12.15	0.00	0.00	0.00	0.76	-0.40
slr0487		hypothetical protein	43.38	7.19	0	17.21	9.13	0.00	0.00	0.00	0.40	-1.33
slr0488		virulence factor MviN I	211.43	47.89	0	156.69	33.83	0.00	0.05	0.00	0.74	-0.43
slr0489		unknown protein	137.92	16.82	0	68.48	20.57	0.00	0.00	0.00	0.50	-1.01
slr0491		hypothetical protein	26.26	2.55	0	17.38	12.39	0.00	0.23	0.20	0.66	-0.60
slr0492	menE	O-succinylbenzoic acil	160.70	44.51	0	200.08	37.48	0.00	0.12	0.00	1.25	0.32
slr0493		similar to mannose-1- $\alpha$	40.17	3.58	0	16.73	12.18	0.00	0.01	0.00	0.42	-1.26
slr0495		HetI protein homolog	37.73	18.37	4.9E-07	52.20	29.73	0.00	0.63	0.57	1.38	0.47
slr0496		unknown protein	9.55	1.75	0	7.36	12.02	0.13	0.06	0.03	0.77	-0.38
slr0498		unknown protein	58.76	7.34	0	42.07	22.08	0.00	0.12	0.09	0.72	-0.48
slr0500	hisB	imidazoleglycerol-phos	125.75	19.93	0	113.58	21.68	0.00	0.32	0.18	0.90	-0.15
slr0502	cobW	cobalamin synthesis p	122.67	16.56	0	96.51	25.46	0.00	0.06	0.02	0.79	-0.35
slr0503	ycf66	hypothetical protein Yf	278.64	31.29	0	266.92	51.23	0.00	0.57	0.49	0.96	-0.06
slr0505		hypothetical protein	26.51	6.38	0	23.48	9.59	0.00	0.44	0.37	0.89	-0.18
slr0506	por	light-dependent NADP	270.18	57.61	0	243.08	43.55	0.00	0.41	0.17	0.90	-0.15
slr0509		hypothetical protein	23.54	4.81	0	35.96	8.74	0.00	0.01	0.00	1.53	0.61
slr0510		hypothetical protein	25.34	2.92	0	61.05	24.90	0.00	0.00	0.00	2.41	1.27
slr0511		putative transposase [	90.24	11.25	0	449.75	180.43	0.00	0.00	0.00	4.98	2.32
slr0513		periplasmic iron-bindin	420.30	67.55	0	303.83	72.63	0.00	0.02	0.00	0.72	-0.47

Table A-1 Gene expression profiles for *Synechocytis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sr0514		unknown protein	135.64	23.82	0	45.99	13.85	0.00	0.00	0.00	0.34	-1.56
sr0516		hypothetical protein	51.07	8.11	0	61.61	3.50	0.00	0.02	0.00	1.21	0.27
sr0517		hypothetical protein	37.38	8.92	0	28.22	11.14	0.00	0.13	0.06	0.75	-0.41
sr0518		similar to alpha-L-arab	41.15	11.30	0	10.43	12.09	0.03	0.02	0.01	0.25	-1.98
sr0519		hypothetical protein	42.04	5.20	0	29.95	17.02	0.00	0.10	0.07	0.71	-0.49
sr0520	purL	phosphoribosyl formylt	47.82	4.77	0	75.77	12.92	0.00	0.00	0.00	1.58	0.66
sr0521		unknown protein	59.90	10.99	0	81.83	21.11	0.00	0.05	0.00	1.37	0.45
sr0522		unknown protein	18.14	3.50	0	15.94	14.32	0.01	0.19	0.16	0.88	-0.19
sr0523		similar to dethiobiotin t	53.04	13.42	0	56.56	15.60	0.00	0.68	0.52	1.07	0.09
sr0525	chlM	Mg-protoporphyrin IX i	163.40	37.05	0	223.80	57.32	0.00	0.07	0.00	1.37	0.45
sr0526	panB	3-methyl-2-oxobutanon	93.91	28.67	1.11E-15	107.50	23.83	0.00	0.34	0.09	1.14	0.19
sr0527		transcription regulator	84.90	26.39	3.33E-15	52.22	13.32	0.00	0.02	0.00	0.62	-0.70
sr0528	murE	UDP-N-acetylmuramo	229.42	46.92	0	172.53	68.28	0.00	0.07	0.02	0.75	-0.41
sr0529	gggB	glucosylglycerol trans	89.10	31.07	2.13E-12	156.76	22.72	0.00	0.00	0.00	1.76	0.81
sr0530	gggC	glucosylglycerol trans	27.28	6.48	0	77.00	13.96	0.00	0.00	0.00	2.82	1.50
sr0531	gggD	glucosylglycerol trans	70.04	11.57	0	82.78	21.06	0.00	0.31	0.22	1.18	0.24
sr0533		two-component senso	1034.94	163.52	0	1007.18	227.83	0.00	0.73	0.67	0.97	-0.04
sr0534		probable transglycosyl	187.41	37.09	0	129.58	38.61	0.00	0.03	0.00	0.69	-0.53
sr0535		protease	407.88	55.37	0	375.42	79.27	0.00	0.42	0.34	0.92	-0.12
sr0536	hemE	uroporphyrinogen deca	151.24	18.90	0	169.18	34.17	0.00	0.35	0.25	1.12	0.16
sr0537		putative sugar kinase	184.30	42.41	0	240.61	73.86	0.00	0.23	0.11	1.31	0.38
sr0541		probable amidotransfe	40.46	3.03	0	50.53	10.00	0.00	0.04	0.01	1.25	0.32
sr0542	clpP	ATP-dependent prote	164.44	43.71	0	147.97	24.53	0.00	0.55	0.22	0.90	-0.15
sr0543	trpB	tryptophan synthase b	274.57	26.82	0	228.61	21.18	0.00	0.01	0.00	0.83	-0.26
sr0544		ATP-binding protein of	97.41	8.54	0	125.23	21.09	0.00	0.01	0.00	1.29	0.36
sr0545		hypothetical protein	64.14	8.21	0	69.26	16.47	0.00	0.67	0.63	1.08	0.11
sr0546	trpC	indole-3-glycerol phos	199.94	41.17	0	166.22	32.43	0.00	0.11	0.01	0.83	-0.27
sr0549	asd	aspartate beta-semialk	86.46	9.94	0	145.01	10.75	0.00	0.00	0.00	1.68	0.75
sr0550	dapA	dihydrodipicolinate syr	132.00	11.69	0	161.74	31.94	0.00	0.05	0.01	1.23	0.29
sr0551		hypothetical protein	563.34	90.01	0	725.97	174.09	0.00	0.05	0.01	1.29	0.37
sr0552		hypothetical protein	124.63	38.83	3.77E-15	168.42	63.34	0.00	0.22	0.08	1.35	0.43
sr0553		hypothetical protein	59.16	7.40	0	56.64	12.01	0.00	0.59	0.51	0.96	-0.06
sr0554		hypothetical protein	286.43	45.91	0	684.25	182.17	0.00	0.00	0.00	2.39	1.26
sr0556		hypothetical protein	46.31	7.97	0	41.53	10.48	0.00	0.38	0.25	0.90	-0.16
sr0557	valS	valyl-tRNA synthetase	223.20	25.28	0	303.64	35.60	0.00	0.00	0.00	1.36	0.44
sr0559	natB	penicillins binding pr	353.30	26.57	0	469.57	61.49	0.00	0.00	0.00	1.33	0.41
sr0565		hypothetical protein	193.24	35.42	0	242.56	44.72	0.00	0.05	0.00	1.26	0.33
sr0569		unknown protein	293.94	49.06	0	422.96	109.58	0.00	0.02	0.00	1.44	0.52
sr0572		unknown protein	108.35	23.72	0	37.38	20.70	0.00	0.01	0.00	0.34	-1.54
sr0573		unknown protein	21.99	5.35	0	7.02	8.93	0.05	0.03	0.01	0.32	-1.65
sr0574		cytochrome P450	1238.12	361.62	0	1681.02	344.74	0.00	0.04	0.00	1.36	0.44
sr0575		hypothetical protein	96.37	8.39	0	81.11	13.34	0.00	0.03	0.01	0.84	-0.25
sr0579		unknown protein	59.60	11.61	0	63.61	16.38	0.00	0.68	0.60	1.07	0.09
sr0580		aluminum resistance p	376.50	53.34	0	313.99	63.35	0.00	0.12	0.04	0.83	-0.26
sr0581		unknown protein	60.87	7.10	0	85.68	31.19	0.00	0.07	0.03	1.41	0.49
sr0582		unknown protein	74.97	24.03	2.13E-14	90.22	24.92	0.00	0.29	0.11	1.20	0.27
sr0583		similar to GDP-fucose	118.21	13.73	0	110.58	17.34	0.00	0.40	0.28	0.94	-0.10
sr0585	argG	argininosuccinate synt	219.15	53.46	0	275.58	83.68	0.00	0.23	0.09	1.26	0.33
sr0586		hypothetical protein	86.07	10.89	0	57.56	10.47	0.00	0.00	0.00	0.67	-0.58
sr0587		unknown protein	153.41	23.85	0	105.28	28.89	0.00	0.02	0.00	0.69	-0.54
sr0588		hypothetical protein	86.56	23.90	0	46.86	37.99	0.00	0.16	0.13	0.54	-0.89
sr0589		hypothetical protein	32.29	5.64	0	67.96	7.56	0.00	0.00	0.00	2.10	1.07
sr0590		hypothetical protein	38.84	7.01	0	115.71	32.08	0.00	0.00	0.00	2.98	1.57
sr0591		ribonucleoside-diphos	247.11	59.87	0	142.99	34.10	0.00	0.00	0.00	0.58	-0.79
sr0592		hypothetical protein	232.68	6.35	0	236.12	32.82	0.00	0.89	0.89	1.01	0.02
sr0593	samp	cAMP binding membr	129.19	6.45	0	134.21	11.20	0.00	0.39	0.30	1.04	0.05
sr0594		hypothetical protein	158.72	67.08	6.81E-09	132.43	37.02	0.00	0.63	0.33	0.83	-0.26
sr0596		hypothetical protein	114.45	17.14	0	98.76	21.47	0.00	0.17	0.07	0.86	-0.21
sr0597	purH	phosphoribosyl aminoi	215.36	31.52	0	260.29	44.45	0.00	0.06	0.00	1.21	0.27
sr0598		hypothetical protein	123.68	22.25	0	84.77	26.12	0.00	0.02	0.00	0.69	-0.54
sr0599		serine/threonine kinas	315.86	37.51	0	342.52	71.41	0.00	0.47	0.37	1.08	0.12
sr0600		NADP-thioredoxin red	118.22	16.16	0	118.13	28.55	0.00	0.88	0.86	1.00	0.00
sr0601		unknown protein	57.36	8.02	0	77.08	25.69	0.00	0.15	0.09	1.34	0.43
sr0602		unknown protein	29.21	5.61	0	17.93	19.38	0.02	0.11	0.08	0.61	-0.70
sr0603	dnaE	DNA polymerase III al	164.61	14.89	0	123.72	13.17	0.00	0.00	0.00	0.75	-0.41
sr0604		GTP-binding protein	335.79	40.09	0	434.52	45.47	0.00	0.00	0.00	1.29	0.37
sr0605		hypothetical protein	65.61	9.24	0	78.75	9.54	0.00	0.03	0.00	1.20	0.26
sr0606		hypothetical protein	115.35	22.11	0	137.46	20.50	0.00	0.12	0.00	1.19	0.25
sr0607		hypothetical protein	193.12	41.48	0	200.19	51.28	0.00	0.85	0.80	1.04	0.05
sr0608	hisIE	histidine biosynthesis I	182.38	23.31	0	147.68	18.29	0.00	0.02	0.00	0.81	-0.30
sr0609		hypothetical protein	372.42	77.79	0	215.97	42.51	0.00	0.00	0.00	0.58	-0.79
sr0610		hypothetical protein	22.86	4.17	0	45.84	26.07	0.00	0.03	0.01	2.01	1.00
sr0611	sds	solaneyl diphosphate	140.83	33.07	0	124.66	38.89	0.00	0.42	0.27	0.89	-0.18
sr0612		probable pseudouridin	53.80	17.68	8.99E-14	32.24	12.77	0.00	0.04	0.01	0.60	-0.74
sr0613		hypothetical protein	70.48	3.16	0	44.50	15.09	0.00	0.01	0.00	0.63	-0.66
sr0615		ATP-binding protein of	150.38	12.53	0	175.32	16.95	0.00	0.01	0.00	1.17	0.22
sr0616		unknown protein	150.41	11.77	0	122.46	9.96	0.00	0.00	0.00	0.81	-0.30
sr0617		unknown protein	112.00	11.46	0	158.50	21.45	0.00	0.00	0.00	1.42	0.50



Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf.	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
sir0618	cobQ	cobyrac acid synthase	47.94	6.82	0	47.64	9.63	0.00	0.88	0.85	0.99	-0.01
sir0619		hypothetical protein	71.53	11.16	0	79.25	25.22	0.00	0.65	0.60	1.11	0.15
sir0623	trxA	thioredoxin	751.16	215.23	0	422.60	100.84	0.00	0.00	0.00	0.56	-0.83
sir0624		UDP-N-acetylglucosar	107.04	21.50	0	167.34	32.47	0.00	0.00	0.00	1.56	0.64
sir0625		hypothetical protein	69.06	12.15	0	87.09	18.59	0.00	0.08	0.01	1.26	0.33
sir0626		probable glycosyltrans	42.10	4.94	0	76.97	20.70	0.00	0.00	0.00	1.83	0.87
sir0628	rps14	30S ribosomal protein	685.44	78.49	0	712.13	186.46	0.00	0.92	0.91	1.04	0.06
sir0630		hypothetical protein	71.00	14.61	0	78.40	10.06	0.00	0.29	0.03	1.10	0.14
sir0633	thiG	thiamine biosynthesis	239.09	55.55	0	173.22	24.90	0.00	0.03	0.00	0.72	-0.46
sir0634		unknown protein	30.87	6.38	0	31.14	9.23	0.00	0.95	0.94	1.01	0.01
sir0635		hypothetical protein	102.09	21.55	0	114.88	32.80	0.00	0.52	0.42	1.13	0.17
sir0636		probable cobalamin [5	104.62	13.79	0	100.23	18.90	0.00	0.60	0.52	0.96	-0.06
sir0637		hypothetical protein	87.30	11.21	0	137.76	25.83	0.00	0.00	0.00	1.58	0.66
sir0638	glyQ	glycyl-tRNA synthetas	86.59	7.16	0	129.23	6.21	0.00	0.00	0.00	1.49	0.58
sir0639		mechanosensitive ion	128.21	44.34	1.42E-12	70.34	17.39	0.00	0.01	0.00	0.55	-0.87
sir0640		two-component senso	117.81	10.38	0	101.39	13.85	0.00	0.04	0.00	0.86	-0.22
sir0642		hypothetical protein	163.58	25.05	0	279.26	47.56	0.00	0.00	0.00	1.71	0.77
sir0643		hypothetical protein	272.72	32.74	0	223.59	30.20	0.00	0.02	0.00	0.82	-0.29
sir0644		nitrogen regulation prc	84.72	50.76	4.34E-05	96.92	54.44	0.00	0.65	0.50	1.14	0.19
sir0645		hypothetical protein	101.62	16.29	0	83.08	29.10	0.00	0.15	0.08	0.82	-0.29
sir0646		probable D-alanyl-D-al	203.64	30.14	0	172.31	51.46	0.00	0.15	0.08	0.85	-0.24
sir0649	metS	methionyl-tRNA synth	145.69	30.34	0	188.19	44.51	0.00	0.08	0.01	1.29	0.37
sir0650		hypothetical protein	112.53	20.43	0	88.13	34.62	0.00	0.11	0.06	0.78	-0.35
sir0651		hypothetical protein	67.97	17.18	0	48.77	27.87	0.00	0.17	0.12	0.72	-0.48
sir0652	hisA	phosphorylformimi	234.84	86.19	2.49E-11	168.65	94.56	0.00	0.16	0.07	0.72	-0.48
sir0653	sigA	principal RNA polymer	454.23	153.74	4.58E-13	265.42	82.26	0.00	0.01	0.00	0.58	-0.78
sir0654		unknown protein	184.39	32.15	0	180.55	52.45	0.00	0.76	0.72	0.98	-0.03
sir0655		hypothetical protein	82.00	13.82	0	66.42	24.54	0.00	0.16	0.09	0.81	-0.30
sir0656		hypothetical protein	161.42	60.55	6.6E-11	58.11	48.71	0.00	0.10	0.06	0.36	-1.47
sir0657		aspartate kinase	229.10	46.79	0	153.83	22.29	0.00	0.00	0.00	0.67	-0.57
sir0658		unknown protein	103.00	25.65	0	54.51	10.61	0.00	0.00	0.00	0.53	-0.92
sir0659		oligopeptidase A	210.98	19.82	0	178.74	14.79	0.00	0.01	0.00	0.85	-0.24
sir0661	proC	pyrroline-5-carboxylate	278.35	38.57	0	220.94	40.91	0.00	0.02	0.00	0.79	-0.33
sir0662		arginine decarboxylase	148.57	30.00	0	106.26	30.24	0.00	0.03	0.00	0.72	-0.48
sir0664		hypothetical protein	10.65	3.07	0	4.07	7.61	0.19	0.01	0.00	0.38	-1.39
sir0665		aconitate hydratase 2	176.52	50.41	0	116.27	13.55	0.00	0.02	0.00	0.66	-0.60
sir0666		unknown protein	51.36	11.19	0	25.58	20.53	0.00	0.11	0.08	0.50	-1.01
sir0667		unknown protein	16.11	5.68	3.77E-12	11.00	12.90	0.04	0.07	0.04	0.68	-0.55
sir0668		unknown protein	3.37	1.18	2.6E-12	0.73	1.75	0.31	0.00	0.00	0.22	-2.20
sir0670		hypothetical protein	124.19	35.52	0	200.73	24.56	0.00	0.00	0.00	1.62	0.89
sir0676	cysC	adenylsulfate kinase	289.48	74.04	0	323.34	51.38	0.00	0.32	0.04	1.12	0.16
sir0677		biopolymer transport E	102.53	11.02	0	101.47	14.18	0.00	0.85	0.81	0.99	-0.02
sir0678		biopolymer transport E	146.35	17.89	0	150.32	15.49	0.00	0.68	0.52	1.03	0.04
sir0679		sun protein	170.96	17.98	0	190.73	25.86	0.00	0.14	0.04	1.12	0.16
sir0680		hypothetical protein	62.71	10.95	0	48.31	30.41	0.00	0.22	0.19	0.77	-0.38
sir0681		probable sodium/calcii	182.82	28.76	0	239.18	15.98	0.00	0.00	0.00	1.31	0.39
sir0682	hisD	histidinol dehydrogena	94.45	18.80	0	118.60	15.14	0.00	0.03	0.00	1.26	0.33
sir0686		hypothetical protein	58.50	15.61	0	37.16	15.25	0.00	0.03	0.00	0.64	-0.65
sir0687		probable two-componk	96.54	27.77	0	94.52	15.44	0.00	0.99	0.99	0.98	-0.03
sir0688		hypothetical protein	205.00	26.37	0	163.98	23.60	0.00	0.02	0.00	0.80	-0.32
sir0689		hypothetical protein	648.52	59.80	0	743.61	104.96	0.00	0.08	0.01	1.15	0.20
sir0692	ycf45	hypothetical protein Yf	182.73	37.17	0	202.68	41.74	0.00	0.40	0.20	1.11	0.15
sir0695		hypothetical protein	78.67	12.90	0	75.29	16.44	0.00	0.64	0.56	0.96	-0.06
sir0697		5-oxoprolinase homolo	196.39	23.26	0	194.72	28.01	0.00	0.88	0.84	0.99	-0.01
sir0698		hypothetical protein	89.89	10.33	0	45.89	1.39	0.00	0.00	0.00	0.51	-0.97
sir0699		unknown protein	15.32	3.98	0	9.17	7.53	0.00	0.13	0.10	0.60	-0.74
sir0700		probable amino acid p	64.31	23.18	1.09E-11	107.29	14.85	0.00	0.00	0.00	1.67	0.74
sir0701		transcriptional regulat	26.70	6.80	0	49.18	10.13	0.00	0.00	0.00	1.84	0.88
sir0702		unknown protein	86.74	35.06	1.36E-09	73.60	27.36	0.00	0.63	0.42	0.85	-0.24
sir0703		putative transposase [	123.32	10.73	0	694.94	293.81	0.00	0.00	0.00	5.64	2.49
sir0704		putative transposase [	153.99	40.59	0	1108.00	377.77	0.00	0.00	0.00	7.20	2.85
sir0707	polA	DNA polymerase I	79.63	14.56	0	120.88	45.23	0.00	0.07	0.02	1.52	0.60
sir0708		unknown protein	164.77	20.80	0	82.05	8.07	0.00	0.00	0.00	0.50	-1.01
sir0709		hypothetical protein	271.25	34.78	0	229.03	66.45	0.00	0.17	0.11	0.84	-0.24
sir0710	gdhA	glutamate dehydrogen	190.12	39.05	0	169.33	37.13	0.00	0.38	0.18	0.89	-0.17
sir0711		hypothetical protein	66.29	19.96	4.44E-16	26.53	24.18	0.01	0.08	0.05	0.40	-1.32
sir0712		hypothetical protein	75.50	14.98	0	91.08	22.74	0.00	0.19	0.06	1.21	0.27
sir0713	tgt	tRNA-guanine transgl	139.54	18.16	0	161.25	17.52	0.00	0.06	0.00	1.16	0.21
sir0719		unknown protein	119.70	19.85	0	166.72	51.23	0.00	0.06	0.01	1.39	0.48
sir0721		malic enzyme	244.91	28.95	0	187.44	26.76	0.00	0.00	0.00	0.77	-0.39
sir0722		hypothetical protein	164.17	12.68	0	89.30	7.62	0.00	0.00	0.00	0.54	-0.88
sir0723		hypothetical protein	294.06	82.91	0	298.95	101.40	0.00	1.00	1.00	1.02	0.02
sir0724		HtaR suppressor prote	41.39	5.53	0	29.02	16.92	0.00	0.11	0.08	0.70	-0.51
sir0725		hypothetical protein	16.14	9.87	6.2E-05	16.80	9.22	0.00	0.49	0.47	1.04	0.06
sir0727		unknown protein	87.92	22.96	0	62.62	50.88	0.00	0.16	0.13	0.71	-0.49
sir0728		hypothetical protein	167.35	24.65	0	215.65	61.23	0.00	0.09	0.04	1.29	0.37
sir0729		hypothetical protein	47.07	7.65	0	33.55	10.83	0.00	0.03	0.00	0.71	-0.49
sir0730		hypothetical protein	177.42	20.00	0	183.34	35.34	0.00	0.81	0.78	1.03	0.05

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0731		hypothetical protein	200.49	20.72	0	189.63	23.39	0.00	0.40	0.26	0.95	-0.08
slr0732		hypothetical protein	233.89	35.20	0	737.37	163.77	0.00	0.00	0.00	3.15	1.66
slr0733		integrase-recombinase	85.62	23.25	0	90.81	19.69	0.00	0.63	0.39	1.06	0.08
slr0734		hypothetical protein	102.29	24.17	0	68.98	23.37	0.00	0.04	0.00	0.67	-0.57
slr0737	psaD	photosystem I subunit	6462.27	1012.11	0	3152.31	710.82	0.00	0.00	0.00	0.49	-1.04
slr0738	trpE	anthranilate synthetase	226.98	27.94	0	237.04	47.54	0.00	0.72	0.67	1.04	0.06
slr0739	crtE	geranylgeranyl pyrophosphatase	285.97	51.67	0	202.56	33.58	0.00	0.01	0.00	0.71	-0.50
slr0740		hypothetical protein	43.31	6.15	0	39.04	13.98	0.00	0.42	0.38	0.90	-0.15
slr0741		transcriptional regulator	27.27	5.38	0	22.75	14.47	0.00	0.32	0.29	0.83	-0.26
slr0742		hypothetical protein	73.54	8.80	0	99.31	24.75	0.00	0.04	0.01	1.35	0.43
slr0743		similar to N utilization factor	121.28	28.28	0	177.75	22.42	0.00	0.00	0.00	1.47	0.55
slr0744	infB	initiation factor IF-2	372.38	106.69	0	406.31	87.81	0.00	0.52	0.29	1.09	0.13
slr0746	stpA	glucosylglycerol phosphatase	185.00	39.76	0	172.48	36.70	0.00	0.62	0.44	0.93	-0.10
slr0747	ggTA	glucosylglycerol transferase	103.49	30.95	2.22E-16	140.99	29.20	0.00	0.07	0.00	1.36	0.45
slr0748		hypothetical protein	236.06	46.75	0	265.46	99.92	0.00	0.68	0.63	1.12	0.17
slr0749	chlL	light-independent protochlorophyllide reductase	511.71	327.11	0.000127	759.96	256.02	0.00	0.10	0.00	1.49	0.57
slr0750	chlN	protochlorophyllide reductase	155.13	27.82	0	232.84	22.68	0.00	0.00	0.00	1.50	0.59
slr0751		hypothetical protein	53.08	17.42	8.5E-14	83.28	38.02	0.00	0.12	0.03	1.57	0.65
slr0752		enolase	272.12	34.25	0	278.56	43.15	0.00	0.81	0.75	1.02	0.03
slr0753		probable transport protein	101.36	12.17	0	130.83	38.42	0.00	0.11	0.06	1.29	0.37
slr0755		hypothetical protein	14.96	3.15	0	29.08	17.37	0.00	0.75	0.75	1.94	0.96
slr0756	kaiA	circadian clock protein	91.62	12.92	0	68.65	13.58	0.00	0.02	0.00	0.75	-0.42
slr0757	kaiB1	circadian clock protein	16.46	4.64	0	10.35	14.30	0.08	0.07	0.04	0.63	-0.67
slr0758	kaiC1	circadian clock protein	102.80	13.40	0	119.58	15.56	0.00	0.07	0.00	1.16	0.22
slr0765		hypothetical protein	284.91	84.60	2.22E-16	669.21	79.35	0.00	0.00	0.00	2.35	1.23
slr0769		hypothetical protein	216.15	59.56	0	186.52	43.06	0.00	0.38	0.17	0.86	-0.21
slr0770		hypothetical protein	35.49	8.38	0	17.92	14.04	0.00	0.07	0.04	0.51	-0.99
slr0771		hypothetical protein	13.26	6.20	1.58E-07	8.23	14.91	0.18	0.05	0.02	0.62	-0.69
slr0772	chlB	protochlorophyllide reductase	458.27	96.76	0	339.74	51.44	0.00	0.02	0.00	0.74	-0.43
slr0773		hypothetical protein	86.36	18.51	0	87.44	18.10	0.00	0.92	0.89	1.01	0.02
slr0774	secD	protein-export membrane protein	250.32	33.64	0	229.89	35.86	0.00	0.32	0.17	0.92	-0.12
slr0775	secF	protein-export membrane protein	154.07	18.95	0	101.41	6.15	0.00	0.00	0.00	0.66	-0.60
slr0776		UDP-3-O-[3-hydroxymercaptopyruvate] lyase	157.57	19.67	0	154.22	19.56	0.00	0.77	0.68	0.98	-0.03
slr0779		hypothetical protein	126.98	43.84	1.29E-12	134.66	48.06	0.00	0.78	0.69	1.06	0.08
slr0780		hypothetical protein	167.71	39.65	0	86.48	20.84	0.00	0.00	0.00	0.52	-0.96
slr0782		putative flavin-containing monooxygenase	148.28	13.97	0	151.49	18.55	0.00	0.77	0.71	1.02	0.03
slr0783	tpi	triosephosphate isomerase	90.67	14.56	0	125.16	45.18	0.00	0.12	0.06	1.38	0.47
slr0784		hypothetical protein	110.12	13.09	0	128.47	42.04	0.00	0.40	0.34	1.17	0.22
slr0786		methionine aminopeptidase	70.33	13.14	0	63.61	6.23	0.00	0.38	0.03	0.90	-0.15
slr0787		hypothetical protein	40.37	5.68	0	52.46	14.25	0.00	0.12	0.07	1.30	0.38
slr0788		similar to pre-B cell enzyme	54.86	17.77	3.89E-14	61.40	13.99	0.00	0.42	0.14	1.12	0.16
slr0789		hypothetical protein	55.91	6.93	0	29.63	11.94	0.00	0.01	0.00	0.53	-0.92
slr0790		similar to ultraviolet light-inducible protein	13.81	3.29	0	9.88	10.37	0.02	0.12	0.09	0.72	-0.48
slr0793		unknown protein	44.07	7.13	0	36.79	13.16	0.00	0.22	0.16	0.83	-0.26
slr0794		cation efflux system protein	267.17	25.98	0	139.78	32.45	0.00	0.00	0.00	0.52	-0.93
slr0795		hypothetical protein	13.30	2.58	0	23.54	12.09	0.00	0.53	0.51	1.77	0.82
slr0796		nickel resistance protein	465.01	85.83	0	392.80	113.55	0.00	0.23	0.14	0.84	-0.24
slr0797	coaT	Cobalt transporter CoaT	88.12	13.26	0	42.56	33.54	0.00	0.07	0.04	0.48	-1.05
slr0798	ziaA	Zinc exporter ZiaA	82.24	1.30	0	135.35	12.62	0.00	0.00	0.00	1.65	0.72
slr0799		putative transposase [gamma]	30.93	8.32	0	63.63	18.21	0.00	0.00	0.00	2.06	1.04
slr0800		putative transposase [gamma]	36.18	6.41	0	44.27	14.16	0.00	0.40	0.33	1.22	0.29
slr0801		hypothetical protein	235.98	57.19	0	308.46	126.30	0.00	0.24	0.15	1.31	0.39
slr0804		probable D-alanyl-D-alanine ligase	151.72	22.91	0	164.41	39.94	0.00	0.60	0.53	1.08	0.12
slr0806		hypothetical protein	168.53	30.62	0	123.37	23.65	0.00	0.02	0.00	0.73	-0.45
slr0807		probable alpha-sialoglycoprotein	444.85	92.10	0	470.98	149.15	0.00	0.82	0.78	1.06	0.08
slr0808		16S rRNA processing protein	48.15	5.66	0	29.45	13.41	0.00	0.05	0.02	0.61	-0.71
slr0809	rfbB	dTDP-glucose 4,6-dehydratase	220.30	201.61	0.007438	169.05	111.62	0.00	0.62	0.39	0.77	-0.38
slr0810		hypothetical protein	21.72	6.21	0	3.89	5.33	0.07	0.02	0.00	0.18	-2.48
slr0812		hypothetical protein	339.10	29.21	0	340.61	34.20	0.00	0.95	0.94	1.00	0.01
slr0813		hypothetical protein	329.76	19.23	0	286.88	26.68	0.00	0.01	0.00	0.87	-0.20
slr0815		hypothetical protein	20.86	2.17	0	17.11	11.58	0.00	0.31	0.29	0.82	-0.29
slr0816		hypothetical protein	35.44	10.77	8.88E-16	27.71	7.04	0.00	0.21	0.07	0.78	-0.35
slr0817		salicylate biosynthesis protein	182.03	46.51	0	192.67	62.41	0.00	0.82	0.78	1.06	0.08
slr0818		hypothetical protein	131.34	28.50	0	88.85	26.05	0.00	0.03	0.00	0.68	-0.56
slr0819		apolipoprotein N-acyltransferase	138.03	27.80	0	197.49	29.36	0.00	0.00	0.00	1.43	0.52
slr0820		probable glycosyltransferase	122.67	30.32	0	55.53	12.33	0.00	0.00	0.00	0.45	-1.14
slr0821		hypothetical protein	228.56	54.70	0	132.49	23.90	0.00	0.00	0.00	0.58	-0.79
slr0822		cation-transporting ATPase	297.28	39.42	0	310.06	50.00	0.00	0.67	0.56	1.04	0.06
slr0823	ycf3	photosystem I assembly protein	117.61	13.08	0	112.18	13.32	0.00	0.49	0.32	0.95	-0.07
slr0825		probable peptidase	217.56	48.53	0	165.85	37.33	0.00	0.08	0.00	0.76	-0.39
slr0827		alanine racemase	222.68	17.48	0	274.57	30.12	0.00	0.00	0.00	1.23	0.30
slr0829		unknown protein	230.53	28.66	0	242.89	21.52	0.00	0.39	0.12	1.05	0.08
slr0833	dnaB	replicative DNA helicase	39.37	10.84	0	61.73	15.70	0.00	0.01	0.00	1.57	0.65
slr0835		MoxR protein homolog	164.92	42.10	0	256.53	68.44	0.00	0.01	0.00	1.56	0.64
slr0836	rfbB	dTDP-glucose 4,6-dehydratase	47.60	9.08	0	67.07	13.53	0.00	0.02	0.00	1.41	0.49
slr0838	purM	phosphoribosyl formyltransferase	169.82	36.28	0	113.80	18.99	0.00	0.01	0.00	0.67	-0.58
slr0839	hemH	ferrochelatase	438.71	98.62	0	495.27	147.52	0.00	0.52	0.40	1.13	0.17
slr0841		unknown protein	81.23	13.58	0	128.24	25.78	0.00	0.00	0.00	1.58	0.66

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0842		hypothetical protein	104.54	17.06	0	100.17	20.94	0.00	0.67	0.58	0.96	-0.06
slr0844	ndhF1	NADH dehydrogenase	422.57	66.93	0	448.68	57.52	0.00	0.46	0.19	1.06	0.09
slr0845		hypothetical protein	120.45	27.56	0	71.17	16.33	0.00	0.00	0.00	0.59	-0.76
slr0846		hypothetical protein	59.39	9.62	0	39.73	15.25	0.00	0.02	0.00	0.67	-0.58
slr0847		phosphopantetheine a	47.10	11.31	0	30.63	22.82	0.00	0.21	0.17	0.65	-0.62
slr0848		hypothetical protein	354.32	29.67	0	317.64	28.51	0.00	0.06	0.00	0.90	-0.16
slr0851	ndaA	type 2 NADH dehydrog	132.00	17.18	0	125.73	29.40	0.00	0.57	0.49	0.95	-0.07
slr0852		hypothetical protein	70.60	8.63	0	79.61	12.21	0.00	0.17	0.06	1.13	0.17
slr0853		ribosomal-protein-alan	46.76	6.70	0	62.26	9.70	0.00	0.01	0.00	1.33	0.41
slr0854	phrA	DNA photolyase	97.80	9.85	0	148.00	35.85	0.00	0.01	0.00	1.51	0.60
slr0856		putative transposase [	59.67	14.10	0	452.73	137.05	0.00	0.00	0.00	7.59	2.92
slr0857		putative transposase [	233.80	61.53	0	542.88	170.70	0.00	0.00	0.00	2.32	1.22
slr0861	purT	glycinamide ribonucleo	126.16	20.38	0	119.38	21.49	0.00	0.57	0.41	0.95	-0.08
slr0862		probable sugar kinase	52.46	14.52	0	54.68	12.90	0.00	0.73	0.58	1.04	0.06
slr0863		hypothetical protein	382.57	95.52	0	334.25	117.10	0.00	0.37	0.26	0.87	-0.19
slr0864		ATP-binding protein of	468.15	51.92	0	462.09	91.08	0.00	0.80	0.76	0.99	-0.02
slr0865		hypothetical protein	155.98	78.42	1.1E-06	231.12	96.45	0.00	0.15	0.03	1.48	0.57
slr0867		unknown protein	56.81	7.07	0	36.12	6.59	0.00	0.00	0.00	0.64	-0.65
slr0868		unknown protein	9.57	2.00	0	5.57	7.83	0.08	0.05	0.03	0.58	-0.78
slr0869		hypothetical protein	195.52	52.22	0	206.74	40.92	0.00	0.64	0.46	1.06	0.08
slr0870		hypothetical protein	11.59	13.15	0.030824	9.81	14.70	0.10	0.12	0.08	0.85	-0.24
slr0871		unknown protein	4.44	2.50	1.32E-05	4.27	6.03	0.08	0.10	0.07	0.96	-0.06
slr0872		hypothetical protein	100.19	28.32	0	144.23	45.55	0.00	0.09	0.01	1.44	0.53
slr0875		large-conductance me	74.41	14.88	0	58.71	20.26	0.00	0.17	0.09	0.79	-0.34
slr0876		hypothetical protein	222.14	57.06	0	178.97	69.73	0.00	0.19	0.09	0.81	-0.31
slr0877		glutamyl-tRNA(Gln) an	168.85	12.84	0	292.30	48.43	0.00	0.00	0.00	1.73	0.79
slr0878		hypothetical protein	78.18	8.69	0	113.03	22.19	0.00	0.00	0.00	1.45	0.53
slr0879		glycine decarboxylase	67.73	17.75	0	74.18	16.64	0.00	0.49	0.25	1.10	0.13
slr0880		similar to fibronectin bi	142.35	39.61	0	122.24	43.05	0.00	0.40	0.23	0.86	-0.22
slr0881		unknown protein	124.34	50.09	1.2E-09	106.12	37.08	0.00	0.48	0.31	0.85	-0.23
slr0882	ycf84	hypothetical protein Yc	339.64	107.50	9.99E-15	303.68	97.71	0.00	0.54	0.39	0.89	-0.16
slr0883		hypothetical protein	324.02	45.45	0	259.16	41.35	0.00	0.03	0.00	0.80	-0.32
slr0884	gap1	glyceraldehyde 3-phos	127.99	26.75	0	137.04	31.89	0.00	0.68	0.57	1.07	0.10
slr0885		hypothetical protein	59.53	6.66	0	53.84	17.00	0.00	0.34	0.29	0.90	-0.14
slr0886		3-oxoacyl-[acyl-carrier	109.35	18.49	0	104.22	30.86	0.00	0.61	0.54	0.95	-0.07
slr0887		hypothetical protein	129.70	39.49	8.88E-16	119.28	24.12	0.00	0.74	0.53	0.92	-0.12
slr0888		hypothetical protein	309.00	50.75	0	89.44	19.11	0.00	0.00	0.00	0.29	-1.79
slr0889		hypothetical protein	191.11	26.62	0	125.10	23.61	0.00	0.00	0.00	0.65	-0.61
slr0890		unknown protein	13.66	2.30	0	6.56	5.63	0.00	0.10	0.07	0.48	-1.06
slr0891		N-acetylmuramoyl-L-al	186.52	31.59	0	134.68	16.13	0.00	0.01	0.00	0.72	-0.47
slr0895		transcriptional regulat	23.32	6.33	0	34.15	6.23	0.00	0.02	0.00	1.46	0.55
slr0896		multi-drug efflux transp	204.96	28.72	0	208.11	16.05	0.00	0.75	0.53	1.02	0.02
slr0897		probable endoglucana	241.65	73.76	1.11E-15	136.33	28.89	0.00	0.01	0.00	0.56	-0.83
slr0898	nirA	ferredoxin-nitrite redu	458.23	47.52	0	536.91	113.94	0.00	0.19	0.12	1.17	0.23
slr0899	cynS	cyanate lyase	56.49	13.82	0	27.89	25.24	0.01	0.10	0.07	0.49	-1.02
slr0900	moaA	molybdopterin biosynt	251.69	54.57	0	266.96	33.15	0.00	0.49	0.19	1.06	0.08
slr0901	moaA	molybdenum cofactor	30.00	6.11	0	17.53	12.20	0.00	0.17	0.14	0.58	-0.77
slr0902	moaC	molybdenum cofactor	60.59	12.89	0	102.50	24.15	0.00	0.00	0.00	1.69	0.76
slr0903	moaE	molybdopterin (MPT) c	31.34	8.21	0	33.91	11.72	0.00	0.77	0.72	1.08	0.11
slr0904		competence protein C	111.15	8.33	0	158.12	19.74	0.00	0.00	0.00	1.42	0.51
slr0905	bchE	Mg-protoporphyrin IX r	30.13	4.81	0	36.53	12.81	0.00	0.39	0.33	1.21	0.28
slr0906	psbB	photosystem II core lig	4365.40	928.40	0	5873.01	1487.86	0.00	0.05	0.00	1.35	0.43
slr0907		unknown protein	185.34	26.42	0	250.61	44.74	0.00	0.02	0.00	1.35	0.44
slr0909		unknown protein	94.00	24.20	0	122.06	13.25	0.00	0.03	0.00	1.30	0.38
slr0912		unknown protein	62.84	7.52	0	79.89	35.13	0.00	0.42	0.39	1.27	0.35
slr0913		unknown protein	20.94	7.03	2.94E-13	19.27	14.85	0.00	0.34	0.31	0.92	-0.12
slr0914		unknown protein	50.34	7.34	0	57.67	24.02	0.00	0.65	0.62	1.15	0.20
slr0915		putative endonuclease	3035.57	569.89	0	8871.85	4210.49	0.00	0.00	0.00	2.92	1.55
slr0917	bioF	7-keto-8-aminopelargi	329.78	54.52	0	455.57	134.18	0.00	0.08	0.03	1.38	0.47
slr0918		methionine aminopept	99.71	33.77	4.77E-13	167.37	24.13	0.00	0.00	0.00	1.68	0.75
slr0919		hypothetical protein	45.84	9.30	0	30.78	14.41	0.00	0.07	0.04	0.67	-0.57
slr0920		mutator MuT protein	19.35	2.46	0	12.98	14.96	0.03	0.09	0.06	0.67	-0.58
slr0921		hypothetical protein	37.40	4.66	0	27.20	14.67	0.00	0.11	0.08	0.73	-0.46
slr0922	pth	peptidyl-tRNA hydrolat	66.00	10.71	0	68.89	19.26	0.00	0.85	0.82	1.04	0.06
slr0923	ycf65	hypothetical protein Yc	72.96	5.33	0	44.87	25.19	0.00	0.12	0.09	0.61	-0.70
slr0924		hypothetical protein	440.88	102.82	0	618.52	139.48	0.00	0.03	0.00	1.40	0.49
slr0925	ssb	single-stranded DNA-t	216.33	57.72	0	115.91	19.16	0.00	0.00	0.00	0.54	-0.90
slr0926	ubiA	4-hydroxybenzoate-oc	121.26	18.85	0	118.65	21.45	0.00	0.80	0.74	0.98	-0.03
slr0927	psbD2	photosystem II reactio	2913.36	264.75	0	3665.83	1157.63	0.00	0.16	0.12	1.26	0.33
slr0929		chromosome partitioni	93.36	22.96	0	103.55	37.67	0.00	0.71	0.64	1.11	0.15
slr0930		hypothetical protein	118.47	11.29	0	126.70	17.24	0.00	0.37	0.25	1.07	0.10
slr0935		hypothetical protein	42.17	8.33	0	23.65	12.69	0.00	0.04	0.02	0.56	-0.83
slr0936	nadC	nicotinate-nucleotide p	155.31	58.70	9.12E-11	139.01	35.87	0.00	0.72	0.51	0.90	-0.16
slr0937		unknown protein	117.38	25.40	0	73.52	17.40	0.00	0.01	0.00	0.63	-0.67
slr0938		probable UDP-N-acety	129.55	12.03	0	127.27	16.62	0.00	0.75	0.69	0.98	-0.03
slr0940	crtQ-2	zeta-carotene desatur	244.26	45.56	0	308.34	54.14	0.00	0.05	0.00	1.26	0.34
slr0941		hypothetical protein	23.48	6.26	0	11.43	7.68	0.00	0.08	0.05	0.49	-1.04
slr0942		alcohol dehydrogenas	223.86	18.55	0	218.12	16.19	0.00	0.59	0.41	0.97	-0.04

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr0943	fda	fructose-bisphosphate	111.99	12.78	0	90.63	19.17	0.00	0.05	0.01	0.81	-0.31
slr0944		multidrug-efflux transp	98.38	4.93	0	89.48	14.92	0.00	0.16	0.11	0.91	-0.14
slr0945		arsenical resistance pi	32.94	11.52	2.52E-12	19.81	11.88	0.00	0.24	0.20	0.60	-0.73
slr0946	arsC	arsenate reductase	40.50	4.72	0	46.40	11.51	0.00	0.32	0.24	1.15	0.20
slr0947	rpaB	response regulator for	161.90	14.78	0	189.35	30.11	0.00	0.07	0.02	1.17	0.23
slr0948		hypothetical protein	78.70	6.22	0	66.25	8.13	0.00	0.01	0.00	0.84	-0.25
slr0949	natD	Integral membrane pro	139.59	33.20	0	94.90	21.67	0.00	0.02	0.00	0.68	-0.56
slr0950		hemolysin-like protein	169.67	16.58	0	99.45	23.42	0.00	0.00	0.00	0.59	-0.77
slr0951		4-diphosphocytidyl-2C	191.40	22.98	0	179.66	12.30	0.00	0.33	0.03	0.94	-0.09
slr0952	fbpII	fructose-1,6-bisphosph	104.19	8.84	0	139.70	20.11	0.00	0.00	0.00	1.34	0.42
slr0953		sucrose-phosphate ph	45.09	9.46	0	37.40	11.66	0.00	0.22	0.09	0.83	-0.27
slr0954		hypothetical protein	125.99	34.97	0	100.60	53.81	0.00	0.30	0.25	0.80	-0.32
slr0955		probable tRNA/rRNA r	174.83	33.26	0	195.08	50.36	0.00	0.44	0.32	1.12	0.16
slr0957		hypothetical protein	70.81	10.31	0	49.08	7.52	0.00	0.00	0.00	0.69	-0.53
slr0958	cysS	cysteinyI-tRNA synthet	120.12	14.94	0	185.76	32.25	0.00	0.00	0.00	1.55	0.63
slr0959		hypothetical protein	147.04	17.34	0	243.82	41.09	0.00	0.00	0.00	1.66	0.73
slr0960		unknown protein	623.62	92.62	0	332.66	88.08	0.00	0.00	0.00	0.53	-0.91
slr0962		unknown protein	385.90	60.32	0	389.68	39.87	0.00	0.84	0.72	1.01	0.01
slr0963	sir	ferredoxin-sulfite reduct	216.43	52.09	0	249.14	75.52	0.00	0.47	0.33	1.15	0.20
slr0964		hypothetical protein	98.99	30.79	3.33E-15	115.09	26.83	0.00	0.31	0.07	1.16	0.22
slr0965	dnaN	DNA polymerase III be	95.94	14.80	0	124.47	24.29	0.00	0.03	0.00	1.30	0.38
slr0966	trpA	tryptophan synthase a	114.70	17.16	0	150.94	23.61	0.00	0.01	0.00	1.32	0.40
slr0967		hypothetical protein	189.16	69.71	3E-11	576.16	222.80	0.00	0.00	0.00	3.05	1.61
slr0969	cobJ	precorrin methylase	448.81	46.64	0	311.10	32.99	0.00	0.00	0.00	0.69	-0.53
slr0971		hypothetical protein	307.09	59.26	0	257.53	65.16	0.00	0.21	0.09	0.84	-0.25
slr0974	infC	initiation factor IF-3	132.21	26.36	0	129.01	20.11	0.00	0.88	0.79	0.98	-0.04
slr0975		hypothetical protein	156.80	11.80	0	199.18	22.46	0.00	0.00	0.00	1.27	0.35
slr0976		hypothetical protein	127.25	12.28	0	87.73	16.87	0.00	0.00	0.00	0.69	-0.54
slr0977		ABC transporter, perme	56.47	17.02	4.44E-16	44.60	33.19	0.00	0.24	0.20	0.79	-0.39
slr0978		hypothetical protein	67.63	14.31	0	30.03	21.36	0.00	0.13	0.10	0.44	-1.17
slr0980		hypothetical protein	49.21	9.70	0	43.21	23.31	0.00	0.35	0.30	0.88	-0.19
slr0981		hypothetical protein	66.58	17.84	0	49.69	8.29	0.00	0.06	0.00	0.75	-0.42
slr0982		probable polysacchari	174.11	20.91	0	182.03	51.24	0.00	0.88	0.87	1.05	0.06
slr0983	rfbF	glucose-1-phosphate r	99.20	7.00	0	43.39	9.87	0.00	0.00	0.00	0.44	-1.19
slr0984	rfbG	CDP-glucose 4,6-dehy	96.37	31.46	6.22E-14	48.60	23.57	0.00	0.02	0.00	0.50	-0.99
slr0985	rfbC	dTDP-4-dehydrohamr	40.50	4.23	0	20.33	14.20	0.00	0.03	0.01	0.50	-0.99
slr0989		hypothetical protein	113.29	27.23	0	92.56	25.86	0.00	0.22	0.06	0.82	-0.29
slr0990		hypothetical protein	152.72	15.26	0	160.72	37.55	0.00	0.73	0.70	1.05	0.07
slr0992		probable tRNA/rRNA r	29.52	4.27	0	41.68	8.39	0.00	0.01	0.00	1.41	0.50
slr0993		putative peptidase	682.16	64.48	0	655.42	124.48	0.00	0.56	0.49	0.96	-0.06
slr0994		lipoate-protein ligase E	102.26	29.22	0	124.51	40.91	0.00	0.36	0.20	1.22	0.28
slr1019		phenazine biosynthetic	66.08	9.67	0	51.01	10.73	0.00	0.03	0.00	0.77	-0.37
slr1020		sulfolipid biosynthesis	542.80	76.19	0	572.05	35.55	0.00	0.38	0.02	1.05	0.08
slr1022	argD	N-acetylmethionine amin	541.48	84.72	0	539.67	85.09	0.00	0.98	0.97	1.00	0.00
slr1023		unknown protein	25.78	6.88	0	23.29	15.80	0.00	0.38	0.34	0.90	-0.15
slr1024		fibrillin	34.87	1.72	0	31.18	7.29	0.00	0.19	0.16	0.89	-0.16
slr1025		hypothetical protein	13.30	5.13	2.19E-10	6.63	10.29	0.11	0.02	0.00	0.50	-1.00
slr1028		unknown protein	399.60	68.02	0	360.87	77.27	0.00	0.35	0.21	0.90	-0.15
slr1030	chlI	magnesium-chelatase	228.13	34.01	0	336.84	31.20	0.00	0.00	0.00	1.48	0.56
slr1031	tyrS	tyrosyl-tRNA synthetase	86.14	24.84	0	137.77	29.93	0.00	0.01	0.00	1.60	0.68
slr1032		unknown protein	35.33	2.31	0	17.55	9.28	0.00	0.01	0.00	0.50	-1.01
slr1033		unknown protein	42.72	6.23	0	63.40	30.57	0.00	0.18	0.13	1.48	0.57
slr1034	ycf41	hypothetical protein YC	153.09	16.12	0	121.63	35.44	0.00	0.06	0.02	0.79	-0.33
slr1035		hypothetical protein	36.24	3.39	0	38.22	6.34	0.00	0.58	0.51	1.05	0.08
slr1037		two-component respon	25.84	10.17	4.92E-10	5.73	7.80	0.07	0.02	0.01	0.22	-2.17
slr1039		hypothetical protein	45.38	9.82	0	24.20	22.34	0.01	0.11	0.08	0.53	-0.91
slr1041		two-component respon	171.41	49.94	0	157.59	35.43	0.00	0.73	0.54	0.92	-0.12
slr1042		two-component respon	80.44	16.66	0	59.36	15.39	0.00	0.07	0.02	0.74	-0.44
slr1043	cheW	similar to chemotaxis p	71.18	16.21	0	71.83	17.47	0.00	0.96	0.95	1.01	0.01
slr1044		methyl-accepting chen	354.83	43.39	0	355.66	44.56	0.00	0.98	0.98	1.00	0.00
slr1045	ycf63	hypothetical protein YC	128.61	33.29	0	108.40	24.38	0.00	0.34	0.10	0.84	-0.25
slr1046		hypothetical protein	56.98	8.93	0	26.13	10.49	0.00	0.01	0.00	0.46	-1.12
slr1047		hypothetical protein	76.69	16.90	0	117.62	27.74	0.00	0.01	0.00	1.53	0.62
slr1048		hypothetical protein	51.64	7.65	0	99.51	18.21	0.00	0.00	0.00	1.93	0.95
slr1050		hypothetical protein	187.33	32.15	0	237.05	62.48	0.00	0.13	0.05	1.27	0.34
slr1051		enoyl-facyl-carrier-prot	103.55	15.14	0	69.10	17.34	0.00	0.01	0.00	0.67	-0.58
slr1052		hypothetical protein	73.72	7.59	0	66.24	9.29	0.00	0.14	0.05	0.90	-0.15
slr1053		unknown protein	169.28	36.78	0	172.15	54.83	0.00	0.97	0.96	1.02	0.02
slr1055	chlH	magnesium-protoporpi	463.36	54.15	0	558.12	105.38	0.00	0.07	0.02	1.20	0.27
slr1056		unknown protein	87.37	18.61	0	55.45	40.84	0.00	0.12	0.09	0.63	-0.66
slr1062		unknown protein	7.65	4.24	9.99E-06	4.55	6.63	0.09	0.05	0.02	0.59	-0.75
slr1063		probable glycosyltrans	466.01	54.18	0	484.29	75.38	0.00	0.68	0.59	1.04	0.06
slr1064		probable glycosyltrans	54.81	7.69	0	20.54	9.67	0.00	0.00	0.00	0.37	-1.42
slr1065		probable glycosyltrans	58.77	13.49	0	33.11	25.66	0.00	0.18	0.15	0.56	-0.83
slr1066		unknown protein	39.72	9.31	0	28.87	23.40	0.00	0.16	0.13	0.73	-0.46
slr1067		UDP-glucose 4-epimeri	90.82	18.34	0	79.71	18.51	0.00	0.33	0.20	0.88	-0.19
slr1068		hypothetical protein	4.53	1.54	6.29E-13	2.23	3.68	0.14	0.02	0.01	0.49	-1.03
slr1069		hypothetical protein	5.85	1.25	0	5.28	5.68	0.02	0.14	0.10	0.90	-0.15

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1070		unknown protein	19.03	7.63	9.87E-10	8.02	11.06	0.08	0.04	0.01	0.42	-1.25
slr1071		unknown protein	30.93	9.53	2E-15	19.58	16.31	0.00	0.14	0.11	0.63	-0.66
slr1072		GDP-D-mannose dehy	62.95	24.40	2.61E-10	51.39	14.73	0.00	0.35	0.14	0.82	-0.29
slr1073		unknown protein	59.29	19.23	4.22E-14	57.16	9.40	0.00	0.98	0.94	0.96	-0.05
slr1074		unknown protein	35.05	10.01	0	36.70	16.77	0.00	0.89	0.87	1.05	0.07
slr1075		putative transposase [	133.45	19.16	0	961.04	430.74	0.00	0.00	0.00	7.20	2.85
slr1076		probable glycosyltrans	52.61	15.45	0	53.97	7.27	0.00	0.69	0.35	1.03	0.04
slr1077		probable glycosyltrans	103.49	22.32	0	148.39	27.02	0.00	0.01	0.00	1.43	0.52
slr1078		similar to UDP-glucosyl	79.90	6.04	0	50.38	11.58	0.00	0.00	0.00	0.63	-0.67
slr1079		unknown protein	303.98	35.53	0	194.41	30.90	0.00	0.00	0.00	0.84	-0.84
slr1081		hypothetical protein	136.20	13.29	0	75.69	29.09	0.00	0.01	0.00	0.56	-0.85
slr1082		unknown protein	245.28	33.68	0	177.73	21.00	0.00	0.00	0.00	0.72	-0.46
slr1083		hypothetical protein	63.73	13.07	0	36.58	25.70	0.00	0.15	0.12	0.57	-0.80
slr1084		unknown protein	67.85	15.62	0	69.88	21.89	0.00	0.93	0.91	1.03	0.04
slr1085		probable glycosyltrans	98.30	37.93	2.18E-10	93.54	38.33	0.00	0.79	0.71	0.95	-0.07
slr1087		hypothetical protein	92.00	8.62	0	51.38	7.47	0.00	0.00	0.00	0.56	-0.84
slr1090		GTP-binding protein	273.32	26.53	0	207.77	25.00	0.00	0.00	0.00	0.76	-0.40
slr1093	folK	2-amino-4-hydroxy-6-t	157.23	38.78	0	179.49	31.57	0.00	0.27	0.04	1.14	0.19
slr1094		hypothetical protein	122.30	8.41	0	200.98	44.64	0.00	0.00	0.00	1.64	0.72
slr1095		hypothetical protein	104.53	10.72	0	91.14	17.25	0.00	0.13	0.06	0.87	-0.20
slr1096		dihydroliipoamide dehy	302.91	64.88	0	350.92	111.92	0.00	0.42	0.31	1.16	0.21
slr1097		hypothetical protein	61.30	11.14	0	76.44	15.85	0.00	0.07	0.01	1.25	0.32
slr1098		hypothetical protein	162.69	36.87	0	159.26	28.69	0.00	0.92	0.86	0.98	-0.03
slr1099	ubiX	3-octaprenyl-4-hydroxy	77.23	29.99	2.82E-10	127.50	34.01	0.00	0.02	0.00	1.65	0.72
slr1100		hypothetical protein	41.64	8.62	0	24.46	17.76	0.00	0.18	0.15	0.59	-0.77
slr1101		hypothetical protein	269.49	55.28	0	287.73	60.40	0.00	0.57	0.41	1.07	0.09
slr1102		hypothetical protein	159.96	27.91	0	186.95	16.88	0.00	0.06	0.00	1.17	0.22
slr1103		hypothetical protein	198.01	52.67	0	178.10	38.90	0.00	0.53	0.33	0.90	-0.15
slr1104		hypothetical protein	464.87	97.05	0	478.44	89.53	0.00	0.78	0.67	1.03	0.04
slr1105		GTP-binding protein T	513.43	101.09	0	681.35	77.71	0.00	0.01	0.00	1.33	0.41
slr1106		prohibitin	131.68	16.60	0	137.24	14.85	0.00	0.54	0.34	1.04	0.06
slr1107		unknown protein	196.37	17.27	0	150.52	17.02	0.00	0.00	0.00	0.77	-0.38
slr1109		similar to ankyrin	218.64	116.29	4.12E-06	181.05	49.81	0.00	0.55	0.27	0.83	-0.27
slr1110		hypothetical protein	70.21	10.84	0	71.70	13.87	0.00	0.88	0.84	1.02	0.03
slr1113		ATP-binding protein of	111.24	14.82	0	101.07	11.13	0.00	0.21	0.04	0.91	-0.14
slr1114		hypothetical protein	557.25	84.15	0	572.76	93.94	0.00	0.76	0.66	1.03	0.04
slr1115		probable methyltransfe	52.80	3.84	0	42.97	22.23	0.00	0.27	0.24	0.81	-0.30
slr1116		hypothetical protein	25.65	3.27	0	10.98	7.00	0.00	0.13	0.09	0.43	-1.22
slr1117		hypothetical protein	40.83	9.78	0	50.47	8.14	0.00	0.07	0.00	1.24	0.31
slr1118		probable UDP-N-acety	80.20	118.90	0.098484	60.94	67.01	0.03	0.93	0.89	0.76	-0.40
slr1119		hypothetical protein	81.15	8.88	0	84.96	21.51	0.00	0.81	0.78	1.05	0.07
slr1120		type 4 prelin-like prot	103.65	18.24	0	175.96	39.75	0.00	0.00	0.00	1.70	0.76
slr1122		hypothetical protein	95.33	20.67	0	60.40	8.88	0.00	0.00	0.00	0.63	-0.66
slr1123		guanylate kinase	45.49	10.34	0	30.58	11.34	0.00	0.04	0.01	0.67	-0.57
slr1124		phosphoglycerate mut	141.41	18.20	0	133.15	16.80	0.00	0.45	0.26	0.94	-0.09
slr1125		probable glucosyl tran	72.35	11.40	0	73.56	13.42	0.00	0.89	0.85	1.02	0.02
slr1127		unknown protein	319.32	50.59	0	340.81	67.42	0.00	0.57	0.45	1.07	0.09
slr1128		hypothetical protein	191.52	44.10	0	141.36	43.48	0.00	0.07	0.01	0.74	-0.44
slr1129	rne	ribonuclease E	287.37	37.51	0	371.20	109.67	0.00	0.08	0.03	1.29	0.37
slr1130	rhnB	ribonuclease HII	73.89	27.87	8.31E-11	100.72	29.09	0.00	0.15	0.01	1.36	0.45
slr1133	argH	L-argininosuccinate ly	140.90	13.79	0	134.93	14.77	0.00	0.47	0.33	0.96	-0.06
slr1134		mutator MutT homolog	48.22	6.45	0	22.50	20.83	0.01	0.05	0.03	0.47	-1.10
slr1135		unknown protein	29.20	6.11	0	51.81	16.03	0.00	0.01	0.00	1.77	0.83
slr1136	ctaC	cytochrome c oxidase	325.06	62.12	0	298.18	61.32	0.00	0.44	0.27	0.92	-0.12
slr1137	ctaD	cytochrome c oxidase	317.48	56.01	0	397.33	172.56	0.00	0.38	0.32	1.25	0.32
slr1138	ctaE	cytochrome c oxidase	87.88	11.63	0	122.43	32.36	0.00	0.03	0.01	1.39	0.48
slr1139	trxA	thioredoxin	227.24	40.00	0	208.11	41.77	0.00	0.41	0.26	0.92	-0.13
slr1140		DegT/DnrJ/EryC1/Strc	115.03	13.92	0	141.36	23.72	0.00	0.03	0.00	1.23	0.30
slr1142		hypothetical protein	123.55	15.56	0	114.22	13.55	0.00	0.30	0.12	0.92	-0.11
slr1143		hypothetical protein	103.45	50.71	5.82E-07	57.11	22.75	0.00	0.07	0.00	0.55	-0.86
slr1145	gltS	Monocomponent sodi	90.25	10.56	0	145.53	29.85	0.00	0.00	0.00	1.61	0.69
slr1147		two-component senso	154.29	13.17	0	155.78	29.50	0.00	0.97	0.97	1.01	0.01
slr1148		unknown protein	202.23	58.91	0	167.84	75.66	0.00	0.28	0.17	0.83	-0.27
slr1149		ATP-binding protein of	127.30	34.46	0	141.99	28.19	0.00	0.40	0.14	1.12	-0.16
slr1150		unknown protein	59.62	12.95	0	91.98	27.39	0.00	0.02	0.00	1.54	0.63
slr1152		hypothetical protein	549.52	82.76	0	468.80	96.85	0.00	0.13	0.04	0.85	-0.23
slr1159	purD	glycinamide ribonucle	118.24	11.92	0	155.02	14.61	0.00	0.00	0.00	1.31	0.39
slr1160		hypothetical protein	88.69	14.17	0	80.78	22.82	0.00	0.40	0.31	0.91	-0.13
slr1161		hypothetical protein	150.17	23.07	0	170.99	72.26	0.00	0.72	0.69	1.14	0.19
slr1162		unknown protein	51.46	9.16	0	51.91	23.01	0.00	0.73	0.71	1.01	0.01
slr1163		unknown protein	159.11	37.21	0	160.18	35.04	0.00	0.94	0.91	1.01	0.01
slr1164		ribonucleotide reducta	169.20	21.73	0	179.26	29.01	0.00	0.53	0.41	1.06	0.08
slr1165		sulfate adenylyltransfe	127.41	18.79	0	148.76	34.60	0.00	0.24	0.14	1.17	0.22
slr1166		UDP-glucose:tetrahyd	84.59	25.19	2.22E-16	95.85	26.27	0.00	0.48	0.27	1.13	0.18
slr1167	gldA	glycerol dehydrogenas	229.94	24.70	0	246.93	41.35	0.00	0.47	0.38	1.07	0.10
slr1168		unknown protein	64.80	13.45	0	11.41	12.44	0.02	0.02	0.01	0.18	-2.51
slr1169		unknown protein	192.95	34.90	0	94.91	9.44	0.00	0.00	0.00	0.49	-1.02
slr1170		hypothetical protein	244.35	19.22	0	216.00	9.11	0.00	0.01	0.00	0.88	-0.18

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1171	gpx1	glutathione peroxidase	242.39	55.15	0	262.84	68.58	0.00	0.59	0.46	1.08	0.12
slr1173		hypothetical protein	280.57	30.14	0	186.15	51.05	0.00	0.01	0.00	0.66	-0.59
slr1174		hypothetical protein	96.83	10.37	0	99.36	11.09	0.00	0.70	0.59	1.03	0.04
slr1176		glucose-1-phosphate t	438.22	100.62	0	703.82	183.59	0.00	0.01	0.00	1.61	0.68
slr1177		hypothetical protein	84.50	20.24	0	123.07	36.46	0.00	0.05	0.00	1.46	0.54
slr1178		hypothetical protein	55.48	10.19	0	47.85	14.27	0.00	0.32	0.25	0.86	-0.21
slr1179		hypothetical protein	286.44	22.85	0	217.24	43.49	0.00	0.01	0.00	0.76	-0.40
slr1181	psbA1	photosystem II D1 pro	335.18	123.66	3.15E-11	511.32	216.07	0.00	0.13	0.03	1.53	0.61
slr1182		hypothetical protein	76.45	7.42	0	60.87	12.04	0.00	0.02	0.00	0.80	-0.33
slr1183		hypothetical protein	9.66	2.92	6.66E-16	8.92	11.45	0.06	0.09	0.06	0.92	-0.11
slr1184		hypothetical protein	9.61	3.03	7.77E-15	15.04	7.87	0.00	0.70	0.69	1.56	0.65
slr1185		Rieske iron-sulfur prot	163.32	73.96	6.34E-08	164.70	63.39	0.00	0.90	0.84	1.01	0.01
slr1186		hypothetical protein	54.62	9.22	0	45.14	15.43	0.00	0.17	0.11	0.83	-0.28
slr1187		unknown protein	328.28	104.08	1.11E-14	314.75	129.11	0.00	0.72	0.66	0.96	-0.06
slr1188		hypothetical protein	415.77	60.62	0	402.71	55.61	0.00	0.71	0.58	0.97	-0.05
slr1189		unknown protein	72.13	5.07	0	79.64	6.36	0.00	0.05	0.00	1.10	0.14
slr1192		probable alcohol dehy	97.40	22.90	0	141.25	29.80	0.00	0.02	0.00	1.45	0.54
slr1194		hypothetical protein	209.89	30.06	0	102.38	17.69	0.00	0.00	0.00	0.49	-1.04
slr1195		hypothetical protein	85.75	12.33	0	90.24	22.17	0.00	0.78	0.75	1.05	0.07
slr1196		hypothetical protein	278.64	4.95	0	290.85	27.76	0.00	0.35	0.32	1.04	0.06
slr1197		SMF protein	66.28	4.45	0	109.67	12.34	0.00	0.00	0.00	1.65	0.73
slr1198		antioxidant protein	1887.03	283.23	0	1246.02	247.89	0.00	0.00	0.00	0.66	-0.60
slr1199	mutL	DNA mismatch repair	255.07	37.30	0	356.09	132.34	0.00	0.09	0.05	1.40	0.48
slr1200		permease protein of bi	117.93	7.88	0	128.15	15.09	0.00	0.19	0.10	1.09	0.12
slr1201		permease protein of bi	181.27	19.11	0	183.56	29.61	0.00	0.93	0.91	1.01	0.02
slr1202		permease protein of si	58.31	12.52	0	88.77	10.13	0.00	0.00	0.00	1.52	0.61
slr1203		hypothetical protein	24.87	7.29	0	21.42	14.93	0.00	0.33	0.31	0.86	-0.22
slr1204		protease	432.03	86.18	0	614.72	90.91	0.00	0.00	0.00	1.42	0.51
slr1205		similar to chlorobenzei	158.07	36.51	0	161.71	41.70	0.00	0.90	0.86	1.02	0.03
slr1206		hypothetical protein	189.30	21.18	0	211.70	24.29	0.00	0.13	0.02	1.12	0.16
slr1207		hypothetical protein	147.72	32.50	0	134.84	28.79	0.00	0.51	0.30	0.91	-0.13
slr1208		probable oxidoreducta	197.39	38.05	0	143.86	37.25	0.00	0.04	0.00	0.73	-0.46
slr1209		hypothetical protein	21.36	3.26	0	7.22	7.72	0.02	0.05	0.02	0.34	-1.56
slr1210		unknown protein	6.27	1.68	0	3.97	7.38	0.19	0.02	0.01	0.63	-0.66
slr1211	cobN	cobalamin biosynthetic	71.93	20.86	0	39.40	7.55	0.00	0.00	0.00	0.55	-0.87
slr1212		similar to two-compo	60.49	10.13	0	93.59	43.98	0.00	0.11	0.07	1.55	0.63
slr1213		two-component respor	113.26	15.63	0	120.87	37.86	0.00	0.81	0.79	1.07	0.09
slr1214		two-component respor	44.21	10.10	0	38.38	16.54	0.00	0.37	0.31	0.87	-0.20
slr1215		hypothetical protein	39.23	7.13	0	31.10	10.09	0.00	0.15	0.08	0.79	-0.34
slr1216		Mg2+ transport proteir	177.31	30.69	0	211.46	82.03	0.00	0.49	0.43	1.19	0.25
slr1218	ycf39	hypothetical protein YC	85.02	12.38	0	34.33	12.85	0.00	0.00	0.00	0.40	-1.31
slr1219	ureE	urease accessory prot	31.19	6.98	0	20.62	17.47	0.00	0.14	0.11	0.66	-0.60
slr1220		hypothetical protein	245.96	37.58	0	215.66	33.19	0.00	0.17	0.03	0.88	-0.19
slr1222		unknown protein	28.22	7.80	0	30.18	16.56	0.00	0.85	0.83	1.07	0.10
slr1223		hypothetical protein	170.22	10.81	0	208.87	19.73	0.00	0.00	0.00	1.23	0.30
slr1224		ATP-binding protein of	138.56	19.71	0	174.12	14.59	0.00	0.01	0.00	1.26	0.33
slr1225		serine/threonine kinas	138.75	14.54	0	133.98	25.12	0.00	0.61	0.55	0.97	-0.05
slr1226	purC	phosphoribosyl aminoi	242.76	40.77	0	244.24	45.82	0.00	0.97	0.96	1.01	0.01
slr1227		chloroplasmic outer env	381.11	54.49	0	290.30	16.04	0.00	0.00	0.00	0.76	-0.39
slr1228		peptide-chain-release	226.71	24.43	0	379.21	38.96	0.00	0.00	0.00	1.67	0.74
slr1229		sulfate permease	94.65	7.49	0	162.09	28.69	0.00	0.00	0.00	1.71	0.78
slr1230		hypothetical protein	23.53	3.02	0	38.20	8.06	0.00	0.00	0.00	1.62	0.70
slr1232		unknown protein	57.29	12.11	0	25.55	12.62	0.00	0.01	0.00	0.45	-1.16
slr1233		succinate dehydrogen	239.82	41.87	0	147.95	34.63	0.00	0.00	0.00	0.62	-0.70
slr1234		protein kinase C inhibi	47.50	4.41	0	35.57	17.50	0.00	0.10	0.06	0.75	-0.42
slr1235		hypothetical protein	76.58	18.84	0	81.09	16.73	0.00	0.64	0.41	1.06	0.08
slr1236		hypothetical protein	74.22	10.98	0	84.13	18.90	0.00	0.34	0.24	1.13	0.18
slr1237		cytosine deaminase	358.36	74.17	0	546.84	192.11	0.00	0.03	0.00	1.53	0.61
slr1238	gshB	glutathione synthetase	77.97	13.11	0	117.01	17.48	0.00	0.00	0.00	1.50	0.59
slr1239	pntA	pyridine nucleotide tra	472.14	83.99	0	550.00	171.98	0.00	0.36	0.27	1.16	0.22
slr1240		unknown protein	93.69	14.38	0	57.78	12.28	0.00	0.00	0.00	0.62	-0.70
slr1241		hypothetical protein	26.92	6.49	0	15.98	7.91	0.00	0.23	0.20	0.59	-0.75
slr1243		unknown protein	84.70	19.18	0	113.96	26.56	0.00	0.06	0.00	1.35	0.43
slr1245	pys	transcriptional regulat	22.04	6.65	4.44E-16	19.72	17.54	0.01	0.20	0.17	0.89	-0.16
slr1246		putative transposase [	59.56	13.09	0	53.22	16.54	0.00	0.41	0.30	0.89	-0.16
slr1247		phosphate-binding per	60.31	8.92	0	80.70	64.68	0.00	0.89	0.89	1.34	0.42
slr1248		phosphate transport s	65.82	20.25	1.78E-15	76.01	29.88	0.00	0.53	0.38	1.15	0.21
slr1249		phosphate transport s	67.13	16.78	0	104.31	17.16	0.00	0.00	0.00	1.55	0.64
slr1250		phosphate transport A	39.02	11.42	0	65.61	20.13	0.00	0.02	0.00	1.68	0.75
slr1251		peptidyl-prolyl cis-trans	98.28	25.05	0	148.35	46.56	0.00	0.04	0.00	1.51	0.59
slr1253		unknown protein	129.76	22.91	0	120.86	32.26	0.00	0.50	0.40	0.93	-0.10
slr1254	pds	phytoene dehydrogen	249.17	40.14	0	226.35	26.41	0.00	0.25	0.04	0.91	-0.14
slr1255		phytoene synthase	167.71	39.07	0	161.19	28.24	0.00	0.80	0.67	0.96	-0.06
slr1256	ureA	urease gamma subuni	42.35	11.22	0	19.41	21.07	0.02	0.08	0.05	0.46	-1.13
slr1257		unknown protein	104.21	5.38	0	108.19	13.45	0.00	0.58	0.54	1.04	0.05
slr1258		unknown protein	129.12	25.84	0	153.74	28.02	0.00	0.15	0.02	1.19	0.25
slr1259		hypothetical protein	339.60	19.14	0	485.50	22.57	0.00	0.00	0.00	1.43	0.52
slr1260		hypothetical protein	55.12	5.59	0	77.88	24.64	0.00	0.03	0.01	1.41	0.50

Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1261		hypothetical protein	225.22	22.68	0	397.78	61.42	0.00	0.00	0.00	1.77	0.82
slr1262		hypothetical protein	174.18	27.44	0	113.64	17.10	0.00	0.00	0.00	0.65	-0.62
slr1263		hypothetical protein	260.63	41.94	0	151.19	46.28	0.00	0.00	0.00	0.58	-0.79
slr1265	rpoC1	RNA polymerase gamma	502.58	98.35	0	571.46	129.13	0.00	0.36	0.21	1.14	0.19
slr1266		hypothetical protein	67.19	13.28	0	53.30	7.50	0.00	0.05	0.00	0.79	-0.33
slr1267	ftsW	cell division protein Fts	78.34	23.72	6.66E-16	76.71	32.49	0.00	0.80	0.75	0.98	-0.03
slr1269	ggT	gamma-glutamyltransf	293.50	202.77	0.000392	221.36	169.72	0.00	0.38	0.21	0.75	-0.41
slr1270		hypothetical protein	371.28	97.73	0	364.52	130.26	0.00	0.82	0.77	0.98	-0.03
slr1271		probable UDP-N-acety	73.65	14.89	0	54.77	29.73	0.00	0.17	0.13	0.74	-0.43
slr1272		probable porin; major	693.37	83.96	0	564.71	126.85	0.00	0.06	0.01	0.81	-0.30
slr1273		hypothetical protein	262.62	24.74	0	207.12	35.73	0.00	0.01	0.00	0.79	-0.34
slr1274	pilM	probable fimbrial asse	223.64	48.91	0	122.52	33.82	0.00	0.00	0.00	0.55	-0.87
slr1275		hypothetical protein	162.94	20.95	0	89.27	17.11	0.00	0.00	0.00	0.55	-0.87
slr1276		hypothetical protein	233.46	43.85	0	115.59	33.43	0.00	0.00	0.00	0.50	-1.01
slr1277		general secretion path	802.08	73.92	0	700.48	81.22	0.00	0.05	0.00	0.87	-0.20
slr1278	ycf62	hypothetical protein Yc	48.32	17.27	7.16E-12	52.63	27.28	0.00	0.94	0.93	1.09	0.12
slr1279	ndhC	NADH dehydrogenase	100.96	9.37	0	101.65	13.75	0.00	0.96	0.95	1.01	0.01
slr1280	ndhK	NADH dehydrogenase	278.48	56.38	0	230.17	65.86	0.00	0.16	0.06	0.83	-0.27
slr1281	ndhJ	NADH dehydrogenase	104.87	13.70	0	162.85	37.89	0.00	0.00	0.00	1.55	0.63
slr1282		putative transposase [	29.72	6.51	0	39.56	11.47	0.00	0.13	0.04	1.33	0.41
slr1283		putative transposase [	542.51	115.64	0	532.49	138.55	0.00	0.84	0.80	0.98	-0.03
slr1285		two-component senso	202.89	43.79	0	178.45	37.25	0.00	0.35	0.16	0.88	-0.19
slr1287		hypothetical protein	168.37	59.63	4.62E-12	159.49	71.35	0.00	0.73	0.65	0.95	-0.08
slr1288		hypothetical protein	80.04	10.37	0	65.20	4.65	0.00	0.01	0.00	0.81	-0.30
slr1289	icd	isocitrate dehydrogen	179.70	31.90	0	157.55	49.97	0.00	0.32	0.24	0.88	-0.19
slr1290		hypothetical protein	118.13	7.65	0	104.84	15.93	0.00	0.10	0.05	0.89	-0.17
slr1291	ndhD2	NADH dehydrogenase	136.87	15.10	0	183.39	32.90	0.00	0.01	0.00	1.34	0.42
slr1293		similar to phytoene	106.23	10.37	0	141.49	19.02	0.00	0.00	0.00	1.33	0.41
slr1295	futA1	iron transport system	563.68	101.16	0	362.15	47.67	0.00	0.00	0.00	0.64	-0.64
slr1298		unknown protein	1041.77	235.81	0	1127.26	288.76	0.00	0.61	0.48	1.08	0.11
slr1299		UDP-glucose dehydro	131.70	6.54	0	141.64	10.54	0.00	0.08	0.02	1.08	0.10
slr1300		similar to 2-octaprenyl	279.18	50.21	0	274.05	45.93	0.00	0.86	0.80	0.98	-0.03
slr1301		hypothetical protein	189.47	29.07	0	209.19	56.77	0.00	0.52	0.44	1.10	0.14
slr1302	cupB	protein involved in con	387.72	25.99	0	278.47	52.08	0.00	0.00	0.00	0.72	-0.48
slr1303		hypothetical protein	89.27	16.30	0	128.79	28.51	0.00	0.01	0.00	1.44	0.53
slr1305		two-component respon	106.48	10.84	0	131.31	26.50	0.00	0.06	0.02	1.23	0.30
slr1306		hypothetical protein	158.58	24.78	0	135.33	50.08	0.00	0.28	0.22	0.85	-0.23
slr1307		hypothetical protein	50.86	4.37	0	47.03	7.09	0.00	0.27	0.19	0.92	-0.11
slr1311	psbA2	photosystem II D1 pro	11695.82	1522.32	0	12512.54	3215.35	0.00	0.74	0.71	1.07	0.10
slr1312		arginine decarboxylas	195.72	25.74	0	114.34	13.67	0.00	0.00	0.00	0.58	-0.78
slr1315		hypothetical protein	109.92	24.44	0	74.99	27.37	0.00	0.04	0.01	0.68	-0.55
slr1316		iron-uptake system pe	184.56	36.72	0	218.23	27.94	0.00	0.08	0.00	1.18	0.24
slr1317		iron-uptake system pe	70.06	11.85	0	101.72	13.17	0.00	0.00	0.00	1.45	0.54
slr1318		iron-uptake system AT	122.82	24.12	0	109.15	39.36	0.00	0.38	0.29	0.89	-0.17
slr1319		iron-uptake system bir	459.33	36.48	0	490.94	18.01	0.00	0.08	0.00	1.07	0.10
slr1322	tlpD	putative modulator of l	254.33	48.65	0	271.00	31.72	0.00	0.45	0.13	1.07	0.09
slr1324		two-component hybrid	587.44	52.35	0	533.27	81.20	0.00	0.19	0.11	0.91	-0.14
slr1325		GTP pyrophosphokina	1216.91	100.95	0	817.38	97.68	0.00	0.00	0.00	0.67	-0.57
slr1327		hypothetical protein	28.85	3.46	0	9.93	5.71	0.00	0.00	0.00	0.34	-1.54
slr1329	atpB	ATP synthase beta su	1270.48	315.25	0	1817.88	773.16	0.00	0.12	0.05	1.43	0.52
slr1330	atpE	ATP synthase epsilon	205.40	42.68	0	318.68	60.24	0.00	0.00	0.00	1.55	0.63
slr1331		processing protease	163.04	44.76	0	154.05	44.06	0.00	0.79	0.67	0.94	-0.08
slr1332		beta ketoacyl-acyl can	76.83	9.50	0	92.47	11.69	0.00	0.03	0.00	1.20	0.27
slr1334		phosphoglucomutase/	114.20	19.60	0	158.54	25.77	0.00	0.01	0.00	1.39	0.47
slr1336		H+/Ca2+ exchanger	106.79	11.04	0	107.10	26.42	0.00	0.86	0.84	1.00	0.00
slr1338		hypothetical protein	78.83	20.61	0	42.76	23.75	0.00	0.16	0.13	0.54	-0.88
slr1339		hypothetical protein	34.91	6.03	0	28.19	9.18	0.00	0.11	0.04	0.81	-0.31
slr1340		unknown protein	15.81	2.75	0	6.06	8.08	0.07	0.03	0.01	0.38	-1.38
slr1342		hypothetical protein	111.43	24.42	0	126.28	48.83	0.00	0.63	0.56	1.13	0.18
slr1343		hypothetical protein	120.21	47.55	5.91E-10	167.83	43.91	0.00	0.08	0.00	1.40	0.48
slr1344		hypothetical protein	104.36	18.38	0	109.43	23.97	0.00	0.73	0.63	1.05	0.07
slr1347	icfA	carbonic anhydrase	185.76	30.59	0	129.96	18.41	0.00	0.00	0.00	0.70	-0.52
slr1348	cysE	serine acetyltransfer	263.99	40.77	0	272.18	32.05	0.00	0.67	0.49	1.03	0.04
slr1349		glucose-6-phosphate i	223.34	21.20	0	270.93	50.53	0.00	0.05	0.01	1.21	0.28
slr1350	desA	fatty acid desaturase	197.31	27.42	0	181.41	33.81	0.00	0.36	0.24	0.92	-0.12
slr1351	murF	UDP-N-acetylmuramo	152.80	32.66	0	199.63	31.89	0.00	0.03	0.00	1.31	0.39
slr1353		hypothetical protein	100.92	12.87	0	142.85	18.30	0.00	0.00	0.00	1.42	0.50
slr1356	rps1a	30S ribosomal protein	519.39	65.60	0	603.09	56.68	0.00	0.04	0.00	1.16	0.22
slr1357		putative transposase [	97.60	24.38	0	622.93	227.65	0.00	0.00	0.00	6.38	2.67
slr1362		hypothetical protein	19.98	2.79	0	26.17	6.88	0.00	0.09	0.04	1.31	0.39
slr1363		hypothetical protein	183.24	49.87	0	160.36	39.42	0.00	0.48	0.28	0.88	-0.19
slr1364	bioB	biotin synthetase	198.92	34.95	0	249.68	35.53	0.00	0.03	0.00	1.26	0.33
slr1365		hypothetical protein	62.67	7.82	0	108.99	15.22	0.00	0.00	0.00	1.74	0.80
slr1366		lipoprotein signal pepti	86.13	21.61	0	79.81	32.82	0.00	0.54	0.50	0.93	-0.11
slr1367		glycogen phosphorylat	147.42	33.27	0	255.10	93.73	0.00	0.03	0.00	1.73	0.79
slr1368	cobL	precoarnin decarboxyl	67.77	22.99	5.16E-13	144.75	30.12	0.00	0.00	0.00	2.14	1.09
slr1369	cdsA	phosphatidate cytidyl	318.25	43.67	0	357.87	71.91	0.00	0.29	0.16	1.12	0.17
slr1376		hypothetical protein	80.88	21.27	0	60.30	35.86	0.00	0.18	0.13	0.75	-0.42

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1377		signal peptidase I	105.47	14.35	0	105.88	17.39	0.00	0.99	0.99	1.00	0.01
slr1378		hypothetical protein	107.39	20.57	0	63.31	20.94	0.00	0.00	0.00	0.59	-0.76
slr1379	cydA	cytochrome oxidase d	150.15	16.47	0	235.35	88.90	0.00	0.03	0.01	1.57	0.65
slr1380	cydB	cytochrome oxidase d	143.51	32.39	0	148.85	20.78	0.00	0.66	0.38	1.04	0.05
slr1383		unknown protein	74.72	25.82	1.36E-12	58.50	33.98	0.00	0.24	0.15	0.78	-0.35
slr1384		hypothetical protein	66.83	10.86	0	101.37	40.58	0.00	0.07	0.02	1.52	0.60
slr1385		unknown protein	102.80	12.32	0	79.35	13.14	0.00	0.01	0.00	0.77	-0.37
slr1390	ftsH	cell division protein Fts	390.34	57.86	0	395.10	73.03	0.00	0.92	0.89	1.01	0.02
slr1391		unknown protein	45.87	3.72	0	63.70	24.49	0.00	0.10	0.06	1.39	0.47
slr1392	feoB	ferrous iron transport p	218.54	26.97	0	210.23	54.41	0.00	0.62	0.57	0.96	-0.06
slr1393		two-component senso	438.56	67.07	0	434.18	61.97	0.00	0.91	0.87	0.99	-0.01
slr1394		hypothetical protein	61.84	9.18	0	46.71	9.46	0.00	0.02	0.00	0.76	-0.40
slr1395		hypothetical protein	66.08	14.92	0	42.13	13.14	0.00	0.02	0.00	0.64	-0.65
slr1396		unknown protein	83.93	24.78	0	86.49	27.74	0.00	0.92	0.90	1.03	0.04
slr1397		unknown protein	215.91	77.27	7.67E-12	160.09	96.59	0.00	0.20	0.12	0.74	-0.43
slr1398		unknown protein	26.41	6.14	0	25.04	14.88	0.00	0.46	0.43	0.95	-0.08
slr1400		two-component hybrid	160.06	17.17	0	171.81	14.68	0.00	0.22	0.04	1.07	0.10
slr1403		unknown protein	702.95	111.58	0	803.10	191.57	0.00	0.33	0.21	1.14	0.19
slr1406		hypothetical protein	125.70	18.48	0	38.85	6.34	0.00	0.00	0.00	0.31	-1.89
slr1407		unknown protein	87.92	13.06	0	79.82	30.77	0.00	0.43	0.38	0.91	-0.14
slr1409		WD-repeat protein	691.23	67.29	0	749.44	96.40	0.00	0.28	0.15	1.08	0.12
slr1410		WD-repeat protein	510.55	81.98	0	560.84	92.75	0.00	0.34	0.16	1.10	0.14
slr1411		hypothetical protein	99.89	16.30	0	117.12	15.62	0.00	0.10	0.01	1.17	0.23
slr1413		hypothetical protein	190.75	25.56	0	172.29	34.63	0.00	0.30	0.16	0.90	-0.15
slr1414		two-component senso	149.31	20.79	0	117.74	19.58	0.00	0.03	0.00	0.79	-0.34
slr1415		hypothetical protein	133.47	28.70	0	212.49	34.88	0.00	0.00	0.00	1.59	0.67
slr1416		similar to MorR protein	155.02	41.18	0	122.99	25.56	0.00	0.20	0.02	0.79	-0.33
slr1417	ycf57	hypothetical protein Yc	247.97	62.62	0	214.11	47.10	0.00	0.35	0.11	0.86	-0.21
slr1418	pyrD	dihydroorotate dehydr	73.70	8.04	0	109.21	21.83	0.00	0.00	0.00	1.48	0.57
slr1419		hypothetical protein	54.14	7.71	0	50.21	7.30	0.00	0.37	0.20	0.93	-0.11
slr1420		probable sugar kinase	104.35	17.12	0	53.95	9.80	0.00	0.00	0.00	0.52	-0.95
slr1421		unknown protein	19.45	6.18	1.24E-14	7.21	8.59	0.04	0.03	0.01	0.37	-1.43
slr1423	murC	UDP-N-acetylmuramat	279.47	29.19	0	303.35	47.87	0.00	0.36	0.26	1.09	0.12
slr1424		UDP-N-acetylenolpyru	189.40	20.51	0	133.90	15.73	0.00	0.00	0.00	0.71	-0.50
slr1425		hypothetical protein	35.34	5.03	0	20.57	11.52	0.00	0.03	0.01	0.58	-0.78
slr1426	recR	recombination protein	66.62	11.39	0	43.84	15.75	0.00	0.04	0.01	0.66	-0.60
slr1428		hypothetical protein	203.29	66.11	5E-14	183.29	46.31	0.00	0.66	0.46	0.90	-0.15
slr1429		hypothetical protein	86.83	26.61	1.33E-15	77.26	12.18	0.00	0.50	0.14	0.89	-0.17
slr1431		hypothetical protein	313.23	52.31	0	293.18	66.25	0.00	0.54	0.42	0.94	-0.10
slr1434	pntB	pyridine nucleotide tra	375.89	46.84	0	416.11	82.72	0.00	0.38	0.27	1.11	0.15
slr1435		PmbA protein homoloq	101.99	32.47	1.44E-14	124.93	48.63	0.00	0.43	0.29	1.22	0.29
slr1436		unknown protein	41.69	9.02	0	60.01	16.42	0.00	0.03	0.00	1.44	0.53
slr1437		unknown protein	129.13	49.58	1.77E-10	36.36	7.11	0.00	0.00	0.00	0.28	-1.83
slr1438		hypothetical protein	140.51	18.40	0	124.28	23.34	0.00	0.19	0.09	0.88	-0.18
slr1440		hypothetical protein	95.67	27.72	0	65.87	25.62	0.00	0.09	0.03	0.69	-0.54
slr1441		hypothetical protein	24.95	5.44	0	28.66	9.96	0.00	0.63	0.57	1.15	0.20
slr1442		hypothetical protein	234.89	75.24	2.04E-14	406.82	130.75	0.00	0.02	0.00	1.73	0.79
slr1443		serine/threonine kinas	163.59	59.01	1.12E-11	213.20	55.82	0.00	0.18	0.01	1.30	0.38
slr1444		hypothetical protein	121.78	19.58	0	54.38	16.46	0.00	0.00	0.00	0.45	-1.16
slr1448		fructokinase	108.71	16.47	0	69.79	12.78	0.00	0.00	0.00	0.64	-0.64
slr1449		hypothetical protein	108.88	10.12	0	71.53	22.66	0.00	0.01	0.00	0.66	-0.61
slr1450		unknown protein	17.61	3.38	0	5.93	10.31	0.16	0.02	0.01	0.34	-1.57
slr1451		hypothetical protein	76.52	3.42	0	63.98	12.83	0.00	0.04	0.02	0.84	-0.26
slr1452	sbpA	sulfate transport syste	520.19	52.02	0	542.78	132.55	0.00	0.87	0.86	1.04	0.06
slr1453	cysT	sulfate transport syste	76.45	11.21	0	131.70	36.55	0.00	0.00	0.00	1.72	0.78
slr1454	cysW	sulfate transport syste	651.61	95.47	0	576.68	132.58	0.00	0.27	0.16	0.89	-0.18
slr1455	cysA	sulfate transport syste	324.34	79.93	0	339.66	84.87	0.00	0.78	0.70	1.05	0.07
slr1456		unknown protein	37.50	6.13	0	54.25	8.50	0.00	0.00	0.00	1.45	0.53
slr1457		chromate transport pr	76.49	11.82	0	172.89	18.15	0.00	0.00	0.00	2.26	1.18
slr1459	apcF	phycobilisome core co	1008.81	162.47	0	1099.64	63.69	0.00	0.19	0.00	1.09	0.12
slr1461		hypothetical protein	75.25	14.82	0	90.66	11.45	0.00	0.05	0.00	1.20	0.27
slr1462		hypothetical protein	256.04	80.07	4.66E-15	213.52	60.01	0.00	0.38	0.19	0.83	-0.26
slr1463	fus	elongation factor EF-C	1258.15	84.63	0	1226.02	28.31	0.00	0.44	0.01	0.97	-0.04
slr1464		hypothetical protein	27.33	2.59	0	42.03	7.33	0.00	0.00	0.00	1.54	0.62
slr1467		precorrin isomerase	81.96	19.86	0	71.34	14.78	0.00	0.36	0.12	0.87	-0.20
slr1468		hypothetical protein	28.01	3.18	0	16.03	10.09	0.00	0.20	0.17	0.57	-0.80
slr1469	mpA	protein subunit of ribo	131.51	23.08	0	140.11	19.40	0.00	0.47	0.22	1.07	0.09
slr1470		hypothetical protein	190.07	42.62	0	175.91	30.55	0.00	0.59	0.34	0.93	-0.11
slr1471		hypothetical protein	672.36	203.55	6.66E-16	513.64	145.52	0.00	0.13	0.01	0.76	-0.39
slr1472		hypothetical protein	55.96	9.86	0	41.69	16.48	0.00	0.09	0.05	0.74	-0.42
slr1474		hypothetical protein	67.45	11.87	0	85.76	6.24	0.00	0.01	0.00	1.27	0.35
slr1476	pyrB	aspartate carbamoyltr	257.35	43.43	0	224.39	66.31	0.00	0.30	0.20	0.87	-0.20
slr1478		hypothetical protein	165.67	21.85	0	112.26	21.93	0.00	0.00	0.00	0.68	-0.56
slr1484		unknown protein	261.68	29.96	0	315.93	76.92	0.00	0.14	0.07	1.21	0.27
slr1485		unknown protein	52.68	11.76	0	33.36	26.34	0.00	0.14	0.11	0.63	-0.66
slr1488		ATP-binding protein of	1120.98	206.88	0	1081.54	170.55	0.00	0.74	0.60	0.96	-0.05
slr1489		transcriptional regulat	55.85	7.05	0	79.50	10.19	0.00	0.00	0.00	1.42	0.51
slr1490		ferriochrome-iron recep	136.28	35.57	0	103.42	25.06	0.00	0.10	0.00	0.76	-0.40



Table A-1 Gene expression profiles for *Synechococcus* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1491		iron(III) dicitrate-bindin	102.60	26.27	0	121.64	42.37	0.00	0.50	0.40	1.19	0.25
slr1492		iron(III) dicitrate-bindin	580.96	123.67	0	527.17	189.85	0.00	0.46	0.38	0.91	-0.14
slr1493		hypothetical protein	32.97	5.06	0	17.66	16.96	0.01	0.10	0.07	0.54	-0.90
slr1494		ATP-binding protein of	228.89	30.36	0	199.79	34.73	0.00	0.14	0.04	0.87	-0.20
slr1495		hypothetical protein	216.73	7.05	0	189.21	25.11	0.00	0.03	0.01	0.87	-0.20
slr1498	hypD	hydrogenase isoenzyn	74.79	10.28	0	114.68	26.90	0.00	0.01	0.00	1.53	0.62
slr1501		probable acetyltransfe	46.28	8.49	0	40.57	26.65	0.00	0.33	0.29	0.88	-0.19
slr1503		hypothetical protein	150.67	38.46	0	195.56	56.21	0.00	0.13	0.03	1.30	0.38
slr1505		unknown protein	206.50	66.73	3.46E-14	197.46	86.21	0.00	0.68	0.62	0.96	-0.06
slr1506		hypothetical protein	603.45	67.45	0	489.62	82.58	0.00	0.02	0.00	0.81	-0.30
slr1507		hypothetical protein	181.92	27.83	0	131.81	13.30	0.00	0.00	0.00	0.72	-0.46
slr1508		probable glycosyltrans	246.34	34.11	0	181.31	26.26	0.00	0.00	0.00	0.74	-0.44
slr1509		V-type sodium ATP sy	197.80	56.22	0	130.33	17.62	0.00	0.01	0.00	0.66	-0.60
slr1510	plsX	fatty acid/phospholipid	166.91	26.23	0	217.53	50.77	0.00	0.06	0.01	1.30	0.38
slr1511	fabH	3-oxoacyl-acyl-carrier	85.27	10.13	0	103.61	14.58	0.00	0.02	0.00	1.22	0.28
slr1512		hypothetical protein	64.45	13.39	0	96.79	37.08	0.00	0.09	0.03	1.50	0.59
slr1513		hypothetical protein	44.07	4.81	0	46.76	19.78	0.00	0.98	0.97	1.06	0.09
slr1515		hypothetical protein	154.36	30.96	0	173.48	43.35	0.00	0.43	0.28	1.12	0.17
slr1516	sodB	superoxide dismutase	1005.94	248.37	0	3141.21	682.56	0.00	0.00	0.00	3.12	1.64
slr1517	leuB	3-isopropylmalate deh	141.22	12.33	0	261.83	26.32	0.00	0.00	0.00	1.85	0.89
slr1518	menA	1,4-dihydroxy-2-napht	115.28	14.75	0	153.34	16.49	0.00	0.00	0.00	1.33	0.41
slr1519		hypothetical protein	111.00	8.73	0	115.28	13.72	0.00	0.57	0.48	1.04	0.05
slr1520		oxidoreductase, aldo/k	65.47	12.78	0	82.36	12.56	0.00	0.04	0.00	1.26	0.33
slr1521		GTP-binding protein	146.99	27.84	0	73.69	13.76	0.00	0.00	0.00	0.50	-1.00
slr1522		putative transposase [	173.49	58.63	4.24E-13	397.72	90.14	0.00	0.00	0.00	2.29	1.20
slr1523		putative transposase	14.42	2.92	0	10.66	7.79	0.00	0.25	0.22	0.74	-0.44
slr1524		putative transposase [	64.86	14.89	0	474.81	119.80	0.00	0.00	0.00	7.32	2.87
slr1529		nitrogen assimilation r	1732.56	223.85	0	2640.36	881.82	0.00	0.02	0.00	1.52	0.61
slr1530		hypothetical protein	80.22	14.52	0	49.00	18.61	0.00	0.01	0.00	0.61	-0.71
slr1531	fhf	signal recognition parti	229.41	18.90	0	219.52	32.38	0.00	0.50	0.42	0.96	-0.06
slr1533		hypothetical protein	15.18	2.58	0	9.02	8.25	0.01	0.17	0.14	0.59	-0.75
slr1534		hypothetical protein	107.57	10.33	0	116.17	9.14	0.00	0.16	0.02	1.08	0.11
slr1535		hypothetical protein	342.84	20.33	0	549.91	119.10	0.00	0.00	0.00	1.60	0.68
slr1536	recQ	ATP-dependent DNA I	96.59	12.07	0	174.92	36.57	0.00	0.00	0.00	1.81	0.86
slr1537		unknown protein	65.54	10.29	0	55.02	18.04	0.00	0.20	0.13	0.84	-0.25
slr1538		cobalamin biosynthesi	58.83	5.46	0	84.74	20.10	0.00	0.01	0.00	1.44	0.53
slr1540		mRNA-binding protein	138.54	28.11	0	109.23	31.81	0.00	0.11	0.03	0.79	-0.34
slr1541		hypothetical protein	59.49	11.23	0	46.53	18.37	0.00	0.14	0.08	0.78	-0.35
slr1542		2-C-methyl-D-erythrit	37.42	4.62	0	36.93	12.33	0.00	0.71	0.69	0.99	-0.02
slr1543		DNA-damage-inducibl	551.34	139.75	0	399.80	119.06	0.00	0.10	0.02	0.73	-0.46
slr1544		unknown protein	183.08	38.28	0	242.67	46.16	0.00	0.02	0.00	1.33	0.41
slr1545	sigG	group3 RNA polymera	1506.81	266.77	0	1161.27	199.57	0.00	0.03	0.00	0.77	-0.38
slr1546		hypothetical protein	215.13	33.50	0	225.21	22.81	0.00	0.52	0.20	1.05	0.07
slr1547		hypothetical protein	166.74	47.41	0	153.01	86.82	0.00	0.48	0.42	0.92	-0.12
slr1549		polypeptide deformylas	136.17	24.57	0	179.29	46.77	0.00	0.06	0.01	1.32	0.40
slr1550	lysS	lysyl-tRNA synthelase	133.99	28.60	0	166.34	28.09	0.00	0.10	0.00	1.24	0.31
slr1552		unknown protein	123.09	16.78	0	117.73	40.17	0.00	0.58	0.54	0.96	-0.06
slr1556		2-hydroxyacid dehydroc	65.70	11.13	0	58.44	19.16	0.00	0.36	0.29	0.89	-0.17
slr1557		hypothetical protein	143.00	10.71	0	188.19	29.56	0.00	0.00	0.00	1.32	0.40
slr1559	aroE	shikimate 5-dehydroge	95.58	17.58	0	84.60	24.90	0.00	0.32	0.20	0.89	-0.18
slr1560	hisS	histidyl tRNA syntheta	500.99	58.31	0	526.20	59.01	0.00	0.46	0.28	1.05	0.07
slr1562		glutaredoxin	45.53	3.31	0	29.06	11.12	0.00	0.01	0.00	0.64	-0.65
slr1563		hypothetical protein	68.56	6.91	0	76.88	6.99	0.00	0.07	0.00	1.12	0.17
slr1564	sigF	group3 RNA polymera	147.44	16.63	0	131.34	12.54	0.00	0.09	0.00	0.89	-0.17
slr1565		hypothetical protein	103.88	11.46	0	96.05	18.59	0.00	0.34	0.25	0.92	-0.11
slr1566		hypothetical protein	189.49	34.91	0	120.09	21.23	0.00	0.00	0.00	0.63	-0.66
slr1567		unknown protein	223.66	29.64	0	244.72	54.60	0.00	0.45	0.35	1.09	0.13
slr1568		hypothetical protein	49.50	11.26	0	23.20	19.46	0.00	0.10	0.07	0.47	-1.09
slr1570		hypothetical protein	79.29	6.43	0	88.48	8.47	0.00	0.06	0.00	1.12	0.16
slr1571		unknown protein	77.80	22.40	0	70.94	18.51	0.00	0.61	0.42	0.91	-0.13
slr1572		hypothetical protein	399.89	105.52	0	278.56	54.54	0.00	0.02	0.00	0.70	-0.52
slr1573		hypothetical protein	197.63	38.05	0	193.90	27.45	0.00	0.90	0.83	0.98	-0.03
slr1575		probable potassium ef	214.51	15.56	0	203.59	14.22	0.00	0.24	0.07	0.95	-0.08
slr1576		unknown protein	32.04	8.41	0	18.37	14.74	0.00	0.18	0.14	0.57	-0.80
slr1577		hypothetical protein	136.97	15.70	0	146.05	17.44	0.00	0.40	0.23	1.07	0.09
slr1579		hypothetical protein	195.31	14.03	0	252.79	22.90	0.00	0.00	0.00	1.29	0.37
slr1583		hypothetical protein	155.47	30.13	0	173.69	15.04	0.00	0.20	0.00	1.12	0.16
slr1584		two-component transc	189.35	48.19	0	129.66	31.30	0.00	0.03	0.00	0.68	-0.55
slr1585		putative transposase [	29.85	6.45	0	48.90	15.13	0.00	0.01	0.00	1.64	0.71
slr1586		putative transposase [	28.81	6.98	0	22.69	9.47	0.00	0.17	0.09	0.79	-0.34
slr1588		two-component transc	175.71	38.84	0	144.64	56.60	0.00	0.25	0.17	0.82	-0.28
slr1590		hypothetical protein	124.71	27.89	0	122.30	19.81	0.00	0.94	0.90	0.98	-0.03
slr1591		hypothetical protein	183.23	41.82	0	74.71	16.48	0.00	0.00	0.00	0.41	-1.29
slr1592		probable pseudouridin	110.20	38.49	2.32E-12	131.27	49.58	0.00	0.47	0.33	1.19	0.25
slr1593		hypothetical protein	779.78	149.88	0	773.82	172.64	0.00	0.91	0.88	0.99	-0.01
slr1594		two-component respor	59.00	14.82	0	73.05	21.22	0.00	0.19	0.06	1.24	0.31
slr1595	nhaS4	Na <sup>+</sup> /H <sup>+</sup> antiporter	466.29	85.40	0	521.08	169.65	0.00	0.52	0.44	1.12	0.16
slr1596	pxcA	a protein in the cytopl	84.37	6.15	0	128.25	44.84	0.00	0.04	0.01	1.52	0.60

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1597		chromosome partitioni	58.35	11.80	0	156.70	38.75	0.00	0.00	0.00	2.69	1.43
slr1598		lipoic acid synthetase	130.99	18.31	0	100.49	21.76	0.00	0.03	0.00	0.77	-0.38
slr1599		hypothetical protein	59.83	10.58	0	73.27	6.28	0.00	0.02	0.00	1.22	0.29
slr1600		hypothetical protein	130.89	15.89	0	138.33	25.42	0.00	0.60	0.50	1.06	0.08
slr1601		hypothetical protein	98.36	32.42	1.07E-13	89.35	37.44	0.00	0.57	0.45	0.91	-0.14
slr1603		hypothetical protein	254.14	63.72	0	395.02	136.45	0.00	0.03	0.00	1.55	0.64
slr1604	ftsH	cell division protein Fts	675.67	201.14	2.22E-16	711.96	276.15	0.00	0.86	0.82	1.05	0.08
slr1608		hypothetical protein	122.35	34.01	0	96.07	15.67	0.00	0.16	0.00	0.79	-0.35
slr1609		long-chain-fatty-acid C	870.43	132.30	0	894.52	155.95	0.00	0.78	0.70	1.03	0.04
slr1610		putative C-3 methyl tr	149.32	26.55	0	108.25	13.49	0.00	0.00	0.00	0.72	-0.46
slr1611		hypothetical protein	82.12	18.28	0	28.52	16.28	0.00	0.12	0.09	0.35	-1.53
slr1612		hypothetical protein	144.43	46.67	3.44E-14	78.87	29.70	0.00	0.02	0.00	0.55	-0.87
slr1613		hypothetical protein	43.93	16.32	4.36E-11	6.32	8.66	0.07	0.01	0.00	0.14	-2.80
slr1614		hypothetical protein	4.57	2.78	5.56E-05	0.90	1.37	0.11	0.01	0.00	0.20	-2.34
slr1615	rfbE	perosamine synthetas	74.79	14.70	0	69.71	23.30	0.00	0.56	0.49	0.93	-0.10
slr1616		unknown protein	78.43	20.16	0	56.40	32.44	0.00	0.13	0.07	0.72	-0.48
slr1617		similar to UDP-glucose	162.54	39.89	0	86.58	21.21	0.00	0.00	0.00	0.53	-0.91
slr1618		unknown protein	62.94	19.17	8.88E-16	49.48	39.69	0.00	0.22	0.18	0.79	-0.35
slr1619		hypothetical protein	101.89	17.55	0	55.10	10.73	0.00	0.00	0.00	0.54	-0.89
slr1622	ppa	soluble inorganic pyro	275.29	28.75	0	171.78	49.63	0.00	0.00	0.00	0.62	-0.68
slr1623		hypothetical protein	110.18	16.28	0	54.22	12.20	0.00	0.00	0.00	0.49	-1.02
slr1624		hypothetical protein	448.03	50.78	0	354.32	42.81	0.00	0.01	0.00	0.79	-0.34
slr1626		dihydroneopterin aldol	42.02	4.19	0	38.36	17.02	0.00	0.41	0.38	0.91	-0.13
slr1627		unknown protein	114.09	37.44	8.33E-14	79.35	64.76	0.00	0.16	0.12	0.70	-0.52
slr1628		hypothetical protein	36.11	6.38	0	21.98	16.34	0.00	0.18	0.15	0.61	-0.72
slr1629		ribosomal large subun	107.50	32.63	6.66E-16	82.35	18.57	0.00	0.16	0.01	0.77	-0.38
slr1634		hypothetical protein	1085.16	379.07	2.35E-12	427.47	112.50	0.00	0.00	0.00	0.39	-1.34
slr1635		putative transposase [	357.36	47.92	0	577.93	57.83	0.00	0.00	0.00	1.62	0.69
slr1636		unknown protein	2374.80	256.77	0	1228.94	259.44	0.00	0.00	0.00	0.52	-0.95
slr1638		hypothetical protein	329.56	28.08	0	281.87	43.55	0.00	0.05	0.01	0.86	-0.23
slr1639		SsrA-binding protein	32.10	2.75	0	14.92	15.85	0.02	0.08	0.05	0.46	-1.10
slr1641		ClpB protein	331.21	73.79	0	422.82	109.64	0.00	0.13	0.03	1.28	0.35
slr1643	petH	ferredoxin-NADP oxid	1016.29	237.00	0	1316.39	270.18	0.00	0.06	0.00	1.30	0.37
slr1644		hypothetical protein	225.05	36.44	0	171.44	30.11	0.00	0.02	0.00	0.76	-0.39
slr1645	psbZ	photosystem II 11 kD	147.00	40.04	0	152.39	30.92	0.00	0.74	0.59	1.04	0.05
slr1646	rnc	ribonuclease III	77.91	9.49	0	126.36	20.86	0.00	0.00	0.00	1.62	0.70
slr1647		hypothetical protein	77.43	9.56	0	93.21	15.00	0.00	0.06	0.01	1.20	0.27
slr1648		hypothetical protein	84.86	11.11	0	139.11	30.90	0.00	0.00	0.00	1.64	0.71
slr1649		hypothetical protein	135.81	36.00	0	125.31	16.95	0.00	0.65	0.27	0.92	-0.12
slr1651		ABC transporter ATP-	321.30	42.35	0	304.96	37.65	0.00	0.51	0.30	0.95	-0.08
slr1652		hypothetical protein	45.44	4.27	0	64.22	10.74	0.00	0.00	0.00	1.41	0.50
slr1653		N-acyl-L-amino acid a	250.23	10.95	0	230.80	36.82	0.00	0.20	0.15	0.92	-0.12
slr1655	psaL	photosystem I subunit	2466.43	81.74	0	2564.49	345.24	0.00	0.59	0.56	1.04	0.06
slr1656	murG	UDP-N-acetylglucosar	52.37	8.23	0	80.09	19.20	0.00	0.00	0.00	1.53	0.61
slr1657		hypothetical protein	92.34	28.14	8.88E-16	107.93	30.56	0.00	0.42	0.16	1.17	0.22
slr1658		unknown protein	95.30	17.79	0	66.81	15.76	0.00	0.02	0.00	0.70	-0.51
slr1659		hypothetical protein	47.00	8.62	0	25.06	17.58	0.00	0.12	0.09	0.53	-0.91
slr1660		hypothetical protein	127.04	12.70	0	148.21	21.85	0.00	0.07	0.02	1.17	0.22
slr1661		hypothetical protein	141.52	38.92	0	182.14	38.23	0.00	0.12	0.01	1.29	0.36
slr1664		hypothetical protein	103.56	9.12	0	85.12	8.13	0.00	0.00	0.00	0.82	-0.28
slr1665	dapF	diaminopimelate epime	216.68	14.72	0	262.02	16.10	0.00	0.00	0.00	1.21	0.27
slr1666		pleiotropic regulatory r	265.38	52.48	0	396.11	59.31	0.00	0.00	0.00	1.49	0.58
slr1667		hypothetical protein (t	56.18	11.06	0	22.49	13.34	0.00	0.02	0.00	0.40	-1.32
slr1668		hypothetical protein (t	93.53	14.36	0	109.03	18.66	0.00	0.14	0.02	1.17	0.22
slr1670		unknown protein	121.18	36.37	4.44E-16	208.86	34.86	0.00	0.00	0.00	1.72	0.79
slr1672	glpK	glycerol kinase	109.58	29.00	0	197.80	29.30	0.00	0.00	0.00	1.81	0.85
slr1673		probable tRNA/rRNA r	68.70	11.24	0	124.87	36.53	0.00	0.00	0.00	1.82	0.86
slr1674		hypothetical protein	134.90	18.30	0	169.17	17.96	0.00	0.01	0.00	1.25	0.33
slr1675	hypA	hydrogenase expressi	15.20	3.19	0	46.16	27.92	0.00	0.01	0.00	3.04	1.60
slr1676		hypothetical protein	71.55	15.03	0	89.21	18.37	0.00	0.10	0.01	1.25	0.32
slr1677		hypothetical protein	95.02	22.24	0	162.68	29.96	0.00	0.00	0.00	1.71	0.78
slr1678	rpl21	50S ribosomal protein	403.07	86.15	0	266.96	35.13	0.00	0.00	0.00	0.66	-0.59
slr1679		hypothetical protein	114.71	22.17	0	93.52	13.21	0.00	0.08	0.00	0.82	-0.29
slr1681		unknown protein	69.48	17.26	0	59.89	25.26	0.00	0.38	0.26	0.86	-0.21
slr1682		putative transposase [	53.38	9.23	0	58.64	17.68	0.00	0.68	0.64	1.10	0.14
slr1683		putative transposase [	29.53	8.21	0	38.72	23.87	0.00	0.97	0.96	1.31	0.39
slr1684		putative transposase [	169.16	26.64	0	192.81	52.44	0.00	0.45	0.36	1.14	0.19
slr1686		hypothetical protein	73.35	9.48	0	106.55	10.80	0.00	0.00	0.00	1.45	0.54
slr1687		hypothetical protein	63.20	12.13	0	90.27	31.11	0.00	0.07	0.02	1.43	0.51
slr1689	fpg	formamidopyrimidine-C	356.62	46.43	0	246.45	30.53	0.00	0.00	0.00	0.69	-0.53
slr1690		hypothetical protein	56.12	5.71	0	99.91	33.06	0.00	0.01	0.00	1.78	0.83
slr1691		glutamine-dependent t	128.02	9.70	0	105.38	13.88	0.00	0.01	0.00	0.82	-0.28
slr1692		hypothetical protein	98.84	10.58	0	63.40	30.30	0.00	0.05	0.02	0.64	-0.64
slr1693		two-component respor	125.89	28.64	0	87.95	14.70	0.00	0.01	0.00	0.70	-0.52
slr1694		expression activator a	34.86	3.46	0	13.22	14.15	0.02	0.05	0.03	0.38	-1.40
slr1697		serine/threonine kinas	267.13	57.73	0	241.25	62.05	0.00	0.45	0.29	0.90	-0.15
slr1699		hypothetical protein	64.93	8.24	0	61.71	6.94	0.00	0.48	0.27	0.95	-0.07
slr1702		hypothetical protein	78.06	10.14	0	72.05	7.43	0.00	0.27	0.07	0.92	-0.12

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1703	serS	seryl-tRNA synthetase	209.59	31.67	0	199.72	53.40	0.00	0.59	0.52	0.95	-0.07
slr1704		hypothetical protein	139.72	18.99	0	745.48	412.36	0.00	0.00	0.00	5.34	2.42
slr1705		aspartoacylase	176.64	15.67	0	146.80	9.06	0.00	0.00	0.00	0.83	-0.27
slr1706		dihydroflavonol 4-redu	99.74	10.73	0	114.69	11.83	0.00	0.05	0.00	1.15	0.20
slr1708		probable peptidase	411.00	100.24	0	394.80	118.39	0.00	0.76	0.68	0.96	-0.06
slr1710		penicillin-binding prote	166.77	19.00	0	104.93	21.96	0.00	0.00	0.00	0.63	-0.67
slr1712		hypothetical protein	275.05	72.06	0	507.43	162.99	0.00	0.02	0.00	1.84	0.88
slr1715		putative transposase [	57.53	8.12	0	425.51	176.77	0.00	0.00	0.00	7.40	2.89
slr1716		putative transposase [	60.02	10.32	0	456.62	113.86	0.00	0.00	0.00	7.61	2.93
slr1717		hypothetical protein	76.83	12.60	0	76.42	8.81	0.00	0.99	0.99	0.99	-0.01
slr1718		hypothetical protein	235.35	56.65	0	224.72	57.24	0.00	0.71	0.62	0.95	-0.07
slr1719		DrgA protein homolog	963.51	562.21	2.69E-05	982.25	547.71	0.00	0.77	0.73	1.02	0.03
slr1720	aspS	aspartyl-tRNA synthet	328.50	47.44	0	328.08	40.18	0.00	0.99	0.98	1.00	0.00
slr1721		hypothetical protein	163.69	17.24	0	213.46	49.64	0.00	0.03	0.00	1.30	0.38
slr1722		inosine-5'-monophosph	384.75	85.68	0	505.25	153.98	0.00	0.14	0.05	1.31	0.39
slr1723		permease protein of st	216.18	54.26	0	185.36	101.27	0.00	0.35	0.29	0.86	-0.22
slr1724		hypothetical protein	101.96	22.38	0	87.67	27.36	0.00	0.33	0.20	0.86	-0.22
slr1726		unknown protein	104.69	22.71	0	155.76	28.21	0.00	0.00	0.00	1.49	0.57
slr1727		Na+/H+ antiporter	158.20	24.75	0	145.94	25.01	0.00	0.45	0.27	0.92	-0.12
slr1728	kdpA	potassium-transportin	233.92	77.71	1.67E-13	804.04	214.18	0.00	0.00	0.00	3.44	1.78
slr1729	kdpB	potassium-transportin	205.56	12.37	0	521.88	196.18	0.00	0.00	0.00	2.54	1.34
slr1730	kdpC	potassium-transportin	31.02	6.00	0	81.28	23.27	0.00	0.00	0.00	2.62	1.39
slr1731	kdpD	potassium-transportin	156.97	40.73	0	95.73	35.06	0.00	0.02	0.00	0.61	-0.71
slr1732		hypothetical protein	34.62	5.68	0	58.12	5.98	0.00	0.00	0.00	1.68	0.75
slr1734	opcA	putative OxPPCycle pi	152.68	35.96	0	114.41	28.88	0.00	0.07	0.00	0.75	-0.42
slr1735	bgTA	ATP-binding subunit o	187.10	12.48	0	171.93	22.41	0.00	0.17	0.09	0.92	-0.12
slr1736		homogenisate phytyle	104.96	22.62	0	87.10	23.37	0.00	0.17	0.05	0.83	-0.27
slr1737		hypothetical protein	51.80	9.09	0	85.60	8.15	0.00	0.00	0.00	1.65	0.72
slr1738		transcription regulator	43.71	14.00	2.04E-14	68.61	31.11	0.00	0.26	0.19	1.57	0.65
slr1739	psbW	photosystem II reactio	49.19	9.94	0	31.29	25.96	0.00	0.14	0.11	0.64	-0.65
slr1740		oligopeptide binding pr	320.15	21.03	0	305.95	20.40	0.00	0.26	0.10	0.96	-0.07
slr1742		probable cobyrinic acid	114.71	33.97	2.22E-16	52.59	33.89	0.00	0.03	0.01	0.46	-1.13
slr1743	ndbB	type 2 NADH dehydro	138.82	28.93	0	174.30	40.46	0.00	0.13	0.03	1.26	0.33
slr1744		N-acetylmuramoyl-L-al	404.31	64.09	0	441.60	110.70	0.00	0.52	0.43	1.09	0.13
slr1746		glutamate racemase	283.01	46.08	0	240.12	65.29	0.00	0.21	0.12	0.85	-0.24
slr1747		cell death suppressor	69.04	6.62	0	101.92	18.05	0.00	0.00	0.00	1.48	0.56
slr1748		probable phosphoglyc	72.55	10.94	0	137.54	34.67	0.00	0.00	0.00	1.90	0.92
slr1751		carboxyl-terminal prote	432.58	55.89	0	671.63	93.90	0.00	0.00	0.00	1.55	0.63
slr1752		hypothetical protein	114.74	6.95	0	88.74	26.42	0.00	0.04	0.02	0.77	-0.37
slr1753		hypothetical protein	87.76	17.33	0	67.32	21.05	0.00	0.10	0.03	0.77	-0.38
slr1755		NAD+ dependent glyco	138.55	22.80	0	116.42	14.61	0.00	0.07	0.00	0.84	-0.25
slr1756	glnA	glutamate-ammonia li	1444.68	143.42	0	1018.68	36.57	0.00	0.00	0.00	0.71	-0.50
slr1759		two-component hybrid	277.99	73.96	0	423.64	155.82	0.00	0.07	0.01	1.52	0.61
slr1760		two-component respor	97.87	11.11	0	86.09	18.92	0.00	0.22	0.15	0.88	-0.19
slr1761		FK506-binding protein	221.02	29.65	0	261.24	37.81	0.00	0.07	0.01	1.18	0.24
slr1762		hypothetical protein	60.55	8.56	0	50.35	24.37	0.00	0.25	0.21	0.83	-0.27
slr1763		probable methyltransf	137.95	26.59	0	186.94	50.45	0.00	0.06	0.01	1.36	0.44
slr1764	terE	similar to tellurium resi	940.51	171.70	0	961.30	185.24	0.00	0.83	0.75	1.02	0.03
slr1767		hypothetical protein	18.93	3.45	0	9.17	11.39	0.05	0.05	0.02	0.48	-1.05
slr1768		unknown protein	103.76	12.03	0	61.75	25.93	0.00	0.02	0.00	0.60	-0.75
slr1770		hypothetical protein	46.67	11.24	0	23.22	18.78	0.00	0.05	0.02	0.50	-1.01
slr1771		unknown protein	139.68	29.66	0	98.91	20.73	0.00	0.02	0.00	0.71	-0.50
slr1772		probable hydrolase	18.45	3.96	0	8.14	12.54	0.11	0.02	0.00	0.44	-1.18
slr1773		unknown protein	25.20	9.28	2.95E-11	21.43	16.85	0.00	0.20	0.17	0.85	-0.23
slr1774		unknown protein	268.73	50.82	0	237.15	78.48	0.00	0.35	0.24	0.88	-0.18
slr1776		high affinity sulfate tra	570.02	112.18	0	780.42	245.76	0.00	0.10	0.04	1.37	0.45
slr1777	chID	magnesium-chelatase	340.98	41.79	0	382.97	79.98	0.00	0.35	0.26	1.12	0.17
slr1778		unknown protein	255.49	44.50	0	227.31	70.67	0.00	0.36	0.28	0.89	-0.17
slr1779	pdxJ	pyridoxal phosphate bi	201.55	21.43	0	240.87	18.33	0.00	0.01	0.00	1.20	0.26
slr1780	ycf54	hypothetical protein YC	59.31	13.16	0	31.64	21.30	0.00	0.10	0.07	0.53	-0.91
slr1783	ycf29	two-component respor	98.46	17.22	0	123.34	24.36	0.00	0.06	0.00	1.25	0.32
slr1784	bvdR	biliverdin reductase	56.27	6.35	0	53.05	13.20	0.00	0.51	0.47	0.94	-0.08
slr1787		thiamine-monophosph	433.56	51.97	0	514.28	46.54	0.00	0.02	0.00	1.19	0.25
slr1788		unknown protein	45.15	11.47	0	63.21	11.07	0.00	0.02	0.00	1.40	0.49
slr1789		unknown protein	33.82	5.10	0	68.40	17.27	0.00	0.00	0.00	2.02	1.02
slr1790		hypothetical protein	188.70	22.10	0	202.20	30.24	0.00	0.44	0.32	1.07	0.10
slr1791	cysH	phosphoadenosine ph	140.53	25.74	0	146.72	31.97	0.00	0.76	0.69	1.04	0.06
slr1793		transaldolase	385.81	70.50	0	461.45	94.31	0.00	0.11	0.02	1.20	0.26
slr1794		probable anion transp	120.33	23.00	0	136.71	18.26	0.00	0.19	0.01	1.14	0.18
slr1795		peptide methionine sul	1302.82	270.93	0	1100.49	201.24	0.00	0.17	0.03	0.84	-0.24
slr1796		hypothetical protein	105.70	38.31	1.4E-11	89.74	35.71	0.00	0.43	0.24	0.85	-0.24
slr1798		unknown protein	413.46	72.71	0	203.34	38.36	0.00	0.00	0.00	0.49	-1.02
slr1799		hypothetical protein	236.85	21.92	0	228.92	40.12	0.00	0.59	0.53	0.97	-0.05
slr1800		hypothetical protein	103.58	16.92	0	137.86	22.45	0.00	0.02	0.00	1.33	0.41
slr1803		adenine-specific DNA	43.05	6.69	0	43.66	16.81	0.00	0.82	0.80	1.01	0.02
slr1805		two-component senso	127.87	15.34	0	189.73	30.60	0.00	0.00	0.00	1.48	0.57
slr1807		hypothetical protein	50.62	6.49	0	60.65	7.94	0.00	0.04	0.00	1.20	0.26
slr1808	hemA	transfer RNA-Gln redu	283.10	64.37	0	305.15	62.99	0.00	0.55	0.36	1.08	0.11

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments

Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1809		unknown protein	93.81	22.33	0	107.73	37.71	0.00	0.64	0.56	1.15	0.20
slr1811		hypothetical protein	120.40	32.80	0	84.45	37.34	0.00	0.09	0.04	0.70	-0.51
slr1812		hypothetical protein	94.48	33.90	8.67E-12	70.28	19.10	0.00	0.16	0.01	0.74	-0.43
slr1813		hypothetical protein	159.10	54.86	1.21E-12	131.26	57.43	0.00	0.32	0.22	0.83	-0.28
slr1814		hypothetical protein	116.58	28.35	0	95.71	34.06	0.00	0.24	0.13	0.82	-0.28
slr1815		hypothetical protein	130.38	28.15	0	112.46	32.75	0.00	0.30	0.16	0.86	-0.21
slr1816		hypothetical protein	83.84	19.41	0	82.98	22.26	0.00	0.89	0.85	0.99	-0.01
slr1818		hypothetical protein	68.14	15.90	0	34.04	25.00	0.00	0.08	0.05	0.50	-1.00
slr1819		hypothetical protein	134.04	15.90	0	114.77	24.43	0.00	0.10	0.04	0.86	-0.22
slr1820		hypothetical protein	51.49	19.49	9.64E-11	54.25	30.61	0.00	0.86	0.84	1.05	0.08
slr1821		hypothetical protein	498.96	106.80	0	473.90	109.23	0.00	0.68	0.56	0.95	-0.07
slr1822		endonuclease III	46.02	2.74	0	51.05	9.36	0.00	0.29	0.24	1.11	0.15
slr1826		hypothetical protein	20.75	3.92	0	19.89	11.60	0.00	0.39	0.37	0.96	-0.06
slr1827		hypothetical protein	45.84	10.28	0	35.25	14.26	0.00	0.12	0.05	0.77	-0.38
slr1828		ferredoxin, petF-like pr	184.35	8.45	0	200.07	24.03	0.00	0.20	0.14	1.09	0.12
slr1829		unknown protein	98.00	19.58	0	91.45	21.86	0.00	0.52	0.39	0.93	-0.10
slr1830		poly-beta-hydroxybutyl	79.30	32.26	1.72E-09	43.75	35.91	0.00	0.13	0.10	0.55	-0.86
slr1834	psaA	P700 apoprotein subu	1849.97	748.00	1.38E-09	2311.14	864.85	0.00	0.47	0.24	1.25	0.32
slr1835	psaB	P700 apoprotein subu	11090.40	1631.99	0	10705.16	2844.03	0.00	0.67	0.61	0.97	-0.05
slr1837		two-component syste	81.16	2.60	0	53.28	21.75	0.00	0.03	0.01	0.66	-0.61
slr1838	ccmK	carbon dioxide concer	110.39	18.80	0	109.63	14.28	0.00	0.99	0.98	0.99	-0.01
slr1839	ccmK	carbon dioxide concer	104.93	18.52	0	65.98	24.10	0.00	0.01	0.00	0.63	-0.67
slr1840		hypothetical protein	136.85	37.35	0	123.61	26.83	0.00	0.53	0.30	0.90	-0.15
slr1841		probable porin; major r	9068.25	1038.61	0	5562.00	1508.07	0.00	0.00	0.00	0.61	-0.71
slr1842	cysK	cysteine synthase	200.37	21.40	0	131.23	19.90	0.00	0.00	0.00	0.65	-0.61
slr1843	zwf	glucose 6-phosphate r	307.77	46.69	0	190.19	32.88	0.00	0.00	0.00	0.82	-0.69
slr1844	uvrA	excinuclease ABC sut	81.75	17.51	0	92.33	37.46	0.00	0.69	0.63	1.13	0.18
slr1846	ycf64	hypothetical protein Yf	64.70	8.80	0	59.74	18.48	0.00	0.46	0.42	0.92	-0.11
slr1847		hypothetical protein	55.95	9.69	0	62.54	4.86	0.00	0.15	0.00	1.12	0.16
slr1848	hisD	histidinol dehydrogena	156.20	18.97	0	192.28	35.38	0.00	0.05	0.01	1.23	0.30
slr1849		probable mercuric red	78.81	16.69	0	89.56	19.41	0.00	0.35	0.17	1.14	0.18
slr1851		hypothetical protein	103.47	24.06	0	43.12	19.60	0.00	0.00	0.00	0.42	-1.26
slr1852		unknown protein	240.68	55.44	0	80.29	14.02	0.00	0.00	0.00	0.33	-1.58
slr1853		carboxymuconolacton	86.92	14.51	0	13.46	16.74	0.05	0.01	0.00	0.15	-2.69
slr1854		unknown protein	270.09	72.29	0	57.87	34.20	0.00	0.00	0.00	0.21	-2.22
slr1855		unknown protein	398.73	83.54	0	171.06	25.65	0.00	0.00	0.00	0.43	-1.22
slr1856		anti-sigma B factor an	66.90	9.91	0	29.06	18.02	0.00	0.14	0.11	0.43	-1.20
slr1857		isoamylase	217.92	37.50	0	165.71	32.74	0.00	0.03	0.00	0.76	-0.40
slr1859		anti-sigma B factor ant	46.26	14.54	6.44E-15	28.37	26.75	0.01	0.21	0.18	0.61	-0.71
slr1860	icfG	carbon metabolisms re	86.50	16.81	0	85.84	31.66	0.00	0.78	0.74	0.99	-0.01
slr1861		probable sigma regula	21.31	7.28	7.49E-13	5.37	6.44	0.04	0.02	0.01	0.25	-1.99
slr1862		unknown protein	516.12	45.82	0	817.90	189.91	0.00	0.00	0.00	1.58	0.66
slr1863		unknown protein	40.87	16.60	1.65E-09	28.28	21.94	0.00	0.16	0.13	0.69	-0.53
slr1864		hypothetical protein	46.51	5.59	0	66.91	11.92	0.00	0.00	0.00	1.44	0.52
slr1865		unknown protein	55.02	16.54	4.44E-16	51.36	32.91	0.00	0.41	0.38	0.93	-0.10
slr1866		unknown protein	33.82	5.93	0	33.28	11.58	0.00	0.71	0.69	0.98	-0.02
slr1867	trpD	anthranilate phosphori	107.09	21.14	0	136.43	21.86	0.00	0.04	0.00	1.27	0.35
slr1869		unknown protein	194.69	40.58	0	116.99	19.20	0.00	0.00	0.00	0.60	-0.73
slr1870		hypothetical protein	63.37	25.00	5.36E-10	45.85	11.20	0.00	0.17	0.01	0.72	-0.47
slr1871		transcriptional regulat	82.62	19.35	0	60.14	11.91	0.00	0.04	0.00	0.73	-0.46
slr1874		D-alanine-D-alanine li	75.08	31.19	3.73E-09	69.40	23.14	0.00	0.87	0.77	0.92	-0.11
slr1875		hypothetical protein	57.03	6.51	0	49.47	22.59	0.00	0.32	0.28	0.87	-0.21
slr1876		hypothetical protein	97.37	42.68	2.29E-08	92.46	52.92	0.00	0.79	0.72	0.95	-0.07
slr1877		2-hydroxyhepta-2,4-dic	94.43	9.04	0	138.36	21.30	0.00	0.00	0.00	1.47	0.55
slr1878	cpcE	phycocyanin alpha-sul	83.49	7.56	0	85.73	7.01	0.00	0.60	0.41	1.03	0.04
slr1879	cobI	precomin-2 methyltran	30.27	3.11	0	68.40	18.02	0.00	0.00	0.00	2.26	1.18
slr1880		hypothetical protein	66.24	22.19	2.65E-13	64.82	29.52	0.00	0.76	0.71	0.98	-0.03
slr1881	natE	ATP-binding subunit o	148.60	18.29	0	100.12	16.02	0.00	0.00	0.00	0.67	-0.57
slr1882	ribF	riboflavin biosynthesis	81.82	12.22	0	134.07	36.74	0.00	0.00	0.00	1.64	0.71
slr1884	trpS	tryptophanyl-tRNA syn	233.94	38.70	0	269.60	74.47	0.00	0.32	0.21	1.15	0.20
slr1885		hypothetical protein	90.64	20.26	0	92.32	20.89	0.00	0.91	0.87	1.02	0.03
slr1886		hypothetical protein	104.55	14.27	0	122.43	22.44	0.00	0.13	0.03	1.17	0.23
slr1887	hemC	porphobilinogen deam	140.21	10.29	0	157.48	23.40	0.00	0.15	0.08	1.12	0.17
slr1888		4-hydroxybutyrate coe	184.30	55.83	6.66E-16	165.63	34.79	0.00	0.62	0.36	0.90	-0.15
slr1890		bacterioferritin	265.01	44.21	0	194.74	59.80	0.00	0.05	0.01	0.73	-0.44
slr1894		probable DNA-binding	1206.50	139.67	0	1797.29	340.42	0.00	0.00	0.00	1.49	0.57
slr1895		hypothetical protein	209.16	18.78	0	168.63	32.12	0.00	0.02	0.00	0.81	-0.31
slr1896		hypothetical protein	65.51	23.90	1.89E-11	43.93	18.68	0.00	0.16	0.07	0.67	-0.58
slr1897		periplasmic sugar-binc	114.43	24.58	0	105.39	23.18	0.00	0.55	0.35	0.92	-0.12
slr1898	argB	N-acetylglutamate kin	119.56	20.35	0	72.67	18.47	0.00	0.00	0.00	0.61	-0.72
slr1899	ureF	urease accessory prot	92.60	13.30	0	40.12	30.71	0.00	0.13	0.10	0.43	-1.21
slr1900		hypothetical protein	102.92	19.91	0	137.82	30.48	0.00	0.06	0.01	1.34	0.42
slr1901		ATP-binding protein of	69.65	4.94	0	73.96	23.34	0.00	0.90	0.90	1.06	0.09
slr1902		putative transposase [	63.63	16.97	0	117.21	34.83	0.00	0.00	0.00	1.84	0.88
slr1903		putative transposase [	89.57	15.42	0	159.01	54.44	0.00	0.01	0.00	1.78	0.83
slr1906		hypothetical protein	70.57	8.37	0	48.14	16.71	0.00	0.04	0.01	0.68	-0.55
slr1907		hypothetical protein	108.06	19.63	0	82.08	16.51	0.00	0.03	0.00	0.76	-0.40
slr1908		probable porin; major r	3761.00	849.07	0	4200.24	1720.15	0.00	0.69	0.62	1.12	0.16

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr1909		two-component respor	94.63	19.41	0	55.56	16.41	0.00	0.00	0.00	0.59	-0.77
slr1910		probable N-acetylmure	140.66	36.94	0	138.87	42.03	0.00	0.88	0.84	0.99	-0.02
slr1911		hypothetical protein	83.34	4.08	0	67.68	25.38	0.00	0.11	0.08	0.81	-0.30
slr1912		anti-sigma F factor ani	89.75	13.55	0	56.75	7.48	0.00	0.00	0.00	0.63	-0.66
slr1913		hypothetical protein	42.19	6.91	0	25.10	11.82	0.00	0.03	0.01	0.60	-0.75
slr1914		hypothetical protein	76.66	15.59	0	79.55	17.80	0.00	0.77	0.69	1.04	0.05
slr1915		hypothetical protein	25.17	3.86	0	17.15	15.52	0.01	0.14	0.11	0.68	-0.55
slr1916		probable esterase	103.71	26.35	0	74.07	17.46	0.00	0.07	0.00	0.71	-0.49
slr1917		hypothetical protein	75.45	14.47	0	92.88	28.95	0.00	0.21	0.12	1.23	0.30
slr1918		hypothetical protein	178.11	14.82	0	145.77	13.25	0.00	0.00	0.00	0.82	-0.29
slr1919		hypothetical protein	195.39	22.89	0	239.81	33.74	0.00	0.02	0.00	1.23	0.30
slr1920		unknown protein	67.53	11.26	0	74.42	42.04	0.00	0.92	0.92	1.10	0.14
slr1923		hypothetical protein	33.31	5.88	0	25.47	14.81	0.00	0.16	0.12	0.76	-0.39
slr1924		D-alanyl-D-alanine car	112.15	10.65	0	177.05	41.70	0.00	0.00	0.00	1.58	0.66
slr1925	cobD	cobalamin biosynthesi	119.04	25.64	0	102.69	19.02	0.00	0.21	0.04	0.86	-0.21
slr1926		hypothetical protein	123.86	13.83	0	144.13	27.94	0.00	0.18	0.10	1.16	0.22
slr1927		hypothetical protein	144.62	16.14	0	130.87	20.13	0.00	0.21	0.10	0.90	-0.14
slr1928		unknown protein	219.86	56.91	0	192.98	80.05	0.00	0.38	0.27	0.88	-0.19
slr1929	pilin	type 4 pilin	109.78	16.27	0	44.34	12.39	0.00	0.00	0.00	0.40	-1.31
slr1930		unknown protein	66.48	13.39	0	59.66	34.30	0.00	0.40	0.35	0.90	-0.16
slr1931		unknown protein	215.64	19.57	0	215.67	47.92	0.00	0.87	0.85	1.00	0.00
slr1932		unknown protein	87.24	31.69	1.56E-11	144.85	76.50	0.00	0.19	0.10	1.66	0.73
slr1933	rfbC	dTDP-4-dehydrohamr	35.24	11.10	7.55E-15	27.29	21.60	0.00	0.18	0.14	0.77	-0.37
slr1934		pyruvate dehydrogena	210.06	29.39	0	229.16	44.26	0.00	0.46	0.35	1.09	0.13
slr1935		hypothetical protein	154.60	45.27	0	194.84	44.27	0.00	0.15	0.01	1.26	0.33
slr1936		putative transposase [	74.83	12.11	0	484.24	171.66	0.00	0.00	0.00	6.47	2.69
slr1937		putative transposase [	185.45	41.86	0	505.24	180.64	0.00	0.00	0.00	2.72	1.45
slr1938		putative translation init	216.03	29.84	0	202.24	37.09	0.00	0.47	0.33	0.94	-0.10
slr1939		unknown protein	117.20	14.34	0	186.39	53.68	0.00	0.01	0.00	1.59	0.67
slr1940		hypothetical protein	206.62	38.05	0	144.79	25.48	0.00	0.01	0.00	0.70	-0.51
slr1942	kaiC3	circadian clock protein	193.30	25.67	0	140.94	20.30	0.00	0.00	0.00	0.73	-0.46
slr1943		probable glycosyltrans	93.96	64.78	0.000381	100.46	45.00	0.00	0.65	0.47	1.07	0.10
slr1944		hypothetical protein	118.81	19.01	0	110.34	15.58	0.00	0.43	0.23	0.93	-0.11
slr1945		2,3-bisphosphoglycere	447.05	63.53	0	590.08	79.48	0.00	0.00	0.00	1.32	0.40
slr1946		hypothetical protein	162.38	11.31	0	129.35	23.20	0.00	0.01	0.00	0.80	-0.33
slr1949		hypothetical protein	149.47	12.86	0	130.51	6.61	0.00	0.01	0.00	0.87	-0.20
slr1950	ctaA	copper-transporting Ci	326.31	90.08	0	174.13	19.81	0.00	0.00	0.00	0.53	-0.91
slr1951		hypothetical protein	51.37	9.86	0	35.65	16.64	0.00	0.14	0.09	0.69	-0.53
slr1956		unknown protein	34.32	11.51	2.76E-13	26.27	21.14	0.00	0.18	0.15	0.77	-0.39
slr1957		hypothetical protein	281.54	39.00	0	38.56	10.97	0.00	0.00	0.00	0.14	-2.87
slr1958		unknown protein	73.32	8.00	0	46.11	13.06	0.00	0.01	0.00	0.63	-0.67
slr1959		unknown protein	27.40	6.14	0	45.57	8.05	0.00	0.00	0.00	1.66	0.73
slr1962		probable extracellular	110.43	20.82	0	91.50	31.35	0.00	0.21	0.11	0.83	-0.27
slr1963		water-soluble carotenc	773.10	152.02	0	1413.65	379.00	0.00	0.00	0.00	1.83	0.87
slr1964		hypothetical protein	148.28	41.14	0	82.40	26.77	0.00	0.00	0.00	0.56	-0.85
slr1966		hypothetical protein	123.01	13.86	0	91.16	10.22	0.00	0.00	0.00	0.74	-0.43
slr1968		unknown protein	184.98	39.58	0	235.32	76.11	0.00	0.15	0.06	1.27	0.35
slr1969		two-component senso	176.87	42.05	0	106.81	6.75	0.00	0.00	0.00	0.60	-0.73
slr1970		hypothetical protein	48.53	7.18	0	22.11	21.52	0.01	0.03	0.01	0.46	-1.13
slr1971		hypothetical protein	414.35	189.63	8.69E-08	555.88	162.98	0.00	0.14	0.01	1.34	0.42
slr1972	ycf81	hypothetical protein Yt	369.77	66.07	0	240.18	34.38	0.00	0.00	0.00	0.65	-0.62
slr1974		GTP binding protein	186.33	55.35	2.22E-16	132.85	36.66	0.00	0.11	0.01	0.71	-0.49
slr1975		N-acylglucosamine 2-t	95.74	23.23	0	91.61	26.09	0.00	0.74	0.64	0.96	-0.06
slr1977		hypothetical protein	149.24	31.01	0	76.83	10.45	0.00	0.00	0.00	0.51	-0.96
slr1978		hypothetical protein	246.86	29.46	0	214.13	32.86	0.00	0.12	0.03	0.87	-0.21
slr1979	trpE	anthranilate synthase	67.64	6.69	0	109.71	20.51	0.00	0.00	0.00	1.62	0.70
slr1980		unknown protein	218.37	26.18	0	206.22	36.78	0.00	0.47	0.36	0.94	-0.08
slr1982		two-component respor	162.36	56.14	1.4E-12	79.29	48.17	0.00	0.01	0.00	0.49	-1.03
slr1983		two-component hybrid	84.60	19.15	0	78.83	15.42	0.00	0.59	0.42	0.93	-0.10
slr1984	nbp1	nucleic acid-binding pr	331.03	93.70	0	228.60	89.25	0.00	0.06	0.01	0.69	-0.53
slr1986	apcB	allophycocyanin beta s	5025.38	809.04	0	4247.28	455.29	0.00	0.08	0.00	0.85	-0.24
slr1990		hypothetical protein	209.20	23.82	0	243.36	34.72	0.00	0.09	0.02	1.16	0.22
slr1991	cya1	adenylate cyclase	168.24	28.41	0	180.59	25.71	0.00	0.44	0.24	1.07	0.10
slr1992	gpx2	glutathione peroxidase	161.85	22.58	0	192.10	29.16	0.00	0.08	0.01	1.19	0.25
slr1993	phaA	PHA-specific beta-ket	173.88	34.22	0	118.02	12.08	0.00	0.00	0.00	0.68	-0.56
slr1994	phaB	PHA-specific acetoace	2028.38	280.66	0	2166.62	293.71	0.00	0.42	0.24	1.07	0.10
slr1998		hypothetical protein	204.83	10.17	0	135.46	17.06	0.00	0.00	0.00	0.66	-0.60
slr1999		hypothetical protein	44.72	8.78	0	48.11	24.53	0.00	0.93	0.92	1.08	0.11
slr2000		hypothetical protein	160.48	38.30	0	130.05	30.31	0.00	0.16	0.04	0.81	-0.30
slr2001		cyanophycinase	228.48	34.54	0	191.80	31.22	0.00	0.09	0.01	0.84	-0.25
slr2002		cyanophycin synthetas	333.03	58.59	0	241.92	52.63	0.00	0.02	0.00	0.73	-0.46
slr2003		hypothetical protein	69.35	8.03	0	69.48	14.24	0.00	0.91	0.89	1.00	0.00
slr2004		unknown protein	125.20	51.77	3.14E-09	173.34	35.88	0.00	0.07	0.00	1.38	0.47
slr2005		hypothetical protein	108.83	17.82	0	121.61	11.48	0.00	0.15	0.00	1.12	0.16
slr2006		hypothetical protein	7.42	0.83	0	8.41	8.50	0.02	0.32	0.29	1.13	0.18
slr2007	ndh5	NADH dehydrogenase	68.64	16.09	0	68.50	10.96	0.00	0.93	0.87	1.00	0.00
slr2008		hypothetical protein	42.57	6.46	0	46.21	29.71	0.00	0.61	0.60	1.09	0.12
slr2009	ndh6	NADH dehydrogenase	153.28	34.67	0	160.42	22.47	0.00	0.61	0.28	1.05	0.07

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr2010		hypothetical protein	23.61	1.45	0	36.44	12.19	0.00	0.04	0.02	1.54	0.63
slr2011		hypothetical protein	61.17	8.77	0	70.06	7.75	0.00	0.08	0.00	1.15	0.20
slr2012		hypothetical protein	82.02	20.34	0	85.32	35.70	0.00	0.99	0.99	1.04	0.06
slr2013		hypothetical protein	165.66	15.35	0	154.10	12.52	0.00	0.20	0.04	0.93	-0.10
slr2015		unknown protein	189.70	5.19	0	169.07	37.69	0.00	0.15	0.11	0.89	-0.17
slr2016		unknown protein	44.56	9.93	0	30.20	5.80	0.00	0.01	0.00	0.68	-0.56
slr2017		unknown protein	197.60	30.47	0	112.28	16.16	0.00	0.00	0.00	0.57	-0.82
slr2018		unknown protein	179.82	41.41	0	138.58	76.83	0.00	0.21	0.16	0.77	-0.38
slr2019		ATP-binding protein of	180.90	26.71	0	214.10	45.00	0.00	0.18	0.06	1.18	0.24
slr2023	fabD	malonyl coenzyme A-ε	48.02	5.08	0	71.02	10.66	0.00	0.00	0.00	1.48	0.56
slr2024		two-component respon	95.23	22.38	0	94.38	23.45	0.00	0.93	0.90	0.99	-0.01
slr2025		hypothetical protein	157.96	36.88	0	134.34	24.49	0.00	0.27	0.05	0.85	-0.23
slr2026	folP	dihydropterolate synth	143.00	17.09	0	100.41	22.89	0.00	0.01	0.00	0.70	-0.51
slr2027		unknown protein	124.96	23.88	0	92.33	31.13	0.00	0.06	0.01	0.74	-0.44
slr2030		hypothetical protein	95.31	8.70	0	128.12	7.02	0.00	0.00	0.00	1.34	0.43
slr2031		hypothetical protein	132.06	25.84	0	136.82	27.40	0.00	0.78	0.68	1.04	0.05
slr2032	ycf23	hypothetical protein YC	390.38	61.19	0	366.23	46.30	0.00	0.50	0.26	0.94	-0.09
slr2033	rub	rubredoxin	142.18	9.97	0	93.21	33.32	0.00	0.02	0.00	0.66	-0.61
slr2034	ycf48	photosystem II stabilit	267.37	67.86	0	240.17	66.00	0.00	0.45	0.27	0.90	-0.15
slr2035	proB	glutamate 5-kinase	55.46	13.47	0	56.91	10.18	0.00	0.76	0.56	1.03	0.04
slr2036		putative transposase [	257.98	27.90	0	491.16	113.10	0.00	0.00	0.00	1.90	0.93
slr2037		unknown protein	9.83	4.47	7.05E-08	14.79	13.82	0.01	0.55	0.53	1.50	0.59
slr2038		hypothetical protein	41.82	8.86	0	20.63	16.80	0.00	0.11	0.08	0.49	-1.02
slr2041		probable two-compont	166.15	19.57	0	142.77	22.19	0.00	0.08	0.02	0.86	-0.22
slr2042		hypothetical protein	74.86	8.85	0	91.82	22.25	0.00	0.13	0.06	1.23	0.29
slr2043		periplasmic solute bind	52.67	17.23	7.15E-14	45.65	24.13	0.00	0.43	0.36	0.87	-0.21
slr2044		ABC transporter ATP-	113.83	32.97	0	102.30	27.04	0.00	0.58	0.37	0.90	-0.15
slr2045		permease protein of A	69.18	18.77	0	57.20	13.43	0.00	0.31	0.06	0.83	-0.27
slr2046		unknown protein	106.63	28.74	0	97.96	22.62	0.00	0.59	0.41	0.92	-0.12
slr2047		PhoH like protein	174.14	45.57	0	110.24	43.89	0.00	0.03	0.00	0.63	-0.66
slr2048		unknown protein	148.14	14.78	0	225.64	54.14	0.00	0.00	0.00	1.52	0.61
slr2049	ycf58	hypothetical protein YC	86.05	18.10	0	92.11	40.73	0.00	0.93	0.92	1.07	0.10
slr2051	cpcG1	phycobilisome rod-con	6565.35	560.59	0	4436.76	933.50	0.00	0.00	0.00	0.68	-0.57
slr2052		hypothetical protein	407.26	105.70	0	285.97	125.28	0.00	0.07	0.01	0.70	-0.51
slr2053		putative hydrolase	91.41	7.23	0	87.21	14.00	0.00	0.47	0.40	0.95	-0.07
slr2057		water channel protein	431.98	51.67	0	169.07	39.56	0.00	0.00	0.00	0.39	-1.35
slr2058	topA	DNA topoisomerase I	200.88	41.88	0	201.19	19.71	0.00	0.87	0.70	1.00	0.00
slr2059		iron-sulfur cluster bind	503.62	102.96	0	528.85	137.62	0.00	0.79	0.73	1.05	0.07
slr2060		hypothetical protein	105.05	8.82	0	107.34	24.53	0.00	0.98	0.98	1.02	0.03
slr2062		putative transposase [	1096.46	196.07	0	1135.32	272.81	0.00	0.83	0.78	1.04	0.05
slr2067	apcA	allophycocyanin alpha	6388.71	383.10	0	5058.37	925.85	0.00	0.01	0.00	0.79	-0.34
slr2070		hypothetical protein	149.38	22.03	0	113.62	31.22	0.00	0.04	0.01	0.76	-0.39
slr2071		unknown protein	70.38	14.24	0	65.30	41.98	0.00	0.42	0.38	0.93	-0.11
slr2072	ilvA	L-threonine deaminase	285.80	71.10	0	385.19	98.42	0.00	0.05	0.00	1.35	0.43
slr2073	ycf50	hypothetical protein YC	603.52	121.82	0	312.01	50.11	0.00	0.00	0.00	0.52	-0.95
slr2074		similar to mannose-1-φ	30.23	4.78	0	18.90	16.35	0.00	0.14	0.11	0.63	-0.68
slr2075	groES	10kD chaperonin	1106.28	264.94	0	1163.59	360.27	0.00	0.80	0.75	1.05	0.07
slr2076	groEL	60kD chaperonin	564.19	202.75	9.35E-12	1159.88	540.91	0.00	0.01	0.00	2.06	1.04
slr2077		probable ABC transpo	376.70	99.63	0	376.53	63.43	0.00	0.91	0.83	1.00	0.00
slr2078		hypothetical protein	34.22	8.88	0	31.62	22.91	0.00	0.32	0.29	0.92	-0.11
slr2079		putative glutaminase	104.14	31.61	6.66E-16	111.76	32.57	0.00	0.71	0.58	1.07	0.10
slr2080		hypothetical protein	28.20	8.18	0	22.23	17.72	0.00	0.22	0.19	0.79	-0.34
slr2081	tyrA	prephenate dehydroge	59.20	7.56	0	59.39	11.44	0.00	0.95	0.94	1.00	0.00
slr2082	ctaDII	cytochrome c oxidase	320.13	60.78	0	217.85	33.59	0.00	0.00	0.00	0.68	-0.56
slr2083	ctaEII	cytochrome c oxidase	64.95	10.65	0	51.62	11.65	0.00	0.08	0.02	0.79	-0.33
slr2084		hypothetical protein	100.16	16.65	0	75.72	7.91	0.00	0.01	0.00	0.76	-0.40
slr2087	ccs1	c-type cytochrome bio	173.66	24.87	0	230.35	38.22	0.00	0.02	0.00	1.33	0.41
slr2088	ilvG	acetohydroxy acid syn	602.10	108.89	0	696.72	215.40	0.00	0.38	0.28	1.16	0.21
slr2089	shc	squalene-hopene-cycl	157.41	26.37	0	209.32	32.13	0.00	0.02	0.00	1.33	0.41
slr2092		hypothetical protein	44.73	10.29	0	53.20	17.45	0.00	0.47	0.37	1.19	0.25
slr2094	fbpI	fructose-1,6-/sedohep	891.89	195.44	0	931.98	149.34	0.00	0.64	0.40	1.04	0.06
slr2095		putative transposase [	71.30	24.45	9.04E-13	134.25	32.17	0.00	0.00	0.00	1.88	0.91
slr2096		putative transposase [	104.10	22.85	0	183.73	42.52	0.00	0.00	0.00	1.77	0.82
slr2097	glbN	cyanoglobin	45.20	10.04	0	40.56	27.34	0.00	0.34	0.31	0.90	-0.16
slr2098		two-component hybrid	250.07	24.59	0	286.46	46.74	0.00	0.12	0.04	1.15	0.20
slr2099		two-component hybrid	781.99	77.15	0	496.71	63.99	0.00	0.00	0.00	0.64	-0.65
slr2100		two-component respon	59.97	3.93	0	78.28	14.78	0.00	0.02	0.00	1.31	0.38
slr2101		hypothetical protein	34.80	4.93	0	34.80	7.91	0.00	0.88	0.86	1.00	0.00
slr2102	ftsY	cell division protein Fts	339.44	54.00	0	384.99	62.90	0.00	0.23	0.08	1.13	0.18
slr2103		hypothetical protein	134.12	16.16	0	103.32	24.55	0.00	0.04	0.01	0.77	-0.38
slr2104		two-component hybrid	98.03	9.55	0	62.70	23.89	0.00	0.01	0.00	0.64	-0.64
slr2105		hypothetical protein	184.86	25.50	0	255.57	43.52	0.00	0.00	0.00	1.38	0.47
slr2107		probable polysacchari	363.25	49.96	0	321.06	98.25	0.00	0.31	0.25	0.88	-0.18
slr2108		probable polysacchari	219.42	57.77	0	169.62	56.61	0.00	0.14	0.05	0.77	-0.37
slr2110		unknown protein	4.50	1.70	9.22E-11	1.68	2.64	0.12	0.01	0.00	0.37	-1.42
slr2111		unknown protein	3.79	1.65	2.01E-08	2.79	5.11	0.18	0.03	0.01	0.74	-0.44
slr2112		putative transposase [	45.85	12.27	0	332.14	102.32	0.00	0.00	0.00	7.24	2.86
slr2113		putative transposase [	55.99	12.33	0	420.85	164.58	0.00	0.00	0.00	7.52	2.91

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
slr2114		perosamine synthetase	16.50	3.00	0	31.72	20.72	0.00	0.70	0.69	1.92	0.94
slr2115		unknown protein	29.73	9.53	2.2E-14	54.40	34.82	0.00	0.14	0.08	1.83	0.87
slr2116		probable glycosyltrans	35.24	43.94	0.049494	30.51	58.67	0.20	0.08	0.05	0.87	-0.21
slr2117		hypothetical protein	6.24	1.98	1.15E-14	4.34	5.21	0.04	0.08	0.05	0.69	-0.53
slr2118		unknown protein	29.54	6.79	0	33.94	8.91	0.00	0.45	0.34	1.15	0.20
slr2119		unknown protein	83.98	12.66	0	50.60	16.38	0.00	0.01	0.00	0.60	-0.73
slr2120		hypothetical protein	120.13	39.97	1.82E-13	70.71	31.67	0.00	0.04	0.00	0.59	-0.76
slr2121		hypothetical protein	97.25	32.12	1.2E-13	155.87	79.25	0.00	0.10	0.03	1.60	0.68
slr2122		hypothetical protein	68.83	6.96	0	33.07	9.29	0.00	0.00	0.00	0.48	-1.06
slr2123		similar to D-3-phospho	70.10	12.00	0	80.46	10.67	0.00	0.14	0.01	1.15	0.20
slr2124		3-oxoacyl-[acyl-carrier	56.30	9.64	0	30.08	13.51	0.00	0.01	0.00	0.53	-0.90
slr2125		hypothetical protein	46.07	15.99	1.69E-12	26.51	20.54	0.00	0.07	0.03	0.58	-0.80
slr2126		probable glycosyltrans	89.23	14.28	0	100.54	30.85	0.00	0.51	0.45	1.13	0.17
slr2127		hypothetical protein	52.75	6.28	0	54.45	11.63	0.00	0.88	0.86	1.03	0.05
slr2128		hypothetical protein	28.96	7.13	0	6.48	9.99	0.11	0.01	0.00	0.22	-2.16
slr2130	aroB	3-dehydroquininate synt	154.38	23.09	0	156.82	33.55	0.00	0.96	0.95	1.02	0.02
slr2131		RND multidrug efflux t	282.74	23.39	0	413.65	54.36	0.00	0.00	0.00	1.46	0.55
slr2132		phosphotransacetylase	126.57	9.46	0	90.83	24.28	0.00	0.01	0.00	0.72	-0.48
slr2135		hydrogenase accessori	126.28	19.66	0	179.17	32.48	0.00	0.01	0.00	1.42	0.50
slr2136		GcpE protein homolog	214.34	39.92	0	200.02	36.09	0.00	0.54	0.34	0.93	-0.10
slr2141		hypothetical protein	126.13	38.01	4.44E-16	100.07	70.00	0.00	0.26	0.22	0.79	-0.33
slr2143		L-cysteine/cystine lyas	186.74	28.31	0	114.20	26.38	0.00	0.00	0.00	0.61	-0.71
slr2144		hypothetical protein	160.23	35.57	0	130.43	28.48	0.00	0.14	0.03	0.81	-0.30
smI0001	psbI	photosystem II reactio	804.67	65.08	0	496.80	140.34	0.00	0.00	0.00	0.62	-0.70
smI0002	psbX	photosystem II PsbX f	189.80	20.12	0	174.36	30.41	0.00	0.31	0.22	0.92	-0.12
smI0003	psbM	photosystem II reactio	100.03	39.26	4.36E-10	137.88	91.58	0.00	0.79	0.76	1.38	0.46
smI0004	petN	cytochrome b6-f comp	134.06	25.75	0	85.15	44.27	0.00	0.07	0.03	0.64	-0.65
smI0005	psbK	photosystem II PsbK f	377.87	54.53	0	330.79	56.72	0.00	0.16	0.07	0.88	-0.19
smI0006	rpl36	50S ribosomal protein	38.02	12.76	2.9E-13	23.65	23.68	0.01	0.12	0.09	0.62	-0.68
smI0007	psbY	photosystem II protein	3.10	1.75	1.46E-05	1.28	2.30	0.17	0.02	0.00	0.41	-1.28
smI0008	psaJ	photosystem I subunit	1346.11	318.22	0	660.47	143.08	0.00	0.00	0.00	0.49	-1.03
smr0001	psbT	photosystem II PsbT f	451.06	103.06	0	267.64	122.09	0.00	0.03	0.01	0.59	-0.75
smr0002		putative transposase [	235.79	34.15	0	461.48	75.89	0.00	0.00	0.00	1.96	0.97
smr0003	petM	cytochrome b6-f comp	22.45	8.00	6.07E-12	11.19	11.41	0.02	0.06	0.03	0.50	-1.00
smr0004	psaI	photosystem I subunit	53.94	5.25	0	58.22	23.83	0.00	0.98	0.98	1.08	0.11
smr0005	psaM	photosystem I subunit	686.36	254.22	3.76E-11	451.53	273.18	0.00	0.11	0.05	0.66	-0.60
smr0006	psbF	cytochrome b559 b su	236.96	72.38	1.11E-15	186.53	40.02	0.00	0.23	0.02	0.79	-0.35
smr0007	psbL	photosystem II PsbL f	406.03	108.55	0	303.01	69.12	0.00	0.10	0.00	0.75	-0.42
smr0008	psbJ	photosystem II PsbJ p	131.76	38.03	0	119.67	35.86	0.00	0.57	0.42	0.91	-0.14
smr0009	psbN	photosystem II PsbN f	84.56	17.75	0	39.72	8.64	0.00	0.00	0.00	0.47	-1.09
smr0010	petG	cytochrome b6-f comp	39.92	26.17	0.000187	36.35	37.74	0.02	0.40	0.36	0.91	-0.13
smr0011	rpl34	50S ribosomal protein	58.42	22.35	1.54E-10	32.39	23.54	0.00	0.11	0.07	0.55	-0.85
ssi0020	petF	ferredoxin I	2161.70	322.38	0	2168.48	415.93	0.00	0.97	0.96	1.00	0.00
ssi0172		putative transposase [	130.41	22.09	0	133.57	41.48	0.00	0.98	0.97	1.02	0.03
ssi0242		hypothetical protein	37.10	8.55	0	32.60	6.46	0.00	0.33	0.13	0.88	-0.19
ssi0259		hypothetical protein	73.03	32.60	4.07E-08	75.00	59.87	0.00	0.51	0.47	1.03	0.04
ssi0294		hypothetical protein	30.94	6.99	0	21.63	12.58	0.00	0.24	0.21	0.70	-0.52
ssi0296		putative transposase [	10.54	5.36	1.46E-06	38.85	22.48	0.00	0.01	0.00	3.69	1.88
ssi0312		hypothetical protein	8.23	1.41	0	1.25	1.96	0.12	0.00	0.00	0.15	-2.72
ssi0331		hypothetical protein	19.08	7.96	4.28E-09	12.14	17.12	0.08	0.06	0.03	0.64	-0.65
ssi0350		unknown protein	6.22	2.39	1.74E-10	2.39	4.77	0.22	0.01	0.00	0.38	-1.38
ssi0352		hypothetical protein	123.97	19.02	0	104.38	16.71	0.00	0.09	0.01	0.84	-0.25
ssi0353		hypothetical protein	477.39	67.26	0	412.62	70.12	0.00	0.16	0.04	0.86	-0.21
ssi0410		unknown protein	27.49	8.02	0	12.35	16.98	0.07	0.04	0.02	0.45	-1.15
ssi0426		putative transposase [	18.37	5.06	0	31.12	14.16	0.00	0.06	0.01	1.69	0.76
ssi0438		similar to 50S ribosom	3.66	1.77	3.9E-07	1.78	2.72	0.11	0.02	0.01	0.49	-1.04
ssi0452	nblA1	phycobilisome degrad	529.82	117.39	0	456.69	97.40	0.00	0.26	0.09	0.86	-0.21
ssi0453	nblA2	phycobilisome degrad	133.77	15.95	0	79.33	30.08	0.00	0.01	0.00	0.59	-0.75
ssi0461		hypothetical protein	36.36	8.03	0	34.71	4.71	0.00	0.76	0.55	0.95	-0.07
ssi0467		unknown protein	68.46	8.86	0	43.47	29.29	0.00	0.08	0.04	0.63	-0.66
ssi0483		hypothetical protein	404.79	96.17	0	275.33	54.86	0.00	0.01	0.00	0.68	-0.56
ssi0511		hypothetical protein	11.59	3.59	2.66E-15	5.53	9.42	0.15	0.02	0.00	0.48	-1.07
ssi0546	minE	septum site-determinir	97.48	33.27	7.12E-13	108.47	78.46	0.00	0.71	0.69	1.11	0.15
ssi0563	psaC	photosystem I subunit	2962.76	423.08	0	2267.73	384.00	0.00	0.02	0.00	0.77	-0.39
ssi0564		transcriptional regulat	91.91	16.69	0	71.15	31.16	0.00	0.17	0.11	0.77	-0.37
ssi0601	rps21	30S ribosomal protein	1130.39	154.70	0	1246.26	542.04	0.00	0.85	0.84	1.10	0.14
ssi0707	glbB	nitrogen regulatory prc	244.40	76.77	6.22E-15	251.20	111.68	0.00	0.87	0.85	1.03	0.04
ssi0738		unknown protein	2.89	2.66	0.007884	1.69	2.97	0.16	0.12	0.04	0.59	-0.77
ssi0750		unknown protein	42.09	9.87	0	26.37	22.62	0.00	0.16	0.13	0.63	-0.67
ssi0769		putative transposase	61.92	19.01	1.55E-15	102.51	27.85	0.00	0.01	0.00	1.66	0.73
ssi0787		unknown protein	521.97	158.59	6.66E-16	491.38	188.88	0.00	0.67	0.58	0.94	-0.09
ssi0788		hypothetical protein	133.45	20.76	0	153.44	35.48	0.00	0.33	0.23	1.15	0.20
ssi0832		hypothetical protein	53.82	12.01	0	28.32	21.50	0.00	0.13	0.10	0.53	-0.93
ssi1004		hypothetical protein	19.54	4.24	0	10.89	13.15	0.04	0.05	0.03	0.56	-0.84
ssi1045		hypothetical protein	81.51	10.22	0	13.34	15.69	0.04	0.02	0.00	0.16	-2.61
ssi1046		hypothetical protein	264.75	38.43	0	74.13	17.01	0.00	0.00	0.00	0.28	-1.84
ssi1255		hypothetical protein	33.77	8.94	0	10.84	10.68	0.01	0.05	0.03	0.32	-1.64
ssi1263		hypothetical protein	150.76	16.82	0	121.66	14.51	0.00	0.01	0.00	0.81	-0.31

Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
ssl1277		putative transposase	42.20	16.82	8.03E-10	26.63	26.81	0.01	0.13	0.10	0.63	-0.66
ssl1300		hypothetical protein	15.87	3.34	0	5.01	7.81	0.12	0.01	0.00	0.32	-1.66
ssl1326		unknown protein	30.81	14.20	1.06E-07	13.00	19.28	0.10	0.03	0.01	0.42	-1.24
ssl1378		hypothetical protein	18.20	4.31	0	10.96	11.65	0.02	0.11	0.07	0.60	-0.73
ssl1417	ycf33	hypothetical protein YC	54.74	8.22	0	40.02	10.45	0.00	0.02	0.00	0.73	-0.45
ssl1426	rpl35	50S ribosomal protein	448.46	63.85	0	312.58	84.27	0.00	0.01	0.00	0.70	-0.52
ssl1464		unknown protein	7.58	3.43	6.34E-08	11.11	13.57	0.04	0.16	0.13	1.47	0.55
ssl1498		hypothetical protein	181.12	29.77	0	210.24	50.30	0.00	0.25	0.12	1.16	0.22
ssl1507		putative transposase [	4.59	1.39	6.66E-16	2.36	3.63	0.11	0.02	0.01	0.51	-0.96
ssl1520		unknown protein	89.20	14.39	0	37.90	17.75	0.00	0.01	0.00	0.42	-1.24
ssl1533		unknown protein	213.46	43.44	0	71.09	15.33	0.00	0.00	0.00	0.33	-1.59
ssl1552		unknown protein	99.26	10.68	0	80.48	16.04	0.00	0.04	0.01	0.81	-0.30
ssl1633	hliC	high light-inducible pot	52.89	20.94	6.09E-10	108.60	70.45	0.00	0.10	0.03	2.05	1.04
ssl1690		hypothetical protein	154.10	26.20	0	89.14	16.83	0.00	0.00	0.00	0.58	-0.79
ssl1707		hypothetical protein	13.35	2.03	0	5.92	8.37	0.08	0.03	0.01	0.44	-1.17
ssl1784	rps15	30S ribosomal protein	146.47	48.97	2.36E-13	119.50	59.61	0.00	0.33	0.20	0.82	-0.29
ssl1792		hypothetical protein	5.68	2.10	3.52E-11	1.49	2.29	0.11	0.01	0.00	0.26	-1.93
ssl1807		hypothetical protein	44.70	2.53	0	17.64	14.70	0.00	0.07	0.05	0.39	-1.34
ssl1911		hypothetical protein	173.53	42.41	0	69.34	13.40	0.00	0.00	0.00	0.40	-1.32
ssl1918		hypothetical protein	52.99	8.16	0	21.46	20.52	0.01	0.08	0.05	0.40	-1.30
ssl1920		putative transposase [	28.37	4.96	0	155.18	35.56	0.00	0.00	0.00	5.47	2.45
ssl1922		putative transposase [	46.49	7.76	0	154.68	55.88	0.00	0.00	0.00	3.33	1.73
ssl1923		hypothetical protein	45.11	12.59	0	20.75	20.34	0.01	0.09	0.06	0.46	-1.12
ssl1972		hypothetical protein	163.71	57.07	2.12E-12	222.32	50.55	0.00	0.05	0.00	1.36	0.44
ssl2009		hypothetical protein	44.01	11.08	0	66.62	21.72	0.00	0.04	0.00	1.51	0.60
ssl2069		hypothetical protein	176.10	49.54	0	142.93	59.73	0.00	0.21	0.11	0.81	-0.30
ssl2084	acp	acyl carrier protein	1423.39	338.53	0	1428.39	232.70	0.00	0.90	0.83	1.00	0.01
ssl2138		unknown protein	24.70	6.81	0	10.94	13.42	0.05	0.04	0.02	0.44	-1.17
ssl2148		hypothetical protein	126.45	23.05	0	137.89	46.73	0.00	0.77	0.73	1.09	0.13
ssl2153		probable ribose phosph	13.31	4.22	1.07E-14	11.53	15.17	0.06	0.09	0.06	0.87	-0.21
ssl2162		unknown protein	20.33	4.80	0	7.64	12.14	0.12	0.01	0.00	0.38	-1.41
ssl2233	rps20	30S ribosomal protein	637.56	171.51	0	593.12	108.61	0.00	0.69	0.47	0.93	-0.10
ssl2245		unknown protein	316.61	47.90	0	319.30	100.48	0.00	0.87	0.85	1.01	0.01
ssl2250		bacterioferritin-associa	252.21	35.03	0	187.81	40.51	0.00	0.01	0.00	0.74	-0.43
ssl2296		pterin-4a-carbinolamin	54.10	3.96	0	62.45	22.22	0.00	0.57	0.55	1.15	0.21
ssl2384		unknown protein	35.59	10.60	2.22E-16	7.12	11.05	0.11	0.01	0.00	0.20	-2.32
ssl2420		unknown protein	264.63	286.97	0.023898	204.74	268.57	0.06	0.42	0.29	0.77	-0.37
ssl2471		hypothetical protein	4.27	3.90	0.007452	3.02	5.76	0.20	0.04	0.02	0.71	-0.50
ssl2501		unknown protein	382.86	40.09	0	319.44	150.50	0.00	0.23	0.19	0.83	-0.26
ssl2542	hliA	high light-inducible pot	13.87	2.94	0	21.96	14.70	0.00	0.97	0.97	1.58	0.66
ssl2559		ferredoxin	6.39	3.47	6.44E-06	4.60	5.67	0.05	0.09	0.06	0.72	-0.47
ssl2595		hypothetical protein	112.35	40.65	1.29E-11	78.95	24.16	0.00	0.09	0.00	0.70	-0.51
ssl2598	psbH	photosystem II PsbH p	537.55	232.97	1.59E-08	622.01	371.87	0.00	0.88	0.86	1.16	0.21
ssl2615	atpH	ATP synthase subunit	557.21	110.51	0	729.96	224.91	0.00	0.13	0.06	1.31	0.39
ssl2667		similar to NifU protein	87.54	30.79	3.3E-12	97.12	49.66	0.00	0.96	0.95	1.11	0.15
ssl2717		hypothetical protein	48.91	8.59	0	18.66	18.15	0.01	0.07	0.04	0.38	-1.39
ssl2733		hypothetical protein	124.15	17.01	0	87.74	17.18	0.00	0.00	0.00	0.71	-0.50
ssl2749		hypothetical protein	18.60	5.29	0	10.06	10.92	0.02	0.09	0.06	0.54	-0.89
ssl2781		hypothetical protein	25.38	3.80	0	14.02	8.66	0.00	0.19	0.16	0.55	-0.86
ssl2789		similar to resolvase	15.47	5.45	3.58E-12	14.69	14.93	0.02	0.20	0.17	0.95	-0.07
ssl2823		hypothetical protein	45.51	11.95	0	29.46	23.43	0.00	0.15	0.11	0.65	-0.63
ssl2874		hypothetical protein	94.54	16.08	0	106.96	14.78	0.00	0.18	0.02	1.13	0.18
ssl2920		hypothetical protein	196.72	81.15	2.88E-09	195.24	112.92	0.00	0.77	0.72	0.99	-0.01
ssl2922	vapB	similar to virulence-as	2.69	3.00	0.02807	5.36	7.83	0.09	0.88	0.83	1.99	1.00
ssl2923	vapC	similar to virulence-as	113.65	18.07	0	615.60	231.39	0.00	0.00	0.00	5.42	2.44
ssl2971		hypothetical protein	15.71	7.82	8.66E-07	9.82	15.30	0.12	0.02	0.01	0.63	-0.68
ssl2982	ycf61	probable DNA-director	112.15	31.67	0	50.96	44.65	0.01	0.10	0.07	0.45	-1.14
ssl3044		probable ferredoxin	770.90	93.29	0	757.18	104.01	0.00	0.79	0.71	0.98	-0.03
ssl3093	cpcD	phycobilisome small rc	930.56	91.58	0	877.38	119.65	0.00	0.39	0.27	0.94	-0.08
ssl3127		similar to permease pr	257.24	42.45	0	231.36	29.80	0.00	0.24	0.05	0.90	-0.15
ssl3177		hypothetical protein	122.60	16.77	0	229.31	64.32	0.00	0.00	0.00	1.87	0.90
ssl3291		hypothetical protein	117.50	35.94	1.11E-15	178.73	99.48	0.00	0.23	0.16	1.52	0.61
ssl3335	secE	preprotein translocase	129.60	16.43	0	125.12	31.48	0.00	0.64	0.59	0.97	-0.05
ssl3364	cp12	CP12 polypeptide	206.12	54.19	0	334.79	59.73	0.00	0.00	0.00	1.62	0.70
ssl3379		hypothetical protein	205.96	21.26	0	175.30	32.94	0.00	0.08	0.03	0.85	-0.23
ssl3382		hypothetical protein	63.88	9.20	0	38.09	25.78	0.00	0.21	0.18	0.60	-0.75
ssl3383		unknown protein	44.93	9.21	0	11.84	13.60	0.03	0.02	0.01	0.26	-1.92
ssl3432	rps19	30S ribosomal protein	91.16	42.84	1.86E-07	169.33	142.67	0.00	0.42	0.35	1.86	0.89
ssl3436	rpl29	50S ribosomal protein	114.29	38.15	2.16E-13	180.73	112.41	0.00	0.32	0.25	1.58	0.66
ssl3437	rps17	30S ribosomal protein	96.63	38.88	1.14E-09	130.68	101.51	0.00	0.95	0.95	1.35	0.44
ssl3441	infA	initiation factor IF-1	1011.23	130.24	0	1201.98	111.19	0.00	0.02	0.00	1.19	0.25
ssl3445	rpl31	50S ribosomal protein	222.28	64.62	0	206.34	41.05	0.00	0.73	0.52	0.93	-0.11
ssl3446		hypothetical protein	3.65	2.42	0.000218	4.70	7.63	0.13	0.07	0.04	1.29	0.36
ssl3451		hypothetical protein	58.56	15.51	0	47.58	38.80	0.00	0.23	0.20	0.81	-0.30
ssl3549		hypothetical protein	266.20	70.17	0	157.77	27.00	0.00	0.00	0.00	0.59	-0.75
ssl3573		hypothetical protein	20.11	7.10	3.86E-12	3.27	3.31	0.02	0.02	0.01	0.16	-2.62
ssl3580	hypC	hydrogenase expressi	12.13	4.60	9.91E-11	12.79	14.25	0.03	0.29	0.26	1.05	0.08
ssl3615		unknown protein	16.06	3.59	0	14.67	7.87	0.00	0.44	0.40	0.91	-0.13



Table A-1 Gene expression profiles for *Synechocystis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
ssl3692		hypothetical protein	4.03	1.53	1.04E-10	2.10	3.23	0.11	0.02	0.01	0.52	-0.94
ssl3712		hypothetical protein	12.91	3.86	2.22E-16	7.04	11.67	0.14	0.02	0.01	0.54	-0.88
ssl3769		unknown protein	36.56	6.76	0	23.82	23.97	0.01	0.13	0.10	0.65	-0.62
ssl3829		hypothetical protein	24.49	3.56	0	9.64	11.68	0.04	0.05	0.02	0.39	-1.34
ssr0102	ycf40	hypothetical protein YC	21.83	7.51	1.1E-12	16.49	17.33	0.02	0.15	0.12	0.76	-0.40
ssr0109		hypothetical protein	173.50	25.89	0	169.51	31.91	0.00	0.76	0.71	0.98	-0.03
ssr0256		putative transposase [	7.39	4.18	1.51E-05	26.99	14.38	0.00	0.00	0.00	3.65	1.87
ssr0330	ftv	ferredoxin-thioredoxin	17.41	9.85	1.5E-05	11.24	17.40	0.11	0.03	0.01	0.65	-0.63
ssr0332		hypothetical protein	306.56	66.92	0	328.25	90.63	0.00	0.71	0.61	1.07	0.10
ssr0336		hypothetical protein	9.76	2.03	0	1.39	2.12	0.11	0.00	0.00	0.14	-2.81
ssr0349		hypothetical protein	316.40	53.31	0	276.73	34.37	0.00	0.21	0.02	0.87	-0.19
ssr0390	psaK	photosystem I subunit	368.45	111.39	4.44E-16	242.99	35.79	0.00	0.02	0.00	0.66	-0.60
ssr0482	rps16	30S ribosomal protein	227.68	62.01	0	157.61	78.07	0.00	0.11	0.06	0.69	-0.53
ssr0536		unknown protein	298.24	63.52	0	113.34	41.76	0.00	0.00	0.00	0.38	-1.40
ssr0657		hypothetical protein	75.06	12.98	0	77.83	14.87	0.00	0.76	0.68	1.04	0.05
ssr0692		hypothetical protein	195.18	91.01	1.49E-07	70.58	20.42	0.00	0.00	0.00	0.36	-1.47
ssr0693		unknown protein	170.64	24.88	0	81.37	20.08	0.00	0.00	0.00	0.48	-1.07
ssr0756		hypothetical protein	94.40	24.10	0	73.15	34.74	0.00	0.23	0.17	0.77	-0.37
ssr0759		unknown protein	17.43	6.58	8.51E-11	3.50	7.06	0.22	0.00	0.00	0.20	-2.32
ssr0817		putative transposase [	1127.10	214.24	0	1635.15	319.50	0.00	0.01	0.00	1.45	0.54
ssr0871		putative transposase [	304.01	54.61	0	675.24	130.36	0.00	0.00	0.00	2.22	1.15
ssr1038		unknown protein	62.77	13.26	0	39.63	30.64	0.00	0.21	0.18	0.63	-0.66
ssr1041		hypothetical protein	23.12	5.07	0	8.52	11.82	0.08	0.03	0.01	0.37	-1.44
ssr1114		hypothetical protein	28.76	5.70	0	41.53	15.95	0.00	0.13	0.07	1.44	0.53
ssr1169		stress induced hydrop	24.68	3.43	0	13.79	11.28	0.00	0.12	0.09	0.56	-0.84
ssr1175		putative transposase [	28.59	5.90	0	217.79	76.21	0.00	0.00	0.00	7.62	2.93
ssr1176		putative transposase [	41.12	11.22	0	360.17	121.39	0.00	0.00	0.00	8.76	3.13
ssr1256		hypothetical protein	55.20	10.36	0	26.96	22.11	0.00	0.13	0.09	0.49	-1.03
ssr1258		hypothetical protein	3.27	2.40	0.000838	1.10	2.64	0.31	0.01	0.00	0.33	-1.58
ssr1375		hypothetical protein	305.27	31.94	0	86.96	41.56	0.00	0.00	0.00	0.28	-1.81
ssr1386	ndhL	NADH dehydrogenase	491.31	66.37	0	466.50	42.97	0.00	0.47	0.20	0.95	-0.07
ssr1391		hypothetical protein	35.25	7.73	0	11.34	8.53	0.00	0.08	0.05	0.32	-1.64
ssr1398	rpl33	50S ribosomal protein	173.59	27.05	0	75.92	31.96	0.00	0.00	0.00	0.44	-1.19
ssr1399	rps18	30S ribosomal protein	125.36	27.23	0	55.69	47.94	0.00	0.10	0.07	0.44	-1.17
ssr1407		hypothetical protein	55.46	6.01	0	34.12	17.94	0.00	0.09	0.06	0.62	-0.70
ssr1425	ycf34	hypothetical protein YC	63.39	6.75	0	49.18	9.53	0.00	0.02	0.00	0.78	-0.37
ssr1480		RNA-binding protein	200.85	57.46	0	219.61	103.27	0.00	0.97	0.96	1.09	0.13
ssr1499		hypothetical protein	154.10	29.03	0	99.74	33.77	0.00	0.02	0.00	0.65	-0.63
ssr1513		hypothetical protein	110.63	23.76	0	90.70	46.63	0.00	0.27	0.22	0.82	-0.29
ssr1527		probable molybdopteri	43.57	4.21	0	16.09	15.05	0.01	0.07	0.04	0.37	-1.44
ssr1528		hypothetical protein	40.42	4.89	0	23.43	14.96	0.00	0.20	0.17	0.58	-0.79
ssr1558		hypothetical protein	23.26	5.34	0	21.27	16.77	0.00	0.34	0.32	0.91	-0.13
ssr1562		hypothetical protein	73.87	10.21	0	76.69	55.12	0.00	0.53	0.51	1.04	0.05
ssr1600		similar to anti-sigma f1	442.80	54.00	0	473.48	102.06	0.00	0.64	0.59	1.07	0.10
ssr1604	rpl28	50S ribosomal protein	397.85	113.92	0	268.56	82.83	0.00	0.04	0.00	0.68	-0.57
ssr1698		hypothetical protein	24.43	8.56	2.79E-12	23.55	17.05	0.00	0.41	0.38	0.96	-0.05
ssr1720		similar to tyrosyl tRNA	28.22	27.74	0.012703	35.15	42.53	0.04	0.48	0.45	1.25	0.32
ssr1736	rps32	50S ribosomal protein	54.11	13.69	0	25.95	23.95	0.01	0.10	0.07	0.48	-1.06
ssr1765		hypothetical protein	32.88	6.10	0	26.78	21.98	0.00	0.18	0.15	0.81	-0.30
ssr1766		hypothetical protein	2.05	1.23	4.1E-05	0.91	1.51	0.14	0.04	0.01	0.44	-1.17
ssr1768		unknown protein	15.35	5.21	5.1E-13	8.02	12.64	0.12	0.04	0.02	0.52	-0.94
ssr1789	hliD	CAB/ELIP/HLIP-relate	40.01	4.42	0	38.29	12.43	0.00	0.59	0.56	0.96	-0.06
ssr1853		unknown protein	31.60	3.59	0	40.02	18.95	0.00	0.62	0.60	1.27	0.34
ssr1951		hypothetical protein	38.03	4.32	0	13.19	17.76	0.07	0.03	0.01	0.35	-1.53
ssr2009		hypothetical protein	7.38	1.79	0	2.46	4.02	0.13	0.01	0.00	0.33	-1.58
ssr2016		hypothetical protein	3.56	1.55	1.99E-08	2.04	4.03	0.22	0.02	0.01	0.57	-0.81
ssr2047		hypothetical protein	52.60	6.52	0	14.88	12.08	0.00	0.05	0.03	0.28	-1.82
ssr2049		unknown protein	61.24	13.46	0	59.30	31.96	0.00	0.55	0.52	0.97	-0.05
ssr2060		unknown protein	35.16	4.95	0	14.27	12.87	0.01	0.03	0.01	0.41	-1.30
ssr2061		glutaredoxin	395.25	39.62	0	364.37	93.58	0.00	0.39	0.34	0.92	-0.12
ssr2062		hypothetical protein	141.64	26.75	0	50.36	22.36	0.00	0.00	0.00	0.36	-1.49
ssr2067		hypothetical protein	11.63	4.92	6.86E-09	7.49	11.07	0.10	0.06	0.03	0.64	-0.64
ssr2078		putative transposase [	23.00	6.01	0	34.45	7.16	0.00	0.01	0.00	1.50	0.58
ssr2087		hypothetical protein	43.04	6.45	0	20.22	13.25	0.00	0.01	0.00	0.47	-1.09
ssr2130		hypothetical protein	609.98	47.99	0	544.45	94.73	0.00	0.13	0.07	0.89	-0.16
ssr2142	ycf19	hypothetical protein YC	576.75	98.33	0	301.11	59.36	0.00	0.00	0.00	0.52	-0.94
ssr2153		unknown protein	119.22	50.85	9.34E-09	233.85	111.84	0.00	0.07	0.01	1.96	0.97
ssr2194		unknown protein	13.89	5.22	7.37E-11	16.68	11.03	0.00	0.53	0.51	1.20	0.26
ssr2201		unknown protein	13.98	5.61	1.01E-09	1.48	1.99	0.07	0.00	0.00	0.11	-3.24
ssr2227		putative transposase	13.58	4.16	1.33E-15	5.54	8.84	0.12	0.03	0.01	0.41	-1.29
ssr2315		unknown protein	56.71	26.35	1.36E-07	21.54	20.27	0.01	0.08	0.05	0.38	-1.40
ssr2317		unknown protein	26.61	7.16	0	11.14	12.98	0.04	0.05	0.02	0.42	-1.26
ssr2318		unknown protein	57.76	11.59	0	85.08	13.61	0.00	0.00	0.00	1.47	0.56
ssr2333		unknown protein	34.65	7.67	0	39.32	26.13	0.00	0.93	0.92	1.14	0.18
ssr2406		unknown protein	47.20	17.66	5.84E-11	31.75	29.52	0.01	0.12	0.08	0.67	-0.57
ssr2422		unknown protein	15.86	2.99	0	12.15	7.43	0.00	0.29	0.27	0.77	-0.38
ssr2439		hypothetical protein	5.88	2.87	5.05E-07	16.41	9.99	0.00	0.02	0.00	2.79	1.48
ssr2549		unknown protein	54.62	8.38	0	57.38	20.35	0.00	0.98	0.98	1.05	0.07

Table A-1 Gene expression profiles for *Synechocytis* PCC6803 after acclimating to high salt conditions

Results of six replicate experiments												
Orf	Symbol	Product	Ave(Control)	SD(control)	p(Control)	Ave(Exp)	SD(Exp)	p(Exp)	Ts	Ta	ratio(Exp/control)	Log Ratio
ssr2551		hypothetical protein	28.00	6.98	0	12.41	13.08	0.02	0.07	0.04	0.44	-1.17
ssr2554		hypothetical protein	94.51	26.78	0	31.63	13.11	0.00	0.00	0.00	0.33	-1.58
ssr2595	hliB	high light-inducible pol	45.27	9.56	0	87.65	13.15	0.00	0.00	0.00	1.94	0.95
ssr2611		hypothetical protein	20.18	4.31	0	55.14	7.49	0.00	0.00	0.00	2.73	1.45
ssr2699		putative transposase [	151.47	29.82	0	282.89	32.64	0.00	0.00	0.00	1.87	0.90
ssr2708		hypothetical protein	408.74	103.86	0	353.46	113.73	0.00	0.39	0.26	0.86	-0.21
ssr2711		hypothetical protein	298.30	66.27	0	272.43	76.99	0.00	0.46	0.34	0.91	-0.13
ssr2723		hypothetical protein	159.29	9.04	0	101.50	17.64	0.00	0.00	0.00	0.64	-0.65
ssr2781		hypothetical protein	45.73	11.17	0	52.09	30.58	0.00	0.47	0.45	1.14	0.19
ssr2786			34.73	11.47	1.18E-13	19.95	20.70	0.02	0.11	0.08	0.57	-0.80
ssr2799	rpl27	50S ribosomal protein	507.99	96.08	0	296.56	28.41	0.00	0.00	0.00	0.58	-0.78
ssr2802		hypothetical protein	1022.38	108.26	0	1192.56	159.74	0.00	0.05	0.00	1.17	0.22
ssr2803		hypothetical protein	7.75	3.44	3.25E-08	6.54	12.33	0.19	0.05	0.02	0.84	-0.25
ssr2806		hypothetical protein	312.46	54.17	0	376.29	173.87	0.00	0.63	0.59	1.20	0.27
ssr2831	psaE	photosystem I subunit	1417.63	251.98	0	956.01	100.96	0.00	0.00	0.00	0.67	-0.57
ssr2843		hypothetical protein	17.33	4.31	0	9.93	6.84	0.00	0.18	0.14	0.57	-0.80
ssr2848		unknown protein	7.24	2.76	1.37E-10	3.86	5.96	0.11	0.02	0.01	0.53	-0.91
ssr2857		mercuric transport pro	221.09	83.92	1.1E-10	296.98	131.40	0.00	0.22	0.09	1.34	0.43
ssr2898		putative transposase [	30.38	5.67	0	125.22	55.62	0.00	0.00	0.00	4.12	2.04
ssr2912		unknown protein	18.74	1.94	0	56.79	21.38	0.00	0.00	0.00	3.03	1.60
ssr2962		hypothetical protein	10.24	1.93	0	3.73	5.78	0.11	0.01	0.00	0.36	-1.46
ssr2972		unknown protein	4.75	2.16	7.14E-08	4.23	7.47	0.17	0.04	0.02	0.89	-0.17
ssr2998		hypothetical protein	109.59	18.21	0	225.30	75.45	0.00	0.00	0.00	2.06	1.04
ssr3000		hypothetical protein	9.93	2.77	0	13.78	15.89	0.03	0.27	0.24	1.39	0.47
ssr3122		hypothetical protein	127.71	21.40	0	181.41	48.24	0.00	0.03	0.00	1.42	0.51
ssr3129		unknown protein	6.67	5.71	0.004216	4.65	7.32	0.12	0.04	0.02	0.70	-0.52
ssr3184		ferredoxin	109.71	24.27	0	154.37	45.91	0.00	0.07	0.01	1.41	0.49
ssr3188		hypothetical protein	62.08	14.90	0	89.66	56.18	0.00	0.87	0.87	1.44	0.53
ssr3189		hypothetical protein	559.77	119.43	0	520.81	92.38	0.00	0.58	0.39	0.93	-0.10
ssr3300		unknown protein	51.87	19.02	2.41E-11	22.85	23.32	0.02	0.08	0.05	0.44	-1.18
ssr3304		hypothetical protein	13.80	2.91	0	3.95	6.77	0.15	0.01	0.00	0.29	-1.80
ssr3307	secG	probable protein-expo	139.45	28.98	0	76.78	13.57	0.00	0.00	0.00	0.55	-0.86
ssr3341		hypothetical protein	97.63	20.74	0	50.39	6.15	0.00	0.00	0.00	0.52	-0.95
ssr3383	apcC	phycobilisome small c	758.39	103.91	0	713.60	194.35	0.00	0.53	0.46	0.94	-0.09
ssr3402		unknown protein	89.54	17.65	0	95.42	26.45	0.00	0.76	0.71	1.07	0.09
ssr3409		hypothetical protein	24.69	7.97	3.38E-14	13.36	16.33	0.05	0.05	0.03	0.54	-0.89
ssr3410		hypothetical protein	9.19	2.58	0	5.48	8.55	0.12	0.02	0.01	0.60	-0.75
ssr3451	psbE	cytochrome b559 alph	1288.72	354.02	0	1029.16	292.03	0.00	0.16	0.03	0.80	-0.32
ssr3452		putative transposase [	451.14	43.27	0	477.16	58.06	0.00	0.42	0.28	1.06	0.08
ssr3465		unknown protein	133.02	28.34	0	72.14	44.65	0.00	0.07	0.04	0.54	-0.88
ssr3467		unknown protein	37.29	11.41	1.11E-15	35.92	32.52	0.01	0.21	0.18	0.96	-0.05
ssr3532		unknown protein	19.82	3.14	0	10.83	11.27	0.02	0.09	0.06	0.55	-0.87
ssr3570		unknown protein	34.71	11.45	1.11E-13	7.43	10.29	0.08	0.01	0.00	0.21	-2.22
ssr3571		hypothetical protein	31.86	9.28	0	6.31	7.40	0.04	0.02	0.00	0.20	-2.34

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sgl0001		hypothetical protein	error	error	-0.492	error	error	-0.109	0.519	-0.167	0.613	error	0.423	-0.335	0.345
sgl0002		hypothetical protein	-0.432	-0.159	-0.105	error	-0.061	-0.049	error	-0.167	0.405	0.615	0.228	0.344	0.851
slf0002		penicillin-binding protein	0.139	-0.245	-0.146	-0.279	0.072	0.06	0.111	0.05	0.059	-0.045	0.064	-0.152	0.66
slf0005		hypothetical protein	-0.537	-0.265	0.385	1.014	0.096	-0.549	-0.123	-0.181	0.086	0.175	0.49	0.223	-0.977
slf0006		putative aminotransferase	-0.802	-0.709	-0.606	0.007	-1.068	-1.035	-1.122	-0.381	-0.24	-0.092	-0.458	0.032	-0.967
slf0007		hypothetical protein	0.056	-0.155	-0.044	-0.242	0.188	-0.048	-0.476	-0.168	-0.096	error	0.032	-0.64	error
slf0008		unknown protein	error	error	1.304	-0.989	error	0.848	error	-0.134	0.692	0.062	0.471	0.08	1.489
slf0010		unknown protein	error	0.35	-0.002	-1.045	error	error	1.151	0.125	0.327	0.674	0.069	-0.206	1.599
slf0012		putative transposase [ISY5]	0.162	-0.193	0.096	0.018	-0.622	-0.069	-0.344	-0.556	-0.25	0.357	-0.861	-0.306	-0.12
slf0016		probable membrane-bound	0.302	0.443	0.956	0.403	1.093	0.539	0.897	-0.113	0.272	-0.132	-0.147	-0.247	1.138
slf0017	hemL	glutamate-1-semialdehyde	-0.175	-0.126	-0.194	-0.426	-0.321	-0.632	-0.519	-0.029	-0.188	-0.359	-0.013	-0.08	-0.193
slf0018	fbaA, fda	fructose-bisphosphate aldo	-0.611	-0.693	-0.685	0.035	-0.511	-0.427	-0.323	-0.184	-0.341	-0.037	0.356	-0.089	1.428
slf0019		1-deoxy-d-xyulose 5-phosp	error	error	error	error	error	error	error	-0.276	-0.06	-0.692	-0.238	-0.24	0.475
slf0020	clpC	ATP-dependent Clp proteas	error	error	error	error	error	error	error	0.353	1.107	0.904	1.376	1.008	0.002
slf0021		probable exonuclease	0.214	0.606	0.312	0.667	0.095	0.262	-0.363	error	error	error	error	error	error
slf0022		unknown protein	-0.423	-0.545	-0.636	-0.129	-0.642	-0.068	-0.586	-0.366	-0.088	0.066	-0.294	0.015	-0.97
slf0023		hypothetical protein	-0.268	0.384	0.299	-0.251	-0.04	0.121	0.094	-0.358	-0.017	-0.133	-0.683	-0.349	-0.701
slf0024		unknown protein	0.377	-0.023	0.276	-0.471	-0.285	0.208	error	-0.224	-0.036	error	-0.444	-0.125	0.551
slf0026	ndhF4	NADH dehydrogenase subu	error	-0.135	-0.515	error	-0.86	-0.286	-0.639	-0.216	-0.598	0.162	-0.669	-0.624	0.47
slf0027	ndhD4	NADH dehydrogenase subu	-0.533	-0.708	-1.395	-0.296	-0.937	-0.602	-0.047	-0.128	-0.405	-0.681	-0.376	-0.403	-0.644
slf0030	cmpR	cmp operon transcriptional	-0.486	-0.59	-0.397	-0.633	-0.733	-0.532	-0.235	-0.082	0.654	1.178	0.253	0.74	0.152
slf0031		hypothetical protein	-0.353	-0.41	-0.116	0.323	0.056	0.194	0.54	0.071	0.297	0.398	-0.03	0.018	-0.541
slf0033	crtH	carotene isomerase/crtH	error	error	-0.063	-0.769	0.061	0.122	-0.044	-0.005	0.559	error	0.074	0.295	-0.138
slf0034		putative carboxypeptidase	-0.193	0.062	0.392	error	-0.085	0.053	-0.442	-0.092	0.074	error	0.104	0.024	0.556
slf0036		hypothetical protein	-0.016	-0.529	-0.109	-1.067	-0.389	-0.124	-0.216	-0.285	-0.187	-0.533	-0.692	-0.703	-0.386
slf0037		hypothetical protein	0.309	0.301	-0.061	-0.238	-0.791	0.164	-0.363	0.531	0.117	-0.162	-0.118	0.397	0.729
slf0038		two-component response re	-0.394	-0.38	-0.302	0.168	-0.329	-0.186	-0.17	-0.015	0.002	0.159	0.024	0.124	-0.787
slf0039		two-component response re	0.123	-0.41	-0.848	-0.128	0.075	0.351	0.101	0.358	-0.069	0.41	0.384	-0.201	0.355
slf0040		similar to chemotaxis protei	-0.23	-0.212	-0.085	error	-0.281	0.014	0.34	0.014	0.064	-0.098	0.093	-0.12	1.152
slf0041		probable methyl-accepting	0.514	0.615	1.993	2.306	1.263	0.501	0.625	0.311	1.788	2.318	1.062	1.673	0.719
slf0042		probable methyl-accepting	0.811	error	error	-1.204	-0.32	-0.127	error	0.116	0.218	-0.013	-0.334	-0.03	5.81
slf0043		two-component hybrid sens	-0.342	-0.499	-0.385	0.2	-0.666	-0.316	-0.663	-0.031	-0.11	-0.252	-0.09	-0.32	-0.612
slf0044		unknown protein	0.495	0.248	0.18	-0.247	0.109	0.25	0.281	-0.009	0.016	0.835	0.306	-0.383	0.95
slf0045	sps	sucrose phosphate synthas	-0.272	-0.363	-1.139	-0.907	-0.863	-1.13	-0.375	-0.117	-0.131	0.145	-0.585	-0.403	0.11
slf0047	ycf12	hypothetical protein YCF12	0.079	error	-1.486	error	error	-0.346	-0.473	-0.023	0.181	0.207	0.065	0.01	0.075
slf0048		unknown protein	error	-0.316	-0.18	-0.073	-0.043	-0.175	-0.165	-0.158	0.583	error	0.199	0.561	-0.107
slf0051		hypothetical protein	-0.373	-0.09	-0.519	-0.519	-0.434	-0.03	0.045	-0.187	0.05	-0.362	-0.349	-0.12	-0.324
slf0053	accC	biotin carboxylaseaccC	error	error	error	error	error	error	error	-0.611	-0.58	-1.044	-0.938	-1.088	-0.279
slf0055		processing protease	error	error	error	error	error	error	error	error	error	error	error	error	error
slf0057	grpE	heat shock protein GrpEgp	0.169	-0.269	-0.071	-0.381	-0.175	-0.411	-0.164	-0.131	0.101	error	0.328	0.09	error
slf0058	dnaK	DnaK protein/dnaK	0.192	-0.028	-0.628	-1.098	-0.247	0.017	0.298	-0.336	-0.102	-0.097	-0.301	-0.331	1.082
slf0060		hypothetical protein	error	error	0.679	error	error	-0.414	error	error	error	error	error	error	error
slf0062		hypothetical protein	error	-0.143	0.17	0.348	0.335	0.133	0.276	-0.027	0.309	0.751	0.311	0.434	0.141
slf0063		hypothetical protein	-0.26	-0.172	-0.536	-0.052	0.429	error	-0.01	-0.306	-0.044	0.185	0.148	-0.073	-0.51
slf0064		binding protein of ABC tran	-0.321	-0.104	-0.605	-0.677	-0.33	-0.033	-0.087	-0.106	0.087	error	0.019	-0.192	-0.706
slf0065	ilvN	acetolactate synthase smal	error	error	-0.45	-0.76	error	0.582	error	0.425	0.247	0.263	0.325	0.206	0.124
slf0066		unknown protein	0.184	0.541	0.904	0.474	0.567	0.335	error	0.387	1.002	0.411	0.615	0.249	-0.431
slf0067		glutathione S-transferase	0.227	0.172	0.316	0.414	0.541	0.407	1.355	0.04	0.285	0.224	0.532	0.084	0.575
slf0068		unknown protein	0.367	0.495	1.067	0.101	0.166	0.35	0.406	-0.243	0.293	0.446	-0.247	0.146	0.518
slf0069		hypothetical protein	error	error	error	error	error	error	error	0.115	0.335	-0.34	-0.064	0.045	0.523
slf0070	purU	phosphoribosylglycinamide	-0.54	-0.568	-0.508	-0.314	-0.872	0.07	-0.277	-0.201	-0.404	0.035	-0.355	-0.499	-0.672
slf0071		hypothetical protein	0.364	error	0.307	-0.991	-0.652	0.317	0.142	-0.841	-0.438	-0.584	-0.588	-0.761	0.199
slf0072		hypothetical protein	error	0.327	-0.439	-1.08	-0.257	0.238	error	0.02	-0.475	0.944	-0.174	-0.686	-1.122
slf0078	thrS	threonyl-tRNA synthetase/th	0.174	0.851	2.026	1.13	0.862	0.652	0.218	-0.088	0.679	-0.062	0.117	0.307	0.558
slf0080	argC	N-acetyl-gamma-glutamyl-p	-0.13	0.113	0.023	-0.075	-0.13	0.322	0.435	-0.27	-0.372	-0.921	-0.345	-0.607	1.381
slf0082		hypothetical protein	0.128	-0.362	-0.134	-0.362	error	-0.649	-1.119	0.112	0.3	0.398	0.056	0.01	0.631
slf0083		phosphoheptose isomerase	-0.322	-0.637	-0.965	-0.415	-0.78	-0.666	-0.479	0.258	-0.151	-0.567	-0.662	-0.202	-0.482
slf0084		putative phosphatase	0.619	0.45	-0.063	-0.481	-0.105	0.676	0.724	0.294	0.02	0.639	0.033	-0.16	-0.23
slf0085		unknown protein	0.075	1.051	-0.527	-0.646	-0.65	0.107	-0.004	-0.234	-0.172	0.346	-0.279	-0.142	-0.94
slf0086		putative arsenical pump-dri	-0.457	-0.421	0.023	0.276	0.078	0.046	0.084	0.041	0.332	0.06	0.473	0.008	-0.412
slf0088		hypothetical protein	0.805	0.35	0.437	0.504	0.077	0.395	0.021	0.695	0.237	0.049	-0.111	0.371	-0.912
slf0092		putative transposase [ISY3]	-1.522	-1.223	-1.096	-0.4	-0.666	-0.499	0.049	-1.25	-0.305	0.52	-0.866	-0.383	-1.057
slf0094		two-component sensor histi	-0.221	-0.167	0.397	error	-0.193	0.262	0.693	-0.334	-0.24	-0.267	-0.095	-0.533	0.185
slf0095		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slf0096		hypothetical protein	-0.326	-0.271	-0.183	0.178	-0.572	-0.172	-0.229	-0.112	-0.182	-0.017	-0.239	-0.051	-0.91
slf0098		hypothetical protein	error	-0.55	0.005	-0.026	-0.264	0.172	0.149	-0.433	-0.127	-0.147	-0.178	-0.544	-0.861
slf0099	cobL	precoirin-6y c5,15-methyltr	-0.012	0.22	-0.732	-0.825	error	0.267	0.661	-0.068	-0.085	0.581	-0.457	-0.219	-1.025
slf0100		N-acyl-L-amino acid amidoh	error	error	error	error	error	0.048	error	-0.104	-0.06	0.451	-0.322	-0.096	-0.948
slf0101		unknown protein	0.705	-0.389	error	0.379	1.397	0.692	error	0.712	0.396	0.735	1.222	0.325	2.611
slf0102		hypothetical protein	-0.459	-0.68	-0.59	-0.091	-0.672	0.016	-0.692	-0.388	-0.651	error	-0.471	-0.885	-1.325
slf0103		hypothetical protein	-0.182	-0.329	-0.45	0.2	error	0.206	0.15	0.006	-0.227	0.13	0.24	-0.489	-0.575
slf0107		KHG/KDPG aldolase	error	error	0.102	-1.265	0.06	0.375	-0.17	-0.078	0.289	-0.06	0.091	-0.172	-0.497
slf0108	amt1	ammonium/methylammoniu	-0.431	-0.379	-0.241	0.437	-0.18	-0.239	-0.343	-0.305	0.007	-0.38	-0.121	0.121	0.357
slf0109	aroH	chorismate mutase/aroH	0.727	0.337	0.185	-1.503	-0.473	0.295	error	-0.084	0.473	error	-0.065	0.258	error
slf0135		5'-methylthioadenosine pho	0.164	0.189	-0.317	-0.361	-0.046	-0.366	-0.533	0.303	0.118	error	0.019	0.017	-0.632

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl0136		aminopeptidase P	-0.199	0.554	0.681	0.237	0.15	0.435	error	-0.292	0.217	-0.097	0.064	-0.016	-0.404
sl0140		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sl0141		hypothetical protein	error	0.144	0.44	0.356	0.611	0.543	0.877	0.005	0.614	0.266	0.595	0.485	-0.329
sl0142		probable cation efflux syste	0.118	0.411	0.771	1.704	0.306	-0.02	-0.114	0.289	0.602	1.008	0.57	0.655	-0.483
sl0144	pyrH	uridine monophosphate kin	-0.108	-0.12	-0.184	0.096	-0.234	-0.407	0.007	-0.207	-0.007	-0.542	-0.092	-0.21	0.124
sl0145	rf	RNA-binding proteinrf	-0.01	-0.248	-0.705	0.008	-0.222	-0.27	-0.207	-0.184	-0.334	-0.115	-0.242	-0.272	0.718
sl0146	natC	Integral membrane protein	0.546	-0.195	-0.843	0.183	-0.246	-0.006	-0.063	0.226	-0.175	0.148	-0.146	-0.056	-0.396
sl0147		hypothetical protein	error	error	-0.297	-1.521	error	-0.094	error	-0.282	-0.021	error	-0.456	-0.026	0.726
sl0148		hypothetical protein	-0.133	-0.133	-0.055	0.355	-0.311	0.004	-0.244	error	error	error	error	error	error
sl0149		hypothetical protein	0.233	error	0.157	-1.002	error	0.528	error	-0.109	0.164	0.422	0.446	0.23	1.309
sl0154		hypothetical protein	error	error	error	error	error	error	error	-0.278	-0.323	-0.044	-0.092	-0.472	0.239
sl0156		unknown protein	0.385	error	0.257	error	-0.277	-0.257	-0.02	-0.436	0.242	0.42	0	error	0.706
sl0157		hypothetical protein	1.021	error	1.385	error	1.565	0.859	1.088	0.578	2.235	2.228	2.164	2.146	2.929
sl0158	glgB	1,4-alpha-glucan branching	-0.185	-0.831	-1.057	-0.131	-0.327	-0.032	-0.206	-0.174	-0.338	-0.419	-0.355	-0.509	-0.039
sl0160		hypothetical protein	-0.076	-0.26	-0.498	-0.336	-0.128	-0.261	error	0.041	error	-0.216	-0.237	error	0.936
sl0161		putative transposase [ISY5	error	error	-0.777	error	-0.356	-0.541	error	-0.232	-0.071	0.801	-0.232	-0.148	-0.24
sl0162		hypothetical protein	-0.109	-0.36	-0.142	0.406	0.043	-0.094	-0.147	-0.236	-0.429	0.16	-0.083	-0.478	-0.745
sl0163		WD-repeat protein	-0.02	-0.337	0.061	0.519	0.943	0.513	0.648	-0.305	0.066	0.16	0.136	-0.069	-0.163
sl0166	hemD	porphyrin biosynthesis prot	error	error	-0.479	error	-0.445	-0.54	-0.699	error	error	error	error	error	error
sl0167		unknown protein	0.039	error	0.269	0.075	0.411	0.384	-0.203	0.394	0.383	0.827	0.572	0.578	0.311
sl0168		hypothetical protein	-0.066	0.127	0.318	0.549	0.411	0.209	0.06	0.361	0.869	1.114	0.431	1.113	-0.169
sl0169		cell division protein Ftn2 ho	-0.175	-0.331	-0.347	0.458	0.092	-0.223	-0.098	-0.078	-0.134	0.48	0.031	-0.187	-0.212
sl0170	dnaK	DnaK proteindnaK	0.707	1.565	3.011	3.644	2.335	0.839	1.026	2	4.176	3.152	3.319	3.713	1.75
sl0171		probable aminomethyltrans	-0.395	0.301	-0.151	-0.624	-0.329	-0.027	0.136	error	error	error	error	error	error
sl0172		unknown protein	-0.177	-0.077	-0.137	error	0.181	0.113	-0.181	0.521	0.701	-0.587	0.343	0.184	0.379
sl0173		hypothetical protein	-0.362	-0.089	-0.453	error	-0.099	-0.158	-0.374	-0.29	-0.17	0.214	-0.167	-0.301	1.278
sl0174		hypothetical protein	-0.508	-0.332	-0.476	-0.324	0.11	0.207	1.151	-0.087	-0.296	1.017	-0.118	-0.732	-1.03
sl0175		hypothetical protein	-0.377	-0.576	-0.393	-0.417	-0.537	-0.185	-0.039	error	error	error	error	error	error
sl0176		hypothetical protein	0.174	-0.269	error	error	-0.031	-0.22	error	-0.121	-0.084	0.483	0.043	-0.208	0.983
sl0177		hypothetical protein	0.812	0.628	-0.163	error	-0.43	-0.438	0.001	0.446	0.088	0.395	-0.044	-0.209	0.589
sl0178		hypothetical protein	error	error	error	error	error	error	error	-0.634	-0.355	-0.642	-0.231	-0.767	-0.144
sl0179	glx	glutamyl-tRNA synthetaseg	error	error	error	error	error	error	error	-0.268	0.043	0.388	0.511	-0.058	0.049
sl0180		hypothetical protein	-0.802	-0.588	-1.053	error	-0.67	-0.995	-0.924	-0.55	-1.007	error	-0.966	-0.909	-1.257
sl0181		unknown protein	-0.494	-0.288	0.236	0.456	-0.218	-0.218	-0.335	error	error	error	error	error	error
sl0182		ABC transporter ATP-bindin	-0.013	-0.568	error	-0.279	-0.329	-0.273	0.167	0.046	-0.237	0.401	-0.05	-0.013	0.034
sl0183		hypothetical protein	-0.161	-0.691	-0.73	0.129	0.126	0.013	0.19	-0.476	-0.356	-0.673	-0.152	-0.585	0.931
sl0184	sigC	group2 RNA polymerase sig	0.306	error	0.744	0.222	error	0.832	0.561	0.262	0.444	0.129	0.744	0.169	1.389
sl0185		hypothetical protein	error	error	error	error	error	error	error	-0.16	1.109	1.504	1.045	0.698	1.313
sl0188		unknown protein	-0.198	-0.205	-0.073	0.67	0.817	0.081	0.303	-0.314	0.095	0.389	1.004	0.201	1.061
sl0189		hypothetical protein	error	error	error	error	error	error	error	0.071	0.424	-0.566	0.163	-0.176	1.292
sl0191		unknown protein	error	error	0.504	error	-0.166	error	error	-0.361	-0.059	0.358	0.026	-0.267	1.43
sl0192		hypothetical protein	error	-0.042	error	error	-0.287	-0.237	error	-0.406	0.004	-0.202	-0.827	-0.322	0.832
sl0194		putative sec-independent p	-0.073	-0.089	0.093	0.241	0.696	0.182	0.574	-0.236	0.249	0.087	0.7	-0.007	2.175
sl0195		probable ATP-dependent p	-0.15	-0.261	0.072	0.27	0.017	-0.044	-0.085	0.215	0.321	0.234	0.513	0.09	1.645
sl0198		hypothetical protein	-0.306	error	-0.149	-0.424	0.147	0.62	error	-0.153	0.339	0.807	0.363	0.555	-0.289
sl0199	petE	plastocyaninpetE	-0.504	-0.747	-0.712	0.04	-0.519	-0.915	-0.301	0.187	-0.443	-0.343	-0.397	-0.251	-1.583
sl0200		putative transposase [ISY1	0.107	-0.41	0.028	0.212	-0.177	-0.414	0.069	-0.803	0.06	0.659	-0.394	-0.057	-0.077
sl0201		putative transposase [ISY1	-0.448	error	-1.386	error	-1.834	-0.762	-0.169	-1.368	-0.394	0.18	-0.94	-0.843	-0.888
sl0202		glucose inhibited division p	-0.181	-0.155	-0.363	0.363	error	0.128	-0.348	0.138	0.296	-0.126	0.279	0.049	-0.307
sl0204		glucose inhibited division p	-0.105	0.205	0.141	1.486	-0.168	-0.402	-0.699	0.064	0.132	-0.003	-0.09	0.097	-0.756
sl0205		hypothetical protein	error	error	-0.36	error	0.222	0.102	0.111	0.24	0.409	error	0.468	-0.404	0.092
sl0207	rfbA	glucose-1-phosphate thymi	-0.339	-1.019	-0.999	error	-0.365	-0.301	-0.325	-0.014	-0.71	0.467	-0.089	-0.498	0.297
sl0208		hypothetical protein	-0.175	-0.248	0.95	2.553	1.674	0.92	0.96	0.158	1.018	2.586	2.151	0.913	0.967
sl0209		hypothetical protein	-0.232	-0.774	-0.223	1.036	0.023	-0.323	-0.144	-0.197	-0.407	error	0.264	-0.456	-0.784
sl0210		bacitracin resistance protei	error	error	error	error	error	error	error	-0.11	0.046	-0.142	0.137	-0.109	0.159
sl0216		hypothetical protein	0.773	error	-0.015	-0.678	0.131	0.389	error	-0.142	-0.006	-0.157	-0.265	-0.047	0.671
sl0217		flavoprotein	-0.219	-0.027	-0.071	0.276	-0.005	0.234	-0.06	error	error	error	error	error	error
sl0218		hypothetical protein	error	error	error	error	error	error	error	0.364	0.855	0.373	-0.134	0.555	0.212
sl0219		flavoprotein	error	error	0.272	-0.385	error	0.354	0.186	-0.49	0.139	-0.058	-0.291	-0.082	0.667
sl0220	glmS	L-glutamine:D-fructose-6-P	error	error	error	error	error	error	error	-0.264	-0.412	-0.298	0.266	-0.652	0.024
sl0221		bacterioferritin comigratory	-0.018	0.642	0.575	-0.386	0.606	0.201	0.056	0.473	0.665	0.746	0.557	0.722	-0.048
sl0222		putative purple acid phosph	error	error	-0.216	error	error	1.716	error	0.212	-0.185	-0.01	-0.088	-0.122	-0.824
sl0223	ndhB	NADH dehydrogenase subu	-0.655	-0.728	-0.978	0.006	-0.741	-0.795	-0.772	-0.015	-0.245	-0.977	-0.289	-0.267	0.244
sl0224		amino-acid ABC transporte	-0.139	error	-0.586	-1.053	-0.574	0.227	-0.241	-0.086	0.226	0.088	-0.448	0.14	1.454
sl0225		unknown protein	error	-0.145	0.171	-0.44	error	-0.054	-0.023	error	error	error	error	error	error
sl0226	ycf4	photosystem I assembly rel	-0.227	-0.065	-0.029	0.424	0.007	-0.035	-0.321	-0.065	0.217	0.53	0.305	0.249	0.129
sl0227		peptidyl-prolyl cis-trans isom	error	error	error	error	error	error	error	-0.117	-0.187	0.052	0.512	-0.209	0.455
sl0228	speB1	arginasespeB1	0.718	0.342	0.202	0.318	0.252	0.139	0.332	0.234	0.206	-0.492	0.577	-0.183	0.432
sl0230		hypothetical protein	-0.702	-0.886	-1.023	-0.313	-0.707	-0.967	-0.98	error	error	error	error	error	error
sl0236		unknown protein	-0.369	-0.53	-0.696	error	-1.325	-0.334	error	-0.697	-0.479	-0.55	-1.029	-0.64	-0.387
sl0237		unknown protein	error	0.049	-0.603	-0.274	-0.391	-0.116	-0.058	error	error	error	error	error	error
sl0238		unknown protein	-0.01	0.131	-0.419	-0.137	-0.507	-0.062	error	-0.25	-0.331	0.436	-0.189	-0.212	-1.04
sl0240		ABC transporter ATP-bindin	0.925	0.517	0.723	-0.79	0.352	0.113	error	-0.08	0.636	0.45	0.206	0.647	1.331
sl0241		unknown protein	-0.298	-0.325	-0.02	0.129	0.514	0.703	0.489	error	error	error	error	error	error
sl0242		unknown protein	-0.496	-0.254	-0.276	-0.272	-0.428	0.066	-0.151	error	error	error	error	error	error

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1								Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	
slf0243		unknown protein	-0.247	-0.16	-0.201	-0.262	-0.042	0.183	0.2	error	error	error	error	error	error	
slf0244		UDP-glucose 4-epimerase	error	error	error	error	error	error	error	0.045	0.581	0.11	1.251	0.21	1.463	
slf0245		probable GTP binding prote	0.177	error	-0.117	0.801	0.714	0.818	error	0.451	0.629	error	0.492	0.376	0.28	
slf0247	isiA	iron-stress chlorophyll-bind	0.403	0.406	-0.636	-0.618	-1.059	-0.868	-0.644	-0.05	-0.292	-1.955	-1.535	-0.089	-0.675	
slf0248	isiB	flavodoxinisiB	-0.568	-0.576	-1.706	-1.177	-1.532	-0.58	-0.803	-0.373	-0.361	-0.618	-0.644	-0.58	-1.158	
slf0249		hypothetical protein	0.151	0.542	0.658	0.328	0.533	0.535	0.721	error	0.825	error	error	error	error	
slf0250		pantothenate metabolism fl	-0.02	0.197	0.176	0.036	-0.003	0.186	0.038	0.1	0.241	0.159	0.375	0.298	-0.198	
slf0252		unknown protein	0.235	0.063	0.123	-0.462	0.237	0.009	-0.296	0.738	0.643	0.552	0.703	0.365	1.032	
slf0253		hypothetical protein	error	error	-0.853	-0.507	error	-0.2	-1.191	-0.518	-0.488	-1.394	-0.927	-0.655	-1.558	
slf0254		probable phytoene dehydro	0.068	0.622	-0.39	-0.312	-0.367	0.295	0.081	error	error	error	error	error	error	
slf0257		hypothetical protein	error	error	error	error	error	error	error	-0.172	0.247	0.009	0.405	0.096	0.491	
slf0258	psbV	cytochrome c550psbV	-0.206	-0.567	-0.944	-0.643	-1.128	-0.666	-0.789	-0.124	-0.533	-1.386	-0.761	-0.558	-0.604	
slf0260		hypothetical protein	-0.436	error	-0.239	-0.979	-0.738	-0.06	-0.232	-0.429	-0.19	-0.188	-0.597	0.111	1.01	
slf0261		hypothetical protein	-0.307	error	0.077	-0.252	0.101	0.365	-0.242	-0.507	0.047	0.042	-0.317	0.133	0.612	
slf0262	desD	delta-6 desaturasesdesD	-1.091	-0.87	-1.207	-0.793	-1.315	-0.436	-0.444	-0.277	-0.318	error	-0.486	-0.642	-0.618	
slf0263		unknown protein	-0.913	error	-0.344	-1.191	-1.127	-0.194	error	-0.03	-0.015	0.023	-0.551	0.065	0.771	
slf0264		probable dioxygenase Ries	-0.003	0.125	-0.167	-0.469	-0.578	-0.028	0.147	-0.418	-0.599	error	-0.675	-0.788	0.139	
slf0265		unknown protein	0.094	error	-0.781	-1.335	error	0.141	-0.383	-0.137	-0.001	-0.053	-0.369	-0.218	0.836	
slf0266		unknown protein	-0.164	-0.372	0.029	-0.496	-0.547	-0.244	-0.616	-0.744	-0.696	-0.748	-0.832	-0.652	-0.42	
slf0267		unknown protein	-0.081	-0.3	0.012	0.437	-0.022	-0.071	-0.231	error	error	error	error	error	error	
slf0268		hypothetical protein	-0.292	error	-0.004	-0.945	0.281	0.169	0.033	0.025	0.793	-0.179	0.276	0.217	1.349	
slf0269		hypothetical protein	-0.264	0.026	0.053	0.014	-0.106	0.319	-0.07	-0.117	0.536	error	-0.16	0.089	0.698	
slf0270		primosomal protein N'	0.129	-0.262	-0.676	-0.138	error	-0.142	-0.127	-0.153	-0.323	-0.392	-0.583	-0.762	-1.242	
slf0271		N utilization substance prot	-0.999	-1.083	-1.13	-0.738	-0.747	-0.205	-0.566	0.409	-0.444	0.49	-0.289	error	-0.783	
slf0272		hypothetical protein	-0.543	-0.329	-0.575	0.004	-0.57	-0.204	-0.08	-0.195	-0.101	0.082	-0.034	-0.078	0.552	
slf0273	nhaS2	Na+/H+ antiporterahaS2	-0.233	-0.19	-0.041	0.258	-0.145	-0.019	-0.026	-0.307	0.012	0.372	-0.176	-0.046	-0.549	
slf0274		hypothetical protein	error	error	error	error	error	error	error	-0.02	-0.118	-0.058	-0.16	-0.133	0.237	
slf0280		unknown protein	0.846	error	error	-1.537	error	0.117	error	-0.62	-0.355	0.403	-0.57	-0.611	0.291	
slf0281		unknown protein	0.308	0.047	0.102	-0.554	-0.315	0.1	0.08	-0.107	-0.001	-0.436	-0.501	-0.52	-0.243	
slf0282		unknown protein	error	1.604	error	-0.889	error	0.455	error	-0.435	-0.467	0.219	-0.534	-1.221	2.121	
slf0283		hypothetical protein	0.237	-0.42	-0.268	-0.881	-0.885	-0.098	error	-1.018	-0.721	-0.535	-1.497	-1.032	0.277	
slf0284		hypothetical protein	-0.376	-0.502	-0.424	-0.382	-0.755	-0.207	error	-0.464	-0.37	-0.027	-0.412	-0.444	error	
slf0286	ycf52	hypothetical protein YCF52	-0.14	0.2	0.187	-0.86	0.104	0.187	0.135	0.089	0.64	-0.076	0.044	0.342	-0.43	
slf0288	minC	septum site-determining pro	error	error	0.2	-0.594	0.077	0.629	1.135	-0.048	0.45	0.6	0.328	0.628	1.831	
slf0289	minD	septum site-determining pro	1.047	error	error	error	0.264	-0.108	error	0.174	0.411	error	0.289	0.148	-0.088	
slf0290	ppk	polyphosphate kinaseppk	-0.263	-0.195	-0.037	error	-0.67	0.458	-0.053	-0.183	-0.254	-0.505	-0.904	-0.252	0.304	
slf0293		unknown protein	0.382	error	1.768	0.839	1.46	1.235	1.794	1.045	1.541	1.651	1.626	1.295	1.774	
slf0294		hypothetical protein	1.049	1.634	2.181	1.811	1.595	1.774	2.264	0.7	1.325	1.624	0.793	0.959	1.711	
slf0295		hypothetical protein	0.343	0.063	-0.601	-0.726	-1.003	-0.385	error	0.544	-0.245	-0.643	-0.762	-0.128	-0.876	
slf0296		hypothetical protein	error	error	1.439	error	0.799	0.789	0.271	1.005	1.103	0.849	0.85	0.704	0.558	
slf0297		hypothetical protein	0.347	0.553	1.067	1.401	0.794	0.115	0.695	0.562	1.528	1.674	1.219	1.308	0.566	
slf0298		hypothetical protein	0.01	error	0.236	0.1	-0.068	-0.015	-0.415	0.041	0.71	-0.003	0.207	0.645	1.155	
slf0300	ribC	riboflavin synthase alpha ch	-0.388	-0.589	-0.273	-0.786	error	-0.277	0.016	-0.182	-0.217	-0.558	-0.481	-0.268	-0.228	
slf0301		hypothetical protein	error	error	error	error	error	error	error	-0.089	0.562	1.422	0.645	0.206	0.545	
slf0306	sigB	group2 RNA polymerase sig	0.702	1.985	3.017	3.108	2.936	2.042	1.7	2.122	3.894	3.198	3.517	3.759	2.642	
slf0309		unknown protein	error	0.613	0.998	1.132	1.064	1.011	0.55	0.28	1.15	1.09	0.896	1.057	0.628	
slf0310		hypothetical protein	error	error	-0.346	0.133	-0.219	0.055	-0.072	-0.186	-0.577	0.04	0.015	-0.567	-1.116	
slf0312		probable oligopeptides ABC	0.118	0.648	0.216	0.092	0.756	0.25	0.995	0.042	0.291	0.397	0.414	0.227	-0.26	
slf0314		hypothetical protein	error	error	error	1.306	1.236	0.717	1.062	0.81	0.779	1.852	1.62	0.721	0.565	
slf0315		putative transposase [ISY2	error	error	error	error	error	-0.495	error	-1.144	-0.485	0.194	-0.973	-0.626	-1.659	
slf0317		putative transposase [ISY2	error	-1.193	-1.451	-1.151	error	-0.562	-0.424	-0.607	0.06	0.898	-0.565	0.15	-0.535	
slf0318		hypothetical protein	0.253	error	0.483	-0.593	error	0.255	error	0.342	0.165	0.005	0.152	-0.087	1.085	
slf0319		hypothetical protein	-0.612	-0.575	error	error	0.475	0.144	0.254	-0.127	0.141	0.962	0.763	0.15	0.883	
slf0320		probable ribonuclease D	-0.049	-0.241	-0.146	-0.399	0.383	0.438	0.267	0.157	0.301	-0.198	0.308	-0.36	0.209	
slf0321		unknown protein	0.274	error	0.302	error	-0.467	0.057	error	-0.402	-0.084	0.036	-0.386	-0.396	0.372	
slf0322	hypF	hydrogenase maturation pro	-0.165	-0.462	-0.842	-0.756	-0.681	-0.253	0.069	-0.646	-0.286	-0.077	-0.73	-0.167	-1.593	
slf0325		hypothetical protein	0.15	error	-0.253	-0.609	-0.24	-0.292	error	-0.379	-0.139	0.495	-0.435	-0.404	0.351	
slf0327		unknown protein	1.21	error	1.091	error	error	0.708	error	-0.14	0.691	0.542	0.204	0.511	2.29	
slf0328		unknown protein	0.678	error	0.242	-0.254	-0.119	0.227	error	0.069	error	error	0.025	error	1.395	
slf0329		6-phosphogluconate dehyd	-0.282	-0.485	-1.23	error	-0.492	-0.176	-0.37	-0.195	-0.639	-0.587	-0.449	-0.739	-0.951	
slf0330		3-oxoacyl-acyl-carrier prote	error	error	error	error	error	error	error	0.323	0.984	1.841	2.561	0.644	1.694	
slf0335		hypothetical protein	0.001	error	0.593	0.157	0.762	0.613	0.547	-1.049	-0.187	-0.016	-0.229	-0.29	0.628	
slf0336	accD, ycf1	acetyl-CoA carboxylase bet	-0.238	-0.129	-0.323	0.302	0.405	-0.108	0.105	0.002	0.204	0.702	0.554	0.289	-0.099	
slf0337		two-component sensor histi	0.183	-0.124	-0.204	0.283	-0.366	-0.46	0.087	0.089	-0.164	-0.103	-0.192	-0.142	0.167	
slf0350		hypothetical protein	0.576	0.821	0.787	0.846	error	-0.281	0.204	0.852	1.267	1.39	0.706	1.195	1.387	
slf0354		hypothetical protein	error	error	0.731	error	error	0.148	0.362	0.06	error	0.121	5.913	-0.551	error	
slf0355		hypothetical protein	0.739	error	1.061	-0.88	error	0.499	0.864	0.056	0.817	0.175	-0.024	0.638	1.066	
slf0356	trpF	N-(5'-phosphoribosyl)anthra	0.868	0.733	1.625	0.828	0.854	0.526	1.214	0.485	1.262	1.123	0.696	1.134	1.349	
slf0359		hypothetical protein	-0.549	-0.793	-0.591	0.127	-0.647	-0.479	-0.089	-1.06	-1.081	-0.816	-1.092	-1.262	0.828	
slf0360		hypothetical protein	error	error	-0.333	-0.979	-0.076	0.113	0.53	-0.323	0.594	0.095	-0.486	0.193	1.106	
slf0361		hypothetical protein	-0.189	0.091	0.345	0.233	0.116	0.289	0.032	-0.273	0.482	error	0.195	0.116	0.295	
slf0362	alaS	alanyl-tRNA synthetasealaS	-0.157	-0.302	-0.226	0.418	0.416	0.08	0.154	-0.4	-0.314	-0.573	0.07	-0.589	-1.075	
slf0364		hypothetical protein	error	0.31	0.29	-0.51	0.35	0.344	0.922	0.432	1	1.433	1.043	1.038	1.606	
slf0368		uracil phosphoribosyltransf	error	error	error	-1.226	error	0.789	error	-0.085	0.295	error	0.035	0.473	0.776	
slf0369		unknown protein	0.099	error	0.15	-0.474	-0.067	0.077	error	-0.542	error	-0.332	-0.327	error	0.499	

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slI0370	pyrA	carbamoyl-phosphate synth	-0.412	-0.56	-0.429	0.154	-0.442	-0.265	-0.004	-0.238	-0.082	error	-0.195	-0.32	-1.295
slI0371		unknown protein	error	error	error	error	error	error	error	-0.677	-0.424	-0.608	-0.4	-0.851	error
slI0372		hypothetical protein	-0.623	error	-0.628	error	-0.207	-0.06	0.28	-0.046	-0.144	-0.257	-0.106	-0.173	-0.652
slI0373	proA	gamma-glutamyl phosphate	-0.315	0.21	error	-0.429	-0.06	0.597	error	-0.254	0.149	0.19	0.141	-0.076	-0.341
slI0374		probable branched chain A	error	0.18	0.345	0.47	0.297	0.595	0.705	0.346	0.622	0.377	0.561	0.281	-0.208
slI0375		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slI0376		unknown protein	0.362	error	0.607	-0.194	error	0.333	error	0.033	0.354	0.379	0.205	0.049	0.354
slI0377		transcription-repair coupling	-0.22	-0.43	-0.64	-0.002	-0.485	-0.488	-0.497	-0.208	-0.224	-0.673	-0.267	-0.228	0.476
slI0378	cobA	uroporphyrin-III C-methyltra	0.177	0.89	-0.003	0.214	-0.261	0.179	-0.27	-0.444	-0.166	-0.528	-0.755	-0.313	0.215
slI0379		acyl-[acyl-carrier-protein]-L	-0.523	-0.32	-0.638	0.399	-0.393	0.183	-0.115	-0.079	-0.334	-0.125	-0.19	-0.497	0.031
slI0380		probable glycosyltransferas	0.595	-0.331	-1.033	-0.484	-0.852	0.163	-0.172	0.089	-0.5	-0.467	-0.591	-0.347	-0.298
slI0381		hypothetical protein	-0.297	error	-0.574	-1.183	-1.846	-0.942	-1.707	0.245	0.262	-1.133	-0.72	error	-0.62
slI0382		hypothetical protein	error	error	error	error	error	error	error	0.149	0.245	-0.549	-0.075	-0.194	-0.086
slI0383		cobalamin biosynthesis pro	0.153	error	0.306	-0.886	-0.432	0.196	error	0.546	0.415	error	-0.434	0.189	0.442
slI0384		unknown protein	0.75	error	0.467	error	-0.592	0.39	error	0.616	0.628	-0.064	-0.481	0.413	0.411
slI0385		ATP-binding protein of ABC	0.788	0.684	1.164	0.348	0.178	-0.039	error	0.617	0.953	0.273	0.096	0.658	0.586
slI0394		unknown protein	error	error	error	error	error	error	error	-0.552	0.015	error	-0.245	-0.28	0.263
slI0395		phosphoglycerate mutase	0.383	0.166	error	error	0.279	0.291	error	error	error	error	error	error	error
slI0396		two-component response re	-0.214	-0.693	-0.585	-0.779	-0.418	-0.23	-0.009	0	-0.132	-0.151	-0.17	-0.005	-0.98
slI0397		hypothetical protein	0.14	error	0.856	-0.565	error	0.562	error	-0.469	0.449	error	-0.284	-0.054	1.537
slI0398		deoxyguanosinetriphosphat	1.005	0.393	0.46	0.024	0.001	-0.004	error	0.052	-0.051	0.455	-0.55	-0.419	0.33
slI0400		hypothetical protein	0.542	error	0.065	-1.257	error	-0.092	error	error	error	error	error	error	error
slI0401		citrate synthase	-0.314	-0.648	-0.212	-0.145	-0.205	-0.276	-0.009	-0.208	-0.109	-0.562	-0.148	-0.607	0.89
slI0402	aspC	aspartate aminotransferase	0.397	error	-0.471	0.075	0.362	0.698	error	0.258	-0.159	0.316	0.181	-0.045	0.467
slI0403		unknown protein	0.108	0.305	-0.162	-0.332	0.048	0.335	0.203	0.405	0.651	0.318	-0.087	0.298	-0.055
slI0404	glcD	glycolate oxidase subunit G	0.116	0.233	-0.396	-0.068	-0.224	0.017	0.372	error	error	error	error	error	error
slI0405		unknown protein	-0.081	-0.481	-0.281	0.453	-0.196	0.253	0.281	-0.057	0.023	0.907	0.206	0.223	0.301
slI0406		unknown protein	error	error	error	error	error	error	error	0.749	0.36	error	-0.077	-0.085	0.098
slI0408		peptidyl-prolyl cis-trans isom	0.481	1.698	2.847	3.109	2.576	1.913	1.828	1.609	3.303	3.037	2.521	3.222	2.214
slI0409		similar to O-succinylbenzoa	error	-0.192	-0.48	-0.75	-0.786	-0.143	0.028	-0.001	0.064	0.128	-0.491	-0.137	error
slI0410		hypothetical protein	-0.155	0.061	0.644	0.671	0.77	0.654	0.786	0.411	0.818	2.106	0.804	0.593	0.404
slI0412		hypothetical protein	0.067	-0.417	0.234	0.64	0.377	0.313	0.492	0.008	0.12	0.484	0.109	-0.202	-1.238
slI0413		hypothetical protein	0.253	-0.089	1.098	0.348	0.789	0.344	0.221	0.502	1.116	1.837	1.668	0.772	2.112
slI0414		hypothetical protein	error	error	error	error	error	error	error	-0.375	-0.208	-0.665	-0.578	-0.298	0.405
slI0415		ATP-binding protein of ABC	0.159	-0.016	-0.046	-0.334	0.009	-0.031	0.663	-0.016	0.136	0.052	-0.177	-0.166	0.056
slI0416	groEL-2	60kD chaperonin 2groEL-2	0.766	1.453	2.605	1.729	1.614	0.211	0.48	1.857	3.516	3.027	2.685	3.647	1.219
slI0418		delta(24)-sterol C-methyltra	error	error	0.114	0.059	0.951	error	0.311	-0.258	0.362	0.609	1.127	0.122	1.697
slI0419		unknown protein	error	0.007	-0.087	-0.425	0.008	0.124	-0.443	-0.172	-0.037	-0.399	0.239	-0.569	0.155
slI0420	ureB	urease beta subunit ureB	-0.582	-0.548	-0.643	-0.352	-0.185	-0.122	0.012	0.076	-0.04	-0.37	-0.041	-0.188	-0.601
slI0421	purB	adenylosuccinate lyase purB	-0.198	-0.465	-0.861	0.141	-0.635	-0.482	-0.579	-0.057	-0.033	0.585	-0.112	-0.103	-0.993
slI0422		asparaginase	-0.011	0.432	0.416	0.323	0.122	0.109	-0.219	0.353	0.491	-0.207	0.216	0.34	2.02
slI0423		hypothetical protein	error	0.13	0.623	0.668	0.646	-0.127	0.181	0.008	0.547	error	error	0.631	0.067
slI0424		hypothetical protein	error	0.315	0.238	-0.291	0.477	0.205	0.571	0.077	0.244	1.169	0.278	0.14	0.28
slI0426		unknown protein	-0.205	0.19	-0.073	-0.04	0.798	0.529	0.526	0.04	0.116	2.109	0.617	-0.427	-0.246
slI0427	psbO	photosystem II manganese	-0.416	-0.554	error	error	-1.001	-0.823	error	0.036	-0.593	-0.755	-0.785	-0.537	-0.322
slI0428		unknown protein	error	error	-0.3	-1.352	error	0.259	error	0.229	-0.12	error	-0.108	error	0.249
slI0430	htpG	heat shock protein HtpG/htp	-0.381	-0.56	0.268	1.953	0.684	0.092	0.208	-0.026	0.462	2.118	1.728	0.218	-0.746
slI0431		putative transposase [ISY10	-0.318	-0.357	-0.237	0.355	-0.325	0.066	-0.238	-1.154	-0.053	0.922	-0.466	-0.322	-0.692
slI0436		hypothetical protein	error	0.571	error	-0.702	0.048	0.184	error	-0.173	0.015	0.26	-0.05	-0.323	2.04
slI0441		unknown protein	0.197	0.248	-0.552	-1.001	-0.767	0.219	1.013	-0.348	0.027	0.183	-0.225	0.074	-0.269
slI0442		hypothetical protein	-0.084	-0.143	-0.138	-0.338	-0.529	0.283	0.249	0.057	0.533	0.33	-0.078	error	-0.429
slI0443		unknown protein	-0.081	error	-0.03	0.106	-0.022	0.385	0.112	0.034	0.112	0.233	0.146	-0.025	-0.457
slI0444		unknown protein	-0.553	-0.126	-0.787	-0.708	-0.227	0.174	-0.063	-0.086	-0.107	-0.158	-0.036	-0.158	-0.822
slI0445		unknown protein	-0.204	0.038	-0.91	-0.332	-0.801	-0.299	-0.539	-0.172	-0.415	0.188	-0.237	-0.354	-0.587
slI0446		unknown protein	-0.495	error	-0.418	-0.662	-0.466	-0.495	-0.478	-0.463	-0.526	0.154	-0.457	-0.369	-1.006
slI0447		unknown protein	-0.123	-0.26	-0.831	error	-0.98	-0.327	-0.794	-0.141	-0.398	-0.722	-0.513	-0.774	0.165
slI0448		unknown protein	error	-0.306	0.372	error	error	0.229	error	-0.375	0.019	-0.276	-0.473	-0.231	0.68
slI0449		unknown protein	error	error	0.119	error	error	0.453	error	-0.711	-0.357	-0.273	-0.783	-0.586	0.794
slI0450		probable nitric oxide reduct	error	error	-0.291	-0.146	-0.104	-0.501	-0.496	-0.026	0.232	0.971	-0.15	0.184	-0.704
slI0451		hypothetical protein	-0.213	-0.499	-0.498	-0.725	-0.132	-0.187	0.156	0.192	0.116	-1.23	-0.447	-0.915	-0.977
slI0454	pheS	phenylalanyl-tRNA synthet	error	error	-0.249	error	-0.318	-0.676	-0.702	0.192	0.175	0.15	0.353	-0.161	0.583
slI0455	thrA	homoserine dehydrogenase	-0.282	-0.412	-0.562	error	-0.35	-0.033	-0.224	-0.172	-0.34	0.234	-0.269	-0.062	0.24
slI0456		hypothetical protein	-0.19	error	-0.3	-0.322	error	0.109	error	-0.117	0.007	0.422	0.361	-0.283	1.106
slI0459		excinuclease ABC subunit B	-0.246	-0.119	-0.371	0.124	0.218	0.357	0.871	-0.115	-0.423	-0.04	-0.015	-0.393	-1.407
slI0461	proA	gamma-glutamyl phosphate	-0.011	0.535	0.487	-0.189	0.269	0.418	0.773	0.251	0.754	0.083	0.503	0.344	-0.054
slI0462		hypothetical protein	error	error	error	error	error	error	error	1.033	1.472	0.73	1.088	0.92	1.107
slI0467		S-adenosylmethionine:tRNA	-0.364	-0.386	0.005	-0.31	-0.059	0.04	0.613	-0.301	0.369	0.433	-0.272	0.113	-0.456
slI0469		ribose-phosphate pyrophos	-0.49	-0.717	-0.556	0.023	-0.517	-0.508	-0.492	-0.072	-0.247	-0.676	0.12	-0.421	0.03
slI0470		hypothetical protein	0.319	0.233	0.266	1.288	1.662	0.901	0.753	0.955	0.577	1.64	1.83	0.356	1.133
slI0471		hypothetical protein	0.063	-0.14	-0.396	0.237	0.038	-0.178	0.239	-0.336	-0.204	-0.141	0.19	-0.146	-0.397
slI0473		unknown protein	error	0.084	0.125	-0.878	-0.307	0.59	error	-0.236	-0.358	-0.43	-0.327	-0.536	-0.187
slI0474		two-component hybrid sens	error	error	error	-1.71	error	error	error	-0.083	-0.248	-0.019	-0.89	-0.496	0.396
slI0477		putative biopolymer transp	-0.578	0.298	0.032	-0.688	-0.647	0.286	error	0.136	0.256	-0.109	-0.841	-0.216	0.111
slI0478		unknown protein	error	-0.286	-0.229	0.282	-0.3	0.351	-0.037	-0.149	-0.124	0.083	-0.132	-0.255	-1.005
slI0479		unknown protein	error	error	1.596	error	error	0.236	error	0.085	0.942	0.444	0.094	0.565	1.237

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl0480		probable aminotransferase	-0.564	-0.544	0.139	0.84	0.089	0.092	-0.251	-0.096	0.425	0.62	0.691	0.226	0.69
sl0481		unknown protein	error	error	1.227	error	error	0.294	error	0.128	0.449	0.277	0.273	0.182	1.913
sl0482		unknown protein	error	error	error	error	error	error	error	0.074	0.126	0.471	-0.124	-0.379	0.365
sl0484		ATP-binding protein of ABC	error	-0.782	-1.077	-1.199	-0.983	-0.157	-0.304	-0.143	-0.039	-0.26	-0.43	-0.239	-0.25
sl0485		two-component response re	0.493	1.063	1.203	0.177	0.939	0.65	error	-0.371	0.271	0.461	0.137	-0.072	1.046
sl0486	kaiB3	circadian clock protein KaiB	-0.417	error	-0.165	-0.707	-0.278	-0.291	error	-0.149	0.069	-0.096	-0.38	-0.173	-0.289
sl0487		hypothetical protein	-0.61	-0.499	-0.683	-0.508	-0.486	-0.248	-0.053	-0.106	0.016	-0.064	-0.025	-0.055	-0.272
sl0488		hypothetical protein	error	error	error	error	0.55	-0.305	-0.175	-0.112	-0.003	0.128	0.162	-0.18	1.48
sl0489		ATP-binding protein of ABC	-0.256	0.184	0.751	1.069	-0.17	-0.52	-0.79	0.28	0.482	0.137	0.428	0.206	-0.364
sl0493		hypothetical protein	0.218	-0.214	-0.074	error	-0.284	-0.406	error	-0.225	0.18	-0.392	-0.086	-0.098	0.726
sl0494		unknown protein	1.507	1.797	1.27	0.679	0.921	0.523	1.727	0.417	0.765	0.761	0.13	0.595	0.261
sl0495	asnS	asparaginyl-tRNA synthetas	-0.466	-0.536	-0.938	error	-0.603	-0.821	-0.674	-0.018	-0.256	-0.283	-0.072	-0.404	-0.448
sl0496		hypothetical protein	-0.102	error	-0.198	error	error	0.126	error	-0.321	-0.275	error	-0.143	-0.428	0.442
sl0497		hypothetical protein	-0.099	0.468	0.145	error	-0.273	-0.389	-0.488	-0.42	0.101	error	-0.255	-0.285	0.584
sl0498		hypothetical protein	-0.181	error	0.153	-0.157	0.23	0.27	-0.126	0.019	0.303	0.481	0.579	0.342	1.361
sl0499		hypothetical protein	-0.171	0.311	-0.102	-0.052	0.122	-0.033	-0.2	0.157	0.025	-0.306	-0.313	0.182	0.155
sl0501		probable glycosyltransferase	0.088	error	0.023	error	-0.343	0.334	1.302	-0.546	-0.311	-0.177	-0.497	-0.002	1.152
sl0502	argS	arginyl-tRNA-synthetasearg	error	error	error	error	error	error	error	-0.313	-0.352	-0.372	-0.231	-0.4	-0.723
sl0503		hypothetical protein	-0.365	-0.145	-0.195	0.269	-0.154	-0.069	-0.029	-0.743	-0.075	0.412	-0.419	-0.061	0.369
sl0504	lysA	diaminopimelate decarboxy	-0.713	-1.06	-1.423	-0.378	-1.716	-1.107	-1.461	-0.543	-0.622	error	-0.816	-0.687	-1.852
sl0505		hypothetical protein	-0.415	-0.558	-0.632	-0.213	-0.764	-0.315	-0.463	-0.114	-0.169	0.242	-0.336	-0.251	-1.161
sl0506		undecaprenyl pyrophospha	error	error	0.185	error	error	0.026	error	0.14	0.141	error	-0.125	-0.178	1.265
sl0507		probable cation transporter	error	error	error	error	error	error	error	-0.378	-0.73	-0.692	-0.428	-0.634	0.595
sl0508		unknown protein	0.368	error	0.756	error	0.271	-0.003	error	-0.119	0.338	error	0.33	0.259	0.994
sl0509		similar to 5',S'''-P-1,P-4-tetra	0.274	-0.109	0.189	0.378	-0.362	0.34	-0.354	0.026	0.259	-0.19	0.123	0.178	0.015
sl0513		hypothetical protein	0.391	-0.199	0.516	-0.236	-0.373	0.14	error	0.093	0.424	0.315	0.001	-0.057	0.701
sl0514		hypothetical protein	0.65	0.468	0.503	0.014	0.52	0.643	0.952	0.222	0.29	0.04	0.609	0.277	0.325
sl0517	rbpA	RNA binding proteinrbpA	error	error	error	error	error	error	error	-0.016	0.853	-0.369	0.572	0.753	0.813
sl0518		unknown protein	-0.303	-0.312	-1.05	-0.616	-0.713	-0.667	-0.137	-0.219	-0.332	-0.48	-0.518	-0.12	0.819
sl0519	ndhA	NADH dehydrogenase subu	-0.299	-0.509	-0.712	0.256	-0.25	-0.586	-0.234	0.452	0.304	-0.126	0.489	0.361	1.273
sl0520	ndhI	NADH dehydrogenase subu	-0.367	-0.72	-0.8	0.182	-0.453	-0.615	-0.538	-0.091	-0.442	error	0.076	-0.79	0.174
sl0521	ndhG	NADH dehydrogenase subu	-0.552	-0.618	-0.543	0.204	-0.606	-0.591	-0.699	0.099	0.006	-0.228	-0.073	0.112	0.055
sl0522	ndhE	NADH dehydrogenase subu	-0.42	-0.357	-1.161	-0.567	-0.477	-0.097	0.153	-0.098	-0.397	0.427	0.072	0.069	-0.437
sl0524		hypothetical protein	-0.095	-0.15	0.46	0.253	0.043	0.166	0.128	-0.284	0.691	0.136	0.297	0.116	0.637
sl0525		hypothetical protein	-0.106	-0.013	-0.084	error	0.193	-0.178	0.177	0.141	0.549	0.429	0.671	0.188	1.819
sl0528		hypothetical protein	0.192	1.873	2.947	2.113	2.876	1.333	2.031	0.339	1.454	0.919	0.659	1.489	2.646
sl0529		hypothetical protein	-0.733	-0.411	-0.415	-0.738	-0.504	-0.175	0.492	0.022	0.269	-0.181	0.032	-0.158	0.651
sl0532		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sl0533		trigger factor	-0.279	-0.754	-0.611	error	-0.452	-0.421	-0.566	-0.285	-0.339	0.006	0.134	-0.594	-1.393
sl0534	clpP	ATP-dependent Clp protease	-0.03	-0.397	-0.47	0.3	0.158	-0.015	-0.484	0.195	0.374	-0.402	0.467	-0.116	0.338
sl0535	clpX	ATP-dependent protease A	0.245	0.009	-0.214	0.301	0.005	-0.304	-0.34	-0.188	-0.536	-0.652	-0.172	error	0.289
sl0536		probable potassium channel	0.515	0.34	0.339	-0.16	0.044	-0.05	-0.164	0.17	0.525	0.296	0.13	0.232	-0.637
sl0537	amt3	ammonium/methylammonium	error	error	error	error	error	error	error	0.004	0.058	0.348	-0.524	-0.181	-0.138
sl0539		unknown protein	error	error	0.775	error	error	-0.069	error	-0.43	-0.076	0.251	0.138	-0.116	1.146
sl0540		phosphate-binding protein P	error	error	error	error	error	error	error	0.138	0.463	-0.144	0.246	-0.01	0.086
sl0541	desC,desS	acyl-CoA desaturase 1desC	-1.158	-1.346	-1.621	0.189	-0.691	-0.62	-0.037	error	error	error	error	error	error
sl0542		acetyl-coenzyme A synthetase	-0.391	-0.428	0.062	error	-1.311	-0.83	-1.19	-0.414	-0.113	error	-0.87	-0.499	-0.094
sl0543		hypothetical protein	-0.396	-0.313	-0.718	-0.347	-0.935	-0.294	-0.189	0.077	-0.173	-1.387	-0.862	-0.563	-1.867
sl0544		hypothetical protein	-0.065	0.089	-0.017	0.718	0.259	0.242	0.122	0.752	0.413	0.521	0.397	0.457	-0.138
sl0545		hypothetical protein	error	error	error	error	error	error	error	-0.137	0.093	error	-0.287	-0.265	0.33
sl0546		probable translation initiatio	-0.111	error	-0.136	-0.552	-0.041	0.34	0.424	error	error	error	error	error	error
sl0547		unknown protein	0.603	0.583	0.149	-0.701	0.337	0.708	error	-0.071	0.319	0.2	-0.089	0.071	-0.229
sl0549		hypothetical protein	0.37	0.852	0.92	0.686	1.645	0.888	1.52	0.125	1.422	1.133	1.889	1.15	1.905
sl0550		flavoprotein	-1.431	-0.726	-0.284	0.388	0.07	-0.079	-0.244	-0.269	0.005	-0.057	0.593	-0.171	-0.292
sl0552		unknown protein	error	error	0.55	error	0.106	0.322	0.261	0.085	0.829	0.347	0.4	0.395	1.082
sl0553		hypothetical protein	0.188	0.313	0.648	0.798	1.236	0.359	error	-0.148	0.651	error	1.29	0.591	1.183
sl0554	frC	ferredoxin-thioredoxin redu	-0.207	-0.137	0.214	-0.572	-0.021	-0.382	0.292	0.111	0.593	0.361	0.421	0.613	1.03
sl0555		methionine aminopeptidase	-0.503	-0.374	-0.745	0.086	-0.697	-0.853	-0.788	-0.174	0.327	error	0.24	0.185	0.027
sl0556		Na <sup>+</sup> /H <sup>+</sup> antiporter	error	1.314	1.443	-0.169	1.189	0.556	error	1.09	1.477	1.03	1.247	0.995	1.21
sl0558	ycf53	hypothetical protein YCF53	-0.15	0.009	0.191	0.566	0.185	0.125	-0.225	error	error	error	error	error	error
sl0563		unknown protein	error	-0.009	-0.14	0.157	0.193	0.544	error	0.244	-0.101	error	0.276	-0.39	0.139
sl0564		hypothetical protein	-0.814	0.261	-0.749	error	error	-0.165	-0.558	0.107	-0.003	0.292	0.255	0.219	-0.475
sl0565		hypothetical protein	error	0.963	-0.226	-0.506	error	0.028	error	0.512	0.028	0.804	-0.196	-0.173	-0.088
sl0567	fur	ferric uptake regulation pro	0.421	0.34	0.842	0.088	0.168	-0.021	0.85	0.456	1.251	1.104	0.822	1.377	1.521
sl0569	recA	RecA gene productrecA	-0.421	-0.289	-0.158	0.207	-0.29	-0.106	0.237	-0.182	-0.111	0.563	0.105	0.004	-0.474
sl0572		hypothetical protein	0.765	error	-0.476	error	0.298	0.15	error	0.057	0.2	-0.132	-0.195	0.063	0.448
sl0573		carbamate kinase	0.51	0.206	0.886	error	0.12	0.295	0.005	0.192	0.116	-0.052	-0.03	-0.344	0.531
sl0574		probable permease protein	error	error	error	error	error	error	error	-0.222	0.195	0.106	-0.057	0.108	0.397
sl0575		probable lipopolysaccharide	error	error	0.126	error	error	0.05	error	-0.611	-0.27	-0.093	-0.787	-0.274	-1.43
sl0576		putative sugar-nucleotide e	-0.215	error	-0.511	-0.441	error	-0.195	0.141	0.238	-0.278	0.108	-0.44	-0.477	-0.645
sl0577		hypothetical protein	-0.487	-0.537	-0.447	-0.101	-0.614	-0.333	error	-0.399	0.068	-0.448	0.228	-0.58	1.02
sl0578	purK	phosphoribosyl aminoimida	0.457	0.497	0.242	-0.409	-0.31	0.059	0.363	0.444	0.278	0.07	0.13	0.028	error
sl0584	ycf36	hypothetical protein YCF36	-0.411	error	-0.159	-0.182	0.394	-0.458	-0.161	-0.363	-0.042	-0.046	0.358	-0.182	0.82
sl0585		hypothetical protein	error	error	error	error	error	error	error	-0.157	0.001	0.229	-0.231	-0.431	0.329
sl0586		hypothetical protein	0.376	error	0.433	-0.187	0.094	0.267	0.692	error	error	error	error	error	error

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slf0587		pyruvate kinase	-0.69	-0.499	-0.867	0.022	-0.577	-0.08	0.408	error	error	error	error	error	error
slf0588		unknown protein	0.438	error	error	-1.02	-0.509	-0.082	error	-0.206	-0.512	-0.757	-0.684	-0.498	0.684
slf0590		unknown protein	-0.11	-0.643	-0.646	-0.928	-0.465	-0.009	0.722	0.064	-0.278	-0.228	-0.555	-0.626	-0.212
slf0593		glucokinase	-0.048	-0.102	-0.131	-0.35	-0.643	-0.199	0.063	error	error	error	error	error	error
slf0594		transcriptional regulator	0.358	0.688	0.626	0.513	0.267	0.062	-0.414	-0.004	-0.066	-0.006	0.123	-0.026	0.584
slf0595		unknown protein	0.059	-0.077	-0.042	-0.512	0.221	0.248	0.312	0.124	0.244	0.15	0.224	-0.102	-0.461
slf0596		hypothetical protein	error	error	0.347	-1.107	error	0.971	error	error	error	-0.267	0.077	0.31	0.126
slf0597		hypothetical protein	error	error	error	error	error	error	error	-0.78	-0.059	-0.701	-0.459	-0.469	-0.075
slf0601		nitrilase homolog	-0.41	-0.053	0.402	-0.095	-0.531	-0.225	-0.292	-0.157	0.426	error	-0.152	0.125	error
slf0602		hypothetical protein	0.07	0.061	-0.367	-0.663	-0.675	0.833	error	-0.636	-0.034	0.365	-0.642	-0.182	-1.066
slf0603	menD	menaquinone biosynthesis	-0.217	-0.473	-0.402	-0.354	-0.477	-0.3	-0.361	-0.319	-0.331	0.213	-0.535	-0.146	-0.832
slf0606		hypothetical protein	-0.331	-0.338	0.134	error	-0.387	-0.429	-0.53	-0.012	-0.005	-0.24	-0.42	0.034	-0.885
slf0608	ycf49	hypothetical protein YCF49	error	-0.008	0.157	-0.201	0.2	-0.245	-0.276	0.064	0.499	0.373	0.318	0.392	0.652
slf0609		hypothetical protein	-0.403	0.196	0.066	-0.397	0.665	0.452	error	0.209	0.176	0.67	0.078	-0.257	-0.141
slf0611		hypothetical protein	error	error	error	-0.816	error	0.423	error	-0.01	0.31	error	-0.43	-0.152	-0.509
slf0613	ruvB	Holliday junction DNA helic	0.103	-0.121	0.012	-0.105	-0.162	0.151	0.245	-0.186	0.615	0.142	-0.016	0.177	0.405
slf0614		unknown protein	error	error	error	error	error	error	error	-0.226	0.129	0.21	-0.036	-0.249	0.49
slf0615		hypothetical protein	0.184	error	-0.51	-0.238	-0.19	0.138	error	0.623	-0.355	-0.276	-0.088	-0.622	-0.006
slf0616	secA	preprotein translocase Sec	-0.005	-0.414	-0.26	-0.386	-0.379	-0.132	0.067	-0.115	-0.363	0.032	0.058	-0.361	0.668
slf0617		hypothetical protein	-0.344	-0.142	-0.47	-0.475	-0.695	-0.205	-0.426	0.146	0.186	0.359	-0.018	0.308	-0.557
slf0621	ccdA	putative c-type cytochrome	error	error	error	error	error	error	error	error	error	error	error	error	error
slf0622	nadA	quinolinate synthetasenadA	0.313	error	0.553	0.332	0.226	0.268	0.365	0.04	0.084	0.501	-0.227	-0.111	-0.571
slf0623		unknown protein	-0.121	-0.273	-0.044	0.919	0.212	0.03	0.286	-0.021	0.461	1.187	0.757	0.485	-0.214
slf0624		unknown protein	0.063	0.097	0.112	-0.171	-0.01	0.154	0.257	0.19	0.123	0.095	0.071	0.223	-0.456
slf0625		unknown protein	-0.153	error	0.064	-0.513	0.073	0.065	1.5	0.215	0.027	0.962	-0.004	-0.103	0.283
slf0626		putative neutral invertase	error	error	error	error	error	error	error	error	error	error	error	error	error
slf0629	psaK	photosystem I reaction cent	-0.251	-0.123	-0.017	-0.011	-0.019	0.172	0.498	-0.086	0.163	0.274	0.093	0.341	0.047
slf0630		unknown protein	-0.029	0.053	0.099	0.069	0.061	0.307	0.26	0.14	-0.202	-1.004	0.019	0.165	1.668
slf0631	nadB	L-aspartate oxidasenadB	0.327	0.349	-0.119	0.114	0.318	0.114	0.081	0.145	0.227	0.405	0.328	0.312	-0.675
slf0634	btpA	photosystem II biogenesis p	-0.32	-0.116	0.132	0.071	-0.286	-0.302	-0.22	error	error	error	error	error	error
slf0635	thiE	probable thiamine-phospha	0.317	0.138	-0.539	-0.188	-0.194	-0.16	error	-0.009	0.151	-0.037	0.004	0.004	0.872
slf0638		hypothetical protein	error	0.891	0.108	error	-0.069	-0.074	error	0.061	0.243	0.373	-0.158	-0.058	1.012
slf0639		hypothetical protein	0.486	0.358	0.7	0.58	0.674	0.652	0.352	0.615	0.734	1.047	0.764	0.646	-0.003
slf0640		probable sodium/sulfate sy	0.305	0.495	0.467	-0.186	-0.273	error	0.057	-0.411	-0.01	error	-0.438	-0.455	0.684
slf0641		unknown protein	0.397	error	-0.276	error	-0.023	0.106	error	-0.429	-0.247	error	-0.469	-0.469	0.592
slf0643	ureG	urease accessory protein G	-0.346	-0.429	-1.049	-0.667	-0.227	0.219	0.092	-0.444	-0.43	-0.149	-0.3	-0.391	-0.558
slf0644		probable esterase	0.484	error	0.147	-0.931	-0.379	0.074	error	-0.454	error	-0.309	-0.847	error	0.049
slf0645		unknown protein	0.094	0.137	-0.205	-0.547	error	0.412	error	-0.078	0.027	error	0.428	-0.262	0.852
slf0646	cya2	guanylyl cyclasecya2	1.314	error	0.569	-1.373	error	0.287	error	-0.233	0.3	error	-0.414	0.193	-0.262
slf0647		unknown protein	error	error	-0.476	-0.772	-0.842	-0.293	-0.294	-0.157	-0.18	-0.432	-0.671	-0.566	0.908
slf0648		probable glycosyltransfera	-0.335	-0.372	-0.15	0.407	-0.108	-0.193	-0.329	-0.316	-0.156	-0.515	-0.074	-0.291	0.451
slf0649		two-component response re	0.373	0.727	0.33	0.012	-0.161	-0.057	0.055	0.127	0.149	0.169	0.02	0.231	0.563
slf0650		putative transposase [ISY1	0.165	-0.357	0.134	-0.26	-0.213	-0.216	-0.125	-0.757	0.335	0.448	-0.362	0.217	0.105
slf0651		putative transposase [ISY1	-0.513	1.36	-1.086	-0.456	-0.72	-0.79	-0.358	-0.257	-0.492	0.301	-0.377	-0.663	-0.325
slf0654		alkaline phosphatase	error	error	error	error	error	error	error	error	error	error	error	error	error
slf0656		unknown protein	-0.18	-0.135	-1.093	-0.628	-1.575	-1.497	-1.449	0.167	-0.447	-1.282	-1.535	-0.39	-1.536
slf0657		phospho-N-acetylmuramoy	error	error	error	error	error	error	error	-0.191	-0.12	0.481	0.542	-0.196	-0.087
slf0658		hypothetical protein	error	1.393	1.453	0.073	1.585	0.983	error	-0.069	0.619	0.146	0.221	0.418	0.212
slf0659		hypothetical protein	-0.059	error	-0.213	error	-0.095	0.089	0.135	0.069	-0.165	0.518	-0.036	-0.282	0.737
slf0660	pdxA	pyridoxal phosphate biosyn	-0.12	0.682	-0.153	-0.214	-0.647	-0.043	-0.741	-0.097	0.095	-0.557	-0.189	-0.468	0.031
slf0661	ycf35	hypothetical protein YCF35	-0.313	-0.372	-0.46	-0.22	-0.534	-0.593	-0.103	-0.176	-0.166	-0.71	0.217	-0.215	0.828
slf0662		hypothetical protein	-0.005	error	0.392	-0.313	error	0.557	-0.269	0.505	0.792	error	0.327	0.874	1.307
slf0664		unknown protein	error	error	error	-1.065	error	0.877	error	-0.422	-0.1	1.846	0.011	-0.637	-0.063
slf0665		putative transposase [ISY5	0.34	error	0.128	-0.638	-0.1	-0.021	-0.015	-0.379	0.134	0.072	-0.597	-0.003	0.225
slf0666		putative transposase [ISY5	0.726	1.08	1.425	1.447	1.048	0.364	-0.125	error	error	error	error	error	error
slf0667		putative transposase [ISY3	0.21	error	-0.055	-1.39	-0.054	0.04	-0.325	-0.804	0.168	-0.071	-0.268	-0.174	0.656
slf0668		putative transposase [ISY3	0.686	error	-0.148	-0.666	error	0.215	0.471	-0.573	-0.123	0.199	-0.197	-0.409	0.927
slf0669		unknown protein	error	error	error	error	error	error	error	0.285	0.213	0.381	1.238	-0.065	-0.077
slf0670		hypothetical protein	-0.339	0.121	-0.111	-0.701	-0.124	0.069	error	-0.061	0.63	error	0.025	0.484	0.392
slf0671		probable cation transporter	2.325	0.308	0.052	-0.693	-0.102	0.197	error	0.282	0.177	0.084	0.226	0.38	-1.009
slf0672		cation-transporting ATPase	-0.128	-0.391	-0.327	-0.377	-0.53	-0.288	-0.344	-0.094	0.491	0.114	0.739	0.431	0.66
slf0676		hypothetical protein	error	error	error	error	error	error	error	0.285	0.132	0.744	0.498	-0.609	0.729
slf0677		putative transposase [ISY5	-0.072	-0.466	-0.291	0.071	-0.686	-0.375	-0.305	-0.443	-0.315	0.545	-0.84	-0.61	-1.15
slf0678		hypothetical protein	error	0.114	0.132	-0.684	error	0.142	error	-0.113	0.846	0.927	0.208	0.385	1.321
slf0679		periplasmic phosphate-bind	error	error	-0.02	-0.211	0.817	0.391	error	0.255	0.577	0.573	0.068	-0.066	-0.069
slf0680		phosphate-binding periplas	-0.51	-0.728	-0.567	1.229	0.084	-0.174	-0.235	0.289	0.251	1.354	0.917	0.241	0.016
slf0681		phosphate transport system	0.165	-0.245	0.179	0.581	0.347	-0.028	-0.071	error	error	error	error	error	error
slf0682		phosphate transport system	error	error	error	error	error	error	error	0.858	1.085	0.692	0.763	0.937	-0.088
slf0683		phosphate transport ATP-b	0.064	error	0.483	0.463	0.059	-0.097	0.326	-0.134	0.015	-0.036	-0.169	-0.029	0.75
slf0684		phosphate transport ATP-b	error	error	error	error	error	error	error	-0.18	0.072	0.417	-0.08	-0.376	0.335
slf0685		hypothetical protein	error	error	error	error	error	error	error	0.021	0.765	error	-0.082	0.139	0.618
slf0686		probable cytochrome c-type	error	error	0.275	-0.84	error	0.307	error	error	error	error	error	error	error
slf0687	sigI	group3 RNA polymerase sig	error	error	error	error	error	error	error	0.01	0.178	-0.31	0.035	-0.108	0.676
slf0688		unknown protein	error	error	1.211	-0.827	error	0.639	error	-0.722	-0.009	error	-0.376	error	1.128
slf0689	nhaS3	Na <sup>+</sup> /H <sup>+</sup> antiporternhaS3	-0.467	-0.805	-0.641	-0.478	-0.462	-0.246	0.194	-0.488	-0.483	-0.145	-0.385	-0.444	0.829



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sli0690		probable transcription regul	-0.233	error	-0.123	error	0.132	-0.129	error	-0.033	0.215	0.451	0.125	0.436	0.483
sli0691		hypothetical protein	0.493	0.563	0.136	-0.619	-0.302	0.376	error	-0.028	0.458	-0.095	-0.283	0.301	-0.625
sli0696		hypothetical protein	0.827	0.412	0.868	0.256	error	error	1.365	0.366	0.714	0.666	0.851	0.233	1.194
sli0698	dfr	drug sensory protein Adfr	-0.055	0.412	0.358	0.052	0.291	0.436	0.459	-0.075	0.065	1.493	-0.16	0.486	0.184
sli0699		putative transposase [ISY10	-0.225	-0.635	-0.265	-0.022	-0.701	-0.561	-0.916	-0.525	0.157	0.085	-0.48	-0.459	-0.745
sli0700		putative transposase [ISY10	-1.087	-1.097	-1.246	-0.369	-0.97	-0.494	-0.477	-1.105	-0.325	0.743	-0.857	-0.588	-1.483
sli0702		unknown protein	error	error	-0.377	error	error	-0.961	error	-0.054	0.148	-0.305	-0.053	-0.108	-0.366
sli0703		unknown protein	0.411	0.373	0.417	-0.305	0.72	0.655	-	-0.211	-0.045	1.455	0.062	-0.394	0.49
sli0704	nifS	cysteine desulfurase nifS	error	error	error	error	error	error	error	error	error	error	error	error	error
sli0708		dimethyladenosine transfer	error	error	0.222	-0.706	0.092	0.305	0.274	-0.466	-0.031	0.265	-0.261	-0.135	1.038
sli0709		putative endonuclease	-0.608	-0.892	-1.487	-0.918	-1.986	-1.315	-1.108	-0.28	-0.632	error	-0.694	-0.641	-0.478
sli0710		unknown protein	-0.494	-0.952	-0.467	error	-0.912	-0.312	-0.166	-0.532	-0.049	-0.451	-0.4	-0.056	0.218
sli0711		isopentenyl monophosphat	-0.109	-0.042	0.808	0.598	0.014	0.158	0.18	-0.013	1.029	0.95	0.13	1.17	-0.405
sli0712	cysM	cysteine synthase cysM	0.088	-0.051	-0.174	0.175	-0.425	-0.448	-0.301	0.043	-0.002	-0.148	-0.253	-0.177	0.101
sli0716		signal peptidase I	0.554	0.651	0.169	-1.042	error	0.053	error	-0.057	0.326	0.524	-0.139	0.067	1.088
sli0720		RTX toxin activating protein	-0.275	-0.084	0.388	-0.277	0.274	0.138	0.184	0.098	0.655	0.873	0.296	0.268	0.573
sli0721		unknown protein	-0.242	-0.21	-0.286	-0.891	0.128	0.334	1.152	-0.402	-0.244	0.116	-0.548	-0.055	0.652
sli0722		unknown protein	error	-0.504	error	error	-0.979	0.443	error	-0.328	0.103	-0.259	-0.05	-0.397	1.894
sli0723		unknown protein	0.319	error	-0.094	error	-0.367	0.441	1.311	-0.04	0.331	0.201	0.178	-0.018	1.559
sli0726		phosphoglucosyltransferase	-0.308	-0.635	-0.256	-0.077	-0.76	-0.634	-0.577	-0.287	-0.128	-0.471	-0.412	-0.084	-0.081
sli0727		hypothetical protein	error	error	error	error	0.278	0.488	error	-0.358	-0.475	error	-0.494	-0.193	0.913
sli0728	accA	acetyl-CoA carboxylase alp	error	error	error	error	error	error	error	-0.109	0.237	0.265	0.107	0.11	0.458
sli0729		probable DNA methyltransf	-0.408	-0.157	-0.034	0.426	-0.16	-0.006	-0.261	-0.092	0.021	0.179	0.088	-0.494	-0.697
sli0732		hypothetical protein	-0.475	-0.484	error	-0.281	-0.677	-0.325	0.039	0.103	0.433	0.532	-0.167	0.189	-0.728
sli0733		unknown protein	-0.34	-0.037	-0.233	-0.356	-0.583	0.195	0.413	0.096	0.103	0.248	0.034	-0.264	-0.024
sli0735		hypothetical protein	-0.611	-0.107	-0.826	-0.33	-0.649	-0.247	-0.326	-0.527	-0.781	-0.835	-0.395	-0.839	-1.184
sli0736		hypothetical protein	error	error	error	error	error	-0.124	error	-0.008	0.028	error	-0.226	-0.472	0.856
sli0737		hypothetical protein	-0.092	0.225	-0.474	error	-0.667	-0.24	-0.569	-0.235	-0.088	-0.199	-0.328	0.008	-0.635
sli0738		molybdate-binding periplas	0.598	error	1.297	0.926	1.459	1.312	1.127	0.334	0.737	0.703	0.95	0.496	1.796
sli0739		ATP-binding protein of moly	0.441	0.455	-0.128	0.155	-0.119	0.608	0.344	0.134	0.175	0.177	-0.121	0.182	-0.826
sli0740		hypothetical protein	-0.017	-0.213	-0.226	0.078	-0.189	-0.135	0.027	-0.436	-0.029	-0.136	-0.069	-0.041	-0.04
sli0741		pyruvate flavodoxin oxidore	0.164	-0.186	-0.056	error	-0.441	0.225	error	-0.942	error	-0.132	-1.001	error	0.126
sli0742		hypothetical protein	0.07	0.162	0.323	-0.656	0.227	0.534	0.293	-0.387	-0.194	-0.327	-0.237	-0.674	-0.167
sli0743		hypothetical protein	error	-0.03	error	-1.287	0.535	-0.367	error	-0.05	0.226	-0.463	0.013	-0.811	1.449
sli0744		hypothetical protein	-0.887	error	error	error	-0.498	0.36	error	-0.4	-0.638	0.691	-0.23	-0.693	-0.45
sli0745		phosphofructokinase	0.034	-0.03	0.121	0.178	0.462	0.547	1.042	-0.104	0.07	0.074	0.328	0.03	0.348
sli0749		hypothetical protein	0.012	0.331	0.837	0.48	0.825	0.293	0.776	1.033	2.757	2.802	1.569	2.84	0.891
sli0750		two-component sensor hist	-0.599	-0.823	-1.185	-0.646	-1.739	-1.082	-1.3	0.042	-0.43	-0.992	-0.906	-0.747	-1.626
sli0751	ycf22	hypothetical protein YCF22	0.071	0.342	0.111	-0.046	-0.191	0.487	0.671	0.165	0.427	0.004	0.214	0.367	0.361
sli0752		hypothetical protein	-0.205	-0.196	-0.038	0.645	-0.224	-0.142	-0.005	error	error	error	error	error	error
sli0753	folD	FolD bifunctional protein fol	error	error	error	error	error	error	error	-0.447	-0.389	0.08	-0.84	-0.949	-0.576
sli0754		ribosome binding factor A	error	0.034	0.232	0.235	0.792	0.223	0.319	0.241	0.646	0.276	0.665	0.431	0.258
sli0755	tpx, ycf42	thioredoxin peroxidase tpx, y	0.508	-0.048	-0.314	-1.25	0.391	0.263	error	0.075	0.276	0.758	0.553	-0.046	1.632
sli0756		unknown protein	0.306	1.024	-0.141	0.309	0.213	0.03	-0.082	0.533	0.122	0.318	0.512	-0.119	0.087
sli0757	purF	amidophosphoribosyltransf	0.096	0.062	0.56	0.837	0.553	0.348	0.252	0.023	0.378	-0.202	0.398	0.398	1.121
sli0759		ABC transporter ATP-bindin	0.871	0.387	0.489	0.186	0.635	0.341	1.194	0.641	0.563	0.569	0.611	0.351	1.322
sli0760	ycf38	hypothetical protein YCF38	-0.077	-0.436	-0.261	-0.156	0.489	0.255	0.392	-0.279	-0.4	-0.098	0.74	-0.618	1.344
sli0761		unknown protein	0.176	-0.072	0.3	1.439	1.246	0.579	0.748	0.246	0.317	1.095	1.149	0.458	0.488
sli0762		unknown protein	-0.079	0.227	0.849	0.969	1.072	0.37	0.759	0.159	0.48	0.647	0.582	0.549	-0.011
sli0763		hypothetical protein	0.184	-0.128	-0.141	0.437	0.483	0.625	0.729	0.516	0.776	1.326	0.874	0.816	-0.087
sli0764		probable branched-chain ar	0.731	1.353	1.454	1.938	1.031	0.298	0.467	0.835	1.34	1.198	0.964	1.417	-0.159
sli0765		hypothetical protein	-0.067	0.64	0.503	0.018	0.281	0.364	0.043	0.126	0.485	0.273	0.111	0.397	-0.43
sli0766	radC	DNA repair protein RadCra	1.503	1.479	1.45	2.194	1.332	0.542	0.355	1.613	1.451	1.248	1.422	1.539	1.358
sli0767	rpl20	50S ribosomal protein L20	0.109	0.543	0.604	1.417	0.363	-0.269	0.29	0.377	0.379	0.927	0.333	0.252	0.023
sli0771	glcP	glucose transport proteinglc	-0.399	-0.126	-1.033	error	-1.194	-1.06	-1.032	0.187	-1.047	-1.898	-1.896	-1.086	-0.297
sli0772		probable porin; major outer	error	error	0.728	error	-0.048	0.368	-0.222	-0.379	-0.339	0.022	-0.543	-0.516	0.396
sli0775		unknown protein	error	error	1.783	-0.415	error	1.136	error	0.38	1.012	error	-0.376	0.695	-0.194
sli0776		serine/threonine kinase	0.094	error	0.161	-1.22	-0.716	0.434	error	-0.551	-0.133	error	-1.109	-0.503	0.883
sli0777		putative carboxypeptidase	-0.385	-0.001	-0.303	-0.033	-0.076	-0.129	-0.375	-0.069	-0.143	-0.045	0.138	0.07	0.926
sli0778		ABC transporter, ATP-bindi	0.05	0.429	0.227	0.544	0.093	-0.169	-0.666	-0.145	0.116	0.336	-0.179	0.071	0.686
sli0779		unknown protein	error	error	error	error	error	error	error	-0.296	-0.266	0.833	-0.263	-0.327	0.773
sli0780		unknown protein	0.089	0.035	0.133	-0.07	-0.075	0.234	0.151	0.389	0.324	-0.519	0.085	0.024	1.227
sli0781		hypothetical protein	-0.059	error	0.52	-0.37	error	0.489	0.463	-0.117	0.117	error	-0.546	-0.066	error
sli0782		transcriptional regulator	0.932	1.714	error	-1.275	error	0.791	error	-0.091	0.624	error	-0.259	0.635	0.902
sli0783		unknown protein	error	error	1.575	error	1.366	0.814	error	0.48	0.97	error	0.454	0.712	3.174
sli0784	merR	nitrilase merR	-0.573	-0.304	-0.001	0.589	0.007	0.161	-0.127	-0.131	-0.406	0.004	-0.433	-1.007	-0.811
sli0785		unknown protein	0.108	error	0.295	-0.422	-0.095	0.183	-0.063	-0.79	-0.692	error	-0.896	-0.709	0.084
sli0786		unknown protein	error	error	error	-2.585	error	error	error	-0.61	-0.017	error	-0.959	error	error
sli0787		hypothetical protein	-0.485	-0.614	-0.439	0.616	-0.385	-0.011	-0.132	-0.174	-0.649	0.264	-0.486	-1.04	-1.316
sli0788		hypothetical protein	0.547	0.023	-0.159	-0.435	-0.321	-0.314	error	0.032	-0.2	0.483	-0.434	-0.039	-0.476
sli0789		two-component response re	-0.254	-0.255	-0.74	-0.205	-0.546	-0.099	-0.499	-0.137	-0.154	-0.199	-0.784	-0.212	0.829
sli0790															

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl0797	nrsR, rppA	two-component response re	0.024	0.56	0.402	-0.03	0.248	0.508	0.273	-0.224	0.388	0.178	0.067	0.115	1.313
sl0798	nrsS, rppB	two-component sensor histi	-0.278	error	-0.144	-1.308	-0.143	-0.15	error	0.059	0.401	0.626	0.129	0.464	0.863
sl0800		hypothetical protein	error	error	-0.226	0.252	-0.25	-0.277	error	-0.001	0.138	error	-0.299	-0.412	0.08
sl0802		hypothetical protein	-0.156	-0.247	-0.243	0.318	0.028	-0.347	-0.304	-0.076	-0.32	-0.19	0.062	-0.309	0.025
sl0803		hypothetical protein	0.384	error	-0.469	-0.766	0.072	0.554	1.179	0.358	0.437	0.484	0.081	0.167	-0.327
sl0804		hypothetical protein	0.201	-0.469	-1.424	-0.951	-1.014	-0.649	error	-0.26	-0.574	0.227	-0.576	-0.366	-0.366
sl0807	rpe	pentose-5-phosphate-3-epi	-0.579	-0.681	-0.999	-0.512	-0.272	-0.29	-0.167	0.114	-0.138	-0.599	0.392	0.095	1.489
sl0808		putative transposase [ISY5	1.014	0.494	-0.02	-0.011	0.572	0.241	0.978	-0.013	0.274	0.744	0.467	-0.281	1.301
sl0809		hypothetical protein	0.838	error	0.499	error	error	0.517	error	0.601	1.177	error	0.448	0.325	-0.484
sl0810		unknown protein	0.553	error	0.598	-0.127	0.519	0.593	1.843	-0.03	0.135	0.472	0.226	-0.155	2.37
sl0811		unknown protein	error	error	error	error	error	error	error	-0.307	-0.324	error	-0.225	-0.36	0.928
sl0812		hypothetical protein	error	error	0.814	-0.333	0.642	0.886	1.948	error	error	error	error	error	error
sl0813	ctaC	cytochrome c oxidase subu	-0.37	0.073	-0.063	-0.284	-0.081	0.207	0.514	-0.215	-0.018	0.356	-0.021	-0.182	0.005
sl0814		hypothetical protein	-0.512	error	0.552	0.937	0.708	0.566	0.255	0.008	0.908	0.763	1.108	0.799	1.979
sl0815		unknown protein	error	error	error	error	error	error	error	-0.258	0.325	-0.394	0.16	-0.052	1.221
sl0816		probable oxidoreductase	1.704	error	0.567	error	0.401	0.006	1.195	-0.201	0.31	0.411	-0.214	0.047	0.829
sl0817		tRNA delta-2-isopentenylpy	0.093	0.094	-0.188	0.069	0.431	0.171	0.606	-0.214	-0.15	-0.28	-0.201	-0.582	-0.644
sl0818		tetrapyrrole methylase fami	0.488	0.17	0.229	-0.185	0.119	0.186	error	-0.177	0.119	0.156	-0.114	-0.226	1.038
sl0819	psaF	photosystem I reaction cent	-0.431	-0.677	-1.07	-0.113	-1.031	-0.806	-0.662	0.137	-0.737	-1.929	-1.302	-0.689	-0.369
sl0821		hypothetical protein	-0.142	-0.631	-0.101	0.493	0.117	0.123	-0.024	-0.653	-0.06	-0.2	-0.127	0.003	0.405
sl0822		hypothetical protein	-0.322	-0.764	-0.964	0.602	-1.055	-0.735	-0.258	-0.552	-0.736	-0.099	-0.528	-0.732	-1.342
sl0823		probable succinate dehydro	0.545	-0.22	-0.393	-0.494	-0.642	-0.126	-0.215	0.447	-0.03	0.082	-0.06	-0.256	-1.152
sl0825		polyA polymerase	0.13	0.428	-0.193	-0.198	0.153	-0.264	error	0.053	-0.032	1.123	-0.008	-0.02	-0.114
sl0827		hypothetical protein	-0.324	0.061	0.156	-0.246	0.532	0.625	1.464	-0.636	-0.393	0.523	0.004	-0.563	-0.586
sl0828		putative amidase	0.382	0.101	-0.113	error	error	0.317	0.593	0.167	0.243	0.548	0.063	0.011	0.284
sl0829		probable methyltransferase	0.156	-0.443	0.068	-0.451	0.08	0.017	error	-0.248	error	0.074	0.043	error	1.05
sl0830	fus	elongation factor EF-Gfus	-0.482	-0.601	-0.964	-0.526	-0.877	-0.154	-0.513	error	error	error	error	error	error
sl0832		hypothetical protein	0.202	0.145	0.706	-0.314	0.308	0.394	0.259	0.164	0.368	error	0.233	0.089	0.673
sl0833		probable oligopeptides ABC	-0.44	error	-0.484	-0.606	-0.461	-0.063	0.221	-0.262	-0.003	0.555	-0.165	0.001	-0.008
sl0834		low affinity sulfate transport	-0.381	-0.339	-0.003	0.223	-0.213	-0.064	-0.062	-0.209	-0.225	0.07	-0.347	-0.513	0.787
sl0837		hypothetical protein	0.067	error	0.924	-0.558	0.485	error	error	0.1	1.032	1.826	0.965	0.687	1.832
sl0838	pyrF	orotidine 5' monophosphate	0.165	-0.446	0.036	-0.333	-0.078	0.108	0.111	-0.129	0.15	-0.275	-0.373	0.312	0.043
sl0839		hypothetical protein	0.615	error	0.334	-0.531	0.227	0.36	0.438	0.066	0.348	-0.118	0.113	0.324	1.454
sl0842		neopullulanase	0.075	-0.144	0.401	-1.09	-0.429	0.141	error	-0.439	0.045	0.075	-0.485	0.025	1.016
sl0843		unknown protein	0.429	0.39	-0.131	-0.37	-0.167	0.22	error	-0.288	-0.005	-0.06	-0.183	-0.018	1.079
sl0844		tRNA (5-methylaminomethy	error	error	error	error	error	error	error	0.161	0.237	0.366	0.5	0.081	0.704
sl0846		hypothetical protein	1.559	2.037	3.87	2.432	3.738	2.306	-	0.884	2.157	-	2.782	1.792	3.07
sl0847		unknown protein	0.692	error	0.363	0.08	0.072	0.047	0.532	-0.142	0.358	0.239	-0.119	-0.017	1.117
sl0848	dnaA	chromosomal replication ini	0.059	-0.316	-0.132	0.224	-0.221	-0.024	-0.218	-0.216	0.237	-0.453	-0.251	-0.18	-0.072
sl0849	psbD	photosystem II reaction cent	-0.798	-0.825	-0.534	0.752	-0.964	-1.082	-1.074	0.125	0.847	0.413	0.478	0.853	0.951
sl0851	psbC	photosystem II CP43 protei	-0.654	-0.8	-1.471	-0.346	-1.064	-1.042	-0.751	0.116	-0.55	-1.357	-0.579	-0.647	-0.107
sl0853		hypothetical protein	-0.194	-0.312	-0.347	-0.265	-0.34	0.069	0.105	error	0.184	error	error	error	error
sl0854		hypothetical protein	-0.216	-0.23	-0.467	-0.133	-0.444	-0.063	0.045	-0.233	0.046	-0.351	-0.312	-0.214	-0.748
sl0855		putative channel transporte	0.203	-0.076	-0.225	-0.283	0.076	0.178	0.327	-0.265	-0.131	0.351	error	-0.128	-0.466
sl0856	sigH	group3 RNA polymerase sig	0.045	0.139	-0.258	-0.297	-0.092	0.106	-0.096	0.112	0.348	-0.676	0.008	-0.196	-0.125
sl0857		unknown protein	error	error	error	error	error	error	error	0.399	0.725	0.783	0.783	0.674	0.311
sl0858		hypothetical protein	0.013	0.139	0.515	0.532	0.411	0.278	0.325	0.088	0.883	0.929	0.698	0.613	-0.08
sl0860		hypothetical protein	-0.028	-0.493	-0.416	-0.769	-0.974	-1.108	-0.519	-0.124	-0.166	-0.48	-0.227	-0.219	0.916
sl0861		hypothetical protein	0.537	0.203	-0.056	-0.534	-0.242	0.001	0.285	0.544	0.614	0.956	0.247	0.413	-0.422
sl0862		hypothetical protein	-0.208	-0.292	-0.283	0.451	0.159	0.114	-0.255	-0.108	-0.182	0.1	0.014	-0.226	0.645
sl0863		hypothetical protein	0.42	error	0.533	-0.672	0.63	0.684	error	-0.149	0.276	-0.136	-0.039	0.319	0.982
sl0864		hypothetical protein	-0.02	0.282	0.361	0.295	1.017	0.285	0.094	-0.305	-0.158	0.309	0.537	-0.044	1.126
sl0865	uvrC	excinuclease ABC subunit C	0.036	0.211	0.426	0.475	-0.089	0.342	-0.155	-0.337	-0.257	-0.353	-0.453	-0.434	error
sl0867		hypothetical protein	0.275	0.641	0.503	error	error	error	0.712	-0.279	0.369	0.413	0.199	0.072	0.221
sl0868		lipoic acid synthetase	-0.006	0.139	-0.106	-0.481	-0.075	0.138	-0.462	-0.392	-0.255	-1.064	-0.727	-0.829	-0.421
sl0869	aat	Leu/Phe-tRNA-protein trans	0.915	0.263	-0.333	-0.892	0.323	error	error	0.143	0.034	-0.769	0.108	-0.287	0.507
sl0871		hypothetical protein	-0.13	0.172	0.449	0.41	0.623	0.394	1.154	-0.457	error	0.385	0.079	error	-0.378
sl0872		unknown protein	0.075	-0.03	0.274	0.232	0.48	-0.119	0.408	-0.284	0.049	-0.097	0.212	0.062	0.18
sl0873		carboxynorspermidine deca	error	error	error	error	error	error	error	error	error	error	error	error	error
sl0875		hypothetical protein	0.573	error	1.385	-0.097	0.687	0.781	0.228	-0.18	0.489	error	-0.109	0.407	0.954
sl0876	ruvA	Holliday junction DNA heli	-0.557	0.007	-0.898	-0.974	-0.725	-0.477	error	-0.257	-0.206	-0.09	-0.662	-0.469	0.738
sl0877		hypothetical protein	-0.039	0.192	0.292	0.134	0.127	-0.052	-0.141	-0.181	0.56	0.022	0.347	0.309	0.307
sl0886		hypothetical protein	-0.56	-0.224	-0.21	-0.296	-0.32	0.098	-0.021	-0.265	0.112	0.026	-0.164	-0.165	-0.418
sl0887		putative modulator of DNA	error	error	error	error	error	error	error	-0.388	-0.042	-0.437	0.109	-0.26	0.436
sl0888		hypothetical protein	error	error	error	-0.485	error	0.613	error	-0.147	-0.006	0.165	0.217	-0.448	1.388
sl0891		malate dehydrogenase	-0.326	error	-0.257	-0.065	-0.16	0.018	-0.061	0.155	0.336	-0.236	0.256	0.07	-0.347
sl0892	panD	aspartate 1-decarboxylase	0.127	-0.409	-0.776	-1.062	error	-0.196	0.203	0.122	0.105	0.122	-0.163	-0.348	0.783
sl0895		CysQ protein homolog	-0.284	-0.175	-0.021	0.409	0.124	-0.061	-0.276	-0.124	0.073	0.931	0.224	0.121	-0.044
sl0896	ruvC	Holliday junction resolvase	error	error	error	-0.265	error	0.264	error	0.059	0.265	-	0.45	-0.323	0.786
sl0897	dnaJ	DnaJ protein dnaJ	-0.134	0.096	0.834	error	0.195	-0.172	-0.403	0.261	1.029	0.397	0.718	0.777	0.883
sl0898		hypothetical protein	-0.3	-0.356	-0.347	0.533	-0.217	-0.33	-0.186	0.097	0.049	-0.299	0.161	-0.239	-0.952
sl0899		UDP-N-acetylglucosamine	-0.179	-0.259	-0.74	-0.989	-0.566	-0.453	-0.438	-0.381	-0.321	-0.374	-0.358	-0.33	0.829
sl0900	hisG	ATP phosphoribosyltransfe	-0.412	-0.555	-0.448	0.109	-0.752	-0.596	-0.523	0.246	0.083	-0.352	0.144	-0.37	-0.957
sl0901	purE	phosphoribosylaminoimidaz	-0.022	-0.076	0.473	-0.267	-0.357	0.407	0.03	-0.14	0.491	-0.132	0.177	0.014	0.278
sl0902	argF	ornithine carbamoyltransfer	-0.5	-0.526	-0.076	0.216	-0.123	-0.288	-0.632	0.267	0.512	-2.008	-0.086	-1.158	-0.698

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl10905		hypothetical protein	0.427	0.851	1.159	0.821	0.476	-0.076	-0.134	0.484	1.081	1.371	0.328	0.897	1.291
sl10909		unknown protein	error	error	error	error	error	0.519	error	0.115	0.483	1.462	0.32	0.022	error
sl10910		unknown protein	error	error	-0.383	error	error	-0.178	error	0.519	0.844	error	5.167	error	-0.15
sl10911		unknown protein	error	-0.186	0.464	0.94	-0.028	0.05	-0.189	error	error	2.265	error	error	error
sl10912		ABC transporter ATP bindin	0.12	error	-0.536	error	-0.372	0.055	0.334	-0.114	-0.226	0.617	-0.168	-0.317	-0.085
sl10913		hypothetical protein	0.943	error	error	-1.306	error	0.376	error	0.466	0.527	0.272	0.104	0.008	1.11
sl10914		unknown protein	0.532	error	0.096	-0.67	0.35	0.436	error	-0.168	0.197	0.059	-0.191	0.065	1.602
sl10915		putative zinc protease prote	error	error	error	error	error	error	error	error	error	error	error	error	error
sl10916	cobH	precorrin isomerasecobH	error	error	error	error	error	error	error	0.435	0.673	0.2	-0.236	0.134	0.381
sl10920	ppc	phosphoenolpyruvate carboc	-0.591	-0.816	-0.855	-0.098	-0.723	-0.387	-0.227	-0.117	-0.282	-0.698	-0.407	0.045	-1.089
sl10921		two-component response re	-0.005	0.359	0.3	-1.303	-0.294	-0.067	error	-0.087	0.047	-0.211	-0.395	0.119	0.609
sl10922		unknown protein	error	error	error	error	error	error	error	0.298	0.063	0.509	-0.086	-0.286	0.271
sl10923		unknown protein	0.382	0.613	-0.131	0.114	-0.177	-0.166	-0.121	0.513	0.163	-0.005	0.11	0.292	1.191
sl10924		hypothetical protein	0.877	1.185	1.06	0.275	0.924	1.004	1.95	0.629	1.245	0.489	0.742	0.946	-0.102
sl10925		hypothetical protein	0.727	1.345	1.109	0.617	1.349	1.35	1.646	0.801	1.026	0.652	0.507	0.895	error
sl10926		hypothetical protein	error	0.531	error	1.414	1.004	0.167	0.406	error	error	error	error	error	error
sl10927		S-adenosylmethionine synt	-0.303	-0.516	-0.593	0.427	-0.245	-0.58	-0.42	0.094	0.05	0.003	0.284	-0.132	0.615
sl10928	apcD	allophycocyanin-BapcD	-0.241	-0.372	-0.571	0.224	-0.627	-0.743	-0.588	-0.303	-0.557	0.27	-0.581	-0.853	0.203
sl10930		unknown protein	1.098	1.611	1.98	1.248	1.494	1.438	2.262	1.262	2.231	0.703	1.249	1.855	2.51
sl10931		hypothetical protein	-0.546	0.426	0.346	0.533	error	0.287	-0.018	0.191	0.632	error	0.419	0.31	0.365
sl10932		hypothetical protein	0.595	error	1.001	-0.263	0.197	0.451	-0.037	-0.012	0.307	0.066	-0.095	0.581	0.957
sl10933		hypothetical protein	0.03	0.117	0.811	0.779	-0.11	-0.364	-0.251	error	error	error	error	error	error
sl10934	ccmA	carboxysome formation pro	0.18	0.352	0.134	1.014	0.323	0.087	0.166	0.21	0.814	0.564	0.915	0.905	0.803
sl10936		putative oxidoreductase	-0.118	-0.395	-0.215	0.138	-0.192	-0.107	-0.289	-0.56	-0.09	-0.143	-0.342	-0.412	0.07
sl10938		aspartate transaminase	error	error	error	error	error	error	error	2.159	2.878	1.034	1.292	2.675	6.007
sl10939		hypothetical protein	2.186	3.351	3.897	2.177	2.929	1.444	1.965	3.974	4.791	3.33	3.311	4.189	3.399
sl10943		unknown protein	2.584	1.615	0.976	error	error	0.374	error	0.669	0.65	error	0.505	0.185	1.479
sl10944		hypothetical protein	-0.053	-0.017	0.821	0.554	0.207	0.26	1.161	-0.401	0.456	error	-0.197	0.372	0.411
sl10945	glgA	glycogen synthaseglgA	-0.474	-0.248	-0.326	-0.094	-0.323	-0.147	-0.477	-0.04	-0.164	-0.61	-0.244	-0.462	-0.722
sl10947	lrgA	light repressed protein A hc	-0.588	-0.661	-0.824	-0.257	-0.794	-0.305	-0.016	-0.761	-1.042	-1.641	-1.468	-1.179	-0.488
sl10980		unknown protein	0.323	error	0.637	-0.371	0.42	0.675	0.417	0.005	0.154	0.546	-0.196	0.217	-0.599
sl10981		unknown protein	-0.353	error	-0.001	0.895	0.523	0.361	0.355	0.101	0.469	0.744	0.761	0.175	0.622
sl10982		unknown protein	0.925	0.377	0.291	0.068	1.419	0.704	0.939	0.222	0.375	error	1.09	0.029	1.484
sl10983		hypothetical protein	error	error	error	error	error	error	error	-0.116	0.31	-0.52	0.059	-0.117	0.512
sl10984		hypothetical protein	0.543	error	0.772	error	-0.098	0.203	error	-0.394	1.036	error	-0.276	error	0.3
sl10985		unknown protein	error	error	error	error	error	error	error	-0.781	-0.52	-0.371	-0.587	-0.69	-0.035
sl10986		putative transposase [ISY12	-0.059	0.155	0.633	0.624	0.571	0.5	0.463	-0.271	0.357	0.76	0.511	0.04	1.099
sl10990		glutathione-dependent form	0.291	-0.435	0.427	error	error	0.27	0.172	0.006	0.154	0.846	-0.118	-0.145	0.643
sl10992		putative esterase	error	0.658	0.856	error	0.187	-0.184	-0.227	0.448	0.331	0.584	0.006	0.17	0.123
sl10993		potassium channel	-0.179	-0.751	-0.095	-1.146	-0.554	-0.347	-0.459	-0.435	-0.116	-0.066	-0.388	-0.328	1.062
sl10994		hypothetical protein	0.121	0.121	0.103	-0.325	-0.187	0.326	error	-0.372	0.006	0.01	-0.514	-0.367	0.034
sl10995		hypothetical protein	0.354	1.132	0.344	-0.666	1.046	0.739	1.29	0.146	0.088	1.166	0.519	0.156	0.365
sl10996		hypothetical protein	error	error	error	error	error	error	error	-0.145	0.165	0.34	0.181	-0.043	-0.289
sl10997		hypothetical protein	-0.247	0.17	0.057	-0.16	-0.338	0.267	-0.134	-0.225	-0.051	-0.006	-0.57	-0.167	-1.306
sl10998	ycf30	LysR family transcriptional	-0.367	-0.656	-0.828	0.042	-0.522	-0.509	-0.298	-0.084	-0.091	0.147	-0.205	-0.036	-0.948
sl11001		ATP-binding protein of ABC	0.422	0.623	0.855	1.223	0.75	-0.107	0.103	0.396	0.994	1.049	0.612	0.834	0.365
sl11002	ycf22	hypothetical protein YCF22	-0.172	-0.41	-0.874	-0.893	-1.111	-0.713	-0.654	-0.092	-0.268	-0.613	-0.788	-0.246	0.03
sl11003		two-component sensor histi	-0.497	-0.849	-1.262	-0.655	-1.78	-1.144	-1.404	-0.587	-0.755	-0.213	-0.998	-0.956	-1.534
sl11004		hypothetical protein	0.456	0.268	1.712	0.945	0.474	0.271	0.108	-0.304	0.853	0.687	-0.055	0.664	0.59
sl11005		MazG protein homolog	-0.448	-0.57	-0.889	-0.397	-1.317	-1.029	-0.87	0.077	-0.544	-0.811	-1.195	-0.276	-2.026
sl11006		unknown protein	0.336	error	1.091	error	0.156	0.304	error	-0.353	0.791	0.23	-0.005	0.411	0.633
sl11009		unknown protein	0.203	0.126	0.286	0.617	-0.214	-0.673	-0.691	-0.006	-0.271	-0.58	-1.284	-0.533	-1.612
sl11011		hypothetical protein	-0.321	-0.6	0.077	-0.055	-0.421	-0.323	-0.559	error	error	error	error	error	error
sl11017	amt2	ammonium/methylammoniu	error	error	error	error	error	error	error	-0.402	0.128	0.301	-0.231	-0.234	0.697
sl11018	pyrC	dihydroorotasepyrC	0.087	-0.226	-0.322	0.102	-0.264	-0.133	-0.211	-0.012	0.218	1.315	-0.02	0.017	-1.019
sl11019		hydroxyacylglutathione hyd	error	error	error	error	error	error	error	0.147	0.525	-0.126	0.156	0.267	0.458
sl11020		plobable glycosyltransferas	-0.342	-0.487	0.071	-0.472	0.107	0.049	-0.003	error	error	error	error	error	error
sl11021		hypothetical protein	-0.253	error	-1.068	-0.594	-0.909	-0.596	-0.308	-0.29	-0.385	0.19	-0.689	-0.731	-0.871
sl11022		hypothetical protein	-0.245	-0.099	1.401	1.385	0.945	0.546	0.958	error	error	error	error	error	error
sl11023		succinyl-CoA synthetase be	0.346	error	1.037	error	0.446	0.502	error	0.174	0.763	0.447	0.329	0.352	1.138
sl11024		hypothetical protein	0.596	0.329	0.216	0.327	-0.073	0.258	0.201	0.214	0.258	0.299	0.188	0.11	0.033
sl11025		hypothetical protein	error	error	error	-0.2	-0.192	0.009	error	0.3	0.269	0.426	0.189	0.267	-0.39
sl11027	glfD	NADH-dependent glutamat	-0.829	-0.42	-0.471	error	error	-0.782	-0.384	-0.116	0.348	0.25	-0.496	0.36	1.227
sl11028	ccmK	carbon dioxide concentrati	-0.605	-0.94	-1.247	-0.578	-1.473	-1.037	-0.811	0.112	-0.338	-1.372	-1.067	-0.152	-0.608
sl11029	ccmK	carbon dioxide concentrati	-0.741	-0.71	-1.11	-0.816	-1.689	-0.8	-0.943	0.235	-0.276	-1.05	-0.56	-0.127	-1.097
sl11030	ccmL	carbon dioxide concentrati	0.148	-0.54	-1.184	-0.652	-0.891	-0.43	-0.066	-0.072	-0.154	-0.806	-0.51	-0.237	0.552
sl11031	ccmM	carbon dioxide concentrati	-0.835	-1.036	-1.014	0.086	-0.969	-0.833	-0.82	-0.232	-0.282	-0.899	-0.408	-0.151	-0.112
sl11032	ccmN	similar to carbon dioxide co	-0.142	-0.178	-0.383	0.113	-0.721	-0.616	-0.663	0.089	0.095	-0.278	-0.459	-0.365	0.678
sl11033		probable protein phosphata	error	error	error	error	error	error	error	0.063	-0.224	0.544	-0.223	-0.342	0.415
sl11035		uracil phosphoribosyltransf	-0.419	0.038	-0.312	-0.409	-0.426	-0.112	0.183	-0.482	-0.161	-0.107	0.163	-0.583	0.848
sl11036		hypothetical protein	error	error	-0.013	-0.481	error	0.289	error	0.133	-0.31	0.264	-0.233	-0.216	-0.895
sl11037		unknown protein	0.492	0.908	0.495	-0.624	0.654	0.446	error	0.115	0.274	0.281	0.018	0.26	0.994
sl11039		hypothetical protein	-0.423	-0.245	-0.1	error	-0.181	0.087	0.303	-0.153	-0.384	0.448	-0.329	-0.599	-1.109
sl11040		unknown protein	-0.397	error	-0.252	-0.702	error	0.338	1.248	-0.417	-0.404	error	0.596	-0.38	error
sl11041	cysA	similar to sulfate transport	0.472	0.053	0.784	0.472	0.154	-0.154	0.26	-0.086	0.506	0.472	0.293	0.306	1.224

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl11043		polyribonucleotide nucleotid	-0.541	-0.96	-1.556	0.079	-1.198	-1.015	-0.892	-0.225	-0.441	0.245	-0.168	-0.565	-1.16
sl11045		mutator MutT protein	0.094	0.005	-0.084	-0.239	-0.142	0.061	0.426	0.422	0.585	-0.097	-0.181	0.11	-1.14
sl11049		hypothetical protein	-0.318	-0.225	0.448	1.156	0.679	0.382	0.273	0.001	0.221	0.406	0.449	0.131	-0.248
sl11051	cpcF	phycocyanin alpha-subunit	0.348	0.844	0.829	0.223	-0.052	-0.496	0.051	-0.134	0.295	-0.457	-0.049	0.095	-0.537
sl11052		hypothetical protein	error	error	0.888	error	error	0.292	error	-0.198	0.438	0.715	0.425	0.209	1.79
sl11053		hypothetical protein	error	error	error	error	error	-0.062	error	-0.695	0.214	0.399	-0.246	0.113	0.723
sl11054		hypothetical protein	-0.33	-0.298	-0.077	0.188	-0.121	0.055	0.355	-0.304	0.37	0.373	-0.091	0.408	-0.582
sl11056	purL	phosphoribosylformyl glycin	0.055	0.009	0.119	0.371	-0.228	0.018	-0.444	-0.045	0.193	-0.367	-0.041	0.177	-0.451
sl11057	trxM2	thioredoxin MtrxM2	-0.497	-0.513	-0.396	-0.522	-0.713	-0.476	-0.542	-0.369	-0.286	-0.789	-0.425	-0.38	0.834
sl11058	dapB	dihydrodipicolinate reducta	-0.18	-0.418	-0.863	-0.477	-0.614	-0.264	-0.091	0.449	-0.171	0.162	-0.371	error	-0.434
sl11059		adenylate kinase	0.402	-0.078	0.012	-0.533	-0.379	0.223	error	-0.175	-0.286	-0.426	-0.544	-0.864	1.006
sl11060		hypothetical protein	-0.386	-0.445	-0.473	-0.758	-0.628	-0.091	error	-0.721	-0.686	-0.238	-0.54	-0.697	0.54
sl11061		unknown protein	-0.273	-0.738	-0.56	error	error	-0.628	error	0.14	0.432	-1.263	-0.046	-0.322	-1.045
sl11062		unknown protein	error	error	error	error	error	error	error	0.555	0.756	-	1.371	0.323	1.62
sl11063		hypothetical protein	error	error	error	error	-0.493	-0.199	error	-0.257	-0.311	-0.217	-0.683	-0.567	0.798
sl11064		hypothetical protein	0.396	0.731	error	error	0.017	-0.076	1.016	-0.11	0.087	0.669	-0.378	0.228	1.028
sl11068		unknown protein	error	error	0.346	-0.673	0.122	0.915	1.332	0.03	0.56	0.277	0.244	0.29	-0.617
sl11069		3-oxoacyl-[acyl-carrier-prot	error	error	error	error	error	error	error	0.487	0.251	error	0.095	-0.039	-0.249
sl11070		transketolase	-0.663	-0.879	-0.546	0.866	-0.418	-0.544	-0.253	0.008	-0.055	0.316	0.698	0.062	-0.777
sl11071		hypothetical protein	-0.195	error	-0.272	0.373	-0.651	-0.327	-0.589	0.259	0.007	-	-0.046	-0.156	-0.421
sl11072		hypothetical protein	-0.101	0.181	0.366	-0.297	0.166	0.223	0.48	0.013	0.278	0.017	0.187	0.285	-0.485
sl11074	leuS	leucyl-tRNA synthetaseleuS	0.02	-0.007	0.135	0.521	-0.283	-0.243	-0.458	-0.278	-0.263	-0.709	-0.579	error	-0.184
sl11076		cation-transporting ATPase	error	error	-0.617	-0.949	error	-0.211	error	-0.254	-0.232	0.525	-0.433	-0.57	-0.059
sl11077	speB2	agmatinasespeB2	0.8	0.923	1.411	0.986	0.411	0.584	-0.24	-0.235	0.602	0.4	0.272	0.495	0.521
sl11078	hypA	hydrogenase expression/fo	-0.182	0.077	0.152	-0.166	0.299	0.507	-0.042	-0.264	0.307	error	-0.31	-0.127	-0.585
sl11079	hypB	hydrogenase expression/fo	0.001	-0.067	0.147	0.052	-0.417	-0.02	-0.194	-0.503	0.29	0.526	-0.523	-0.241	-0.367
sl11080		ABC transport system subs	0.282	0.029	0.258	-0.424	-0.232	0.381	error	-0.666	0.054	-0.303	-0.247	-0.297	0.436
sl11081		ABC transport system perm	-0.126	0.103	0.654	1.315	0.144	-0.062	0.156	0.173	0.874	0.506	0.132	0.754	-0.654
sl11082		ABC transport system ATP-	error	0.669	0.063	-0.877	error	0.418	error	error	error	error	error	error	error
sl11084		hypothetical protein	error	error	error	error	error	error	error	-0.431	-0.594	-1.024	-0.76	-0.76	-0.704
sl11085	gipD	glycerol-3-phosphate dehyd	error	error	error	error	error	error	error	0.046	0.943	0.93	1.476	0.899	0.902
sl11086		unknown protein	0.088	0.032	0.959	0.343	0.529	0.471	0.307	0.19	1.098	0.64	0.77	0.572	0.943
sl11087		similar to sodium/glucose c	-0.122	-0.029	0.585	1.629	-0.266	-0.366	-0.585	0.351	0.281	-0.068	0.245	0.035	-0.821
sl11089		unknown protein	0.089	0.134	-0.268	error	0.238	-0.104	-0.124	-0.104	0.272	0.099	0.636	-0.161	1.458
sl11091	chpP	geranylgeranyl hydrogensa	error	error	error	error	error	error	error	-0.101	-1.015	-1.038	-1.038	-0.777	-0.327
sl11092		hypothetical protein	-0.441	0.136	-0.214	-0.377	-0.341	-0.027	-0.278	0.217	0.352	error	0.032	-0.445	-0.821
sl11094		putative transposase	error	0.342	0.103	-0.168	error	0.305	error	-0.03	0.222	0.434	0.083	0.12	-0.531
sl11095		hypothetical protein	0.442	0.714	0.79	0.809	0.893	0.933	0.985	0.288	0.684	0.738	0.588	0.157	0.213
sl11096	rps12	30S ribosomal protein S12r	-0.046	-0.062	0.039	1.503	-0.192	-0.789	-0.774	0.405	0.767	0.866	0.537	0.867	-1.003
sl11097	rps7	30S ribosomal protein S7rp	0.085	0.147	0.038	1.308	-0.056	-0.381	-0.715	0.578	0.741	0.728	0.601	0.983	-0.401
sl11098	fus	elongation factor EF-Gfus	0.364	0.16	0.347	error	0.268	0.065	-0.13	0.751	1.042	0.521	1.193	0.999	1.438
sl11099	tufA	elongation factor TufuA	-0.619	-0.926	-1.618	0.149	-1.408	-1.354	-0.936	-0.008	-0.987	-0.82	-0.46	-1.252	-1.357
sl11101	rps10	30S ribosomal protein S10r	-0.498	-0.928	-1.185	0.799	-0.585	-0.902	-0.941	-0.026	0.101	0.043	0.307	-0.128	-1.324
sl11102	gtrA	integral membrane protein	-0.074	0.193	-0.034	-0.123	-0.451	-0.045	0.153	0.237	0.398	0.77	-0.138	0.335	-1.019
sl11103	gtrB	integral membrane protein	-0.277	-0.576	-0.49	0.178	-0.503	-0.091	-0.515	-0.084	-0.758	-0.289	-0.648	-0.719	-1.103
sl11104	gtrC	periplasmic substrate-bindin	0.486	error	0.507	error	0.105	0.005	-0.269	0.196	0.832	error	0.074	0.316	0.636
sl11106		hypothetical protein	0.451	2.169	3.764	2.818	2.564	1.418	1.379	1.677	4.234	4.319	2.503	4.291	1.336
sl11107		type IV pilus biogenesis pro	-0.348	0.383	1.52	0.931	0.597	0.117	0.392	0.688	2.655	1.955	0.988	2.856	0.137
sl11108		stationary-phase survival p	-0.739	error	error	error	-0.177	-0.036	error	-0.26	0.016	0.195	-0.007	-0.216	0.906
sl11109		hypothetical protein	-0.621	-1.122	-1.513	-0.616	-1.253	-1.037	-0.759	-1.01	-1.021	-0.657	-1.249	-1.09	0.522
sl11110	prfA	peptide chain release factor	-0.014	-0.306	-0.6	0.027	-0.522	-0.56	-0.632	0.037	-0.061	error	-0.34	-0.798	-0.06
sl11112	aroQ	3-dehydroquinate dehydrat	1.056	0.565	0.861	0.277	1.242	0.55	error	0.553	0.644	0.871	1.204	0.729	2.112
sl11118		hypothetical protein	error	error	error	error	error	error	error	-0.179	0.466	error	0.156	0.397	1.456
sl11119		hypothetical protein	-0.649	-0.866	-0.011	0.495	0.923	0.988	0.679	-0.222	-0.309	0.345	0.441	-0.248	0.029
sl11120		chromosome segregation p	-0.441	-0.495	-0.506	0.014	-0.592	-0.249	-0.048	-0.281	-0.274	-0.035	-0.575	-0.583	-1.345
sl11121		hypothetical protein	-0.61	-0.541	-0.522	0.157	-0.282	-0.146	-0.49	-0.209	-0.182	0.194	-0.148	-0.343	-0.652
sl11123		hypothetical protein	0.182	-0.129	-0.1	-0.93	0.106	-0.413	-0.328	-0.257	0.11	0.154	0.038	-0.239	0.615
sl11124	plpA	phytochrome like protein Pl	error	-0.401	-0.502	-0.182	-0.845	-0.409	-0.323	-0.092	-0.259	error	-0.542	-0.224	-1.569
sl11127	menB	naphthoate synthasemenB	0.619	0.37	0.392	-0.547	-0.11	0.002	0.337	0.824	1.177	0.015	0.005	0.998	0.905
sl11129		2-hydroxy-6-oxohepta-2,4-d	0.229	0.188	-0.202	-0.486	-0.245	0.169	error	0.082	0.486	0.646	-0.143	0.238	0.653
sl11130		unknown protein	-0.386	-0.486	-0.558	0.02	-0.451	-0.168	-0.622	-0.12	-0.004	-0.887	0.043	-0.058	-0.175
sl11131		unknown protein	-0.319	-0.562	-1.036	-0.571	-0.367	-0.313	-0.386	-0.109	-0.563	-0.49	0.048	-0.589	0.769
sl11132		unknown protein	-0.188	-0.083	0.304	0.511	error	0.136	0.188	-0.372	-0.117	0.046	-0.064	-0.223	-0.149
sl11135		unknown protein	error	2.584	3.494	3.4	2.693	1.822	1.894	error	error	error	error	error	error
sl11138		hypothetical protein	-0.032	-0.359	-0.666	-0.132	-0.769	-0.941	-0.747	0.116	-0.401	-0.572	-0.612	-0.347	-0.131
sl11142		hypothetical protein	-0.404	-0.273	-0.463	0.075	-0.124	-0.113	-0.107	-0.233	-0.071	0.03	-0.114	-0.141	-0.745
sl11143	pcrA	ATP-dependent helicase Pc	-0.279	-0.726	-0.814	-0.207	-0.265	-0.029	0.157	-0.377	-0.576	-0.359	-0.339	-0.745	-1.275
sl11144		hypothetical protein	1.396	0.817	error	0.795	1.579	0.444	0.723	0.279	0.74	0.495	1.085	0.593	1.786
sl11147		glutathione S-transferase	0.297	0.264	-0.227	-0.532	-0.314	0.142	-0.051	-0.1	0.08	-0.098	-0.035	0.027	-0.207
sl11150		hypothetical protein	-0.416	-0.199	-0.079	0.482	-0.058	-0.277	-0.55	error	error	error	error	error	error
sl11151		unknown protein	-0.124	-0.297	0.188	-0.499	error	0.093	error	0.152	0.285	0.334	error	-0.256	0.506
sl11154		putative antibiotic efflux pro	0.27	0.181	-0.194	-0.31	0.047	-0.209	-0.071	0.19	0.228	0.146	0.388	0.164	1.296
sl11155		hypothetical protein	-0.026	-0.014	0.085	error	0.125	-0.381	-0.068	0.067	0.33	error	0.2	-0.062	error
sl11156		putative transposase [ISY1	0.688	0.072	1.028	0.229	0.556	0.265	error	0.18	0.749	1.076	0.684	0.198	1.999
sl11157		putative transposase [ISY1	0.2	0.524	0.622	0.66	0.514	0.413	0.177	0.007	0.784	0.706	0.656	error	1.42

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slI1158		hypothetical protein	error	error	error	error	error	-0.095	error	-0.465	-0.033	0.415	0.434	-0.191	-0.012
slI1159		probable bacterioferritin co	0.645	0.07	0.508	-1.145	-0.146	0.076	error	-0.305	error	error	-0.581	error	5.369
slI1160		hypothetical protein	0.965	1.629	3.385	1.24	2.9	1.834	-	0.438	1.45	-	error	0.801	6.761
slI1161		probable adenylate cyclase	0.396	0.724	error	error	-0.254	0.047	error	-0.089	0.42	-0.471	-0.605	0.095	0.844
slI1162		hypothetical protein	error	error	-0.495	-1.067	error	0.491	error	-0.465	-0.374	-0.372	-0.154	-0.332	-0.499
slI1163		unknown protein	-0.247	0.128	-0.324	0.029	0.036	0.035	-0.14	error	error	error	error	error	error
slI1164		hypothetical protein	error	0.294	-0.256	-1.117	error	0.651	error	-0.245	-0.183	-0.186	-0.283	-0.575	-0.303
slI1165		DNA mismatch repair prote	-0.409	-0.424	-0.403	-0.125	-0.742	0.036	-0.062	-0.569	-0.724	-0.13	-0.637	-0.718	-0.866
slI1166		hypothetical protein	0.132	-0.079	0.057	0.831	-0.027	-0.156	0.023	0.343	0.287	0.604	0.28	0.188	-0.17
slI1167		unknown protein	0.215	0.442	1.794	0.421	1.298	0.243	0.041	0.283	0.574	0.195	0.522	0.795	0.345
slI1169		hypothetical protein	-0.093	error	0.182	error	-0.345	0.399	0.54	-0.613	-0.337	error	-0.584	-0.869	0.25
slI1170		unknown protein	0.499	0.105	0.237	-0.755	0.545	0.382	error	-0.647	-0.372	error	-0.584	-0.344	0.741
slI1172	thrC	threonine synthase thrC	-0.681	-0.578	-0.34	0.073	-0.309	-0.38	-0.36	-0.2	0.226	error	0.396	-0.019	0.107
slI1173		hypothetical protein	0.35	0.54	0.582	0.099	-0.107	0.492	0.8	0.397	0.284	0.437	-0.09	0.344	0.073
slI1174		unknown protein	-0.309	-0.077	0.088	0.846	-0.203	-0.155	-0.498	-0.192	-0.046	0.348	0.101	-0.158	-0.618
slI1178		probable carbamoyl transfe	-0.039	0.509	0.116	0.427	-0.121	-0.472	-0.277	0.167	0.274	-0.321	-0.198	0.144	-0.757
slI1180		toxin secretion ABC transp	-0.418	-0.575	-0.181	0.789	0.069	0.063	0.121	-0.141	0.057	0.223	0.377	0.411	-0.352
slI1181		similar to hemolysin secreti	-0.591	-0.461	-0.304	error	-0.366	-0.025	-0.505	-0.233	-0.06	0.837	0.385	-0.259	-0.837
slI1182		Rieske iron-sulfur protein w	-0.238	-0.196	-0.598	-0.317	0.196	-0.105	0.641	-0.226	-0.344	-0.482	0.309	-0.172	-0.292
slI1184	ho1	heme oxygenase ho1	error	error	error	error	error	error	error	-0.774	-1.857	-2.164	-2.141	-1.735	-1.724
slI1185	hemF	coproporphyrinogen III oxid	-0.346	0.374	-0.395	-0.287	-0.674	-0.47	-0.55	-0.115	-0.28	-1.04	-0.618	-0.638	-0.219
slI1186		hypothetical protein	error	error	error	error	error	error	error	0.31	0.1	error	-0.191	-0.143	0.126
slI1187		polipoprotein diacylglycer	0.07	-0.314	-1.35	-0.753	-0.892	-1.025	-0.876	-0.212	-0.612	-0.564	-0.364	-0.537	0.718
slI1188		hypothetical protein	0.341	error	-0.099	-0.135	0.002	0.231	0.425	0.231	0.14	0.208	-0.069	-0.118	2.089
slI1189	glcE	glycolate oxidase subunit G	-0.184	0.099	-0.017	0.266	0.194	0.335	0.793	-0.125	0.095	-0.103	0.288	0.264	-0.366
slI1191		hypothetical protein	error	0.465	0.684	0.89	error	0.143	0.166	0.085	0.791	0.626	0.335	0.3	1.131
slI1192		hypothetical protein	0.213	0.146	0.018	-0.415	0.01	0.325	-0.026	-0.262	-0.05	-0.515	-0.041	-0.297	0.827
slI1193		hypothetical protein	-0.18	0.109	0.922	0.38	0.295	0.198	0.279	error	error	error	error	error	error
slI1194	psbU	photosystem II 12 kDa extri	-0.406	-0.372	-1.124	error	-0.773	-0.652	-0.371	-0.264	-0.977	-1.066	-0.586	-0.947	1.039
slI1196		phosphofruktokinase	-0.286	0.129	-0.656	-0.559	-0.794	0.325	0.044	-0.241	-0.561	-0.191	-0.818	-0.507	-1.276
slI1198		tRNA (guanine-N1)-methyl	-0.222	error	-0.544	-0.811	-1.024	-0.526	0.028	-0.185	-0.403	-1.203	-1.373	-0.551	-0.13
slI1200		hypothetical protein	error	error	-0.123	error	-0.511	0.077	error	-0.924	-0.314	-0.355	-1.027	-0.609	1.005
slI1201		hypothetical protein	-0.121	0.264	-0.217	error	-0.107	-0.164	-0.173	error	error	error	error	error	error
slI1202		iron(III) dicitrate-binding pr	0.07	error	-0.847	-1.087	error	0.526	0.377	0.07	0.319	1.188	0.073	-0.13	error
slI1203		hypothetical protein	-0.295	-0.201	-0.396	-0.237	-0.352	0.1	0.51	-0.308	-0.055	0.32	-0.762	0.891	-1.496
slI1204		similar to macrolide efflux p	-0.204	-0.249	-0.104	0.48	-0.659	-0.61	-0.761	-0.65	-0.105	-0.099	-0.296	-0.296	-0.207
slI1205		transcriptional regulator	-0.538	-0.815	-1.427	-0.899	-1.735	-0.798	-0.809	-0.261	-0.699	0.323	-0.861	-0.359	-1.06
slI1206		probable ferric aerobactin r	error	error	error	error	error	0.173	error	-0.139	-0.179	0.023	-0.653	-0.441	-0.698
slI1209	lig	DNA ligase lig	error	error	-0.547	error	-0.599	-0.227	-0.153	-0.247	-0.304	0.032	-0.903	-0.088	0.624
slI1212		GDP-mannose 4,6-dehydra	-0.243	-0.612	-0.676	0.15	-0.346	-0.193	0.118	error	error	error	error	error	error
slI1213		GDP-fucose synthetase	-0.188	-0.104	-0.106	-0.736	-0.018	0.109	-0.103	-0.454	-0.315	-0.34	-0.333	-0.782	0.555
slI1214	ycf59	hypothetical protein YCF59	-0.833	-1.238	-1.939	-0.34	-0.992	-1.101	-0.892	error	error	error	error	error	error
slI1217		unknown protein	-0.138	0.615	0.231	0.172	0.374	0.282	0.484	0.067	0.963	0.645	0.43	0.791	0.331
slI1218	ycf39	hypothetical protein YCF39	-0.129	-0.251	-0.213	-0.512	-0.324	-0.159	-0.354	error	error	error	error	error	error
slI1219		hypothetical protein	0.161	0.2	0.329	0.229	0.164	0.017	2.044	-0.467	0.009	0.43	-0.201	-0.064	0.283
slI1220		NADH dehydrogenase I cha	0.527	1.144	1.33	error	0.662	0.011	0.852	1.022	1.251	0.945	0.799	0.532	-0.918
slI1221	hoxF	NADH dehydrogenase I cha	0.037	0.555	0.583	0.068	0.449	0.295	0.67	0.175	0.502	0.925	0.073	0.521	0.348
slI1222		hypothetical protein	error	error	error	error	error	error	error	0.338	error	error	0.374	0.242	0.058
slI1223	hoxU	NAD-reducing hydrogenase	error	error	error	-1.832	0.451	0.413	error	-0.238	-0.104	-0.748	-0.609	-0.327	0.026
slI1224	hoxY	NAD-reducing hydrogenase	error	error	error	-1.858	error	0.623	error	0.046	0.483	error	0.053	0.042	1.398
slI1225		unknown protein	error	error	error	-1.598	error	0.47	error	-0.397	0.202	error	0.353	-0.482	1.175
slI1226	hoxH	NAD-reducing hydrogenase	0.222	1.01	0.909	0.082	0.005	0.211	error	error	error	error	error	error	error
slI1228		two-component hybrid sens	0.197	0.167	0.046	0.052	-0.378	0.157	0.023	0.063	0.136	0.321	-0.206	0.12	-0.737
slI1229		two-component hybrid sens	-0.419	-0.454	-1.208	-0.544	-1.19	-0.82	-0.469	-0.238	-0.521	-0.821	-1.004	-0.638	-1.42
slI1231		mannosyltransferase	error	error	error	error	error	error	error	0.043	0.165	-0.462	-0.209	-0.334	0.465
slI1232		hypothetical protein	error	error	0.726	-0.881	error	0.515	error	0.391	0.813	error	0.595	-0.206	2.299
slI1233		hypothetical protein	error	error	error	error	error	error	error	-0.762	-0.283	-0.606	-0.568	-0.709	0.377
slI1234		adenosylhomocysteinase	error	error	error	error	error	error	error	0.019	-0.282	0.088	1.132	-0.518	0.667
slI1236		unknown protein	1.108	error	2.04	0.404	3.424	2.505	3.592	1.12	2.418	2.013	2.853	1.91	4.418
slI1237	hemG	protoporphyrinogen IX oxid	1.108	1.293	0.879	error	0.848	0.448	0.91	0.697	1.047	0.157	0.798	0.608	1.249
slI1239		unknown protein	0.296	0.624	1.407	0.127	0.452	0.217	error	0.621	1.406	1.186	0.514	1.08	1.237
slI1240		unknown protein	error	error	error	error	error	0.519	error	0.124	0.6	-0.829	0.798	-0.399	0.588
slI1241		unknown protein	error	error	-0.559	-0.834	-0.025	error	error	-0.198	0.467	-	0.085	-0.35	0.169
slI1242		hypothetical protein	-0.504	error	-0.379	-0.103	-0.154	0.146	-0.111	-0.104	-0.191	-0.344	0.19	-0.125	-0.005
slI1244	rpl9	50S ribosomal protein L9rp	-0.013	0.175	0.971	2.044	-0.253	-0.66	-0.774	-0.059	0.394	0.804	0.003	0.467	-0.422
slI1245	cytM	cytochrome CytMcytM	-0.519	-0.286	-1.295	-0.86	-1.67	-1.456	-1.374	0.278	-0.547	-1.425	-1.234	-0.517	-0.698
slI1247		hypothetical protein	error	error	error	error	error	error	error	-0.589	-0.641	-0.405	-0.472	-0.69	0.133
slI1249	panC	pantothenate synthetase/cy	error	-0.106	-0.121	error	-0.48	-0.335	-0.18	0.157	0.092	-0.084	-0.543	-0.297	-0.145
slI1250		hypothetical protein	0.004	0.312	0.405	0.265	-0.116	0.233	0.296	0.128	1.049	0.583	0.242	0.707	-0.627
slI1251		hypothetical protein	1.557	error	error	-1.268	error	0.658	error	-0.02	0	-0.442	-0.068	-0.178	0.921
slI1252		hypothetical protein	error	error	error	error	error	error	error	-0.381	0.083	-0.226	-0.188	-0.255	0.335
slI1253		similar to polyA polymerase	error	0.112	0.095	-0.155	0.034	-0.011	error	-0.06	0.155	0.099	0.177	-0.035	0.187
slI1254		hypothetical protein	-0.561	-0.763	-0.997	error	-0.573	-0.293	-0.379	-0.218	0.032	-0.43	-0.037	0.098	-0.331
slI1255		putative transposase [ISY2	error	error	-1.139	error	-0.789	-0.479	-0.689	-0.979	-0.227	error	-0.659	-0.519	0.386
slI1256		putative transposase [ISY1	0.32	-0.261	-0.475	-0.233	-0.444	-0.259	-0.369	-0.924	-0.143	0.902	-0.478	-0.25	0.954

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl1257		putative transposase [ISY10	-0.575	-0.675	-0.631	0.066	-0.537	-0.495	-0.649	-1.201	-0.427	-0.275	-0.734	-0.604	-0.21
sl1258		dCTP deaminase	-0.299	0.854	-0.091	-0.438	-0.065	0.024	error	0.108	0.377	0.377	0.432	0.42	0.61
sl1260	rps2	30S ribosomal protein S2pr	0.14	0.082	0.528	1.603	0.038	-0.49	-0.194	0.478	0.713	0.855	0.805	0.628	0.656
sl1261	tsf	elongation factor TStsf	0.358	-0.067	-0.474	0.628	-0.154	-0.582	-0.094	0.02	-0.063	0.091	0.154	-0.301	0.361
sl1262		hypothetical protein	-0.328	-0.354	-1.155	-1.016	-0.822	-0.165	0.038	-0.006	-0.082	error	-0.434	-0.455	-0.198
sl1263		cation efflux system protein	0.87	0.063	-0.399	-0.568	-0.674	0.25	0.05	error	0.458	error	-0.007	error	error
sl1265		unknown protein	-0.209	error	-0.012	-0.772	-0.41	0.477	-0.287	-0.164	-0.003	-0.274	-0.408	-0.06	0.427
sl1267		unknown protein	-0.527	-0.645	-0.471	0.548	0.622	0.119	0.182	-0.07	-0.245	0.435	1.211	-0.198	1.392
sl1268		unknown protein	0.638	error	0.635	-0.612	1.161	0.549	error	0.132	0.573	0.415	0.885	0.569	1.696
sl1270	BgtB	Periplasmic substrate-bindin	-0.475	-0.124	-1.026	-0.762	-1.003	-0.155	-0.386	-0.003	-0.228	-0.419	-0.82	-0.386	-0.927
sl1271		probable porin; major outer	-0.378	0.434	-0.05	error	-0.282	0.469	-0.416	error	error	error	error	error	error
sl1272		unknown protein	0.499	-0.233	0	-0.547	0.135	0.125	0.619	-0.262	-0.151	-0.676	-0.298	-0.759	0.837
sl1273		unknown protein	-0.021	-0.417	-0.271	-0.356	-0.168	0.278	1.414	-0.666	-0.356	-0.514	-0.166	error	1.252
sl1274		hypothetical protein	-0.093	-0.119	0.464	0.972	0.763	0.476	0.199	error	error	error	error	error	error
sl1275		pyruvate kinase	-0.677	error	error	error	-1.365	-1.049	error	-0.474	-0.641	-0.465	error	-0.771	-1.198
sl1276		ATP-binding protein of ABC	-0.174	-0.127	-0.061	1.063	-0.516	-0.512	-0.521	0.291	0.091	0.076	0.121	0.354	-0.689
sl1277	recF	RecF proteinrecF	0.288	-0.016	-0.12	-0.354	-0.731	0.279	-0.213	-0.266	-0.014	-0.348	-0.284	-0.416	-0.513
sl1280		hypothetical protein	-0.301	-0.296	-0.14	0.724	-0.129	0.212	0.153	error	error	error	error	error	error
sl1281	ycf9	hypothetical protein YCF9y	-0.406	-0.349	-0.249	-0.294	-0.508	-0.453	-0.372	0.189	0.282	-0.843	-0.024	-0.039	-0.94
sl1282	ribH	riboflavin synthase beta sub	0.508	0.654	0.458	0.591	0.314	0.1	0.423	error	error	error	error	error	error
sl1283		similar to stage II sporulatio	-0.55	-0.684	-0.507	0.255	0.456	0.372	0.751	-0.036	-0.179	0.528	0.233	-0.2	-0.001
sl1284		esterase	0.375	0.121	0.059	-0.206	0.332	0.104	-	-0.054	-0.327	-0.214	-0.04	-0.199	0.554
sl1285		hypothetical protein	0.43	0.422	0.446	0.368	0.642	0.526	0.907	0.097	0.384	0.579	0.212	0.174	0.023
sl1286		transcriptional regulator	-0.67	error	-1.327	-0.951	-1.088	-0.238	-0.778	-1.156	-1.384	-0.733	-1.802	-1.766	-1.895
sl1289		hypothetical protein	-0.137	0.617	0.395	-0.207	0.353	0.642	1.275	error	error	error	error	error	error
sl1290		probable ribonuclease II	-0.039	-0.501	-0.259	0.288	0.175	0.289	0.678	error	error	error	error	error	error
sl1291		two-component response re	-0.346	-0.387	-0.74	-0.878	-1.04	-0.425	-0.661	-0.247	-0.444	-0.46	-0.543	-0.432	-0.291
sl1292		two-component response re	-0.536	-0.971	-1.514	error	-1.284	-0.718	-0.547	-0.304	-0.472	-1.513	-0.983	-0.587	-0.965
sl1293		unknown protein	error	error	error	error	error	error	error	-0.294	0.209	-0.25	-0.116	-0.143	0.712
sl1294		methyl-accepting chemotax	0.257	-0.009	-0.002	-0.443	-0.457	-0.131	0.32	-0.467	-0.53	-0.52	-0.791	-0.261	-0.03
sl1296		two-component hybrid sens	-0.061	0.121	0.165	-0.716	-0.151	0.101	0.173	-0.243	-0.012	0.147	-0.465	0.33	-0.885
sl1297		probable dioxygenase, Ries	-0.604	-0.634	-0.534	-0.542	-0.559	-0.155	error	-0.378	0.095	error	-0.543	0.21	-1.183
sl1298		putative carboxymethylenet	-0.384	-0.851	-0.537	error	-0.169	-0.061	-0.188	error	error	error	error	error	error
sl1299		acetate kinase	error	error	error	error	error	error	error	0.306	0.559	-0.113	0.165	0.306	0.027
sl1300		putative methyltransferase	error	error	error	error	error	error	error	0.079	0.901	1.802	0.341	0.637	0.303
sl1304		unknown protein	error	error	error	error	error	error	error	0.012	0.127	-0.633	-0.938	-0.261	-0.566
sl1305		probable hydrolase	error	-0.344	-0.819	-0.867	-1.101	-0.492	-0.635	-0.229	-0.042	-0.822	-1.255	-0.219	-1.173
sl1306		unknown protein	-0.296	-0.197	-0.269	0.017	-1.033	-0.779	-1.114	0.167	-0.367	-0.514	-1.047	-0.247	-0.576
sl1307		hypothetical protein	0.172	error	error	-2.24	error	0.111	error	0.283	0.016	-0.298	-1.427	-0.453	-0.537
sl1308		probable oxidoreductase	-0.346	-0.502	-0.329	0.712	-0.531	-0.32	-0.288	-1.358	-0.381	0.375	-0.747	-0.384	-1.417
sl1314		hypothetical protein	0.075	0.339	0.244	error	0.236	0.568	0.677	error	error	0.197	error	error	error
sl1315		unknown protein	0.218	error	0.289	0.244	0.195	0.44	0.235	-0.078	-0.178	-0.003	-0.408	-0.69	0.784
sl1316	petC	cytochrome b6-f complex ir	-0.386	-0.341	-0.375	0.479	-0.249	-0.248	-0.094	-0.086	-0.185	-0.082	0.05	0.098	-0.964
sl1317	petA	apocytochrome f, compone	-0.707	-0.444	-0.924	-0.261	-1.3	-0.514	-0.798	0.196	-0.061	-0.973	-0.055	0.026	-1.017
sl1318		error	error	error	error	error	error	error	error	0.148	0.355	error	0.007	0.041	-0.051
sl1319		hypothetical protein	-0.035	0.049	-0.236	0.267	0.046	0.167	-0.078	-0.23	-0.056	0.624	-0.163	0.295	-0.373
sl1321	atp1	ATP synthase protein latp1	-0.886	-1.311	-0.727	0.377	-1.107	-1.004	-0.727	-0.232	0.048	-0.905	-0.296	-0.152	-0.036
sl1322	atpI	ATP synthase subunit aatpI	-1.328	-1.797	-1.185	-0.077	-1.358	-0.817	-0.771	-0.45	-0.403	-0.483	-0.39	-0.245	-0.616
sl1323	atpG	ATP synthase subunit b'atp	-0.556	-0.686	-0.842	0.347	-0.737	-0.614	-0.725	0.278	-0.103	-0.924	-0.365	-0.021	-0.211
sl1324	atpF	ATP synthase subunit batp	-0.397	-0.746	-0.953	0.225	-1.014	-0.962	-0.563	0.056	0.256	-0.204	-0.152	0.105	0.348
sl1325	atpD	ATP synthase d subunitatp	-0.341	-0.849	-1.191	-0.011	-1.193	-0.879	-0.882	0.273	-0.403	-1.221	-0.599	-0.239	0.055
sl1326	atpA	ATP synthase a subunitatp	-0.52	-0.612	-1.153	0.448	-1.054	-0.913	-0.937	0.194	-0.444	-1.127	-0.221	-0.548	-0.486
sl1327	atpC	ATP synthase g subunitatp	-0.515	-0.601	-0.73	-0.02	-0.712	-0.661	-0.68	0.136	-0.391	-0.033	-0.298	-0.417	-0.364
sl1329		inositol monophosphate fan	-0.399	-0.338	0.296	0.185	0.216	-0.117	0.057	-0.088	0.378	0.539	0.515	0.535	-0.418
sl1330		two-component system resp	0.854	1.238	1.64	1.08	1.634	-0.632	1.016	0.515	1.423	error	0.983	1.408	1.349
sl1333		unknown protein	-0.436	-0.337	-0.192	-0.412	error	-0.078	-0.395	-0.255	0.268	error	-0.412	-0.048	0.228
sl1334		two-component sensor histi	-0.321	0.331	-0.036	0.414	0.2	-0.064	-0.132	-0.061	-0.078	0.027	-0.31	-0.095	-0.826
sl1336		hypothetical protein	-0.207	0.157	0.216	0.516	-0.081	-0.298	-0.247	-0.051	0.375	0.802	0.019	0.148	0.505
sl1338		unknown protein	-0.262	-0.151	-0.226	0.571	-0.397	-1.034	-0.967	0.256	0.224	0.177	0.273	0.207	-1.005
sl1340		hypothetical protein	error	error	error	error	error	0.472	error	-0.274	0.149	-0.701	-0.343	-0.114	1.324
sl1341		bacterioferritin	-0.472	-0.328	-0.4	0.521	-0.273	-0.203	0.056	0.098	0.001	0.748	0.284	0.005	-0.136
sl1342	gap2	NAD(P)-dependent glycera	-0.796	-1.002	-0.822	0.031	-0.83	-0.9	-0.815	-0.523	-0.844	error	-0.417	-0.654	-0.078
sl1343		aminopeptidase	0.008	0.029	0.009	-0.209	0.028	0.268	0.225	-0.143	0.144	-0.397	-0.463	-0.031	-0.743
sl1344		unknown protein	-0.231	error	-0.478	-0.406	-0.226	0.146	0.027	-0.504	-0.394	-0.374	-0.229	-0.415	1.397
sl1348		hypothetical protein	2.729	1.29	1.233	0.548	0.9	0.65	error	0.905	0.858	error	0.266	0.621	0.782
sl1349		phosphoglycolate phosphat	error	error	error	error	error	error	error	1.981	2.831	1.536	1.496	2.788	0.034
sl1350		hypothetical protein	0.403	0.476	-0.573	-0.432	-0.115	-0.076	0.252	-0.129	-0.268	0.125	-0.184	-0.336	-1.019
sl1352		unknown protein	-0.324	-0.255	-0.156	0.526	-0.166	-0.014	-0.232	-0.218	-0.33	-0.197	-0.464	-0.443	-1.22
sl1353		two-component sensor histi	-0.609	-0.589	-0.797	-0.771	-1.509	-0.377	-0.214	-0.443	-0.839	-0.781	-0.76	-0.883	-1.1
sl1354	recJ	single-strand-DNA-specific	0.266	0.192	0.526	0.118	0.01	0.218	-0.125	0.111	0.31	0.044	0.034	0.494	-0.036
sl1355		hypothetical protein	0.789	error	error	-0.927	error	0.435	error	0.129	0.35	0.314	0.206	-0.126	1.042
sl1356		glycogen phosphorylase	0.015	0.097	1.224	-0.286	0.023	0.273	0.053	-0.29	-0.006	-0.655	-0.541	-0.116	-0.328
sl1358		hypothetical protein	-0.132	-0.332	-0.783	error	-1.06	-0.278	error	-0.653	-0.855	-1.213	-1.99	-1.145	-0.464
sl1359		unknown protein	0.209	0.143	0.398	-0.462	-0.623	0.251	0.791	error	error	error	error	error	error
sl1360		DNA polymerase III subunit	0.313	0.421	0.183	0.128	0.296	0.351	0.335	0.299	0.305	0.209	0.101	0.354	-0.42

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl11362	ileS	isoleucyl-tRNA synthetase	0.09	-0.068	0.083	-0.307	error	0.457	0.029	-0.134	-0.234	0.032	-0.406	-0.216	0.578
sl11363	ilvC	ketol-acid reductoisomerase	-0.164	-0.193	0.052	0.705	-0.279	-0.775	-0.237	0.127	0.671	1.123	0.325	0.825	1.098
sl11365		unknown protein	-0.363	error	-0.067	-0.039	0.049	-0.245	-0.364	-0.454	-0.305	-0.149	-0.047	-0.597	0.482
sl11366		putative SNF2 helicase	0.14	error	-0.212	-0.721	-1.209	0.164	error	-0.522	-0.24	-0.359	-0.988	-0.273	0.531
sl11367		hypothetical protein	error	error	error	error	error	error	error	-0.123	-0.228	0.443	-0.17	-0.02	-0.088
sl11369		putative peptidase	error	1.014	error	-0.764	0.385	-0.06	error	0.195	0.436	0.21	0.635	0.392	0.959
sl11370	rfbM	mannose-1-phosphate guar	0.33	0.063	error	-0.594	-0.181	0.001	-0.06	0.215	0.364	-0.204	-0.039	0.172	0.893
sl11371	syncr1	cAMP receptor proteinsyncr	-0.056	-0.297	-0.236	-1.073	-0.99	-0.457	-0.47	0.028	-0.152	-0.479	-0.364	0.019	-0.443
sl11372		hypothetical protein	0.596	0.363	0.55	error	error	error	error	0.02	1.056	0.788	0.335	0.721	0.891
sl11373		unknown protein	-0.194	0.004	0.187	0.168	-0.221	-0.206	0.198	-0.071	0.255	-0.065	0.046	-0.243	0.442
sl11374		probable sugar transporter	-0.02	-0.011	0.123	0.353	0.569	0.257	0.544	0.168	0.36	0.299	0.772	0.305	0.638
sl11376		hypothetical protein	-0.341	0.273	-0.045	error	-0.125	-0.367	-0.177	0.235	0.647	0.947	0.304	0.705	1.452
sl11377		probable glycosyltransferas	0.2	0.163	0.085	error	0.539	0.33	0.507	-0.084	0.614	0.57	0.792	0.275	1.073
sl11378		hypothetical protein	0.315	0.2	0.044	0.429	0.228	0.176	0.366	0.147	0.146	0.059	0.404	-0.144	0.449
sl11380		hypothetical protein	-0.027	-0.024	-0.473	0.327	0.425	0.185	0.493	error	error	error	error	error	error
sl11381		hypothetical protein	-0.214	-0.119	-0.133	0.422	-0.034	-0.122	0.013	-0.168	-0.081	0.088	-0.064	0.095	-0.728
sl11382		ferredoxin, petF-like protein	-0.312	-0.37	-0.403	0.348	-0.674	-0.798	-0.715	0.182	0.425	-0.362	-0.175	0.391	-0.37
sl11383		probable myo-inositol-1(or	1.165	1.066	0.942	0.256	0.882	0.522	2.35	0.128	0.864	1.064	0.763	0.834	error
sl11384		similar to DnaJ protein	-0.838	-0.827	-0.765	0.583	-0.991	-0.536	-1.025	-0.676	-0.303	-0.554	-0.402	-0.529	-1.573
sl11386		hypothetical protein	0.459	0.276	0.328	error	0.179	-0.002	-0.116	0.355	0.747	0.752	0.623	0.629	0.788
sl11387	pppA	serine/threonine protein ph	-0.025	-0.055	0.062	-0.181	0.152	-0.504	-0.344	-0.041	-0.091	-0.21	0.217	0.043	0.921
sl11388		hypothetical protein	1.331	1.615	1.164	0.064	0.203	0.11	error	0.91	1.032	error	-0.134	0.814	0.914
sl11389		hypothetical protein	0.869	0.821	0.427	-0.262	0.543	-0.13	0.607	0.394	0.625	0.551	0.31	0.513	0.744
sl11390		hypothetical protein	-0.397	-0.132	-0.016	0.882	-0.173	-0.495	-0.372	-0.095	0.442	-0.088	0.181	0.535	0.861
sl11392		transcriptional regulator	error	error	error	error	error	error	error	0.224	0.973	error	0.428	0.583	1.297
sl11393	glgA	glycogen (starch) synthase	-0.505	-0.789	-0.776	-0.125	-0.24	-0.098	-0.218	-0.287	-0.078	-0.112	-0.005	0.038	-0.419
sl11394		peptide methionine sulfoxid	-0.253	-0.461	0.402	-0.102	1.268	0.737	1.4	-0.201	0.433	1.184	1.03	0.144	1.501
sl11395	rfbD	dTDP-6-deoxy-L-mannose-	-0.09	-0.079	0.637	0.384	0.284	-0.071	-0.04	0.234	0.62	1.252	0.905	0.724	0.526
sl11396		unknown protein	error	error	0.897	error	error	0.449	0.067	0.07	0.3	0.868	0.455	0.174	-0.115
sl11397		putative transposase [ISY10	-0.61	-0.661	-0.387	0.356	-0.508	-0.627	-0.605	-1.042	-0.291	0.258	-0.705	-0.221	-1.143
sl11398	psbW, psb	photosystem II reaction cen	-0.391	-0.291	-0.549	-0.5	-0.641	-0.345	0.185	-0.309	-0.176	0.518	-0.372	-0.046	-0.084
sl11399		hypothetical protein	-0.41	-0.219	-0.259	0.264	-0.906	-0.209	-0.523	-0.194	-0.165	-0.615	-0.408	-0.472	-0.958
sl11400		hypothetical protein	-0.331	-0.314	-0.082	-0.621	error	-0.082	-0.728	0.067	0.214	error	-0.169	-0.697	-0.148
sl11401		unknown protein	0.439	0.234	-0.156	-0.438	-0.189	-0.254	error	-0.151	0.114	0.271	0.214	-0.248	1.73
sl11404		biopolymer transport ExbB	error	error	error	error	error	error	error	0.481	0.823	0.929	0.547	0.727	0.305
sl11405		biopolymer transport ExbD	-0.038	-0.002	0.229	-0.964	0.071	0.403	0.95	-0.223	-0.021	-0.904	-0.74	-0.678	-0.134
sl11406		ferrichrome-iron receptor	-0.149	0.426	0.505	0.076	0.497	0.42	1.29	error	error	error	error	error	error
sl11407		probable methyltransferase	error	error	-0.643	-0.881	error	0.58	error	-0.431	-1.288	error	-1.326	-1.409	-1.389
sl11408		transcriptional regulator	0.26	1.186	0.828	-1.306	-0.11	0.748	1.263	-0.876	-0.133	-0.757	-1.027	-0.631	0.533
sl11409		ferrichrome-iron receptor	-0.559	-0.507	-1.345	-1.059	-2.183	-1.146	-1.286	-0.268	-0.238	error	-0.636	-0.272	-1.326
sl11411		hypothetical protein	error	-0.091	-0.387	-0.777	-0.5	-0.059	-0.128	-0.626	-0.27	0.141	-0.52	-0.407	-0.882
sl11414		hypothetical protein	error	-0.617	-0.131	0.648	-0.129	-0.336	-0.097	-0.348	0.043	0.017	0.062	-0.037	0.545
sl11415		hypothetical protein	0.55	-0.213	0.292	-0.895	-0.276	0.106	error	-0.094	0.073	-0.062	-0.206	-0.074	error
sl11418	psbP	similar to photosystem II ox	error	error	error	error	error	error	error	-0.67	-0.444	-0.019	-0.462	-0.617	0.019
sl11423	ntcA, ycf2	global nitrogen regulatorntc	0.208	0.24	0.778	0.779	0.147	0.152	0.215	0.382	0.885	1.583	0.769	0.93	1.171
sl11424		hypothetical protein	0.689	0.61	0.727	0.496	0.35	0.149	0.336	error	error	error	error	error	error
sl11425	proS	proline-tRNA ligaseproS	error	error	error	error	error	error	error	0.397	0.461	0.212	0.122	0.352	0.504
sl11426		unknown protein	0.72	0.721	0.432	1.53	1.108	0.833	0.509	error	error	error	0.74	error	error
sl11427		protease	0.316	0.312	0.227	0.748	0.318	0.288	0.048	0.176	0.441	-0.097	0.735	0.345	1.004
sl11428		probable sodium-dependent	error	error	0.223	error	error	-0.382	error	-0.254	-0.086	-0.016	-0.236	-0.52	0.278
sl11429		unknown protein	-0.253	-0.09	-0.021	0.353	-0.472	-0.058	-0.348	error	error	error	error	error	error
sl11430		adenine phosphoribosyltran	-0.045	0.097	-0.317	-0.245	0.272	0.179	1.198	-0.007	0.389	0.164	0.006	0.073	-0.875
sl11432	hypB	hydrogenase isoenzymes fo	0.018	-0.348	-0.955	-0.687	-0.173	-0.191	-0.787	-0.62	0.016	0.562	-0.358	-0.623	0.047
sl11433		hypothetical protein	-0.261	-0.19	-0.218	0.376	-0.311	-0.226	-0.458	-0.188	-0.271	0.195	-0.29	-0.644	-1.316
sl11434		penicillin-binding protein	-0.052	-0.406	-0.005	0.943	0.341	0.24	0.104	-0.053	0.164	0.535	0.764	0.097	-0.114
sl11435		glutamyl-tRNA(Gln) amidot	-0.123	-0.238	-0.231	0.284	-0.489	-0.451	-0.165	-0.084	0.18	0.444	0.089	0.078	-0.878
sl11436		putative transposase [ISY10	-0.403	-1.132	-0.19	0.232	-0.741	-0.483	-0.697	-0.193	0.359	0.213	-0.389	-0.177	-0.763
sl11437		putative transposase [ISY10	error	error	-0.621	error	-0.494	-0.285	error	-1.204	-0.467	-0.128	-0.912	-0.886	-0.155
sl11439		unknown protein	error	error	error	-0.883	error	0.687	error	-0.1	0.233	0.358	0.397	-0.043	1.83
sl11440	pdxH	pyridoxamine 5'-phosphate	0.115	0.236	0.042	-0.841	-0.415	-0.283	0.217	0.115	0.368	-0.734	-0.365	-0.011	0.726
sl11441	desB	delta 15 desaturasesdesB	0.216	0.113	-0.195	-1.497	-0.009	error	0.27	-0.097	0.06	0.078	-0.099	-0.28	1.096
sl11442		hypothetical protein	0.503	0.292	0.068	error	-0.5	-0.199	-0.003	-0.176	0.639	0.017	0.197	0.54	1.291
sl11443	pyrG	CTP synthetasepyrG	-0.186	-0.156	-0.032	0.46	0.138	0.025	-0.116	-0.142	0.01	0.308	0.172	-0.039	0.839
sl11444		3-isopropylmalate dehydrat	-0.478	-0.766	-1.136	-0.035	error	0.239	0.293	-0.035	-0.255	0.167	0.276	-0.518	-0.543
sl11446		hypothetical protein	0.419	-0.109	-0.797	-0.462	0.091	0.523	0.6	0.441	0.15	0.664	0.187	0.279	-0.62
sl11447		hypothetical protein	-0.119	-0.278	-0.172	-0.305	error	-0.26	-0.515	-0.09	-0.13	-0.55	-0.41	-0.472	0.157
sl11450	nrtA	nitrate/nitrite transport syste	error	error	error	error	error	error	error	0.675	0.848	0.376	0.837	0.782	0.927
sl11451	nrtB	nitrate/nitrite transport syste	-0.54	-0.514	-0.867	0.341	-0.287	0.058	0.281	-0.084	-0.219	-0.623	-0.051	-0.096	-0.627
sl11452	nrtC	nitrate/nitrite transport syste	-0.031	-0.305	-0.309	0.435	0.127	0.41	0.053	-0.203	0.098	-0.133	-0.175	0.084	1.054
sl11453	nrtD	nitrate/nitrite transport syste	error	-0.101	-0.705	0.336	0.135	0.539	0.825	0.247	0.032	0.062	-0.007	0.042	0.078
sl11454	narB	nitrate reductasenarB	0.043	-0.377	-0.552	-0.112	-0.347	0.041	-0.207	-0.082	-0.318	-0.456	0.059	-0.404	0.492
sl11455		hypothetical protein	0.662	0.557	0.205	0.178	0.355	0.216	-0.015	0.105	0.988	0.416	-0.038	0.23	1.347
sl11456		unknown protein	-0.742	-0.925	-1.308	0.232	-0.395	-0.743	-0.641	-0.374	-0.876	-1.197	-0.21	-1.002	0.495
sl11457		probable glycosyltransferas	0.236	-0.302	0.117	-0.1	-0.172	-0.077	0.669	0.038	0.095	-0.074	-0.138	-0.187	0.588
sl11459		stationary-phase survival pr	1.079	error	0.552	-0.229	1.007	0.641	error	-0.394	0.137	error	0.509	-0.205	1.578



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sil1461		hypothetical protein	0.502	0.266	0.556	error	0.656	-0.08	-0.164	-0.169	0.415	0.281	0.518	0.102	1.063
sil1462	hypE	hydrogenase expression/fo	-0.1	-0.218	-0.129	0.122	0.104	-0.07	-0.085	-0.264	-0.349	error	0.048	-0.386	-1.318
sil1463	ftsH	cell division protein FtsHfts	-0.511	-0.718	-0.193	0.636	-0.022	-0.019	-0.304	-0.33	0.061	0.994	0.32	0.367	-0.722
sil1464		hypothetical protein	0.765	-0.117	0.531	0.546	0.282	-0.229	0.138	error	error	error	error	error	error
sil1466		probable glycosyltransferas	-0.103	0.154	0.513	error	-0.087	-0.117	-0.224	error	error	error	error	error	error
sil1468	crtR	beta-carotene hydroxylased	-0.425	-0.31	0.123	1.097	-0.055	0.021	-0.141	error	error	error	error	error	error
sil1469		hypothetical protein	-0.704	-0.351	0.061	0.354	-0.029	0.305	0.38	-0.32	-0.453	0.098	-0.374	-0.442	error
sil1470	leuC	3-isopropylmalate dehydrat	-0.92	-1.137	-1.215	-0.619	-0.907	-0.599	-0.734	-0.398	-0.115	0.308	-0.129	-0.436	-1.132
sil1471	cpcG2	phycobilisome rod-core link	-0.718	-0.816	-1.204	-1.331	-2.82	-1.314	-2.091	-0.276	-0.921	-1.919	-1.573	-0.892	-1.92
sil1472		unknown protein	-0.035	-0.529	error	-1.494	-1.818	-0.49	-0.637	-0.436	-0.232	-0.874	-0.444	-0.609	0.838
sil1473		hypothetical protein	-0.099	-0.257	-0.148	error	-0.153	0.183	-0.137	-0.217	-0.209	-0.255	-0.158	-0.272	-0.619
sil1474		putative transposase [ISY2]	-0.757	error	-1.263	error	-0.92	-0.438	-0.599	-1.737	-0.312	0.312	-0.805	-0.479	0.554
sil1475		two-component sensor histi	error	error	error	error	error	error	error	0.159	0.078	0.396	0.09	-0.406	-0.959
sil1476		unknown protein	0.735	0.086	0.545	-0.921	error	error	-0.158	-0.167	0.098	0.369	0.388	0.135	1.163
sil1477		hypothetical protein	0.216	0.545	0.635	0.114	0.139	0.059	0.283	0.23	1.316	-0.476	-0.024	0.932	0.492
sil1479		6-phosphogluconolactonas	0.258	-0.071	0.443	error	-0.2	-0.119	-0.061	-0.421	0.184	-0.423	-0.252	-0.182	1.12
sil1481		ABC-transporter membrane	1.801	error	1.016	error	1.194	0.448	1.306	0.261	1.095	1.071	1.406	0.92	2.024
sil1482		ABC transporter permease	0.529	0.723	0.394	error	0.179	0.461	0.804	-0.27	0.285	0.363	0.183	error	1.022
sil1483		hypothetical protein	0.708	2.308	4.885	4.331	5.467	3.405	3.586	1.014	4.965	5.176	5.453	4.41	5.005
sil1484	ndbC	type 2 NADH dehydrogenas	-0.296	0.271	1.332	0.922	0.78	0.571	0.941	-0.206	1.325	0.913	0.758	0.722	0.537
sil1485		hypothetical protein	0.247	0.43	1.121	0.896	0.555	0.799	1.318	0.535	1.629	1.975	1.12	1.63	0.435
sil1486		hypothetical protein	-0.08	0.603	0.906	0.429	0.089	0.161	0.014	0.228	0.818	0.672	0.101	0.654	-0.153
sil1488		hypothetical protein	0.391	0.134	0.376	error	-0.558	0.004	error	-0.365	-0.106	0.821	-0.415	-0.284	1.095
sil1489	cpmA	circadian phase modifier Cp	-0.433	error	-0.355	-0.373	-0.3	-0.145	-0.388	-0.041	-0.038	-0.005	-0.241	-0.151	0.893
sil1491		WD-repeat protein	0.947	1.203	1.193	1.923	0.779	-0.006	0.556	1.289	1.046	1.313	1.067	1.449	-0.416
sil1495		hypothetical protein	0.866	0.919	0.436	error	-0.373	0.18	error	0.171	0.384	0.367	-0.027	-0.073	0.925
sil1496		mannose-1-phosphate guar	0.498	0.377	-0.159	0.046	-0.147	0.099	0.024	0.236	-0.02	0.115	-0.03	-0.173	-0.739
sil1498		carbamoyl-phosphate synth	-0.2	0.358	-0.09	0.405	-0.166	-0.096	-0.14	error	error	error	error	error	error
sil1499	glsF	ferredoxin-dependent gluta	error	error	error	error	error	error	error	0.056	-0.082	-0.713	-0.144	-0.295	-0.245
sil1500		hypothetical protein	0.113	0.661	0.053	error	-0.132	0.65	error	-0.304	-0.258	-0.094	-0.09	-0.008	-1.292
sil1501	cobB	cobyrinic acid a,c-diamide s	error	error	error	error	error	error	error	-0.152	-0.149	0.063	-0.25	-0.284	0.462
sil1502	gltB	NADH-dependent glutamat	-0.503	-0.262	-0.566	-0.187	-0.727	-0.323	-0.61	-0.221	-0.39	-0.514	-0.692	-0.206	0.694
sil1503		unknown protein	-0.378	-0.378	-0.152	0.537	-0.233	0.512	0.055	error	error	error	-0.097	error	error
sil1504		hypothetical protein	0.856	error	0.184	-0.536	error	0.575	2.882	0.404	0.484	0.408	0.27	-0.007	-0.051
sil1505		hypothetical protein	-0.093	-0.08	0.149	-0.067	-0.198	-0.065	-0.355	0.607	0.818	0.303	0.176	0.398	0.142
sil1507		hypothetical protein	0.478	0.916	1.734	0.722	0.859	0.249	error	0.723	2.395	2.525	1.272	1.789	1.572
sil1508		UDP-3-O-acyl N-acetylgluc	-0.179	-0.471	-1.244	-0.617	-1.494	-1.078	-1.054	0.67	0.026	-0.508	-0.548	-0.319	-0.728
sil1509	ycf20	hypothetical protein YCF20	-0.238	-0.168	-0.25	0.45	-0.441	-0.168	-0.135	0.252	0.99	0.848	0.341	0.642	-0.015
sil1510		unknown protein	error	error	error	error	0.505	error	error	0.074	0.285	1.564	0.318	-0.292	1.35
sil1511		unknown protein	error	0.682	1.875	-0.35	0.117	0.292	error	0.334	0.519	0.452	0.454	0.22	0.708
sil1512		hypothetical protein	-0.063	0.007	0.414	0.33	0.528	0.214	0.678	-0.216	0.554	0.298	0.206	0.208	0.003
sil1513	ccsA, ycf5	c-type cytochrome synthesi	-0.095	-0.155	0.195	0.372	0.275	0.076	-0.042	0.141	0.406	-0.047	0.646	0.235	0.852
sil1514	hspA	16.6 kDa small heat shock	error	error	error	error	error	error	error	2.464	4.905	4.391	4.8	4.363	4.459
sil1515		unknown protein	error	0.289	-0.655	0.243	0.092	-0.28	-0.15	error	error	error	error	error	error
sil1516		hypothetical protein	-0.356	-0.385	-0.034	-0.168	-0.121	0.068	-0.18	error	error	error	error	error	error
sil1520	recN	DNA repair protein RecNrec	-0.612	-0.171	-0.238	-0.498	-0.367	-0.01	0.27	-0.04	0.173	0.403	-0.433	-0.213	-0.322
sil1521		flavoprotein	error	error	error	error	error	error	error	-0.254	0.101	0.287	-0.142	0.06	0.145
sil1522		CDP-diacylglycerol-glycer	0.06	0.339	-0.926	-0.814	-0.719	-0.017	-0.042	0.199	0.039	0.482	-0.441	-0.461	-1.091
sil1524		hypothetical protein	error	error	error	error	error	error	error	0.301	0.799	0.019	0.646	0.429	0.483
sil1525	prk	phosphoribulokinaseprk	-0.166	-0.425	-0.527	0.719	-0.296	-0.535	-0.247	0.193	0.021	-0.226	0.241	0.093	0.879
sil1526		hypothetical protein	-0.513	-0.44	-0.33	0.106	-0.052	0.201	0.084	-0.316	-0.465	-0.125	-0.176	-0.53	-0.291
sil1527		unknown protein	-0.333	0.198	-0.199	error	error	0.35	-0.207	-0.295	-0.058	0.491	-0.182	-0.025	error
sil1528		unknown protein	-0.548	-0.591	-0.276	0.365	-0.379	-0.111	-0.177	-0.554	-0.539	-0.517	-0.495	-0.604	-1.272
sil1530		unknown protein	-0.407	-0.356	-0.878	-0.813	-1.229	-0.507	error	-0.389	-0.661	-0.793	-0.929	-0.908	-0.701
sil1531		unknown protein	-0.16	-0.111	-0.085	0.739	-0.453	-0.035	-0.125	error	error	error	error	error	error
sil1532		hypothetical protein	0.335	0.039	-0.369	0.012	0.101	-0.203	error	0.036	0.375	-0.046	0.545	0.314	1.015
sil1533	pilT	twitching mobility proteinpil	-0.434	-0.82	-1.397	-0.672	-1.456	-1.139	-0.967	-0.341	-0.698	-0.536	-1.063	-0.98	0.228
sil1534		probable glycosyltransferas	0.15	-0.488	-0.916	-0.902	-1.848	-0.722	-0.837	error	error	error	-0.507	error	error
sil1535		putative sugar transferase	-0.979	-1.416	-1.233	0.316	-0.756	-0.519	-0.635	-0.525	-1.034	-1.037	-0.451	-1.348	-0.765
sil1536	moeb	molybdopterin biosynthesis	-0.327	error	-0.405	0.418	-0.32	-0.45	-0.824	-0.595	-0.681	-1	0.012	-0.959	-0.135
sil1537		similar to mutator MutT prot	0.274	0.231	0.525	-0.086	0.245	0.337	0.34	-0.026	0.682	0.515	0.107	0.356	0.903
sil1538		similar to beta-hexosaminid	error	error	error	error	error	error	error	-0.042	-0.313	-0.805	-0.413	-0.479	-0.562
sil1540		alpha, alpha-trehalose-phos	0.657	0.533	0.315	0.805	0.926	1.064	0.84	0.298	0.338	1.253	0.88	0.405	0.713
sil1541		hypothetical protein	-0.621	-0.502	-1.374	-0.254	-0.552	-0.954	-0.528	0.209	0.279	1.03	0.772	0.216	-0.198
sil1542		hypothetical protein	error	error	-0.069	0.316	0.393	0.156	error	-0.292	0.127	0.405	0.283	0.094	1.626
sil1543		hypothetical protein	0.373	0.138	-0.19	error	0.145	0.215	0.412	-0.101	0.1	-0.108	0.113	-0.409	1.244
sil1544		two-component response re	0.572	0.091	0.999	-0.132	0.183	-0.077	0.826	0.338	0.755	1.225	0.278	0.395	0.909
sil1545		glutathione S-transferase	-0.245	-0.489	-0.368	-0.154	-0.527	-0.543	-0.394	-0.006	-0.064	-0.403	-0.281	-0.443	0.319
sil1546	ppx	exopolyphosphalaseppx	0.145	-0.395	-0.623	-1.468	-0.916	-0.666	-0.563	error	error	error	error	error	error
sil1547		hypothetical protein	-0.089	-0.07	0.036	0.6	-0.162	0.211	-0.173	-0.057	0.068	-0.588	-0.185	-0.358	-0.879
sil1549		hypothetical protein	-0.45	-0.219	0.383	0.494	-0.033	0.351	0.573	-0.298	0.102	-0.623	-1.006	0.124	-1.083
sil1550		probable porin; major outer	-0.364	-0.33	-0.478	0.128	-0.307	-0.171	-0.679	0.063	-0.322	0.123	-0.091	-0.214	-0.788
sil1552		unknown protein	error	error	0.483	-0.689	error	-0.282	error	-0.139	0.329	0.962	-0.428	0.215	1.159
sil1553	pheT	phenylalanyl-tRNA syntheta	-0.377	-0.683	-1.124	-0.045	-0.941	-0.813	-0.8	0.01	-0.534	-0.804	-0.525	-0.51	-0.536
sil1555		two-component hybrid sens	-0.429	-0.474	-0.818	-0.459	-0.877	-0.249	-0.341	-0.171	-0.256	-0.849	-0.477	-0.411	-0.449



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl11556		isopentenyl-diphosphate d	0.742	0.611	0.792	-0.877	0.722	0.571	error	0.101	0.793	1.519	0.542	0.596	1.351
sl11557		succinyl-CoA synthetase al	0.032	0.421	0.933	0.398	1.282	1.107	2.223	0.086	0.916	0.062	0.725	0.482	1.325
sl11558		mannose-1-phosphate gua	0.023	1.089	2.119	1.838	1.975	1.188	1.426	1.093	2.705	2.025	1.922	2.7	1.146
sl11559		soluble hydrogenase 42 kD	-0.333	0.012	0.379	0.211	0.544	-0.171	-0.126	0.372	0.753	0.949	0.964	0.636	1.322
sl11560		putative transposase [ISY20	-0.732	-0.619	-0.257	error	-0.774	-0.697	-0.724	-0.965	-0.473	0.357	-0.784	-0.734	-1.2
sl11561	putA	proline oxidaseputA	-0.347	-0.314	-0.577	-0.174	-0.728	-0.417	-0.217	-0.338	-0.205	-0.358	-0.552	-0.265	-0.173
sl11562		unknown protein	error	error	error	error	error	0.049	error	error	-0.235	0.079	0.391	0.122	0.019
sl11563		unknown protein	-0.442	-0.159	0.059	0.457	-0.083	-0.041	-0.008	-0.246	0.078	0.212	-0.072	-0.282	-0.895
sl11564		putative lyase	-0.158	-0.209	-0.478	-0.074	-0.777	-0.144	-0.393	0.022	-0.514	-0.67	-0.424	-0.492	-0.902
sl11566	ggpS	glucosylglycerolphosphate	0.133	1.086	2.906	2.571	3.072	1.541	2.456	0.269	2.107	2.329	3.153	2.219	1.553
sl11568		fibrillin	-0.263	-0.106	-0.049	0.018	-0.206	-0.091	0.232	-0.213	0.042	0.408	-0.219	-0.146	0.066
sl11570		unknown protein	-0.2	error	0.141	error	0.169	0.446	error	-0.094	0.226	-0.253	-0.222	0.104	0.099
sl11571		hypothetical protein	-0.852	error	-1.132	-0.859	-0.603	-0.359	-0.353	-0.619	-0.65	-0.484	-0.702	-0.905	-0.801
sl11572	dnaE	DNA polymerase III alpha s	-0.345	error	-0.36	0.416	-0.247	0.269	-0.088	-0.187	-0.419	-0.725	-0.418	-0.467	-0.392
sl11573		hypothetical protein	error	error	error	error	error	0.506	error	0.447	0.524	error	0.304	0.276	1.285
sl11574		similar to serine/threonine k	error	error	error	error	error	error	error	-0.147	0.241	-0.603	-0.1	-0.138	0.512
sl11575		similar to serine/threonine k	-0.31	-0.408	-0.658	-0.273	-0.639	-0.518	-0.547	0.113	0.007	-0.529	-0.292	0.155	-0.711
sl11577	cpcB	phycocyanin beta subunitc	-0.468	-0.74	-2.118	-1.51	-2.901	-2.21	-1.764	0.101	-1.422	-2.97	-3.054	-1.565	-1.901
sl11578	cpcA	phycocyanin alpha subunitc	-0.433	-0.79	-2.345	-1.964	-3.226	-2.531	-1.782	-0.231	-1.407	-3.127	-3.332	-1.464	-1.203
sl11579	cpcC2	phycobilisome rod linker po	-0.586	-1.056	-2.223	-2.021	-3.616	-2.639	-2.042	0.238	-0.805	-2.342	-2.961	-0.866	-2.845
sl11580	cpcC1	phycobilisome rod linker po	-0.76	-1.128	-2.187	-2.117	-3.366	-2.65	-1.82	-0.084	-1.357	-2.596	-3.181	-1.428	-1.139
sl11581		hypothetical protein	-0.387	-0.318	-0.222	0.05	-0.117	0.095	0.39	-0.288	-0.029	-0.239	-0.392	-0.021	0.269
sl11582		unknown protein	-0.314	-0.111	-0.301	error	error	error	-0.19	-0.015	0.073	0.116	0.272	-0.001	0.747
sl11583		unknown protein	-0.336	-0.613	-1.14	-0.308	-1.23	-0.68	-0.784	-1.009	-1.235	-1.592	-1.558	-1.385	-0.133
sl11584		ferredoxin like protein	error	error	error	error	error	error	error	-0.231	0.102	-0.48	-0.403	-0.203	0.208
sl11586		unknown protein	-0.021	0.166	-0.195	0.228	-0.153	0.286	0.207	-0.346	-0.287	0.482	0.028	-0.343	-0.506
sl11590		two-component sensor histi	-0.46	-0.55	-0.749	-0.338	-0.833	-0.323	-0.624	-0.038	-0.16	-0.402	-0.089	-0.026	-0.626
sl11592		two-component response re	0.601	0.368	0.686	-0.291	0.564	0.482	1.149	-0.393	0.39	0.821	-0.43	-0.385	1.455
sl11594	ndhR	ndhF3 operon transcription	0.626	1.429	1.873	-0.081	0.023	-0.191	-0.223	1.315	2.108	0.338	0.382	2.09	0.954
sl11595	kaiC2	circadian clock protein KaiC	0.038	0.066	-0.006	-0.05	-0.153	-0.041	0.226	error	error	error	error	error	error
sl11596	kaiB2	circadian clock protein KaiE	error	error	error	-0.612	error	0.556	0.622	0.203	0.37	0.126	0.04	0.178	-0.174
sl11598	mntC	Mn transporter MntCmntC	-0.404	-0.069	-0.271	0.521	-0.472	-0.106	-0.027	-0.057	0.01	-0.2	-0.136	-0.005	-0.445
sl11599	mntA	manganese transport syste	-0.584	-0.737	0.133	0.446	0.253	0.09	0.194	0.132	0.431	0.073	0.545	0.348	-0.462
sl11600	mntB	manganese transport syste	0.325	0.523	0.284	-0.151	0.314	0.605	0.731	0.154	0.189	0.697	-0.063	0.493	-0.395
sl11601		hypothetical protein	error	0.162	-0.355	-0.623	-0.916	-0.003	error	-0.043	0.231	0.543	-0.133	0.259	-0.503
sl11605		(3R)-hydroxymyristol acyl c	error	error	error	error	error	error	error	-0.341	-0.08	-0.811	-0.667	-0.348	-0.611
sl11606		hypothetical protein	-0.131	-0.229	-0.245	0.791	-0.325	-0.288	0.102	-0.399	-0.048	0.623	-0.179	-0.308	-0.821
sl11608		hypothetical protein	0.054	error	-0.054	-0.272	-0.38	-0.092	0.831	-0.613	-0.201	0.248	-0.464	-0.4	0.79
sl11609		hypothetical protein	0.316	-0.187	error	-0.777	-0.176	0.25	error	-0.037	error	-0.046	-0.043	error	1.41
sl11611		unknown protein	-0.268	-0.142	0.088	-0.77	0.003	0.264	error	-0.204	-0.222	-0.065	-0.393	-0.239	0.87
sl11612	folC	folypolyglutamate synthase	-0.591	-0.697	-0.743	error	-0.736	-0.35	-0.532	-0.197	-0.458	0.462	-0.221	-0.704	-1.537
sl11613		unknown protein	0.789	0.214	error	error	0.177	-0.067	-0.165	0.303	0.694	0.385	-0.109	0.364	1.043
sl11614	pma1	cation-transporting ATPase	0.014	0.565	0.7	0.584	0.451	0.174	0.489	-0.208	0.287	0.067	-0.187	0.357	-0.378
sl11615		thiophen and furan oxidatio	0.085	0.04	0	-0.289	-0.057	-0.4	-0.395	-0.168	0.107	error	0.061	0.208	0.948
sl11618		hypothetical protein	-0.136	0.018	0.08	0.357	0.493	0.254	0.24	-0.236	0.098	-0.152	-0.036	-0.093	-0.707
sl11620		hypothetical protein	0.086	0.119	0.573	0.576	0.335	0.256	error	0.598	1.858	1.331	1.353	1.529	2.065
sl11621		AhpC/TSA family protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sl11623		ABC transporter ATP-binding	-0.036	0.193	0.486	error	0.051	-0.239	0.21	-0.222	0.294	0.103	-0.07	0.105	0.229
sl11624		two-component response re	0.299	0.524	0.28	-1.058	0.38	0.285	0.13	error	error	error	0.571	error	error
sl11625		succinate dehydrogenase in	-0.326	0.084	-0.16	-0.684	0.017	0.011	0.64	-0.085	-0.03	0.127	-0.153	0.029	0.111
sl11626		LexA repressor	-0.712	-0.926	-1.557	-0.537	-0.878	-1.058	-1.05	-0.292	-0.694	-0.671	-1.156	-0.679	0.816
sl11628		hypothetical protein	-0.306	0.049	0.129	-0.025	0.051	-0.074	-0.033	-0.7	-0.183	error	-0.018	-0.08	0.505
sl11629	phr	DNA photolyasephr	0.181	0.259	0.657	1.315	-0.122	0.009	-0.059	-0.395	-0.059	-0.072	-0.559	-0.291	-1.648
sl11630		unknown protein	error	error	error	-0.718	error	0.337	error	-0.268	0.242	0.291	0.027	-0.118	1.073
sl11631		putative cytidine and deoxy	error	error	0.614	error	error	-0.186	error	0.137	0.014	error	-0.074	-0.37	0.938
sl11632		hypothetical protein	-0.183	-0.118	0.035	0.827	-0.113	0.163	-0.231	-0.009	0.042	error	-0.278	-0.182	-0.375
sl11633	ftsZ	cell division protein FtsZfts	0.276	0.143	0.749	0.752	0.474	0.381	error	0.564	0.999	1.071	0.929	1.032	1.038
sl11634		hypothetical protein	1.819	0.757	1.633	0.265	1.589	0.539	2.042	0.358	1.487	1.475	0.921	0.738	1.8
sl11635		Thy1 protein homolog	-0.028	-0.324	-0.179	0.081	-0.266	0.102	-0.105	-0.136	0.002	-0.358	-0.124	-0.146	0.066
sl11636		ferripyochelin binding prote	-0.382	-0.498	-0.514	0.35	-0.567	-0.175	-0.184	-0.089	-0.014	-0.424	-0.38	-0.044	-0.926
sl11638		hypothetical protein	error	-0.649	-1.471	-0.731	-1.273	-0.522	0.23	-0.107	-0.781	-1.682	-1.536	-1.06	0.417
sl11639	ureD	urease accessory protein D	-0.19	-0.523	-0.548	-0.409	-0.577	0.124	-0.126	0.51	0.288	-0.104	-0.148	-0.267	-0.693
sl11640		hypothetical protein	1.1	1.635	1.937	1.731	1.325	0.648	0.326	error	error	error	error	error	error
sl11641		glutamate decarboxylase	-0.064	0.382	-0.361	-0.209	0.346	0.356	1.083	-0.19	-0.025	-0.115	-0.106	-0.32	-0.5
sl11642		hypothetical protein	error	error	0.019	-1.475	error	0.982	error	error	error	error	error	error	error
sl11643		hypothetical protein	-0.197	-0.189	-0.579	-0.033	-0.586	0.052	-0.097	0.204	-0.018	1.675	0.144	0.038	-0.181
sl11647		probable phosphinothricin N	-0.561	-0.258	-0.2	error	-0.161	error	-0.551	error	error	error	error	0.057	error
sl11651		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sl11652		hypothetical protein	error	error	error	error	error	error	error	3.088	2.708	1.519	1.936	2.336	1.422
sl11653		similar to menaquinone bio	2.316	3.473	1.882	0.986	2.134	1.3	1.998	2.427	2.238	1.168	1.289	2.021	1.658
sl11654		hypothetical protein	error	error	error	error	error	error	error	0.913	0.815	0.676	0.274	0.688	0.877
sl11655		similar to biotin [acetyl-CoA	1.017	1.822	0.906	0.545	1.12	1.14	0.715	1.424	1.419	-0.309	0.784	1.274	1.526
sl11656		hypothetical protein	-0.206	0.093	0.31	0.022	0.129	0.081	-0.011	0.494	0.729	-0.085	0.457	0.459	0.36
sl11658		hypothetical protein	error	error	error	error	error	error	error	0.123	0.345	0.059	0.224	-0.347	0.152
sl11659		hypothetical protein	error	-0.328	0.238	error	0.205	0.545	error	-0.199	-0.037	-0.075	-0.094	0.187	-0.62

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl11660		hypothetical protein	0.49	-	0.222	-0.993	0.331	0.566	0.476	-0.113	0.265	-0.268	-0.187	0.104	1.07
sl11662		probable prephenate dehydrogenase	0.01	0.204	0.277	0.209	-0.006	0.16	0.375	-0.055	0.521	0.576	0.479	0.495	-0.275
sl11663		phycoerythrin alpha subunit	-0.575	-0.573	-0.579	-0.357	-0.536	-0.209	-0.165	error	error	error	error	error	error
sl11664		probable glycosyl transferase	0.377	0.073	0.109	0.422	error	0.087	-0.016	0.145	-0.052	-0.389	0.105	-0.397	0.813
sl11665		unknown protein	-0.397	-0.23	-0.948	-0.217	-0.463	-0.361	-0.602	-0.365	-0.637	-0.652	-0.676	-0.773	0.886
sl11666	dnaJ	DnaJ protein	-0.724	-0.519	1.117	0.956	0.109	-0.575	-0.73	0.149	1.534	0.398	0.916	0.377	-0.811
sl11667		hypothetical protein	0.269	0.147	1.213	0.716	0.771	-0.037	0.335	0.375	1.316	1.897	1.064	1.335	0.868
sl11669	aroK	shikimate kinase	0.9	0.891	1.96	0.49	error	0.415	0.664	0.034	1.414	0.944	0.724	1.155	1.349
sl11670		heat-inducible transcription factor	0.02	-0.051	-0.158	0.069	-0.033	-0.054	0.119	error	error	error	error	error	error
sl11671		hypothetical protein	0.283	-0.034	0.465	error	error	0.05	error	-0.219	0.369	0.193	-0.192	0.138	-0.659
sl11672		two-component hybrid sensor	-0.43	-0.406	-1.292	-1.02	-1.476	-1.242	-0.879	-0.149	-0.619	-1.302	-1.201	-0.438	-0.914
sl11673		two-component response regulator	-0.359	-0.425	-0.892	-0.232	-0.674	-1.041	-0.494	-0.187	-0.348	-0.354	-0.397	-0.364	0.353
sl11675		hypothetical protein	0.263	0.138	0.283	error	0.077	0.305	0.513	error	error	error	error	error	error
sl11676		4-alpha-glucanotransferase	-0.086	-0.77	-0.753	-0.417	-0.528	-0.104	0.457	-0.311	-0.452	-0.102	-0.414	-0.389	0.284
sl11677		similar to spore maturation protein	-0.363	0.053	-0.106	0.656	-0.117	0.138	-0.374	0.468	-0.158	-0.309	-0.489	-0.382	-0.447
sl11678		similar to spore maturation protein	0.099	-0.17	-0.317	-0.817	-0.437	-0.703	-0.101	0.103	0.079	-0.222	-0.498	-0.177	0.744
sl11679		protease	0.147	0.158	0.848	1.537	1.422	0.67	0.627	0.089	1.034	0.925	1.344	1.02	1.283
sl11680		hypothetical protein	error	-0.216	1.01	1.724	1.283	0.463	0.444	-0.037	1.539	2.186	1.932	1.112	0.005
sl11681		unknown protein	error	error	error	error	error	error	error	0.134	0.509	0.775	0.985	0.219	0
sl11682		alanine dehydrogenase	-0.611	-0.293	-0.557	-0.86	-1.026	-0.067	-0.102	-0.246	-0.283	-0.236	-0.863	-0.282	-1.116
sl11683		lysine decarboxylase	error	error	error	error	error	error	error	-0.431	-0.104	-0.438	-0.177	-0.566	-0.367
sl11685	pxcA, cotA	protein involved in light-inducible gene expression	-0.122	-0.008	0.038	0.167	0.175	0.175	-0.496	error	error	error	error	error	error
sl11686		hypothetical protein	error	0.303	error	-1.231	-0.526	-0.562	-0.254	-0.49	-0.437	0.08	-0.078	-0.483	0.684
sl11687		unknown protein	error	0.378	0.389	-0.777	-0.848	-0.088	error	-0.618	-0.457	0.078	-1.226	-0.506	0.212
sl11688	thrC	threonine synthase	-0.186	-0.357	0.38	0.335	-0.459	-0.585	-0.179	-0.02	0.072	0.598	0.268	0.057	0.483
sl11689	sigE, rpoD2	group 2 RNA polymerase sigma factor	0.131	0.218	-0.112	0.325	0.079	-0.196	0.373	-0.203	-0.192	0.584	-0.58	-0.303	0.941
sl11691		hypothetical protein	-0.262	-0.436	-0.87	-0.678	-0.377	0.065	0.016	-0.216	-0.143	-0.535	-0.128	-0.472	-0.432
sl11692		hypothetical protein	0.05	error	-0.583	error	-0.177	-0.302	-0.468	0.003	0.23	error	0.12	-0.433	1.197
sl11693		hypothetical protein	0.195	-0.175	-0.528	-0.291	-0.311	0.091	0.184	0.158	0.424	0.818	0.203	0.444	0.099
sl11694	pilA1	pilin polypeptide PilA1	-0.524	-0.762	-1.279	0.072	0.318	0.314	0.58	-0.002	-0.423	0.227	0.824	-0.559	0.378
sl11695	pilA2	pilin polypeptide PilA2	-0.177	-0.473	-0.861	-0.684	0.412	0.549	1.13	0.085	-0.001	0.357	1.18	0.113	0.156
sl11696		hypothetical protein	-0.292	0.033	0.08	0.962	0.557	-0.046	0.253	-0.245	0	0.271	0.798	-0.123	0.17
sl11697		hypothetical protein	-0.193	-0.38	-0.372	error	0.774	0.218	0.395	0.097	-0.082	0.79	0.362	-0.246	0.256
sl11698		hypothetical protein	0.063	0.183	0.024	-0.515	0.171	-0.042	0.583	-0.309	-0.079	-0.595	-0.705	-0.299	-0.814
sl11699		oligopeptide-binding protein	0.376	0.212	0.196	0.547	0.527	0.345	0.252	error	error	error	error	error	error
sl11702	ycf51	hypothetical protein YCF51	error	error	0.391	-0.091	-0.132	0.13	error	-0.054	0.602	0.082	0.292	0.135	0.951
sl11703		protease IV	error	error	error	error	error	error	error	-0.128	-0.062	-0.14	-0.386	-0.452	-0.303
sl11704		probable short chain dehydrogenase	error	error	error	error	error	error	error	error	error	error	error	error	error
sl11708		two-component response regulator	-0.072	error	0.145	-0.314	-0.078	0.092	-0.108	0.043	0.465	-	0.217	0.337	1.127
sl11709		3-ketoacyl-acyl carrier protein	-0.216	0.063	-0.81	-0.388	-0.13	-0.173	-0.067	-0.024	0.019	-0.144	-0.113	-0.388	-0.226
sl11710		putative transposase [ISY52]	-0.185	-0.62	-0.276	0.691	-0.719	-0.41	-0.355	-0.529	-0.35	0.548	-0.821	-0.328	-1.027
sl11712		DNA binding protein HU	error	error	error	error	error	error	error	-0.617	-1.153	-2.009	-1.96	-1.308	-1.141
sl11713	hisC	histidinol-phosphate aminotransferase	0.168	-0.191	-0.299	-0.442	-0.862	-0.515	-0.044	-0.224	-0.188	-0.155	-0.658	-0.277	5.072
sl11714		unknown protein	-0.118	0.134	0.241	0.446	0.156	0.254	0.024	-0.051	0.1	error	0.03	-0.266	-0.469
sl11715		hypothetical protein	1.002	1.129	error	-0.264	0.91	0.39	error	0.059	0.764	0.571	0.415	-0.117	1.599
sl11716		putative transposase [ISY52]	0.087	-0.153	-0.342	0.027	-0.489	-0.254	-0.199	-0.658	-0.379	1.011	-0.909	-0.455	-0.773
sl11717		unknown protein	-0.196	-0.041	0.177	0.022	-0.242	0.258	-0.036	-0.283	-0.048	0.339	-0.154	-0.416	0.291
sl11721		pyruvate dehydrogenase E1	-0.845	-0.508	-0.769	-0.261	-0.587	-0.603	-0.342	error	error	error	error	error	error
sl11722		hypothetical protein	0.263	0.406	0.807	1.653	1.422	0.355	0.971	error	error	error	error	error	error
sl11723		probable glycosyltransferase	-0.341	0.16	0.581	0.71	1.097	0.696	1.075	-0.105	0.214	0.476	0.672	0.116	-0.839
sl11724		probable glycosyltransferase	0.649	error	error	-0.688	error	-0.282	error	-0.27	0.03	0.439	0.088	-0.12	-0.15
sl11725		ATP-binding protein of ABC transporter	0.822	0.453	0.221	1.146	0.225	0.091	-0.168	0.407	0.578	1.041	0.482	0.544	-0.272
sl11726		hypothetical protein	0.863	0.841	0.673	0.223	0.124	0.376	error	0.367	0.426	0.002	0.033	-0.079	0.707
sl11730		unknown protein	0.166	0.54	1.024	0.275	-0.122	0.174	0.526	-0.028	0.848	-0.492	-0.3	0.557	1.368
sl11732	ndhF3	NADH dehydrogenase subunit	0.281	0.861	1.254	-0.699	-0.011	0.322	error	-0.157	0.573	0.339	-0.642	0.396	0.362
sl11733	ndhD3	NADH dehydrogenase subunit	-0.672	-0.996	-1.451	-1.113	-1.92	-0.924	-1.024	-0.431	-0.922	-0.773	-1.341	-0.818	-0.137
sl11734	cupA	protein involved in low CO <sub>2</sub> growth	0.527	1.123	2.062	1.044	0.361	0.044	error	-0.049	1.555	1.91	0.171	1.27	0.94
sl11735		hypothetical protein	-0.058	0.138	0.375	-0.304	0.466	0.326	0.176	0.534	0.306	1.044	0.061	-0.249	-0.229
sl11736		hypothetical protein	-0.204	-0.507	-0.111	-0.23	-0.5	-0.164	0.454	-0.054	0.371	-0.306	-0.097	0.068	0.284
sl11737	ycf60	hypothetical protein YCF60	error	error	error	error	error	error	error	0.383	1.323	1.928	0.783	0.911	-0.237
sl11738		hypothetical protein	0.231	0.098	0.583	0.345	0.385	0.089	error	0.199	1.037	0.529	0.704	0.807	-0.238
sl11739		unknown protein	-0.426	0.24	0.288	0.736	0.223	0.213	0.064	error	error	error	error	error	error
sl11740	rpl19	50S ribosomal protein L19	0.309	error	1.194	0.56	error	-0.219	0.145	0.763	1.282	1.39	0.959	0.973	0.646
sl11742	nusG	transcription antiterminator	0.31	0.341	0.762	0.901	error	-0.426	0.067	0.442	0.508	0.095	0.36	0.645	-1.139
sl11743	rpl11	50S ribosomal protein L11	error	error	error	error	error	error	error	0.445	0.638	error	0.407	0.401	-0.457
sl11744	rpl1	50S ribosomal protein L1r	-0.122	-0.222	0.331	0.99	-0.198	-0.866	-0.802	0.277	0.724	0.859	0.762	0.488	0.012
sl11745	rpl10	50S ribosomal protein L10	-0.239	-0.497	0.168	1.736	-1.068	-1.588	-1.197	0.115	0.511	0.632	0.021	0.209	-2.103
sl11746	rpl12	50S ribosomal protein L12	-0.475	-0.781	-0.371	1.352	-1.256	-1.856	-1.274	-0.263	-0.384	0.216	-0.417	-0.584	-2.494
sl11747	aroC	chorismate synthase	0.051	-0.177	-0.385	0.068	-0.391	-0.398	-0.239	-0.173	0.006	0.377	-0.057	-0.048	-0.607
sl11749		hypothetical protein	error	error	error	-1.424	0.126	0.669	error	0.296	0.124	-0.621	0.367	error	0.644
sl11750	ureC	urease alpha subunit	0.384	-0.447	-0.837	-0.075	-0.414	0.122	-0.202	0.074	-0.308	-0.503	-0.045	-0.089	0.245
sl11751		hypothetical protein	-0.075	-0.023	1.325	-0.251	0.549	0.213	error	-0.006	1.029	0.689	0.312	0.906	0.704
sl11752		hypothetical protein	0.215	-0.051	0.392	0.948	0.536	0.088	0.272	-0.072	0.501	1.007	0.556	0.314	1.019
sl11755		unknown protein	0.27	0.504	-0.042	0.137	0.28	-0.091	0.191	error	error	error	error	error	error
sl11757		hypothetical protein	-0.031	0.04	0.166	0.497	0.298	0.237	0.301	-0.405	-0.19	-0.215	-0.187	-0.141	0.072

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl1758		MrsA protein homolog	-0.162	-0.405	-0.574	0.251	-0.296	0.017	-0.492	error	0.35	error	error	error	error
sl1760	thrB	homoserine kinases thrB	-0.199	error	0.929	-0.43	-0.193	0.027	0.82	-0.05	0.326	-0.141	-0.24	0.277	0.593
sl1761		unknown protein	-0.079	-0.09	-0.362	-0.837	-0.523	0.047	-0.066	-0.169	-0.393	0.131	-0.624	-0.727	-0.927
sl1762		binding protein of ABC tran	-0.487	error	-0.915	-0.988	-0.924	-0.581	-0.656	-0.664	-1.032	-0.324	-1.256	-1.156	0.403
sl1763		unknown protein	0.294	error	0.562	-1.077	-0.793	0.119	error	-0.344	0.258	-0.584	-0.514	-0.132	0.116
sl1764		unknown protein	0.228	-0.198	-0.743	error	error	-0.711	error	-0.296	-0.077	-0.052	-0.614	0.311	0.197
sl1765		unknown protein	0.319	0.063	-0.345	0.333	-0.134	-0.021	-0.071	0.24	0.3	error	-0.178	-0.168	1.087
sl1766		hypothetical protein	-0.013	0.032	-0.129	-0.056	-0.145	0.179	-0.394	-0.314	-0.709	-0.129	-0.64	-0.652	0.346
sl1767	rps6	30S ribosomal protein S6rp	-0.303	-0.112	-0.031	0.59	-0.638	-1.017	-0.815	0.274	0.241	-0.021	-0.362	-0.21	-0.007
sl1768		probable oligopeptides ABC	error	error	error	error	error	error	error	0.167	0.478	error	0.308	0.555	0.422
sl1769		hypothetical protein	0.435	error	1.141	0.18	0.799	0.476	0.146	error	error	error	error	error	error
sl1770		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sl1771	pphA	protein serin-threonin phos	0.225	error	0.218	-0.219	-0.627	-0.016	0.451	0.261	0.417	0.255	0.507	0.446	0.424
sl1772	mutS	DNA mismatch repair prote	-0.164	0.113	-0.081	-0.339	-0.699	-0.198	-0.083	0.024	0.021	0.031	-0.021	-0.025	-0.834
sl1773		hypothetical protein	0.259	1.225	2.673	0.339	0.9	0.455	0.316	error	2.249	error	error	error	error
sl1774		hypothetical protein	-0.004	-0.435	-0.742	-0.151	-0.597	-0.291	-0.005	-0.382	-0.422	-0.069	-0.61	-0.731	-0.674
sl1775		hypothetical protein	error	error	error	error	error	error	error	-0.051	-0.008	0.09	-0.464	-0.076	0.139
sl1776		deoxyribose-phosphate ald	0.012	-0.611	0.141	-1.319	-0.774	-0.07	error	0.036	-0.08	-0.245	-0.652	-0.082	0.115
sl1780		putative transposase [ISY2	-0.621	error	-0.309	error	-0.322	-0.59	-0.466	-1	0.017	0.625	-0.429	-0.335	0.893
sl1783		hypothetical protein	-0.282	-0.795	-0.761	-0.639	-1.328	-0.763	-0.665	-0.475	-0.701	0.05	-0.971	-0.521	-0.303
sl1784		unknown protein	error	error	error	error	error	error	error	-0.426	-0.837	-1.561	-1.695	-0.939	-1.656
sl1785		unknown protein	error	-0.612	-1.406	-0.67	-1.41	-0.883	-0.973	-0.296	-0.898	-1.624	-1.798	-1.017	-2.1
sl1786	taiD	similar to Sec-independent	0.732	1.101	1.379	2.136	1.239	0.346	0.386	error	error	error	error	error	error
sl1787	rpoB	RNA polymerase beta subu	0.039	-0.238	-0.261	0.914	-0.198	-0.163	-0.732	0.465	0.347	0.129	0.485	0.362	-1.216
sl1789	rpoC2	RNA polymerase beta prime	0.178	-0.4	-0.199	0.607	-0.405	-0.448	-0.471	0.247	error	-0.61	-0.115	-0.331	-1.043
sl1791		putative transposase [ISY8	error	0.361	0.264	0.746	-0.01	-0.21	-0.188	0.168	0.352	error	-0.028	0.152	-0.901
sl1792		putative transposase [ISY8	0.721	0.652	0.696	-0.152	0.34	0.365	1.157	-0.177	0.171	0.523	0.106	0.214	5.751
sl1796	petJ	cytochrome c553petJ	0.445	0.209	0.141	-0.009	0.073	-0.235	0.13	0.082	0.353	-0.334	0.225	0.267	0.243
sl1797	ycf21	hypothetical protein YCF21	0.581	1.106	2.36	1.746	2.299	1.386	1.725	0.84	2.065	1.863	2.005	2.187	1.628
sl1799	rpl3	50S ribosomal protein L3rp	1.13	1.295	1.817	2.891	1.326	0.755	0.389	2.208	3.035	2.072	2.06	3.003	0.755
sl1800	rpl4	50S ribosomal protein L4rp	0.259	0.593	1.404	1.899	0.769	0.019	0.236	1.385	2.199	1.569	1.877	1.99	1.559
sl1801	rpl23	50S ribosomal protein L23r	-0.142	0.097	0.858	error	0.147	-0.323	-0.263	0.813	1.29	1.306	1.163	1.245	-0.627
sl1802	rpl2	50S ribosomal protein L2rp	-0.026	0.228	0.934	2.053	0.275	-0.434	-0.303	0.737	1.635	1.226	1.13	1.274	0.109
sl1803	rpl22	50S ribosomal protein L22r	0.352	error	0.738	1.64	0.212	0.005	error	0.773	1.131	1.085	0.552	1.103	-0.045
sl1804	rps3	30S ribosomal protein S3rp	-0.048	0.072	0.94	2.134	-0.143	-0.507	-0.747	0.858	1.454	1.357	1.067	1.468	-0.359
sl1805	rpl16	50S ribosomal protein L16r	-0.167	-0.433	0.074	1.418	-0.272	-0.632	-0.635	0.181	0.774	0.25	0.436	error	-0.404
sl1806	rpl14	50S ribosomal protein L14r	-0.107	-0.265	0.332	1.378	-0.32	-0.691	-0.359	0.445	0.943	0.558	0.666	0.493	-0.619
sl1807	rpl24	50S ribosomal protein L24r	-0.19	-0.397	-0.098	1.287	-0.347	-0.745	-0.689	0.229	0.499	1.129	0.327	0.773	-1.17
sl1808	rpl5	50S ribosomal protein L5rp	-0.065	-0.264	0.504	1.671	-0.279	-0.858	-0.805	0.234	0.861	0.732	0.479	0.447	-0.255
sl1809	rps8	30S ribosomal protein S8rp	-0.453	-0.449	0.382	1.762	-0.559	-0.85	-0.801	0.169	0.375	0.874	0.396	0.255	-1.015
sl1810	rpl6	50S ribosomal protein L6rp	-0.256	-0.329	0.123	1.291	-0.394	-0.811	-0.617	0.074	0.247	1.059	0.286	0.037	-0.176
sl1811	rpl18	50S ribosomal protein L18r	-0.03	-0.302	0.155	0.988	-0.324	-0.751	-0.509	0.264	0.868	-0.016	0.252	0.334	0.135
sl1812	rps5	30S ribosomal protein S5rp	-0.086	-0.48	-0.413	1.358	-0.64	-0.924	-0.86	0.166	0.264	0.578	0.176	0.158	-1.165
sl1813	rpl15	50S ribosomal protein L15r	0.192	-0.536	0.196	0.863	-0.374	-0.408	-0.246	0.56	0.491	0.432	0.6	0.513	-0.117
sl1814	secY	preprotein translocase Sec	-0.262	-0.728	-0.782	0.124	-0.927	-0.788	-0.974	0.048	0.057	0.379	0.025	0.201	-1.157
sl1815		adenylate kinase	0.372	-0.014	0.139	0.363	-0.301	-0.115	-0.477	0.296	0.479	0.341	0.235	0.159	-0.281
sl1816	rps13	30S ribosomal protein S13r	-0.102	0.11	0.35	1.803	-0.374	-0.825	-0.834	0.968	1.25	1.096	0.914	1.279	-0.547
sl1817	rps11	30S ribosomal protein S11r	-0.169	0.1	0.361	1.59	-0.251	-0.464	-0.63	0.717	0.872	0.674	0.621	0.906	-1.004
sl1818	rpoA	RNA polymerase alpha sub	-0.109	-0.219	-0.149	1.392	-0.718	-1.237	-0.979	0.693	0.772	0.167	0.527	0.413	-1.191
sl1819	rpl17	50S ribosomal protein L17r	0.24	0.012	0.029	0.996	-0.115	-0.423	-0.314	0.526	0.875	error	0.621	0.679	0.506
sl1820		tRNA pseudouridine syntha	-0.136	-0.381	-0.258	0.726	error	0.021	-0.773	0.325	0.489	-0.257	0.339	0.295	0.185
sl1821	rpl13	50S ribosomal protein L13r	error	error	error	error	error	error	error	-0.08	-0.011	0.441	-0.029	-0.152	-0.85
sl1822	rps9	30S ribosomal protein S9rp	0.394	error	-0.143	1.586	-0.076	-0.512	error	0.569	0.961	0.813	0.723	0.833	-0.508
sl1823	purA	adenylosuccinate synthetas	0.826	1.486	2.117	1.59	0.748	-0.212	-0.127	2.076	2.855	1.744	1.408	2.961	-0.861
sl1824	rpl25	50S ribosomal protein L25r	0.229	0.816	1.264	1.678	0.128	-0.203	error	0.795	1.761	1.488	0.88	1.662	0.5
sl1825		hypothetical protein	-0.264	-0.8	error	-0.939	-0.76	-0.169	error	-0.318	-0.309	-0.701	-0.811	-0.683	0.241
sl1830		unknown protein	-0.529	-0.741	-0.626	-1.006	-1.783	-0.71	-0.977	-1.044	-0.541	-1.256	-1.615	-0.641	-0.707
sl1831		glycolate oxidase subunit, (	-0.297	error	-0.397	0.369	1.182	0.43	1.188	error	error	error	error	error	error
sl1832		hypothetical protein	error	error	error	error	error	error	error	-0.197	-0.309	-1.127	0.113	-0.534	1.042
sl1833		penicillin-binding protein	-0.058	-0.463	-0.118	-0.17	0.079	0.204	0.135	-0.122	-0.048	-0.341	-0.078	error	0.776
sl1834		hypothetical protein	-0.084	error	0.02	error	0.341	0.101	0.45	0.218	0.406	0.615	0.287	0.069	-0.774
sl1835		hypothetical protein	-0.472	-1.104	-1.365	-0.132	-0.592	-0.533	-0.627	error	error	error	error	error	error
sl1837		unknown protein	error	-0.686	-1.141	-0.544	-0.978	-0.425	-0.548	0.342	0.115	error	-0.14	-0.213	error
sl1841		pyruvate dehydrogenase di	-0.278	-0.146	0.504	0.849	0.076	-0.167	-0.054	error	error	error	error	error	error
sl1845		hypothetical protein	error	error	1.459	0.776	error	0.731	error	0.281	0.611	1.339	0.441	0.304	0.872
sl1848		putative acyltransferas	error	error	1.072	error	0.732	0.344	1.085	0.047	0.798	0.756	0.413	0.538	1.283
sl1849		probable dioxygenase Ries	error	error	1.596	error	1.154	0.923	-	0.155	1.188	error	0.811	0.666	1.404
sl1851		unknown protein	1.306	2.003	1.347	0.624	0.616	0.389	0.305	error	error	error	error	error	error
sl1852		nucleoside diphosphate kin	0.743	error	error	0.833	1.701	0.923	error	0.027	1.67	1.693	1.651	1.699	6.684
sl1853		unknown protein	0.16	0.464	0.795	0.75	0.408	0.125	0.114	-0.105	0.251	-0.607	-1.481	-0.136	0.887
sl1854		exodeoxyribonuclease III	0.348	0.307	0.889	0.521	error	0.4	0.163	0.445	0.713	0.125	0.631	0.217	-0.54
sl1858		unknown protein	-0.208	0.236	-0.027	0.169	0.088	0.089	-0.096	-0.048	0.267	0.36	0.316	0.27	0.701
sl1860		putative transposase [ISY5	-0.122	-0.109	0.136	-0.216	-0.561	-0.366	-0.592	-0.657	-0.097	1.208	-0.754	-0.212	0.175
sl1861		putative transposase [ISY5	error	0.096	0.435	-0.376	0.734	0.385	error	-0.358	0.061	1.648	-0.346	-0.162	0.685
sl1862		unknown protein	error	error	error	error	error	error	error	5.891	6.976	6.95	6.227	6.477	7.237

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl1863		unknown protein	3.78	4.509	4.667	4.773	error	3.221	4.693	4.267	5.559	error	5.365	5.481	error
sl1864		probable chloride channel p	0.589	0.485	0.722	1.907	0.306	-0.013	0.174	0.615	0.981	1.019	0.753	0.911	0.071
sl1865	prfB	peptide chain release factor	0.591	0.078	0.445	0.388	0.247	0.366	0.149	-0.065	0.106	-0.437	0.118	-0.292	0.73
sl1866		hypothetical protein	0.681	0.529	0.344	error	0.105	-0.145	0.198	0.343	0.539	-0.035	0.527	0.544	0.887
sl1867	psbA3	photosystem II D1 proteinps	-0.581	-0.197	0.777	1.381	-0.192	-0.606	-0.589	0.703	1.666	0.222	0.784	1.335	0.333
sl1868	dnaG	DNA primasednaG	-0.196	0.366	0.171	0.549	0.195	0.013	0.321	0.063	0.373	error	0.155	0.19	-0.693
sl1869		probable dioxxygenase, Ries	error	error	error	error	error	error	error	-0.222	0.133	-0.437	0.057	-0.194	1.589
sl1870		ATP-binding protein of ABC	0.42	error	0.893	0.135	0.287	0.038	0.7	0.412	0.587	1.108	0.311	0.37	0.566
sl1871		two-component system sen	-0.228	-0.338	-1.354	error	-1.46	-0.922	-0.854	-0.305	-0.674	-1.152	-1.381	-0.885	-0.485
sl1872		transcriptional regulator	-0.246	-0.341	-0.502	-0.323	-0.054	-0.039	-0.272	-0.478	-0.55	-0.494	-0.469	-0.195	0.734
sl1873		unknown protein	-0.553	-0.771	-1.293	-0.615	-1.122	-0.846	-0.864	-0.51	-0.597	-0.896	-0.838	-0.623	0
sl1874		hypothetical protein	-0.622	-0.586	-0.89	-0.005	-0.767	-0.327	-0.553	-0.402	-0.748	-1.426	-0.976	-0.735	-1.552
sl1875	ho2	heme oxygenaseho2	0.067	error	0.213	-0.854	0.325	-0.023	-0.039	-0.46	0.471	error	-0.603	-0.49	-0.177
sl1876	hemN	oxygen independent coprop	error	-0.438	-0.827	-1.309	-1.02	0.086	-0.55	-0.506	-0.494	-0.175	-1.18	-0.489	-1.487
sl1878		iron(III)-transport ATP-bind	-0.512	0.171	1.358	error	0.407	-0.205	0.362	0.181	1.345	0.567	0.02	1.63	0.24
sl1879	ycf55	two-component response re	-0.011	0.222	-0.035	-0.277	-0.469	0.09	-0.203	0.151	0.307	-0.328	-0.298	0.087	-0.44
sl1880		hypothetical protein	error	0.496	error	-1.063	error	0.203	error	0.328	0.275	error	0.294	-0.325	1.364
sl1882		unknown protein	error	-0.826	-0.228	-0.555	-1.387	-0.296	error	-0.997	-0.588	-0.98	-1.095	-0.757	-0.157
sl1883	argJ	arginine biosynthesis bifunc	-0.136	-0.117	0.37	0.566	0.339	0.42	0.315	0.393	0.482	-0.303	0.479	-0.013	0.832
sl1884		hypothetical protein	1.426	2.464	2.606	2.923	2.284	0.915	1.16	2.355	error	3.005	2.414	error	0.424
sl1885		unknown protein	-0.399	-0.583	-0.583	0.042	-0.549	-0.314	-0.05	-0.405	-0.027	0.057	-0.309	0.024	-1.056
sl1886		hypothetical protein	0.082	0.401	0.361	-0.123	0.651	0.436	0.136	0.199	0.481	0.525	0.554	0.351	-0.312
sl1888		two-component sensor histi	-0.084	-0.172	-0.098	0.82	0.143	-0.124	-0.174	0.131	-0.085	0.352	0.456	0.083	-0.421
sl1890	cobN	similar to cobalamin biosyn	error	error	error	error	error	error	error	-0.066	-0.03	error	-0.376	-0.153	0.182
sl1891		unknown protein	error	error	error	error	error	error	error	-0.6	-0.534	-0.386	0.569	-0.823	0.696
sl1892		unknown protein	error	error	error	error	error	error	error	-0.835	-0.479	-0.916	-0.704	-0.997	0.016
sl1893	hisF	cyclasehisF	0.412	0.206	-0.238	-0.227	-0.212	0.333	0.259	-0.066	-0.276	0.92	-0.252	-0.162	-0.257
sl1894	ribA	riboflavin biosynthesis prot	error	error	error	error	error	error	error	0.211	0.441	1.106	0.502	0.429	-0.211
sl1895		hypothetical protein	-0.364	-0.77	-0.575	-0.402	0.128	0.168	0.306	-0.308	-0.44	0.88	-0.004	-0.574	-0.93
sl1897		hypothetical protein	0.155	error	-0.119	-1.491	-0.282	-0.073	error	-0.087	0.3	-0.164	-0.051	0.299	0.498
sl1898		hypothetical protein	-0.223	-0.067	0.847	1.003	1.548	1.002	1.686	-0.796	0.206	error	0.5	0.086	1.879
sl1899	ctaB	cytochrome c oxidase foldin	-0.661	-0.68	-0.878	-0.006	-0.701	-0.688	-0.715	-0.185	-0.275	-0.907	-0.108	-0.142	-0.319
sl1900	act	acetyltransferaseact	error	0.719	0.899	-0.052	0.009	0.108	error	0.295	0.833	-0.084	0.244	0.534	0.838
sl1902		hypothetical protein	1.088	error	0.662	error	0.267	0.264	error	-0.209	0.374	error	-0.278	-0.298	0.958
sl1905		two-component hybrid sens	-0.082	-0.362	-0.283	-0.675	-0.866	-0.54	-1.014	-0.23	-0.32	-0.647	-0.425	-0.198	-0.787
sl1906		hypothetical protein	-0.017	-0.114	0.064	0.54	0.108	0.137	0.437	-0.238	0.034	0.263	0.081	-0.04	0.785
sl1908	serA	D-3-phosphoglycerate dehy	-0.415	-0.504	-0.257	0.425	-0.193	-0.118	-0.381	-0.155	-0.22	-0.703	0.059	-0.436	0.104
sl1909		probable methyltransferase	error	error	error	error	error	error	error	0.349	-0.053	0.382	0.227	0.083	-0.215
sl1910	zam	protein conferring resistanc	-0.283	-0.167	0.089	error	-0.38	-0.754	-0.558	-0.076	0.204	-0.041	-0.046	0.279	0.655
sl1911		hypothetical protein	error	error	error	error	error	error	error	0.017	0.996	0.441	1.338	0.568	1.361
sl1912		hypothetical protein	error	error	error	error	error	error	error	0.003	0.409	-0.487	-0.085	-0.17	0.247
sl1913		hypothetical protein	error	error	-0.469	-0.647	-0.232	0.16	error	-0.319	-0.086	-0.048	-0.256	-0.044	-1.414
sl1915		hypothetical protein	0.151	0.517	0.611	0.019	0.34	0.191	0.228	0.716	1.4	1.685	0.588	1.145	-0.032
sl1916		hypothetical protein	0.199	0.579	0.344	error	0.114	0.24	0.11	-0.064	-0.002	-0.381	-0.216	-0.074	-0.521
sl1917	hemN	oxygen independent coprop	0.732	0.589	0.251	-0.415	0.074	0.39	-0.211	0.714	0.725	0.95	0.554	0.631	0.301
sl1920	pacS	copper transporting CPx-ty	0.103	-0.045	-0.041	0.837	-0.016	0.033	0.015	-0.129	0.047	0.29	0.077	0.332	-0.375
sl1921		hypothetical protein	0.094	error	0.563	error	0.193	0.262	error	-0.077	0.369	0.263	-0.07	0.155	-0.361
sl1924	syrcp2	cAMP receptor protein syrc	error	error	error	-0.092	-0.175	-0.135	error	0.105	0.669	-0.117	-0.412	0.583	0.255
sl1925		hypothetical protein	error	-0.342	-0.304	-0.724	-0.03	0.198	-0.14	0.029	0.212	error	-0.312	-0.248	0.252
sl1926		hypothetical protein	-0.06	0.038	-0.147	-0.86	-0.182	0.177	-0.203	0.059	0.502	0.055	0.269	0.177	0.453
sl1927		ABC transporter ATP-bindin	0.49	0.752	0.91	1.454	0.609	-0.003	0.41	1.029	0.925	1.21	0.639	1.139	-0.315
sl1929	comE	competence protein ComEc	-0.648	-0.429	-0.563	0.047	-0.641	-0.276	-0.57	-0.232	-0.159	0.363	-0.034	-0.189	-0.631
sl1930		putative transposase [JSY1	-0.797	-1.344	-1.443	-0.738	-1.635	-0.707	error	-1.285	-0.348	0.381	-0.803	-0.781	-0.542
sl1931	gylA	serine hydroxymethyltransfe	-0.447	-0.592	-0.772	-0.17	-0.831	-1.118	-0.604	0.004	-0.23	-0.806	-0.517	-0.387	0.411
sl1932	dnaK	DnaK proteindnaK	0.693	error	-0.309	error	-0.035	-0.252	error	-0.32	0.034	0.323	-0.192	0.431	error
sl1933	dnaJ	DnaJ proteindnaJ	0.543	0.548	-0.274	-0.899	0.048	-0.065	0.194	-0.191	0.247	0.176	-0.15	0.081	-0.023
sl1934		hypothetical protein	error	error	0.754	error	0.877	0.245	1.606	0.068	-0.677	0.163	0.592	-0.866	-0.35
sl1937		ferric uptake regulation prot	0.05	0.021	0.116	-0.857	-0.196	-0.06	0.259	-0.138	0.392	-0.019	-0.056	0.341	0.13
sl1938		hypothetical protein	error	-0.067	error	error	0.419	0.122	error	-0.09	0.191	-0.248	error	-0.265	0.222
sl1939		unknown protein	0.11	error	-0.34	-0.793	-0.636	-0.274	0.262	-0.227	-0.384	-1.311	-1.115	-0.807	0.374
sl1940		hypothetical protein	0.341	-0.308	-0.418	-0.361	error	0.196	-0.168	error	error	error	error	error	error
sl1941	gyrA	DNA gyrase A subunitgyrA	0.164	-0.235	0.023	0.02	0.359	0.056	0.577	-0.449	-0.045	-0.061	-0.245	-0.41	0.343
sl1942		unknown protein	-0.776	-0.931	-1.14	-0.469	-0.882	-0.186	-0.34	error	error	error	error	error	error
sl1945		1-deoxyxylulose-5-phospha	-0.318	-0.505	0.267	0.979	-0.167	-0.182	-0.33	error	error	error	error	error	error
sl1946		hypothetical protein	0.606	0.654	0.147	0.067	error	0.648	0.861	-0.134	0.181	0.264	-0.03	0.164	-0.476
sl1949		unknown protein	-0.428	-0.484	error	error	-0.434	-0.451	-0.581	0.249	0.191	error	-0.092	0.009	0.7
sl1950		unknown protein	0.67	0.32	0.638	0.423	0.529	0.566	0.517	0.366	0.773	0.645	0.97	0.59	2.074
sl1951		unknown protein	-0.141	-0.552	-1.722	0.127	-0.884	-0.86	-0.718	0.378	-0.643	-1.536	-0.371	-0.582	0.32
sl1954		unknown protein	error	error	-0.275	error	-0.728	-0.159	error	-0.644	0.027	0.401	-0.242	-0.139	1.23
sl1956		hypothetical protein	0.918	error	-0.627	-0.32	0.008	0.6	error	0.003	-0.153	0.239	-0.269	-0.287	-0.285
sl1957		transcriptional regulator	0.229	0.032	-0.068	-0.665	-0.076	-0.074	0.771	-0.094	0.121	-0.064	0.201	0.108	1.317
sl1958	hisC	histidinol phosphate aminot	-0.153	-0.006	0.479	0.081	-0.67	-0.295	-0.365	0.187	0.631	0.158	0.02	0.604	-1.073
sl1959		probable inositol monophos	-0.096	-0.161	0.13	0.658	-0.405	-0.208	-0.201	-0.14	0.038	-0.084	-0.22	0.087	-1.122
sl1960		hypothetical protein	0.29	0.319	0.585	error	0.38	0.105	0.391	0.279	0.678	0.223	0.137	0.466	0.798
sl1961		hypothetical protein	0.066	-0.123	-0.834	-0.548	-0.786	-0.024	-0.151	-0.082	-0.245	-0.205	-0.5	-0.143	-0.454

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sl1965		hypothetical protein	0.31	0.993	1.165	0.44	0.339	0.282	0.736	0.48	1.546	1.09	0.371	1.441	error
sl1967		probable RNA methyltransf	-0.023	error	0.934	-0.1	0.787	0.42	0.183	-0.33	0.511	0.973	0.158	0.516	1.28
sl1968	pmgA	photomixotrophic growth re	0.043	0.568	0.385	0.686	0.985	0.584	0.763	0.433	0.634	0.875	0.843	0.172	0.852
sl1969		hypothetical protein	-0.009	0.158	0.211	1.097	0.41	0.398	-0.05	0.189	0.047	0.089	0.7	-0.451	-0.537
sl1971		probable hexosyltransferas	-0.007	0.063	0.209	error	0.017	0.093	error	-0.397	error	0.282	-0.462	error	0.977
sl1973		hypothetical protein	-0.56	-0.571	-1.129	-2.007	-1.189	-0.483	-0.527	0.09	0.109	-0.169	error	-0.192	-0.625
sl1979		hypothetical protein	0.441	-0.084	0.208	-1.226	-0.122	-0.043	1.033	0.376	0.784	error	0.364	0.22	0.794
sl1980	trxA	thiol:disulfide interchange p	-0.151	-0.696	0.214	0.367	0.908	0.413	0.454	0.178	0.661	-0.274	1.402	0.13	0.491
sl1981	ilvB	acetolactate synthaseilvB	0.644	0.764	1.005	1.078	0.991	0.423	0.367	0.62	1.124	0.824	1.04	1	1.147
sl1982		putative transposase [ISY3	-0.555	-0.535	-0.838	-0.324	-0.183	-0.085	0.247	-0.696	-0.317	0.402	-0.417	-0.415	-0.594
sl1983		putative transposase [ISY10	-0.236	-0.071	0.017	0.683	-0.186	-0.379	-0.243	-0.46	0.077	error	-0.288	0.134	-1.047
sl1984		putative transposase [ISY10	error	error	-0.954	error	error	-0.029	error	-0.894	-0.433	0.561	-0.967	-0.607	0.565
sl1985		putative transposase [ISY3	0.042	-0.106	-0.015	-0.173	-0.846	-0.179	-0.217	-0.672	-0.446	0.575	-0.44	-0.485	0.164
sl1987	cpx, katG	catalase peroxidasecpx, ka	-0.135	-0.484	-0.344	-0.474	-0.74	-0.252	0.076	-0.072	-0.15	error	-0.296	-0.189	0.785
sl1988	hsp33	33 kDa chaperoninhsp33	-0.017	0.292	0.359	0.593	0.168	0.204	0.026	error	error	error	0.393	error	error
sl1994	hemB	porphobilinogen synthaseh	-0.51	-0.762	-0.584	-0.096	-0.875	-0.5	-0.664	-0.54	-0.753	-1.138	-0.797	-0.817	0.062
sl1995		hypothetical protein	-0.236	-0.099	-0.759	-0.497	-0.725	-0.358	-0.697	-0.177	-0.237	-0.344	-0.469	-0.207	-0.979
sl1997		putative transposase [ISY20	error	error	-0.161	error	-0.265	0.549	-0.473	-0.224	0.498	0.943	0.207	0.314	0.867
sl1998		putative transposase [ISY10	-0.224	-0.493	-0.603	0.116	-0.55	-0.529	-0.336	-0.99	-0.052	1.647	-0.538	0.012	-0.888
sl1999		putative transposase [ISY20	-0.753	-0.542	-0.592	-0.689	-0.907	-0.542	-0.836	-0.254	0.225	0.351	-0.552	0.062	-0.976
sl2001		leucine aminopeptidase	error	error	error	error	error	error	error	0.071	0.61	0.262	0.066	0.465	-0.393
sl2002		hypothetical protein	-0.391	error	-1.019	-1.054	-0.843	-0.335	-0.508	-0.202	-0.085	-0.786	-0.6	-0.103	0.686
sl2003		hypothetical protein	-0.206	-0.062	-0.111	-0.212	-0.075	0.056	0.018	-0.184	-0.167	-0.416	-0.202	-0.107	0.846
sl2005	gyrB	DNA gyrase B subunit [Con	0.074	-0.398	-0.408	error	-0.488	-0.344	-0.257	-0.369	-0.777	-0.953	-0.434	-0.684	0.543
sl2006		hypothetical protein	error	error	error	error	error	error	error	error	0.604	error	error	error	error
sl2007		hypothetical protein	0.21	-0.156	-0.564	error	-0.391	-0.163	-0.031	0.103	0.179	0.403	-0.275	-0.312	-0.656
sl2008		processing protease	error	error	error	error	error	error	error	-0.009	0.012	-0.185	0.04	0.036	-0.468
sl2009		processing protease	0.174	-0.103	-0.306	error	error	0.324	0.565	0.059	-0.168	-0.278	0.011	-0.549	-0.668
sl2010	murD	UDP-N-acetylmuramoylalar	0.076	-0.067	-0.514	-0.724	-0.474	-0.058	-0.062	-0.089	-0.03	0.553	-0.322	0.125	-0.388
sl2011		hypothetical protein	error	error	0.828	-1.025	error	0.639	error	0.179	0.88	0.339	0.174	0.314	1.034
sl2012	sigD	group2 RNA polymerase sig	0.921	error	3.62	2.611	2.471	1.53	1.824	2.508	4.538	2.439	2.737	4.194	1.906
sl2013		hypothetical protein	0.047	0.376	1.154	0.756	0.119	0.091	error	-0.326	0.543	0.37	-0.135	0.438	0.332
sl2014		sugar fermentation stimulato	-0.078	0.577	-0.009	-0.643	-0.323	-0.016	0.06	-0.08	0.304	0.672	-0.289	0.347	1.44
sl2015		hypothetical protein	error	error	error	error	error	error	error	0.047	0.172	0.848	0.769	0.051	0.33
slr0001		hypothetical protein	-0.196	-0.016	0.053	0.453	0.743	0.404	0.528	error	error	error	error	error	error
slr0006		unknown protein	-0.336	-0.606	-0.105	0.463	0.336	0.191	0.296	-0.151	-0.014	0.187	0.144	-0.16	1.707
slr0007		probable sugar-phosphate	-0.303	-0.239	-0.005	0.006	-0.017	0.095	error	-0.131	0.177	0.682	-0.032	0.154	1.432
slr0008	ctpA	carboxyl-terminal processin	-0.134	0.614	1.088	1.422	1.073	0.116	0.276	0.843	2.207	2.141	1.703	2.183	0.764
slr0009	rbcL	ribulose bispophosphate carb	-0.953	-1.166	-1.48	-0.511	-1.652	-1.337	-1.266	-0.276	-1.06	-1.989	-1.599	-0.952	-0.374
slr0011	rbcX	hypothetical proteinrbcX	error	error	error	error	error	error	error	error	error	error	error	error	error
slr0012	rbcS	ribulose bispophosphate carb	-0.715	-0.874	-1.884	-1.216	-2.003	-1.223	-1.338	-0.454	-1.121	-1.36	-1.408	-1.118	-0.234
slr0013		hypothetical protein	error	-0.379	error	-0.672	-0.271	-0.198	-0.036	-0.052	0.08	error	-0.044	-0.196	0.967
slr0014		Mg2+ transport ATPase	0.472	0.623	0.419	-0.257	-0.049	0.279	0.57	error	error	error	error	error	error
slr0015		lipid A disaccharide synthas	-0.206	error	-0.573	0.199	-0.332	0.293	error	-0.011	0.038	0.596	0.09	0.083	0.306
slr0016		hypothetical protein	-0.244	error	-0.032	error	0.24	0.111	0.161	-0.274	0.211	0.107	0.059	-0.132	1.1
slr0017	murZ	UDP-N-acetylglucosamine	-0.259	-0.278	0.175	0.233	-0.699	-0.549	-0.719	0.035	0.735	-	-0.494	0.644	0.325
slr0018		fumarase	error	error	-0.251	error	error	0.599	error	0.236	-0.317	-0.208	0.181	-0.34	0.563
slr0019		unknown protein	-0.177	0.108	-0.413	-0.194	-0.498	0.192	error	-0.174	0.767	0.62	-0.13	0.686	1.344
slr0020	recG	DNA recombinaserecG	0.306	-0.153	error	-0.601	-0.217	0.022	error	-1.173	-0.652	0.264	-0.949	-0.944	-0.454
slr0021		protease	-0.077	0.018	-0.266	-0.418	0.016	-0.044	error	-0.036	0.017	0.122	0.092	0.325	-0.342
slr0022		hypothetical protein	0.082	0.361	0.188	error	0.057	-0.295	error	-0.219	0.119	error	-0.239	0.124	0.699
slr0023		unknown protein	1.015	error	0.013	-1.131	error	0.868	1.876	0.077	0.099	-0.114	0.386	-0.039	2.077
slr0031		hypothetical protein	0.701	0.359	0.346	-0.101	0.282	0.161	error	-0.453	-0.23	0.104	-0.128	-0.164	0.945
slr0032		probable branched-chain a	-0.293	-0.491	-0.065	0.122	-0.219	-0.262	-0.227	0.032	0.412	1.162	0.23	0.799	-0.718
slr0033		glutamyl-tRNA(Gln) amidotr	-0.028	0.341	0.115	-0.058	-0.138	-0.118	-0.234	-0.064	-0.086	error	-0.224	-0.048	0.848
slr0036	aspC	aspartate aminotransferase	-0.263	-0.188	-0.319	0.114	-0.695	-0.092	-0.392	0.05	-0.262	-0.255	-0.187	-0.118	-1.089
slr0038		hypothetical protein	-0.128	error	-0.32	-0.443	-0.21	-0.315	error	error	0.769	-0.11	0.22	-0.463	-0.391
slr0039		hypothetical protein	-0.063	0.124	0.173	0.697	0.13	-0.003	0.048	0.306	0.457	0.941	0.211	0.467	-0.422
slr0040	cmpA	bicarbonate transport syste	0.612	0.736	0.99	0.129	0.405	0.32	error	error	error	error	error	error	error
slr0041	cmpB	bicarbonate transport syste	error	error	error	error	error	error	error	0.02	0.496	0.388	0.082	0.402	0.375
slr0042		probable porin; major outer	-0.179	-0.241	-0.615	error	-0.755	-0.508	-0.68	-0.312	-0.464	-0.408	-0.437	-0.652	-0.001
slr0043	cmpC	bicarbonate transport syste	0.078	0.044	-0.078	-0.345	0.234	0.233	0.829	-0.186	-0.442	0.297	-0.373	-0.488	-0.777
slr0044	cmpD	bicarbonate transport syste	0.401	error	-0.264	-0.449	0.272	0.76	2.284	error	error	error	error	error	error
slr0049		hypothetical protein	-0.644	-1.093	-1.04	-0.443	-0.407	-0.274	-0.739	error	error	error	error	error	error
slr0050	ycf56	hypothetical protein YCF56	0.197	error	0.191	-0.23	-0.066	0.255	-0.085	error	error	error	error	error	error
slr0051	icfA	carbonic anhydraseicfA	-0.467	-0.565	-0.605	0.117	-0.654	-0.736	-0.569	-0.051	-0.191	-0.598	-0.307	-0.271	0.122
slr0053		hypothetical protein	error	error	error	error	error	error	error	-0.162	0.279	0.421	0.371	-0.138	0.356
slr0054		diacylglycerol kinase	-0.413	error	0.725	0.126	0.68	0.095	0.593	0.013	0.569	0.405	0.298	0.318	-0.218
slr0055	trpG	anthranilate synthasecmp	1.334	0.765	0.42	-1.086	0.98	0.238	error	0.13	0.394	error	0.377	0.31	6.18
slr0056	chlG	chlorophyll a synthasechlG	0.139	0.14	0.788	error	0.532	0.368	0.287	0.207	0.359	0.384	0.755	0.45	1.352
slr0058		hypothetical protein	0.178	0.019	0.056	0.161	1.433	0.768	0.953	0.095	0.244	0.683	1.163	0.002	1.909
slr0059		unknown protein	-0.247	0.116	-0.038	error	-0.001	0.136	-0.337	-0.196	-0.049	-0.296	0.033	-0.247	-0.414
slr0060		unknown protein	error	0.501	0.044	-0.497	0.184	0.304	error	0.011	-0.041	0.309	0.324	0.233	-0.325
slr0061		unknown protein	error	error	error	error	error	error	error	-0.657	0.04	-0.69	-0.405	-0.642	0.069
slr0063		general secretion pathway	-0.249	-0.555	-0.642	0.093	-0.095	0.029	-0.26	-0.267	-0.329	0.048	-0.039	-0.123	-0.678

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sir0064		hypothetical protein	0.271	0.321	0.057	0.105	0.031	0.243	-0.042	0.178	0.24	error	0.036	0.234	1.055
sir0065		hypothetical protein	error	error	error	error	error	error	error	-0.345	-0.036	-0.644	-0.234	-0.481	0.24
sir0066	ribD	riboflavin biosynthesis prote	-0.091	-0.418	-0.68	-1.495	-0.604	-0.039	error	-0.335	-0.306	-0.265	-0.706	-0.348	-1.168
sir0067		MRP protein homolog	-0.204	-0.008	0.111	-0.187	-0.346	-0.064	-0.175	0.079	0.031	-0.26	-0.058	0.088	-0.703
sir0069		unknown protein	-0.049	error	error	-0.739	error	0.346	error	error	error	error	error	error	error
sir0070	fmt	methionyl-tRNA formyltrans	error	error	error	error	error	error	error	-0.16	-0.146	-0.112	-0.472	-0.658	-0.309
sir0072	gidB	glucose inhibited division p	0.278	0.097	0.152	-0.062	-0.249	0.382	0.045	0.071	0.124	-0.123	-0.057	0.045	-0.045
sir0073		two-component sensor histi	-0.113	-0.419	-0.5	0.082	-0.602	-0.38	-0.418	0.127	0.208	-0.141	-0.203	0.405	-0.46
sir0074	ycf24	ABC transporter subunitycf2	0.045	0.388	-0.231	-0.602	-0.315	-0.586	-0.59	0.506	-0.046	0.076	-0.245	0.184	5.182
sir0075	ycf16	ABC transporter ATP-bindin	-0.637	-0.798	-0.537	0.659	0.445	-0.08	-0.261	-0.444	-0.119	0.77	0.54	-0.171	-0.211
sir0076		hypothetical protein	-0.601	-0.503	-0.574	0.618	0.235	-0.125	-0.329	-0.249	-0.596	1.659	0.854	-0.454	-0.508
sir0077	nifS	cysteine desulfurasenifS	-0.19	0.064	0.299	0.683	0.025	-0.117	-0.182	0.026	0.414	0.104	0.286	0.136	-0.432
sir0078		putative 6-pyrrovoyl tetrahy	0.693	error	0.277	error	-0.573	0.767	error	-0.215	0.15	-0.086	0.248	-0.496	5.099
sir0079		probable general secretion	-0.569	-0.707	-0.765	0.345	-0.604	-0.391	-0.573	-0.007	-0.235	0.678	-0.013	-0.349	-0.478
sir0080	mhA	ribonuclease HmhA	0.33	0.437	0.456	0.041	0.591	0.68	0.767	0.278	0.926	0.672	0.651	0.578	1.139
sir0081		two-component response re	-0.549	-0.657	-1.863	-1.062	-1.773	-2.076	-1.489	-0.292	-0.997	-1.954	-1.72	-1.048	-0.525
sir0082		hypothetical protein	0.538	error	1.632	error	0.821	0.255	0.519	1.262	1.882	1.784	1.478	1.895	0.734
sir0083	chrR	RNA helicase LightchrR	-0.386	-0.339	1.061	1.831	0.08	-0.47	-0.452	0.032	0.614	1.942	0.86	0.372	-0.211
sir0084	hisH	amidotransferase HisHhisH	0.743	0.3	-0.142	-0.049	-0.352	0.245	-0.011	0.35	0.259	0.448	0.276	0.564	0.534
sir0086		similar to DnaK protein	-0.168	-0.286	-0.387	0.575	-0.513	-0.275	-0.226	-0.079	0.195	0.17	0.042	0.048	-0.317
sir0088	crfO	beta-carotene ketolasecrfO	0.066	0.5	0.138	-0.47	-0.335	0.022	0.778	error	error	error	error	error	error
sir0089		gamma-tocopherol methyltr	error	-0.418	0.147	-0.015	0.573	0.407	0.668	-0.015	0.551	0.38	0.599	0.523	-0.07
sir0090		probable 4-hydroxyphenylp	error	error	error	error	error	error	error	-0.32	-0.351	-0.779	-0.357	-0.712	-0.323
sir0091		aldehyde dehydrogenase	-0.614	0.476	2.092	0.896	1.859	1.208	3.181	-0.075	0.523	0.719	0.71	0.631	-0.163
sir0092		hypothetical protein	-0.223	0.443	0.5	0.372	0.613	0.341	error	error	error	error	error	error	error
sir0093	dnaJ	DnaJ proteindnaJ	error	1.824	2.107	1.374	2.755	2.193	error	1.78	2.938	2.573	3.141	2.636	2.502
sir0095		O-methyltransferase	0.615	1.487	1.795	1.085	2.348	1.901	-	0.488	1.474	1.295	1.389	1.018	2.386
sir0096		low affinity sulfate transport	-0.106	error	0.297	-0.738	1.173	1.051	6.61	0.116	0.308	0.209	0.472	0.122	0.998
sir0099		putative transposase [ISY3	-0.752	-1.012	-1.078	-0.115	-0.335	-0.305	0.035	-1.206	-0.047	-0.001	-0.465	-0.231	0.587
sir0103		unknown protein	error	error	error	-1.124	0.74	0.097	error	-0.349	0.463	0.894	0.088	0.477	1.595
sir0104		hypothetical protein	-0.261	-0.059	-0.542	-0.57	-0.296	0.093	0.041	-0.552	-0.507	error	-0.459	-0.487	-0.403
sir0105		hypothetical protein	-0.399	error	-0.751	-0.694	-0.081	0.584	1.055	error	error	error	error	error	error
sir0106		unknown protein	0.733	-0.06	0.355	-0.428	error	0.107	error	-0.47	-0.229	-0.471	-0.225	-0.625	0.765
sir0108		unknown protein	0.044	0.121	0.342	0.394	0.014	0.209	0.184	0.155	0.719	0.393	0.339	0.559	0.402
sir0109		unknown protein	1.004	error	error	-1.26	error	0.622	error	-0.323	-0.016	0.107	-0.156	-0.485	0.327
sir0110		hypothetical protein	-0.456	-0.541	-0.617	-0.313	-0.825	-0.525	-0.569	error	error	error	error	error	error
sir0111		unknown protein	error	error	error	error	error	error	error	-0.109	0.22	-0.339	-0.471	-0.554	0.878
sir0112		unknown protein	0.227	0.283	0.642	0.368	1.093	0.524	error	error	error	error	1.019	error	error
sir0114		unknown protein	error	error	error	-1.172	error	error	error	-0.056	0.157	0.38	0.068	-0.148	1.398
sir0115	rpaA, ycf27	response regulator for ener	-0.293	-0.186	-0.129	-0.623	-0.274	0.136	0.22	-0.067	0.364	0.315	0.125	0.501	0.602
sir0116		phycocyanobilin:ferredoxin	0.164	-0.584	0.018	error	error	0.492	error	-0.139	-0.634	0.034	-0.582	-0.404	0.502
sir0118	thiC	thiamine biosynthesis prote	-0.586	-0.677	-1.005	-0.62	-0.91	-0.666	-0.552	-0.12	-0.4	-0.382	-0.251	-0.475	0.202
sir0119		hypothetical protein	-0.443	-0.231	-0.392	-0.141	-0.638	-0.671	-0.419	-0.012	0.439	-0.048	-0.166	0.072	0.131
sir0120		probable tRNA/rRNA methy	-0.295	error	0.417	-0.092	0.169	-0.103	0.343	0.033	0.409	0.819	0.218	0.334	-0.025
sir0121		hypothetical protein	-0.567	-1.045	-1.409	-1.021	-1.322	-0.398	-0.485	error	error	error	error	error	error
sir0142		hypothetical protein	-0.525	-0.23	-0.524	-0.276	-1.194	-0.53	-0.787	-0.124	0.107	0.394	0.03	0.206	-0.039
sir0143		WD-repeat protein	-0.334	0.026	0.071	0.017	-0.128	-0.084	-0.289	-0.275	0.046	0.164	-0.534	0.129	0.316
sir0144		hypothetical protein	-0.786	-0.82	-1.259	-0.61	-1.578	-1.098	-1.11	-1.129	-1.295	-1.699	-1.763	-1.177	-1.405
sir0145		unknown protein	0.036	error	error	-0.868	-0.394	-0.244	-0.45	0.181	0.165	0.392	0.163	-0.142	-0.321
sir0146		hypothetical protein	error	-0.65	-1.234	-0.838	-1.93	-0.389	-0.847	0.017	-0.384	-0.466	-0.938	-0.332	-1.344
sir0147		hypothetical protein	error	error	error	error	error	error	error	-0.371	-0.786	-0.583	-0.954	-0.931	-1.157
sir0148		hypothetical protein	-0.341	-0.629	-1.035	-0.566	-1.275	-0.47	-0.288	-0.121	-0.316	-0.373	-0.732	-0.313	0.032
sir0149		hypothetical protein	error	error	error	error	error	error	error	0.609	0.114	-0.135	-0.24	-0.244	1.067
sir0150		ferredoxin, petF-like protein	-0.354	-0.622	-1.52	-0.997	-1.853	-1.279	-1.208	0.173	-0.591	-0.861	-1.138	-0.622	-0.942
sir0151		unknown protein	-0.317	-0.328	-0.798	-0.245	-0.818	-0.85	-0.678	-0.078	-0.244	-0.33	-0.509	-0.439	0.597
sir0152		serine/threonine protein kin	0.022	-0.266	-0.369	-0.595	-0.52	-0.118	-0.233	0.05	-0.224	0.061	-0.374	-0.351	error
sir0156	clpB	ClpB proteincipB	-0.084	-0.385	0.198	error	error	-0.415	-0.371	-0.17	0.001	0.596	0.271	-0.033	-0.881
sir0157		unknown protein	-0.022	-0.016	0.105	-0.566	-0.219	-0.053	-0.03	error	error	error	error	error	error
sir0161	pilT	twitching motility protein Pil	error	error	error	error	error	error	error	error	error	error	error	error	error
sir0162	pilC	similar to fimbrial assembly	0.04	-0.425	-1.18	-0.693	-0.609	0.102	-0.255	0.003	-0.258	-0.245	-0.411	-0.521	error
sir0163	pilC	similar to fimbrial assembly	0.237	0.213	0.383	-0.025	-0.126	-0.322	-0.394	0.566	0.944	0.258	0.331	1.047	0.279
sir0164	clpP	ATP-dependent Clp proteas	-0.194	0.189	0.629	0.826	0.293	-0.158	-0.685	-0.042	-0.288	-0.821	0.514	-0.651	0.141
sir0165	clpP	ATP-dependent Clp proteas	-0.046	-0.254	-0.94	-0.161	-0.079	-0.554	-0.102	0.392	-0.247	-0.664	0.333	-0.641	0.784
sir0166		putative transposase [ISY5	-0.02	-0.135	-0.205	-0.427	-0.721	0.247	-0.401	-0.357	0.207	1.223	-0.218	0.45	0.046
sir0168		unknown protein	0.78	0.165	-0.202	-0.44	0.233	0.745	0.891	0.157	-0.281	0.281	0.013	-0.271	1.098
sir0169		hypothetical protein	0.452	0.026	0.851	1.687	0.262	0.152	0.28	0.219	1.78	1.603	1.21	1.799	1.304
sir0171	ycf37	photosystem I assembly rel	-0.255	-0.197	-0.254	-0.336	-0.379	0.102	-0.256	-0.352	-0.152	-0.423	-0.344	-0.256	0.138
sir0172		hypothetical protein	-0.754	-1.227	-1.167	-0.524	-0.902	-0.987	-0.83	-0.803	-0.914	-0.973	-0.644	-0.932	0.506
sir0179		hypothetical protein	0.066	1.248	2.001	2.154	1.962	1.408	1.109	0.654	1.474	2.585	1.385	1.346	1.26
sir0180		putative transposase [ISY2	-0.481	0.488	1.319	1.083	0.789	0.197	1.074	-0.069	1.637	1.099	0.348	1.635	-0.223
sir0181		hypothetical protein	error	0.357	-0.186	0.075	0.384	-0.026	0.411	0.227	0.487	0.297	0.399	0.536	-0.596
sir0184		unknown protein	error	error	0.422	-2.451	error	0.291	error	-0.057	0.854	error	0.386	0.037	1.677
sir0185		orotate phosphoribosyltrans	0.534	0.194	0.224	-0.453	-0.054	0.031	-0.09	0.318	0.246	0.299	0.151	0.217	2.019
sir0186	leuA	2-isopropylmalate synthase	-0.379	-0.611	-1.127	0.313	-0.062	-0.42	-0.517	0.044	-0.655	-0.448	0.119	-0.36	-0.031
sir0191		similar to amidase enhance	error	-0.36	0.106	0.879	0.361	0.422	0.207	-0.237	error	0.803	0.945	error	0.78



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios		Data set 1							Data set 2					
Orf	Symbol Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr0306	unknown protein	-0.044	-0.01	0.095	0.105	-0.481	0.042	-0.275	-0.127	-0.208	error	-0.378	-0.212	-1.006
slr0309	probable methyltransferase	-0.301	error	0.353	error	-0.283	-0.183	0.141	-0.449	-0.175	0.355	-0.929	-0.36	0.636
slr0311	two-component sensor hist	0.476	error	0.109	error	0.221	0.414	0.39	-0.267	-0.249	-0.039	-0.489	0.204	1.016
slr0312	two-component response re	-0.066	0.036	0.209	-0.105	-0.177	-0.062	0.094	0.01	0.35	-0.077	-0.076	0.237	0.894
slr0313	hypothetical protein	0.288	0.369	0.18	error	-0.179	-0.144	-0.423	0.341	0.904	-0.04	0.113	0.214	1.004
slr0314	non-heme chloroperoxidase	error	error	error	error	error	error	error	error	error	error	error	error	error
slr0315	probable oxidoreductase	error	error	-0.018	error	-0.014	-0.226	error	-0.49	0.153	1.986	-0.131	-0.247	1.617
slr0316	hypothetical protein	error	error	error	-1.326	error	0.822	error	-0.34	0.279	0.059	-0.119	-0.264	1.047
slr0317	hypothetical protein	error	error	1.054	-1.154	error	0.847	error	-0.131	0.329	0.117	-0.096	-0.179	0.672
slr0318	unknown protein	error	0.266	0.396	0	0.031	0.051	0.22	0.138	0.491	0.026	-0.089	0.09	0.398
slr0319	beta-lactamase	-0.031	error	0.341	-0.061	0.247	0.371	1.5	-0.017	0.22	0.319	0.05	0.189	0.113
slr0320	hypothetical protein	-0.013	1.532	0.859	0.148	0.711	0.2	0.137	0.211	1.162	1.12	0.852	0.764	1.03
slr0321	GTP-binding protein ERA h	0.715	0.492	0.054	-0.731	0.286	0.209	1.071	0.525	0.507	0.481	0.353	0.815	-0.013
slr0322	two-component hybrid sens	error	error	error	error	error	error	error	-0.393	-0.663	-0.113	-0.564	-0.595	-1.374
slr0323	putative alpha-mannosidas	-0.347	-0.35	-0.55	0.253	-0.288	0.02	-0.237	-0.177	-0.398	-0.178	-0.036	-0.741	-0.779
slr0324	probable oligopeptides ABC	0.727	0.847	0.807	0.767	0.57	0.555	0.342	error	error	error	error	error	error
slr0325	hypothetical protein	-0.019	error	0.131	-0.292	0.163	0.075	error	-0.267	0.216	0.065	-0.053	-0.053	1.283
slr0326	hypothetical protein	0.203	0.928	1.777	1.613	1.081	1.013	0.595	0.536	1.718	0.891	1.156	2.372	1.626
slr0327	iron(III) ABC transporter, pe	0.077	0.019	0.302	error	0.259	0.457	0.478	-0.13	0.492	0.131	0.206	0.151	0.889
slr0328	low molecular weight phosph	error	error	0.699	error	1.06	0.86	error	0.056	0.288	0.292	0.218	-0.317	-0.217
slr0329	glucokinase	0.423	0.74	0.319	-0.07	-0.043	-0.013	-0.206	0.207	0.37	-0.276	-0.019	0.05	0.805
slr0331	ndhD1	-0.854	-0.692	-1.095	-0.675	-0.464	-0.473	0.158	-0.226	-0.381	-1.076	-0.149	-0.279	-0.483
slr0333	unknown protein	error	error	error	-1.451	error	0.313	error	0.163	0.402	-0.395	0.17	-0.489	-0.17
slr0334	unknown protein	0.334	0.027	-0.439	-0.764	-0.359	-0.152	error	0.028	-0.034	0.538	-0.382	-0.138	-0.843
slr0335	apcE	-0.76	-1.047	-2.17	-1.381	-2.214	-1.719	-1.358	-0.187	-1.219	-2.505	-2.014	-1.293	-2.02
slr0337	hypothetical protein	0.871	1.426	-0.396	-0.647	0.29	0.351	error	0.286	-0.28	0.21	-0.464	-0.373	-0.596
slr0338	probable oxidoreductase	-0.48	-0.359	-0.419	0.406	0.026	-0.134	0.818	-0.23	0.09	0.026	0.517	-0.178	5.474
slr0341	unknown protein	0.095	-0.008	0.17	0.353	-0.004	0.406	0.01	-0.017	0.3	0.36	-0.235	0.295	-0.555
slr0342	petB	-0.736	-1.051	-1.436	-0.176	-0.908	-0.711	-0.206	-0.179	-0.354	-0.856	-0.154	-0.244	-0.352
slr0343	petD	-0.436	-0.783	-1.399	-0.326	-0.8	-0.4	0.12	-0.14	-0.679	-0.428	-0.251	-0.596	0.346
slr0344	probable glycosyltransferas	error	error	-0.364	-1.134	error	0.075	error	-0.825	-0.706	0.721	-0.627	-0.658	-1.088
slr0345	unknown protein	error	error	-0.055	error	-0.219	-0.005	error	0.227	0.706	-0.104	0.184	0.232	1.562
slr0346	rcn	0.448	-0.121	error	-1.221	-0.521	-0.268	2.066	-0.121	-0.308	-0.685	-0.722	-0.587	1.163
slr0347	probable permease protein	error	error	error	error	1.276	error	error	0.053	0.203	0.065	0.125	-0.499	1.303
slr0348	hypothetical protein	-0.409	-0.245	-0.17	-0.302	0.052	0.001	0.601	error	error	error	error	error	error
slr0350	putative transposase [ISY5	-0.195	-0.218	-0.154	0.65	-0.561	-0.3	-0.313	-0.417	-0.23	1.001	-0.729	-0.232	-0.882
slr0351	hypothetical protein	0.232	error	-0.182	-0.415	-1.004	-0.255	error	-0.285	0.004	-0.115	-0.754	-0.271	0.783
slr0352	putative transposase [ISY1	-0.562	-0.716	-0.468	0.368	-0.6	-0.589	-0.598	-1.03	-0.21	0.659	-0.675	-0.516	-1.274
slr0353	unknown protein	0.588	error	0.628	error	0.584	0.526	error	1.118	2.204	1.599	1.772	2.079	2.857
slr0354	ATP-binding protein of ABC	1.38	1.189	0.797	0.453	0.956	0.281	0.198	0.949	0.908	0.501	0.594	0.78	1.116
slr0355	hypothetical protein	0.627	0.62	0.014	0.444	0.384	-0.141	-0.332	0.921	0.883	1.108	0.612	0.781	-0.295
slr0356	hypothetical protein	0.012	0.286	0.341	1.318	0.887	0.47	0.569	0.648	1.196	1.28	0.903	1.14	0.357
slr0357	hisS	0.124	error	0.057	0.17	0.548	0.038	1.13	-0.17	0.127	-0.184	0.104	0.076	0.881
slr0358	unknown protein	-0.009	-0.397	-0.773	0.169	0.084	0.091	-0.065	-0.15	-0.39	0.405	-0.096	-0.536	-0.354
slr0359	hypothetical protein	0.329	0.321	-0.121	-0.893	error	-0.193	error	-0.059	-0.181	0.719	-0.623	-0.281	0.51
slr0360	hypothetical protein	-0.44	-0.627	-0.376	0.009	-0.382	-0.244	0.062	-0.747	-0.781	-0.764	-0.791	-0.688	0.922
slr0361	probable ribosomal large su	0.057	0.2	0.457	error	-0.168	0.285	error	error	error	error	error	error	error
slr0362	hypothetical protein	error	error	error	error	error	error	error	-0.373	-0.244	-0.677	-0.335	-0.49	0.258
slr0363	hypothetical protein	-0.18	0.312	0.332	0.246	0.109	0.317	error	-0.193	0.353	0.49	0	0.18	0.929
slr0364	hypothetical protein	-0.295	-0.106	-0.018	0.317	-0.42	-0.197	-0.056	error	error	error	error	error	error
slr0366	unknown protein	-0.143	error	0.198	-0.226	0.058	0.429	error	-0.651	error	-0.07	-0.512	error	0.588
slr0368	unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slr0369	RND multidrug efflux transp	-0.477	-0.461	-0.507	0.321	-0.364	-0.617	-0.51	-0.56	-0.607	-0.768	-0.626	-0.456	0.309
slr0370	succinate-semialdehyde de	0.128	0.244	-0.079	-0.004	-0.136	0.076	-0.034	0.147	0.217	0.701	0.273	error	0.054
slr0373	hypothetical protein	-0.345	-0.105	1.181	1.605	0.755	0.169	-0.305	0.075	0.763	2.102	0.573	0.806	-0.182
slr0374	hypothetical protein	0.162	-0.293	0.295	1.158	-0.031	-0.591	-0.281	0.294	-0.057	0.593	-0.087	0.028	-0.123
slr0376	hypothetical protein	0.559	0.382	0.744	1.076	0.545	0.144	0.225	0.546	0.538	0.46	0.584	0.257	-0.146
slr0377	unknown protein	error	error	-0.474	-0.286	-0.153	-0.101	-0.28	0.052	-0.038	1.061	0.026	0.003	0.003
slr0378	similar to 7-beta-(4-carboxy	-0.036	0.48	0.289	0.486	0.117	0.013	-0.158	-0.236	0.168	0.082	-0.031	-0.082	0.611
slr0379	thymidylate kinase	-0.259	0.16	-0.172	0.316	-0.022	0.113	-0.183	0.177	0.498	0.76	0.181	0.511	-0.032
slr0380	hypothetical protein	-0.442	0.58	1.112	1.218	1.464	0.876	0.386	0.002	0.66	1.642	1.075	0.884	0.396
slr0381	lactoylglutathione lyase	error	error	error	error	error	error	error	-0.011	0.688	1.88	1.908	0.348	1.935
slr0383	hypothetical protein	0.055	error	0.263	-0.277	-0.052	0.272	1.892	0.135	0.32	0.685	0.077	0.106	-0.583
slr0384	sulfolipid sulfoquinovosylidi	0.073	0.392	0.802	1.215	1.114	0.857	0.759	0.003	0.985	1.152	0.692	0.845	0.27
slr0386	unknown protein	-0.061	error	0.152	error	-0.182	0.047	error	-0.384	error	0.33	-0.089	error	0.662
slr0387	nifS	0.163	0.766	1.424	0.958	1.417	0.942	1.428	-0.318	0.656	1.062	0.45	0.395	1.162
slr0388	hypothetical protein	error	error	error	error	error	0.415	error	-0.079	0.478	error	0.196	0.492	1.445
slr0392	unknown protein	error	error	error	error	error	error	error	0.229	-0.16	1.359	0.123	-0.543	0.522
slr0393	unknown protein	-0.392	error	error	0.403	-0.164	-0.154	-0.391	error	error	error	error	error	error
slr0394	pgk	-0.58	-0.777	-1.022	0.58	-0.052	-0.089	0.365	0.078	-0.327	-0.281	0.555	-0.332	1.711
slr0395	nltB	0.586	0.049	-0.275	-0.318	-0.468	0.303	1.358	-0.065	-0.255	0.087	-0.52	-0.486	-0.745
slr0397	hypothetical protein	error	error	0.059	-0.927	error	0.344	error	-0.173	0.57	0.272	0.042	0.365	1.195
slr0398	unknown protein	-0.297	-0.365	-0.129	0.249	-0.082	0.089	0.036	-0.147	-0.023	error	0.011	-0.127	5.584
slr0399	ycf39	0.135	-0.039	0.45	0.019	-0.091	-0.427	-0.331	-0.088	0.305	-0.008	-0.018	0.269	1.2
slr0400	hypothetical protein	0.161	error	0.079	-0.47	-0.821	-0.115	-0.221	error	error	error	error	error	error



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr0401		periplasmic polyamine-bind	0.005	-0.065	0.067	0.844	-0.565	-0.41	-0.273	0.197	-0.101	0.599	0.111	-0.178	-0.704
slr0402		hypothetical protein	0.037	0.604	0.611	-1.235	-0.091	0.212	error	0.178	0.298	-	0.004	0.094	-0.146
slr0404		hypothetical protein	-0.463	-0.207	0.127	error	1.017	0.303	0.071	-0.095	0.572	0.745	1.391	0.555	1.707
slr0406	pyrC	dihydroorotasepyrC	-0.188	-0.092	0.055	1.443	-0.375	-0.558	-0.713	-0.068	-0.006	-0.069	-0.293	-0.047	-1.176
slr0407		hypothetical protein	error	0.666	0.611	-0.663	0.289	0.399	error	error	error	error	error	error	error
slr0408		unknown protein	error	error	0.065	0.129	-0.349	-0.512	-0.19	0.498	1.292	0.977	0.446	1.209	1.246
slr0415	nhaS5	Na <sup>+</sup> /H <sup>+</sup> antiporternhaS5	-0.013	0.372	-0.148	0.354	0.057	0.312	0.552	-0.139	-0.008	0.061	-0.036	-0.085	-0.663
slr0416		unknown protein	error	error	error	-0.977	error	0.67	error	-0.642	0.253	-0.513	0.242	-0.511	1.27
slr0417	gyrA	DNA gyrase A subunitgyrA	-0.152	-0.181	0.309	0.055	-0.269	-0.209	-0.356	-0.243	0.06	-0.558	-0.327	-0.316	-0.061
slr0418		putative transcription factor	error	error	error	error	error	error	error	0.118	0.299	error	-0.108	0.181	0.651
slr0420		hypothetical protein	-	error	-0.906	-0.697	error	-0.186	error	-0.15	-0.199	0.493	0.145	-0.15	-0.494
slr0421		unknown protein	0.094	error	0.016	-0.229	-0.177	0.046	error	-0.201	0.132	-0.092	-0.128	0.147	0.411
slr0423		hypothetical protein	error	error	error	error	error	error	error	0.604	0.702	1.746	2.529	0.288	0.096
slr0426	folE	GTP cyclohydrolase IfolE	0.108	0.795	0.783	0.919	-0.072	-0.386	-0.528	0.439	1.279	0.819	0.173	0.914	0.286
slr0427		putative competence-dama	0.667	0.444	1.58	error	0.457	0.273	error	0.021	0.504	-0.108	-0.178	0.142	0.958
slr0431		hypothetical protein	0.142	-0.106	error	error	-0.027	0.116	0.619	0.062	0.375	-0.036	0.351	0.279	0.78
slr0434	efp	elongation factor Pefp	-0.358	-0.419	-0.125	0.289	-0.129	-0.227	-0.463	-0.13	-0.013	-0.288	0.093	-0.23	0.719
slr0435	accB	biotin carboxyl carrier prote	0.166	error	-0.191	0.017	-0.188	-0.231	-0.243	error	error	error	error	error	error
slr0436	ccmK	carbon dioxide concentratin	0.351	0.108	-0.216	error	error	-0.139	-0.186	error	error	error	error	error	error
slr0438		hypothetical protein	-0.102	-0.001	0.131	0.113	-0.194	0.16	0.224	-0.05	0.407	0.185	-0.095	0.106	-0.45
slr0439		unknown protein	error	error	error	error	error	error	error	-0.309	-0.182	-0.569	-0.556	-0.712	0.184
slr0440		hypothetical protein	error	error	error	error	error	error	error	-0.166	0.179	-0.08	0.094	-0.372	0.628
slr0442		unknown protein	0.772	error	-0.526	-0.734	-0.061	-0.313	-0.532	-0.237	-0.029	0.378	0.052	0.029	1.384
slr0443		hypothetical protein	0.629	1.703	1.319	0.472	1.026	0.698	0.418	1.177	1.282	0.999	1.015	1.088	1.806
slr0444	aroA	3-phosphoshikimate 1-carb	0.169	-0.073	-0.048	0.373	-0.229	0.156	-0.104	-0.1	0.183	0.104	-0.135	0.282	0.043
slr0445		hypothetical protein	error	0.343	0.567	-0.409	0.648	0.62	error	0.382	0.448	0.125	0.466	0.347	0.681
slr0446	dnaX	DNA polymerase III delta' s	0.324	0.359	0.642	0.64	0.208	0.064	0.291	0.127	0.447	0.192	0.011	0.305	-0.614
slr0447		substrate-binding protein of	-0.521	-0.742	-1.509	-0.682	-2.018	-1.677	-1.454	0.099	-0.657	-0.875	-0.924	-0.495	-0.871
slr0448	radA	DNA repair protein RadAra	error	error	0.362	error	-0.133	error	error	-0.097	0.028	-0.082	-0.053	-0.047	0.6
slr0449		probable transcriptional reg	0.181	error	0.594	-1.096	error	0.575	0.177	-0.419	-0.056	-0.009	-0.644	-0.207	0.8
slr0451		putative helicase	0.069	error	0.149	error	0.093	0.241	0.35	-0.4	0.169	error	-0.284	-0.204	0.6
slr0452	ilvD	dihydroxyacid dehydrataseil	-0.713	-0.81	-1.566	-0.946	-1.411	-0.946	-0.705	-0.291	-0.878	-0.657	-0.858	-0.898	-0.932
slr0453		hypothetical protein	-0.267	-0.061	-0.304	-0.041	-0.017	-0.059	-0.245	-0.062	-0.143	0.286	0.114	-0.432	-0.414
slr0454		RND multidrug efflux transp	0.193	0.511	0.661	0.868	0.488	0.155	0.209	0.304	0.952	0.875	0.51	0.835	-0.159
slr0455		hypothetical protein	error	-0.13	0.235	-0.742	0.067	0.099	error	0.144	0.097	1.74	0.436	0.303	1.114
slr0456		unknown protein	0.103	error	error	error	-0.018	-0.051	0.712	0.1	0.362	0.418	0.179	0.488	1.271
slr0457		tRNA pseudouridine syntha	0.235	0.412	0.221	0.077	0.047	-0.071	-0.306	-0.322	-0.325	-0.418	-0.605	error	-0.069
slr0458		unknown protein	2.076	error	error	-0.924	error	error	error	0.136	0.349	1.956	0.529	-0.4	0.901
slr0459		hypothetical protein	-0.149	error	-0.203	0.063	-0.168	-0.068	0.281	-0.438	-0.224	error	-0.381	-0.081	0.238
slr0460		putative transposase [ISY33	-0.258	error	-0.789	error	error	-0.984	-0.811	-0.623	-0.323	-0.064	-0.437	-0.147	0.102
slr0462		putative transposase [ISY33	-0.603	-0.748	-0.166	0.169	-0.33	-0.036	-0.012	-0.782	-0.028	0.195	-0.217	-0.392	-0.477
slr0467	natA	conserved component of Ase	-0.12	0.097	-0.068	-0.68	-0.761	0.358	error	error	error	error	error	error	error
slr0468		unknown protein	-0.377	error	-1.156	-0.461	-0.879	-0.322	0.21	-0.886	-0.926	-0.741	-0.488	-0.83	0.593
slr0469	rps4	30S ribosomal protein S4rp	0.132	0.464	0.735	1.903	0.492	-0.132	0.223	0.824	1.316	0.809	1.106	1.19	-0.375
slr0473	phy	phytochromophy	-0.019	-0.135	-0.034	1.542	1.748	0.82	1.039	0.058	0.459	1.413	1.702	0.615	0.214
slr0474		two-component response re	0.471	error	0.146	-1.196	-0.355	0.293	-0.282	-0.206	-0.163	0.255	-0.406	-0.425	0.798
slr0476		unknown protein	error	error	error	error	error	error	error	-0.418	-0.576	-1.019	-0.848	-0.703	0.419
slr0477	purN	phosphoribosylglycinamide	0.659	-0.335	0.461	-0.834	-0.274	-0.074	error	-0.021	0.316	-0.25	-0.498	0.011	0.323
slr0479		hypothetical protein	0.569	error	1.356	-0.105	0.239	0.441	0.524	0.15	0.873	0.272	0.404	0.746	1.259
slr0480	ycf46	hypothetical protein YCF46	0.054	-0.326	-0.654	-0.665	-0.832	-0.428	-0.215	-0.34	-0.217	-0.072	-0.489	-0.398	0.395
slr0482		unknown protein	error	error	0.329	-0.666	-0.207	-0.305	-0.318	-0.168	0.283	0.172	-0.182	0.26	-0.514
slr0483		hypothetical protein	0.007	0.034	-0.941	0.294	-0.067	0.109	0.334	-0.067	-0.575	-0.783	-0.472	-0.527	0.286
slr0484		two-component sensor histi	-0.25	-0.581	-0.537	0.379	-0.673	-0.489	-0.407	-0.271	-0.434	-0.536	-0.499	-0.296	-0.579
slr0487		hypothetical protein	error	1.096	0.487	-0.489	0.343	0.189	error	0.377	0.616	0.613	-0.189	0.267	-0.263
slr0488		virulence factor MviN homo	-0.359	-0.163	-0.51	-0.495	-0.629	-0.798	-0.437	-0.278	-0.153	-0.219	-0.333	-0.164	-0.964
slr0489		unknown protein	error	error	-0.333	-0.115	0.951	0.209	error	-0.241	0.006	0.504	0.378	-0.172	-0.457
slr0491		hypothetical protein	error	-0.01	0.332	-0.314	0.144	0.095	error	0.047	0.273	0.044	0.095	0.232	0.088
slr0492	menE	O-succinylbenzoic acid-Co	-0.124	error	-0.777	-0.854	-0.934	-0.357	-1.045	-0.203	-0.416	0.527	-0.559	-0.358	-0.569
slr0493		similar to mannose-1-phosp	-0.473	-0.285	-0.352	0.027	0.662	0.193	0.421	-0.156	0.225	0.305	0.397	-0.08	-0.539
slr0495		Hell protein homolog	error	-0.119	error	-0.914	0.502	0.598	0.47	0.229	0.185	0.277	-0.093	-0.189	0.846
slr0496		unknown protein	0.3	1.514	0.161	-0.559	-0.132	-0.142	0.992	0.269	0.17	-0.605	-0.428	0.08	-0.426
slr0498		unknown protein	-0.163	-0.26	-0.234	0.189	-0.005	0.466	0.479	0.003	0.072	0.341	0.155	0.243	-0.412
slr0500	hisB	imidazoleglycerol-phospha	error	error	error	error	1.151	error	error	0.664	1.927	1.626	1.31	1.808	1.849
slr0502	cobW	cobalamin synthesis protei	error	error	error	error	error	error	error	-0.012	-0.026	-0.156	-0.039	-0.198	-0.058
slr0503	ycf66	hypothetical protein YCF66	-0.59	-0.475	-0.755	-0.328	-0.233	-0.108	0.091	0.056	0.047	error	0.478	-0.062	-0.41
slr0505		hypothetical protein	-0.175	0.185	0.054	0.167	0.476	0.254	-0.154	0.223	0.253	-0.07	0.389	-0.318	1.091
slr0506	por	light-dependent NADPH-pro	-0.629	-0.462	-0.837	-0.628	-1.053	-0.542	-0.527	-0.185	-0.373	-0.738	-0.72	-0.155	-1.396
slr0509		hypothetical protein	0.58	error	0.258	error	-0.155	0.46	error	error	error	error	error	error	error
slr0510		hypothetical protein	error	error	error	error	error	error	error	-0.25	0.008	-0.354	-0.761	-0.382	-0.595
slr0511		putative transposase [ISY53	0.132	-0.222	0.056	-0.248	-0.403	-0.213	-0.399	-0.59	0.147	0.366	-0.686	-0.095	-0.058
slr0513		periplasmic iron-binding pro	-1.608	-1.485	0.231	-0.006	-0.786	-0.215	0.022	0.05	-0.048	-1.579	-1.579	-0.097	-1.416
slr0514		unknown protein	-0.32	0.283	0.277	0.593	-0.046	0.302	-0.131	0.46	0.378	0.296	-0.368	-0.047	-0.732
slr0516		hypothetical protein	0.92	-0.053	0.435	-1.083	-0.299	0.119	error	error	error	error	error	error	error
slr0517		hypothetical protein	-0.322	-0.371	-0.45	0.007	-0.485	0.25	0.189	-0.072	-0.102	-0.068	-0.384	-0.249	-1.07
slr0518		similar to alpha-L-arabinofu	-0.589	-0.807	-0.477	0.573	-0.034	0.138	0.013	-0.262	-0.506	-0.842	-0.137	-0.934	-0.697

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis PCC6803*

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sir0519		hypothetical protein	-0.4	-0.665	-0.639	0.028	error	-0.214	0.095	-0.143	-0.155	0.014	-0.158	-0.226	-1.041
sir0520	purl	phosphoribosyl formylglycyl	0.32	-0.039	-0.17	-0.187	-0.233	0.132	error	-0.027	-0.092	-0.027	-0.387	-0.169	1.05
sir0521		unknown protein	-0.059	0.082	-0.135	-0.004	-0.526	0.512	0.064	-0.18	-0.265	-0.354	-0.292	-0.443	-1.608
sir0522		unknown protein	error	error	error	error	error	0.755	error	-0.304	-0.258	-0.156	0.11	-0.624	-0.71
sir0523		similar to dethiobiotin synth	-0.019	-0.072	0.198	0.5	0.183	0.231	0.158	0.083	0.531	0.285	0.362	0.543	0.929
sir0525	chlM	Mg-protoporphyrin IX methyl	-0.111	0.32	0.799	0.13	0.197	0.355	-0.311	0.276	0.875	0.984	0.719	0.893	0.693
sir0526	panB	3-methyl-2-oxobutanoate hy	0.711	0.467	0.588	-0.181	0.029	-0.056	error	-0.007	0.428	0.06	0.223	0.013	1.592
sir0527		transcription regulator ExsE	0.497	-0.003	0.376	-0.918	-0.613	0.093	-0.236	-0.058	0.138	-0.246	-0.525	-0.094	-0.172
sir0528	murE	UDP-N-acetylmuramoylalan	-0.321	-0.364	-0.676	error	-0.779	0.014	-0.208	0.112	0.015	-0.218	-0.354	-0.261	-0.694
sir0529	gggB	glucosylglycerol transport s	error	0.812	1.546	0.183	1.241	0.693	error	-0.491	0.614	0.532	0.433	0.511	1.189
sir0530	gggC	glucosylglycerol transport s	0.83	0.838	1.238	1.001	0.602	0.6	0.787	0.476	0.644	0.85	0.393	0.579	-0.251
sir0531	gggD	glucosylglycerol transport s	error	0.05	0.057	0.314	-0.282	0.104	0.105	0.758	0.614	1.647	0.341	0.283	0.261
sir0533		two-component sensor histi	-0.032	0.191	0.123	-0.29	0.236	0.285	0.361	-0.29	0.114	0.198	-0.115	error	-0.346
sir0534		probable transglycosylase	0.364	-0.134	-0.414	-0.421	-0.364	-0.606	-0.223	0.061	0.014	-0.312	-0.101	-0.118	0.67
sir0535		protease	error	error	error	error	error	error	error	0.205	0.098	error	0.212	0.209	0.604
sir0536	hemE	uroporphyrinogen decarbox	-0.337	-0.485	-0.637	0.212	-0.811	-0.909	-0.968	-0.052	-0.081	-0.607	-0.276	-0.437	0.04
sir0537		putative sugar kinase	error	error	-0.084	error	error	0.253	1.182	-0.065	0.134	0.132	0.082	0.293	1.728
sir0541		probable amidotransferase	error	0.243	-0.02	-0.74	0.185	0.523	error	-0.265	-0.179	1.605	0.127	-0.52	-0.9
sir0542	cipP	ATP-dependent protease C	-0.495	-0.264	0.191	0.858	0.168	0.016	-0.354	0.201	0.513	-0.445	0.527	0.11	0.421
sir0543	trpB	tryptophan synthase beta s	-0.074	-0.725	-0.892	-0.614	-0.608	-0.712	-0.307	-0.42	-0.421	0.801	-0.163	-0.515	5.341
sir0544		ATP-binding protein of ABC	0.718	0.825	0.908	0.543	1.32	0.777	0.898	error	error	error	error	error	error
sir0545		hypothetical protein	-0.104	-0.138	-0.173	-0.274	0.147	0.343	-0.037	0.133	0.384	0.549	0.219	0.307	-0.317
sir0546	trpC	indole-3-glycerol phosphate	0.512	0.332	1.27	0.06	0.493	0.177	0.099	-0.105	0.417	0.075	-0.079	0.227	0.019
sir0549	asd	aspartate beta-semialdehyd	0.536	0.613	0.559	0.72	0.081	0.064	0.324	0.785	0.939	-	0.649	0.817	-0.409
sir0550	dapA	dihydrodipicolinate synthas	1.076	0.202	0.282	0.486	-0.105	0.14	0.006	0.475	0.425	0.484	0.367	0.858	0.147
sir0551		hypothetical protein	0.074	-0.101	0.746	2.329	0.438	0.216	0.42	0.414	0.762	1.484	1.158	0.829	-0.163
sir0552		hypothetical protein	-0.257	-0.333	-0.308	0.291	0.07	-0.193	0.189	0.287	-0.164	1.209	0.475	-0.402	0.423
sir0553		hypothetical protein	0.104	-0.084	-0.016	0.872	-0.104	-0.21	-0.12	0.194	0.315	-0.083	0.205	0.101	-0.748
sir0554		hypothetical protein	0.3	0.355	0.058	0.567	0.231	0.281	0.201	0.363	0.884	1.064	0.428	0.783	-0.433
sir0556		hypothetical protein	0.842	0.577	0.826	0.119	0.335	0.531	error	0.048	0.537	0.344	0.367	0.147	0.252
sir0557	valS	valyl-tRNA synthetasevalS	0	-0.296	-0.574	0.065	-0.226	-0.365	-0.22	0.101	-0.164	-0.371	-0.13	-0.205	0.475
sir0559	nalB	periplasmic binding protein	0.108	-0.072	0.059	0.212	0.107	-0.021	-0.292	0.082	0.555	0.63	0.994	0.454	0.757
sir0565		hypothetical protein	0.063	-0.061	0.276	0.455	0.848	0.451	0.372	0.038	0.642	1.136	1.486	0.525	0.98
sir0569		unknown protein	-0.044	-0.272	-0.29	-0.283	-0.011	0.274	0.102	-0.022	-0.361	-0.043	0.048	-0.158	-0.88
sir0572		unknown protein	0.293	error	error	-0.892	-0.699	0.484	error	0.385	-0.224	-0.768	-1.126	-0.532	-1.54
sir0573		unknown protein	-0.291	-0.09	-0.418	-0.332	-0.333	0.442	0.092	-0.1	0.217	-0.447	-0.232	-0.227	0.009
sir0574		cytochrome P450	error	error	-0.77	error	-1.028	-0.486	-0.254	-0.28	-0.433	0.158	-0.718	-0.647	0.56
sir0575		hypothetical protein	0.006	0.03	-0.124	error	0.256	-0.359	error	-0.043	0.178	-0.023	0.057	0.098	1.485
sir0579		unknown protein	error	0.161	-0.129	error	0.047	0.085	0.079	0.052	0.398	0.383	0.454	-0.105	1.262
sir0580		aluminum resistance protein	-0.602	-0.326	-0.212	0.804	0.26	0.059	-0.248	error	error	error	error	error	error
sir0581		unknown protein	-	1.366	1.613	0.321	error	1.062	error	0.522	1.107	1.304	1.584	1.181	1.804
sir0582		unknown protein	0.057	0.126	0.289	0.976	0.878	0.264	0.519	-0.02	0.398	0.284	0.952	0.055	0.79
sir0583		similar to GDP-fucose synth	-0.288	-0.993	-0.902	-0.742	-0.819	-0.338	-0.187	-0.884	-0.841	-0.896	-0.74	-1.018	0.322
sir0585	argG	argininosuccinate synthetase	-0.065	-0.259	0.073	0.646	0.621	0.059	0.162	-0.011	0.415	-0.144	0.565	0.139	0.943
sir0586		hypothetical protein	0.133	0.308	-0.259	error	-0.385	0.159	-0.068	0.178	0.285	0.441	-0.091	-0.02	-1.195
sir0587		unknown protein	error	-0.036	0.007	-0.016	-0.579	-0.29	-0.424	0.451	0.979	0.451	0.211	0.935	-0.143
sir0588		hypothetical protein	0.331	-0.313	0.1	-0.348	0.019	-0.113	error	0.064	0.08	1.514	0.567	0.044	1.101
sir0589		hypothetical protein	error	error	error	error	error	-0.269	error	-0.171	0.205	0.286	0.208	0.213	0.586
sir0590		hypothetical protein	0.343	-0.264	-0.17	-0.764	-0.266	0.343	1.485	0.356	0.475	0.856	0.752	0.296	1.381
sir0591		ribonucleoside-diphosphate	-0.498	-0.454	-0.222	0.741	0.257	0.263	0.323	-0.484	-0.393	0.008	0.545	-0.502	1.395
sir0592		hypothetical protein	-0.123	0.005	-0.326	0.071	-0.346	-0.087	0.362	-0.458	-0.161	-0.082	-0.254	-0.376	0.53
sir0593	samp	cAMP binding membrane p	-0.485	-0.913	-1.778	-1.851	-2.833	-2.314	-1.729	0.089	-0.542	-1.069	-1.882	-0.727	-1.015
sir0594		hypothetical protein	0.444	0.157	0.69	error	0.53	0.037	error	0.189	0.518	0.686	0.745	0.473	1.345
sir0596		hypothetical protein	-0.22	error	0.716	0.137	-0.195	0.172	-0.058	-0.072	0.473	0.45	-0.101	0.676	-0.872
sir0597	purH	phosphoribosyl aminoimida	-0.152	-0.14	0.159	0.261	-0.403	-0.262	-0.156	0.142	0.4	-0.171	0.019	0.381	-0.05
sir0598		hypothetical protein	-0.351	error	-0.078	0.353	-0.43	-0.036	-0.231	0.106	0.23	1.77	0.405	0.356	-0.095
sir0599		serine/threonine kinase	-0.125	0.031	0.091	0.168	-0.274	-0.292	-0.518	-0.065	-0.081	-0.083	-0.188	-0.157	0.568
sir0600		NADP-thioredoxin reductase	0.293	0.705	1.277	error	0.692	-0.301	0.045	0.205	0.479	0.313	0.415	0.527	-0.338
sir0601		unknown protein	0.308	1.047	2.249	2.317	1.328	1.039	0.963	0.348	1.53	1.937	0.936	1.287	0.356
sir0602		unknown protein	-0.428	error	-0.371	error	0.044	0.277	-0.22	0.036	0.088	0.289	0.434	-0.006	-0.166
sir0603	dnaE	DNA polymerase III alpha s	-0.4	-0.613	-0.708	-0.282	-0.356	0.289	0.048	-0.825	-1.076	-0.585	-0.174	-1.012	-0.582
sir0604		GTP-binding protein	-0.378	-0.359	-0.133	0.867	-0.231	-0.484	-0.345	-0.026	0.13	-0.488	-0.082	0.141	0.83
sir0605		hypothetical protein	error	error	error	error	error	-0.116	error	0.71	1.469	1.349	0.752	0.793	1.204
sir0606		hypothetical protein	error	error	error	error	error	error	error	-0.181	-0.156	-0.1	0.239	-0.604	0.912
sir0607		hypothetical protein	0.386	0.049	-0.226	-0.589	-0.111	0.068	0.512	0.075	0.103	-0.214	0.239	-0.334	1.364
sir0608	hisIE	histidine biosynthesis bifun	-0.414	-0.341	-0.68	-0.183	-0.66	-0.336	-0.292	-0.16	-0.191	0.114	-0.21	-0.353	-1.035
sir0609		hypothetical protein	-0.483	-0.592	-0.559	0.022	0.137	0.023	-0.127	-0.471	-0.608	-0.06	0.408	-0.005	1.142
sir0610		hypothetical protein	error	error	error	error	error	error	error	0.032	0.676	0.765	0.353	0.384	1.233
sir0611	sds	solaneyli diphosphate synt	-0.468	-0.449	-0.366	0.198	-0.644	-0.78	-0.688	0.169	1.758	1.052	0.778	1.605	0.232
sir0612		probable pseudouridine syr	1.395	error	1.377	-0.642	error	0.472	error	-0.072	0.717	error	0.002	0.502	0.869
sir0613		hypothetical protein	0.206	0.303	0.668	0.38	0.245	0.097	0.51	0.249	0.642	0.646	0.275	0.524	-0.581
sir0615		ATP-binding protein of ABC	-0.24	-0.11	-0.04	-0.008	error	-0.105	error	0.244	0.487	-0.106	0.284	0.007	-0.478
sir0616		unknown protein	0.332	-0.179	-0.128	-0.292	0.212	-0.358	-0.074	-0.356	-0.116	0.746	-0.393	-0.318	1.135
sir0617		unknown protein	-0.318	0.515	-0.216	-0.155	-0.018	-0.016	-0.421	-0.276	0.028	-0.056	-0.077	-0.19	-0.145
sir0618	cobQ	cobryic acid synthasecobQ	0.056	0.165	0.246	0.355	-0.204	0.029	error	-0.082	-0.001	-0.196	-0.277	error	0.292

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sir0619		hypothetical protein	-0.162	-0.34	-0.362	error	-0.301	-0.116	0.088	-0.19	-0.613	-0.821	-0.334	-0.932	0.282
sir0623	trxA	thioredoxintrxA	error	error	error	error	error	error	error	-0.691	-0.813	-1.1	-0.54	-0.979	-0.568
sir0624		UDP-N-acetylglucosamine	-0.61	-1.067	-0.976	-0.252	-0.443	-0.348	-0.505	-0.396	-0.472	-0.988	-0.733	-0.789	0.52
sir0625		hypothetical protein	-0.134	-0.153	-0.303	error	-0.926	0.288	0.428	-0.425	-0.7	-0.392	-0.641	-0.176	0.012
sir0626		probable glycosyltransferase	-0.662	-0.092	0.148	-0.097	0.231	0.089	0.395	-0.133	0.431	0.276	0.427	-0.106	-0.344
sir0628	rps14	30S ribosomal protein S14	0.997	1.597	1.884	2.677	1.463	0.631	0.658	1.33	2.244	2.05	1.258	2.141	0.607
sir0630		hypothetical protein	0.889	error	0.677	0.063	0.579	0.578	0.507	0.346	0.539	-0.137	0.339	0.453	1.155
sir0633	thiG	thiamine biosynthesis prote	-0.287	-0.22	-0.19	0.3	-0.206	-0.392	-0.202	-0.142	-0.132	-0.072	-0.304	-0.104	-0.147
sir0634		unknown protein	error	1.678	0.981	-0.553	0.325	0.31	error	-0.092	0.454	error	0.179	0.159	1.214
sir0635		hypothetical protein	-0.269	error	-0.108	error	-0.865	-0.407	-0.349	-0.216	0.033	error	-0.345	-0.077	-0.557
sir0636		probable cobalamin [5'-pho	error	0.142	error	-1.044	-0.917	0.131	error	error	error	error	error	error	error
sir0637		hypothetical protein	0.104	0.18	0.165	0.316	0.323	-0.033	0.356	0.297	0.781	0.409	0.583	0.776	0.261
sir0638	glyQ	glycyl-tRNA synthetase alp	error	error	error	error	error	error	error	0.431	0.35	error	0.365	0.331	-0.245
sir0639		mechanosensitive ion chan	-0.049	-0.268	0.668	-0.087	0.135	0.254	error	-0.239	0.206	-0.122	-0.097	0.101	-0.468
sir0640		two-component sensor histi	error	error	error	error	error	error	error	0.401	-0.691	-0.599	-0.148	-0.475	-1.524
sir0642		hypothetical protein	-0.165	error	0.437	0.61	0.851	0.45	0.739	error	error	error	error	error	error
sir0643		hypothetical protein	0.15	error	0.305	-0.226	0.569	0.152	error	-0.203	0.336	0.795	0.628	-0.163	0.807
sir0644		nitrogen regulation protein	error	error	error	error	error	error	error	-0.37	-0.312	-0.616	-0.619	-0.766	-0.054
sir0645		hypothetical protein	error	error	error	error	error	error	error	-0.074	-0.506	-0.684	-0.607	-0.675	0.379
sir0646		probable D-alanyl-D-alanin	0.321	0.51	0.604	0.617	-0.089	-0.32	-0.355	0.546	1.043	0.38	-0.354	0.811	0.133
sir0649	metS	methionyl-tRNA synthetase	0.144	0.111	-0.219	0.497	-0.161	-0.12	-0.215	0.082	0.017	-0.332	-0.14	-0.309	0.346
sir0650		hypothetical protein	error	error	error	error	error	error	error	-0.295	0.13	-0.844	-0.566	-0.21	0.179
sir0651		hypothetical protein	error	error	1.263	error	0.735	0.337	error	-0.303	0.585	1.055	0.574	0.231	1.524
sir0652	hisA	phosphorybosylformimino-5-	-0.14	0.008	1.101	1.317	0.633	0.076	0.046	-0.239	0.283	0.118	0.195	0.213	0.143
sir0653	sigA,rpoDI	principal RNA polymerase s	-0.142	-0.422	-0.428	0.525	-0.485	-0.677	-0.288	-0.403	-0.789	-0.841	-0.458	-1.197	0.157
sir0654		unknown protein	0.305	error	-0.101	-0.139	-0.172	0.065	-0.268	0.556	0.231	-0.356	-0.231	0.207	1.38
sir0655		hypothetical protein	-0.127	-0.118	-0.341	-0.05	-0.087	-0.425	0.12	-0.068	-0.016	error	-0.348	-0.215	0.389
sir0656		hypothetical protein	-0.193	-0.163	-0.437	error	-0.233	-0.864	-1.061	0.482	0.255	error	0.284	0.263	0.481
sir0657		aspartate kinase	-0.096	-0.315	0.173	0.75	-0.012	0.004	0.061	0.212	0.48	0.267	0.613	0.236	-0.901
sir0658		unknown protein	-0.158	-0.399	-0.353	0.303	-0.127	-0.857	-0.817	-0.044	-0.164	0.487	-0.081	-0.428	-0.441
sir0659		oligopeptidase A	-0.318	-0.506	-0.588	error	-0.397	-0.464	-0.325	-0.233	-0.085	-0.645	-0.439	-0.482	-0.72
sir0661	proC	pyrroline-5-carboxylate red	0.215	0.337	0.226	-0.132	-0.137	0.209	0.017	0.06	0.455	0.201	-0.143	0.464	-0.176
sir0662		arginine decarboxylase	error	error	error	error	error	error	error	0.362	0.406	-0.596	-0.023	0.476	-0.081
sir0664		hypothetical protein	error	error	error	error	error	error	error	error	error	error	5.617	error	error
sir0665		aconitate hydratase 2	-0.365	-0.185	-0.145	0.034	-0.739	-0.287	-0.493	-0.104	0.169	-0.312	-0.069	-0.423	-0.819
sir0666		unknown protein	-0.452	error	error	error	-0.136	-0.131	0.024	-0.195	-0.327	-0.017	-0.156	-0.627	0.611
sir0667		unknown protein	error	-0.225	-0.457	0.352	-0.165	0.322	-0.033	0.3	0.355	0.55	0.138	0.205	-0.324
sir0668		unknown protein	error	error	error	-1.389	error	0.981	error	0.212	0.639	1.555	0.38	error	0.335
sir0670		hypothetical protein	error	-0.092	-0.072	0.226	-0.032	0.244	0.104	error	error	error	error	error	error
sir0675		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sir0676	cysC	adenylsulfate kinasecysC	error	error	error	error	error	error	error	0.693	1.447	1.479	1.357	1.518	-0.077
sir0677		biopolymer transport ExbB	0.428	0.167	0.68	0.507	0.695	0.395	0.565	error	error	error	error	error	error
sir0678		biopolymer transport ExbD	0.648	0.33	0.83	0.378	1	0.46	0.324	0.171	0.579	0.595	1.157	0.338	0.879
sir0679		sun protein	-0.423	-0.496	-0.803	-0.063	-0.365	-0.657	-0.813	-0.288	-0.275	-0.425	-0.251	error	0.153
sir0680		hypothetical protein	-0.131	-0.555	error	error	-1.442	error	-0.771	0.009	-0.376	0.203	-0.649	-0.892	0.756
sir0681		probable sodium/calcium ex	-0.449	0.385	1.073	1.501	0.784	0.349	0.281	0.182	1.581	1.101	0.866	1.537	0.443
sir0682	hisD	histidinol dehydrogenasehis	0.327	0.001	-0.666	-0.428	-0.203	-0.097	0.079	-0.014	0.034	0.62	0.238	0.224	-0.362
sir0686		hypothetical protein	-0.055	-0.065	0.108	-0.197	0.196	0.292	-0.031	-0.338	error	-0.313	0.212	error	0.523
sir0687		probable two-component re	0.757	0.591	0.639	-0.512	0.387	0.379	2.009	0.11	0.386	0.894	0.14	0.164	0.722
sir0688		hypothetical protein	0.468	error	0.185	-0.101	-0.125	0.133	-0.059	-0.062	0.548	-0.022	-0.217	0.213	0.613
sir0689		hypothetical protein	0.042	0.026	0.122	0.51	-0.135	0.024	-0.168	0.162	0.013	0.026	0.088	0.012	-0.914
sir0692	ycf45	hypothetical protein YCF45	-0.452	-0.215	-0.127	0.227	-0.584	-0.131	-0.582	-0.126	-0.203	-0.311	-0.243	-0.445	-0.739
sir0695		hypothetical protein	-0.215	-0.341	-0.332	0.161	-0.198	-0.186	-0.573	0.012	0.119	-0.399	-0.049	0.02	-0.431
sir0697		5-oxoprolinase homolog	-0.254	-0.336	error	-1.352	-0.886	0.014	error	-0.921	-0.214	-0.009	-0.943	-0.282	0.474
sir0698		hypothetical protein	-0.449	0.163	0.998	0.225	0.317	0.767	0.378	0.268	1.015	0.352	0.524	1.16	-0.069
sir0699		unknown protein	error	error	error	-2.409	error	0.794	error	0.196	0.454	error	0.56	error	0.747
sir0700		probable amino acid perme	-0.231	-0.422	-0.307	0.068	-0.626	-0.734	-0.953	-0.162	0.134	0.26	-0.296	-0.103	-0.182
sir0701		transcriptional regulator	0.114	0.311	0.5	-0.322	0.353	0.9	0.803	-0.007	0.368	-0.003	0.042	0.372	0.824
sir0702		unknown protein	0.388	error	error	-0.77	-0.194	0.393	1.309	-0.424	0.198	0.954	-0.168	0.041	0.531
sir0703		putative transposase [ISY5]	-0.038	-0.014	0.043	0.165	-0.182	-0.062	0.14	-0.382	0.184	1.15	-0.127	0.244	-0.978
sir0704		putative transposase [ISY10]	-0.236	-0.65	-0.332	0.163	-0.458	-0.587	-0.686	-1.405	-0.278	0.664	-0.682	-0.18	0.659
sir0707	polA	DNA polymerase IpolA	-0.346	-0.188	-0.24	0.936	-0.429	-0.546	-0.431	-0.104	-0.08	-0.343	-0.399	-0.51	-1.241
sir0708		unknown protein	-0.489	error	-0.197	error	-0.4	-0.566	-0.723	-0.384	-0.604	-0.895	-1.26	-0.424	-0.932
sir0709		hypothetical protein	0.082	0.315	-0.157	-0.789	-0.277	-0.058	error	-0.416	0.255	-0.36	-0.064	0.13	2.372
sir0710	gdhA	glutamate dehydrogenase (	-0.723	-1.101	-1.33	error	-0.825	-0.343	-0.685	-0.058	-0.725	-0.028	-0.421	-0.913	-0.633
sir0711		hypothetical protein	0.077	error	1.933	error	0.457	-0.103	1.687	-0.076	0.485	0.089	0.047	0.377	1.384
sir0712		hypothetical protein	0.137	0.495	0.437	0.128	0.169	0.228	-0.259	0.163	0.175	0.539	-0.285	0.592	0.365
sir0713	tgt	tRNA-guanine transglycosy	error	error	error	error	error	error	error	0.225	0.193	0.017	0.035	0.039	-0.84
sir0719		unknown protein	-0.148	error	0.181	-0.22	-0.061	0.181	0.378	-0.174	0.175	0.108	0.003	0.161	0.428
sir0721		malic enzyme	error	error	error	error	-0.406	-0.167	0.3	error	error	error	error	error	error
sir0722		hypothetical protein	error	error	error	error	error	error	error	-0.051	1.341	1.585	0.497	0.916	0.035
sir0723		hypothetical protein	-0.198	-0.354	-0.425	0.315	-0.11	-0.101	-0.083	-0.237	-0.052	0.474	-0.077	0.1	-1.071
sir0724		HtaR suppressor protein ho	-0.144	0.021	-0.197	-0.585	-0.218	0.258	-0.239	-0.237	-0.079	-0.112	-0.228	-0.199	0.73
sir0725		hypothetical protein	-0.424	error	error	error	error	error	error	0.468	0.76	-0.816	-0.32	-0.215	-0.242
sir0727		unknown protein	0.699	0.569	0.356	error	-0.014	0.213	0.833	0.04	0.532	1.122	0.697	0.041	6.776

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis PCC6803*

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr0728		hypothetical protein	-0.32	-0.625	-0.549	-0.163	-0.46	0.221	-0.062	-0.41	-0.607	0.26	-0.442	-0.745	error
slr0729		hypothetical protein	0.025	-0.174	0.341	-0.361	0.165	0.176	-0.443	-0.148	0.279	-0.42	0.117	-0.083	0.32
slr0730		hypothetical protein	0.111	-0.177	-0.04	-0.554	-0.335	-0.408	-0.197	-0.08	-0.067	-0.185	-0.13	-0.228	0.086
slr0731		hypothetical protein	-0.226	-0.211	-0.015	0.19	-0.488	0.438	-0.051	-0.091	-0.171	-0.123	-0.543	-0.516	-0.289
slr0732		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slr0733		integrase-recombinase prot	0.373	0.658	0.82	0.72	0.153	0.095	0.34	0.846	0.647	-0.063	-0.077	0.231	-0.361
slr0734		hypothetical protein	0.07	-0.09	0.105	-0.347	-0.469	0.051	-0.143	-0.14	0.242	0.133	-0.36	-0.402	0.031
slr0737	psaD	photosystem I subunit lpsa	-0.659	-0.96	-1.508	-0.684	-1.482	-1.138	-1.013	-0.527	-1.424	-2.334	-1.678	-1.43	-0.919
slr0738	trpE	anthranilate synthetase alp	-0.197	-0.493	-0.174	-0.178	-0.795	-0.439	-0.109	-0.173	-0.439	error	-0.463	-0.349	-0.206
slr0739	crfE	geranylgeranyl pyrophosph	-0.219	0.085	-0.266	-0.206	-0.248	-0.169	-0.08	0.236	0.19	-0.159	0.015	0.408	-0.198
slr0740		hypothetical protein	0.294	error	error	-0.911	0.592	0.572	error	-0.027	0.127	-0.146	0.197	-0.444	0.688
slr0741		transcriptional regulator	-0.312	-0.517	-0.707	-0.362	-0.567	-0.343	-0.458	0.23	0.186	0.689	-0.112	-0.238	-0.609
slr0742		hypothetical protein	-0.575	-0.491	1.044	1.721	0.678	0.236	0.171	-0.045	0.751	0.973	1.032	0.7	0.097
slr0743		similar to N utilization subst	-0.054	-0.2	0.634	1.465	0.063	-0.016	-0.246	0.349	0.7	0.606	0.671	0.333	-0.645
slr0744	infB	initiation factor IF-2infB	error	error	error	error	error	error	error	0.12	-0.378	0.291	-0.256	-0.162	-0.095
slr0746	stpA	glucosylglycerolphosphate	-0.376	error	-0.264	-0.324	error	0.005	-0.12	-0.476	0.291	0.31	0.149	-0.031	1.41
slr0747	ggtA	glucosylglycerol transport s	error	error	error	error	error	error	error	0.064	0.207	-0.53	0.331	-0.016	0.368
slr0748		hypothetical protein	-0.107	0.14	0.047	0.604	0.284	0.088	-0.162	-0.099	0.108	0.658	0.156	-0.029	-0.245
slr0749	chlL	light-independent protochlo	error	error	error	error	error	error	error	-1.272	-1.371	-2.443	-1.808	-1.436	-1.263
slr0750	chlN	protochlorophyllide reductas	error	-0.392	-0.93	-1.127	-0.906	-0.467	-0.535	-0.516	-1.142	-1.109	-1.392	-0.763	-1.256
slr0751		hypothetical protein	0.146	0.401	0.905	0.216	0.186	0.418	0.549	0.263	0.669	0.814	0.284	0.512	0.404
slr0752		enolase	-0.341	-0.568	-0.074	error	-0.696	-0.481	-0.534	-0.139	-0.253	-0.721	-0.114	-0.376	0.503
slr0753		probable transport protein	-0.337	-0.408	-0.32	0.472	0.101	-0.155	-0.167	0.031	0.189	0.447	0.39	0.014	-0.577
slr0755		hypothetical protein	-0.09	0.173	0.494	0.93	0.242	0.167	0.341	0.311	0.583	0.536	0.684	0.554	-0.579
slr0756	kaiA	circadian clock protein KaiA	error	0.243	0.502	error	0.119	-0.177	0.591	-0.301	0.061	error	0.516	-0.031	error
slr0757	kaiB1	circadian clock protein KaiB	error	error	error	error	error	error	error	0.152	0.21	0.874	0.92	0.232	1.748
slr0758	kaiC1	circadian clock protein KaiC	-0.141	error	0.064	error	0.102	0.184	error	-0.414	-0.051	0.125	0.405	-0.197	1.564
slr0765		hypothetical protein	-0.628	-0.509	-0.341	error	1.115	0.879	1.557	-0.308	-0.387	0.251	1.362	-0.41	1.07
slr0769		hypothetical protein	-0.509	-0.89	-0.42	0.398	-0.245	-0.011	0.077	-0.181	-0.102	error	0.207	-0.375	0.891
slr0770		hypothetical protein	error	error	error	error	error	error	error	0.383	0.359	error	0.126	error	0.754
slr0771		hypothetical protein	1.947	0.877	1.241	-0.477	error	0.567	error	0.447	0.742	0.841	0.732	0.352	1.952
slr0772	chlB	protochlorophyllide reducta	-0.868	-1.23	-1.606	-1.342	-2.103	-1.204	-1.504	-1.55	-2.307	-2.546	-3.149	-2.349	-0.992
slr0773		hypothetical protein	0.261	error	0.196	0.514	-0.32	-0.043	error	0.295	0.576	error	-0.194	0.324	1.305
slr0774	secD	protein-export membrane p	0.361	0.315	1.204	0.904	0.614	0.33	0.315	1.093	2.087	1.804	1.649	2.086	1.923
slr0775	secF	protein-export membrane p	-0.277	-0.595	-0.402	-0.181	-0.464	-0.137	0.067	-0.067	-0.101	0.116	-0.059	-0.172	-1.108
slr0776		UDP-3-o-[3-hydroxymyristo	-0.285	-0.486	-0.643	-0.376	-0.492	-0.282	-0.075	-0.074	-0.228	0.024	-0.116	-0.485	-0.412
slr0779		hypothetical protein	0.319	0.44	-0.397	-0.024	-0.274	-0.332	-0.411	0.622	0.199	0.593	0.403	0.361	error
slr0780		hypothetical protein	0.116	0.442	-0.086	-0.351	-0.128	0.217	0.915	error	error	error	error	error	error
slr0782		putative flavin-containing m	-0.182	0.055	-0.678	-0.654	-0.657	-0.162	-0.478	-0.07	-0.229	-0.419	-0.805	-0.564	-0.957
slr0783	tpi	triosephosphate isomerase	error	error	error	error	error	error	error	-0.079	-0.113	-0.028	0.118	-0.211	0.683
slr0784		hypothetical protein	-0.083	-0.331	-0.15	-0.53	-0.288	0.105	0.27	-0.124	0.046	0.109	-0.019	0.066	0.187
slr0786		methionine aminopeptidase	error	error	error	error	error	error	error	0.099	0.965	1.517	0.314	0.887	-0.557
slr0787		hypothetical protein	1.982	2.298	2.456	0.678	1.426	1.513	1.945	error	error	error	error	error	error
slr0788		similar to pre-B cell enhanc	0.756	1.047	1.177	-0.162	0.531	0.75	error	-0.719	-0.13	error	-0.837	-0.245	0.424
slr0789		hypothetical protein	0.113	-0.053	-0.025	0.023	0.078	0.384	-0.111	0.56	0.403	0.533	-0.12	0.147	-0.608
slr0790		similar to ultraviolet light res	error	error	0.263	-0.994	error	0.94	error	0.324	0.086	error	0.317	-	-0.012
slr0793		unknown protein	error	error	error	error	error	error	error	0.128	error	error	error	error	error
slr0794		cation efflux system protein	-0.186	-0.438	-0.173	-0.809	-0.308	0.365	0.628	-0.673	-0.484	-0.471	-0.996	-0.716	0.148
slr0795		hypothetical protein	0.342	error	-0.209	-0.218	-0.034	-0.11	error	0.359	0.321	-0.237	-0.234	-0.47	-0.332
slr0796		nickel resistance protein Nr	0.887	1.287	1.299	1.683	1.046	0.271	0.372	1.275	1.259	0.643	0.834	1.166	0.667
slr0797	coaT	Cobalt transporter CoaTcoa	-0.205	-0.041	-0.143	error	-0.352	0.067	0.895	error	error	error	error	error	error
slr0798	ziaA	Zinc exporter ZiaA/ziaA	-0.471	-0.386	-0.244	error	-1.332	-0.654	-1.022	-0.134	0.227	0.281	-0.446	0.152	-0.381
slr0799		putative transposase [ISY8	0.029	0.215	0.194	0.282	-0.212	0.029	0.114	0.02	0.149	0.874	-0.415	0.18	-0.181
slr0800		putative transposase [ISY8	error	error	error	-0.633	error	error	error	-0.809	-0.136	0.65	-0.463	-0.15	-0.988
slr0801		hypothetical protein	-0.56	0.013	0.268	-0.048	0.215	0.074	-0.301	-0.689	-0.352	0.376	-0.79	-0.6	0.193
slr0804		probable D-alanyl-D-alanine	0.69	error	0.471	-0.546	0.739	0.414	0	0.397	0.307	0.016	-0.029	0.218	1.286
slr0806		hypothetical protein	0.103	0.047	-0.627	-0.267	-0.7	-0.323	-0.472	-0.1	-0.387	-0.473	-0.615	-0.334	-0.857
slr0807		probable o-sialoglycoprotei	0.179	-0.067	error	error	error	-0.061	error	error	error	error	error	error	error
slr0808		16S rRNA processing prote	0.063	error	error	-1.481	-0.142	0.332	error	-0.267	-0.193	1.183	-0.387	-0.196	-0.832
slr0809	rfbB	dTDP-glucose 4,6-dehydrat	-0.298	-0.177	-0.375	0.129	-0.06	0.189	-0.239	0.138	0.243	0.237	0.383	0.086	-0.264
slr0810		hypothetical protein	error	error	0.077	-0.511	0.095	0.215	error	-0.066	0.203	0.299	0.138	0.136	0.452
slr0812		hypothetical protein	error	error	error	error	error	error	error	-0.234	0.159	0.3	0.079	-0.076	0.265
slr0813		hypothetical protein	error	error	0.216	0.365	0.281	0.077	error	0.46	1.126	0.772	0.402	1.196	-0.24
slr0815		hypothetical protein	error	error	error	error	error	error	error	0.027	0.452	-0.244	0.111	0.129	1.119
slr0816		hypothetical protein	1.946	1.034	error	-0.217	0.953	0.543	error	0.509	0.675	0.073	0.362	0.249	1.07
slr0817		saicylate biosynthesis isoc	error	error	error	error	error	error	error	error	error	error	0.746	error	error
slr0818		hypothetical protein	0.198	error	0.15	error	error	0.512	error	-0.161	0.434	0.089	0.265	0.164	0.52
slr0819		apolipoprotein N-acyltransf	0.029	0.017	0.037	0.029	-0.227	-0.07	-0.073	-0.216	-0.242	-0.509	-0.689	error	0.213
slr0820		probable glycosyltransferas	-0.343	-0.696	-1.167	-0.645	-1.77	-0.685	-0.522	-0.392	-0.732	-0.379	-1.02	-0.879	-1.218
slr0821		hypothetical protein	-0.368	-0.442	-0.194	0.991	-0.034	-0.302	-0.286	0.093	0.104	-0.1	0.226	-0.106	-0.695
slr0822		cation-transporting ATPase	-0.421	-0.585	-0.845	-0.25	-1.127	-0.566	-0.791	-0.393	0.009	error	-0.264	-0.013	-1.664
slr0823	ycf3	photosystem I assembly rel	-0.391	-0.314	-0.851	-0.324	-0.189	-0.128	0.111	-0.292	-0.346	0.139	-0.113	-0.291	-0.127
slr0825		probable peptidase	error	error	error	error	error	error	error	-0.303	-0.387	-0.239	-0.396	-0.646	0.065
slr0827		alanine racemase	0.026	0.118	-0.37	-0.733	-0.465	-0.178	0.055	0.309	0.488	0.261	0.171	0.412	-0.189
slr0829		unknown protein	-0.044	0.041	-0.226	-0.64	-0.261	0.106	-0.197	-0.377	-0.231	3.294	-0.254	0.29	-0.026

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr0833	dnaB	replicative DNA helicase	0.562	error	0.293	-1.121	-0.22	-0.118	error	-0.247	-0.075	0.029	-0.756	-0.604	-0.208
slr0835		MoxR protein homolog	0.058	-0.053	-0.057	0.077	0.141	-0.14	-0.212	0.142	0.224	-0.014	0.281	0.217	0.536
slr0836	rfbB	dTDP-glucose 4,6-dehydratase	0.884	error	0.559	0.128	error	error	error	0.049	-0.027	0.367	0.036	0.238	-0.661
slr0838	purM	phosphoribosyl formylglycin	-0.108	-0.162	0.157	0.175	-0.158	0.118	0.122	0.12	0.386	0.108	0.113	-0.158	0.064
slr0839	hemH	ferrochelatase	-0.691	-0.386	0.162	0.655	0.229	0.298	0.247	0.171	0.571	0.29	0.936	0.647	0.402
slr0841		unknown protein	-0.391	-0.314	-0.08	0.811	0.245	0.158	0.208	0.16	0.308	0.491	0.802	0.283	-0.13
slr0842		hypothetical protein	0.392	0.129	0.027	-0.195	-0.789	-0.06	-0.361	error	error	error	error	error	error
slr0844	ndhF1	NADH dehydrogenase subunit	-0.612	-0.58	-0.583	0.117	-0.757	-0.477	-0.725	-0.195	-0.21	-0.492	0.505	-0.09	0.66
slr0845		hypothetical protein	-0.09	-0.14	-0.033	0.446	0.041	0.073	0.011	0.056	0.563	0.82	0.4	0.442	-0.881
slr0846		hypothetical protein	error	error	error	error	error	error	error	-0.108	0.29	0.309	-0.044	-0.086	0.295
slr0847		phosphopantetheine adenylyltransferase	-0.257	-0.238	-0.169	-0.012	0.149	0.603	0.551	-0.212	0.067	1.245	0.204	0.01	-0.224
slr0848		hypothetical protein	-0.765	-0.609	-0.645	0.068	-0.479	-0.172	-0.008	-0.308	-0.237	-0.116	-0.098	-0.323	-0.386
slr0851	ndaA	type 2 NADH dehydrogenase	-0.057	0.117	0.702	-0.135	0.464	0.404	0.496	-0.366	0.264	error	0.274	0.14	1.104
slr0852		hypothetical protein	0.987	1.82	2.147	1.275	1.704	0.96	1.473	1.957	2.901	2.642	2.09	2.729	2.047
slr0853		ribosomal-protein-alanine	1.027	1.409	error	error	1.36	0.338	0.621	0.634	1.571	0.786	0.82	1.209	0.421
slr0854	phrA	DNA photolyase	0.441	1.05	1.057	1.078	0.926	0.684	0.716	1.001	1.237	0.436	1.003	1.35	-0.492
slr0856		putative transposase [ISY100]	-0.051	-0.37	-0.125	0.423	-0.516	-0.124	-0.324	-0.462	0.248	0.683	-0.294	0.53	-0.479
slr0857		putative transposase [ISY100]	-0.153	error	-0.621	error	-1.284	-0.745	-0.639	-1.091	-0.2	0.076	-0.83	-0.363	0.481
slr0861	purT	glycinamide ribonucleotide transferase	-0.426	-0.252	0.226	0.927	-0.123	0.15	-0.024	0.155	0.47	0.351	0.457	0.288	-0.292
slr0862		probable sugar kinase	0.214	error	0.275	error	error	0.003	0.4	-0.446	0.142	-0.357	-0.29	-0.001	0.714
slr0863		hypothetical protein	0.318	-0.227	-0.25	error	0.03	-0.654	-0.449	-0.132	0.222	0.161	error	0.055	0.272
slr0864		ATP-binding protein of ABC transporter	0.284	0.488	0.774	1.604	0.253	-0.05	0.374	0.255	0.83	1.571	0.401	0.776	0.519
slr0865		hypothetical protein	-0.276	error	-0.642	error	-0.218	-0.162	0.149	-0.136	0.14	error	0.242	-0.196	1.628
slr0867		unknown protein	1.281	0.828	0.991	error	0.322	-0.116	0.255	0.129	0.823	0.54	0.004	0.302	2.089
slr0868		unknown protein	error	error	error	-1.665	error	0.769	error	0.987	0.874	error	0.72	-0.022	1.459
slr0869		hypothetical protein	-0.649	-0.727	-0.976	-0.531	-0.729	-0.14	error	error	error	error	error	error	error
slr0870		hypothetical protein	error	error	-0.642	-1.367	error	0.722	error	error	error	error	error	error	error
slr0871		unknown protein	-0.084	0.141	0.021	-0.237	0.03	-0.131	0.645	0.019	0.508	0.562	0.025	0.318	-0.38
slr0872		hypothetical protein	-0.145	-0.075	0	0.163	0.258	0.208	0.399	-0.422	-0.192	0.478	-0.058	-0.231	-0.409
slr0875		large-conductance mechanosensitive channel	error	error	error	error	error	error	error	0.682	0.98	error	0.274	0.583	0.477
slr0876		hypothetical protein	-0.196	-0.559	-0.788	-0.194	-0.523	-0.435	-0.426	-0.138	-0.4	-0.469	-0.256	-0.594	-0.666
slr0877		glutamyl-tRNA(Gln) amidotransferase	0.141	0.064	0.373	0.251	-0.013	-0.279	0.089	0.224	0.563	-0.177	0.185	0.222	1.421
slr0878		hypothetical protein	0.698	0.407	0.525	-0.513	0.008	0.36	1.13	0.16	0.692	0.166	-0.112	0.456	-0.918
slr0879		glycine decarboxylase complex	0.219	0.662	0.164	-0.42	0.199	0.183	-0.341	0.097	0.527	-0.462	0.162	-0.005	0.329
slr0880		similar to fibronectin binding protein	error	error	error	error	error	error	error	0.367	0.942	0.446	0.579	0.598	1.432
slr0881		unknown protein	error	error	error	error	error	error	error	-0.047	-0.03	-0.137	0.004	-0.065	-0.25
slr0882	ycf84	hypothetical protein YCF84	error	0.845	1.136	error	1.247	0.14	0.889	0.812	1.391	1.539	1.566	1.191	1.387
slr0883		hypothetical protein	-0.026	0.485	0.238	0.536	0.169	0.007	0.224	0.001	0.478	error	0.17	0.748	0.136
slr0884	gap1	glyceraldehyde 3-phosphate dehydrogenase	error	error	error	error	error	error	error	-0.147	-0.201	-0.641	-0.243	-0.401	0.599
slr0885		hypothetical protein	1.078	1.803	2.356	0.638	1.784	1.108	error	1.004	1.736	1.734	1.092	1.732	1.413
slr0886		3-oxoacyl-acyl-carrier protein	error	error	error	error	error	error	error	-0.254	-0.167	-0.787	-0.353	-0.273	-0.132
slr0887		hypothetical protein	error	error	error	error	error	error	error	0.22	0.462	0.045	0.232	0.287	0.268
slr0888		hypothetical protein	-0.075	-0.397	-0.177	-0.261	-0.587	-0.01	-0.244	-0.506	-0.392	error	-1.065	-0.644	0.085
slr0889		hypothetical protein	-0.263	-	-0.277	-0.366	-0.09	-0.459	-0.631	-0.299	0.008	-0.096	-0.41	-0.57	error
slr0890		unknown protein	-0.325	error	0.106	-1.075	0.178	0.22	0.469	-0.213	0.419	error	-0.223	-0.065	1.233
slr0891		N-acetylmuramoyl-L-alanine amidase	-0.365	-0.564	-1.007	-0.659	-0.94	-0.011	-0.216	-0.377	-0.867	-0.393	-0.58	-1.055	-1.106
slr0895		transcriptional regulator	2.543	3.694	3.374	error	2.02	1.534	4.648	2.281	2.855	0.871	1.091	2.625	2.142
slr0896		multi-drug efflux transporter	0.043	0.401	-0.271	-0.072	0.199	0.196	0.538	0.018	-0.097	-0.134	-0.337	-0.158	-0.101
slr0897		probable endoglucanase	0.577	0.299	error	-0.643	0.301	0.439	error	-0.455	0.025	-0.007	-0.113	0.227	0.62
slr0898	nirA	ferredoxin-nitrite reductase	-0.174	0.056	0.644	-0.29	-0.039	0.08	-0.073	0.427	0.472	-0.131	0.215	0.641	0.896
slr0899	cynS	cyanate lyase	1.655	1.744	error	-0.379	0.125	0.519	error	0.071	0.116	0.188	-0.093	-0.139	1.476
slr0900	moaA	molybdopterin biosynthesis protein	error	error	error	error	error	error	error	0.014	0.092	0.156	-0.093	-0.229	-0.153
slr0901	moaA	molybdenum cofactor biosynthesis protein	error	error	error	error	error	error	error	0.111	-0.069	0.184	0.266	-0.188	0.04
slr0902	moaC	molybdenum cofactor biosynthesis protein	error	error	error	error	error	error	error	-0.182	-0.041	0.869	-0.225	-0.456	0.194
slr0903	moaE	molybdopterin (MPT) conversion protein	-0.3	-0.086	-0.132	-0.948	-0.059	0.235	0.152	-0.168	-0.102	-0.207	-0.266	0.009	-0.654
slr0904		competence protein ComM	-0.201	error	-0.19	-1.632	-0.062	0.003	0.004	0.02	0.283	0.09	0.212	0.263	0.022
slr0905	bchE	Mg-protoporphyrin IX monomethyltransferase	-0.514	-0.791	-1.576	-0.966	-2.111	-1.381	-1.376	0.434	-0.673	0.345	-0.784	-0.837	-1.313
slr0906	psbB	photosystem II core light harvesting protein	-0.914	-1.018	-2.071	-1.537	-1.619	-1.35	-1.268	-0.245	-1.352	-2.866	-1.736	-2.15	-1.741
slr0907		unknown protein	-0.318	-0.302	-0.052	error	-0.231	-0.132	-0.144	error	error	error	error	error	error
slr0909		unknown protein	-0.388	-0.24	-0.595	-0.259	-0.511	0.251	0.783	-0.833	error	-0.486	-0.534	error	1.11
slr0912		unknown protein	-0.397	-0.096	-0.213	0.154	-0.334	-0.092	-0.187	error	error	error	error	error	error
slr0913		unknown protein	-0.02	-0.067	-0.952	-1.056	-0.207	0.621	error	0.045	-0.33	0.622	-0.342	-0.414	-0.116
slr0914		unknown protein	-0.353	error	-0.319	-0.833	-0.781	0.255	error	-0.474	-0.069	0.155	-0.35	-0.157	-0.271
slr0915		putative endonuclease	error	error	error	error	error	error	error	-0.217	0.237	-0.446	0.42	-0.058	1.624
slr0917	bioF	7-keto-8-aminopelargonic acid synthase	-0.111	-0.114	-0.452	-0.062	-1.075	-0.918	-0.853	0.049	0.24	-0.543	-0.509	0.319	-0.405
slr0918		methionine aminopeptidase	0.112	-0.329	0.148	0.286	0.189	0.074	-0.009	0.123	-0.08	-0.499	0.369	-0.228	0.736
slr0919		hypothetical protein	0.423	0.18	0.225	-0.342	-0.096	0.771	error	0.143	0.471	0.809	0.139	0.496	0.778
slr0920		mutator MutT protein	0.126	-0.032	0.052	-0.467	0.024	0.065	1.276	0.075	0.352	0.027	-0.019	0.084	-0.629
slr0921		hypothetical protein	error	-0.068	0.968	-1.07	0.439	0.651	error	0.252	0.345	0.703	0.224	0.017	0.539
slr0922	pth	peptidyl-tRNA hydrolase	0.409	0.459	0.433	0.201	0.573	0.381	0.49	0.129	0.582	0.41	0.438	0.456	-0.36
slr0923	ycf65	hypothetical protein YCF65	0.209	-0.212	0.508	1.486	0.253	error	0.038	0.619	0.86	1.125	1.673	0.701	0.451
slr0924		hypothetical protein	0.206	0.171	0.461	1.616	1.15	0.435	1.114	0.144	1.016	0.81	1.722	0.803	1.762
slr0925	ssb	single-stranded DNA-binding protein	0.33	0.293	-0.106	-0.647	0.355	0.175	0.477	-0.436	0.005	-0.297	-0.52	-0.326	0.366
slr0926	ubiA	4-hydroxybenzoate-octaprenyl transferase	error	-0.043	-0.476	-1.074	-0.202	0.038	0.447	-0.349	-0.667	-0.358	-0.547	-0.699	-1.075
slr0927	psbD2	photosystem II reaction center protein	-0.564	-0.808	-0.139	0.877	-0.625	-0.859	-0.677	0.081	1.027	0.324	0.434	0.916	0.262

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1								Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	
slr0929		chromosome partitioning pr	error	error	error	error	error	0.283	error	0.047	0.403	0.567	0.326	0.034	0.403	
slr0930		hypothetical protein	-0.093	0.023	0.021	0.31	-0.031	-0.024	0.059	0.083	0.299	0.34	-0.05	0.166	-0.516	
slr0935		hypothetical protein	0.421	0.375	0.596	-1.176	0.348	0.266	error	-0.218	0.575	0.446	0.14	error	1.965	
slr0936	nadC	nicotinate-nucleotide pyrop	0.789	error	0.55	-0.682	-0.199	0.001	error	-0.179	0.199	0.02	-0.187	0.153	0.907	
slr0937		unknown protein	-0.138	-0.155	0.142	0.144	-0.098	0.145	0.081	-0.156	0.406	-0.395	-0.274	0.121	0.527	
slr0938		probable UDP-N-acetylmur	0.428	0.464	error	-1.242	-0.937	0.192	error	0.101	0.063	0.23	-0.011	-0.103	0.817	
slr0940	crtQ-2	zeta-carotene desaturase	-0.184	-0.341	-0.045	error	0.21	-0.011	-0.054	0.057	0.297	-0.077	0.508	0.273	1.161	
slr0941		hypothetical protein	0.083	0.303	0.374	-0.608	-0.102	0.255	error	0.029	0.369	-0.441	0.25	-0.124	0.774	
slr0942		alcohol dehydrogenase [NA	-0.493	-0.577	-0.743	0.046	-0.754	-0.549	-0.29	-0.103	-0.239	-0.13	-0.468	-0.118	-0.441	
slr0943	fda	fructose-bisphosphate ald	-0.148	-0.371	-1.293	-0.877	-0.802	-0.894	-0.551	-0.101	-0.753	-0.645	-0.553	-0.907	0.415	
slr0944		multidrug-efflux transporter	error	error	error	error	0.343	0.216	error	-0.198	0.653	error	0.291	0.691	0.449	
slr0945		arsenical resistance protein	-0.343	-0.027	0.154	0.232	-0.046	0.205	-0.261	-0.112	0.214	-0.001	-0.197	0.166	-0.928	
slr0946	arsC	arsenate reductase	0.132	0.769	2.049	2.122	1.071	0.006	0.273	0.254	2.079	2.154	1.44	1.793	0.959	
slr0947	rpaB, ycf27	response regulator for ener	-0.34	-0.443	-0.953	-1.08	-1.077	-0.483	-0.821	0.152	0.23	0.247	-0.418	0.367	1.266	
slr0948		hypothetical protein	0.177	0.981	1.155	1.38	0.877	0.509	0.73	0.857	2.097	2.877	1.267	1.959	0.34	
slr0949	natD	Integral membrane protein	0.186	0.47	0.015	-0.034	-0.123	0.185	0.387	0.096	0.289	0.199	-0.162	0.827	-0.671	
slr0950		hemolysin-like protein	1.093	-0.231	error	-1.055	-1	-0.075	error	-0.667	-0.237	0.545	-0.964	-0.25	0.235	
slr0951		4-diphosphocytidyl-2C-met	error	-0.145	-0.028	0.407	0.065	0.115	0.242	0.021	0.268	-0.303	0.036	-0.137	-1.017	
slr0952	fbpII	fructose-1,6-bisphosphatas	-0.278	-0.01	0.866	error	1.542	0.727	0.809	-0.526	0.19	0.244	1.151	0.096	1.414	
slr0953		sucrose-phosphate phosph	-0.304	0.088	0.189	0.962	0.53	0.232	-0.053	0.316	0.172	0.713	0.377	0.028	-0.836	
slr0954		hypothetical protein	-0.105	-0.421	-0.807	-0.094	0.014	-0.13	-0.213	0.508	0.348	1.073	0.418	0.01	-0.683	
slr0955		probable tRNA/rRNA methy	0.307	-0.102	-0.49	0.64	-0.027	-0.33	-0.439	0.72	-0.17	0.578	0.342	-0.181	-0.943	
slr0957		hypothetical protein	error	-0.315	-0.157	error	0.233	0.037	0.105	0.493	1.006	0.035	0.889	0.121	-0.118	
slr0958	cysS	cysteinyl-tRNA synthetase	0.467	0.812	0.578	0.993	0.88	0.311	0.679	0.658	1.229	0.543	1.041	1.292	-0.36	
slr0959		hypothetical protein	3.172	3.929	4.265	error	3.828	2.512	3.294	3.693	4.802	4.181	3.232	4.929	1.604	
slr0960		unknown protein	0.413	0.938	0.697	-0.081	0.456	0.2	-0.064	0.629	1.094	1.182	0.876	0.624	0.934	
slr0962		unknown protein	error	error	error	error	error	error	error	0.222	0.043	0.197	-0.038	-0.113	0.286	
slr0963	sir	ferredoxin-sulfite reductase	0.022	-0.349	-0.086	0.509	0.002	-0.372	-0.109	0.122	0.299	0.148	0.359	0.414	0.677	
slr0964		hypothetical protein	0.048	error	0.566	-0.731	error	0.39	-0.146	-0.551	0.179	0.043	-0.306	-0.002	0.689	
slr0965	dnaN	DNA polymerase III beta su	0.072	0.017	-0.303	-0.21	-0.017	0.014	0.215	-0.304	0.205	0.058	0.183	0.276	-0.871	
slr0966	trpA	tryptophan synthase alpha	0.239	-0.127	0.133	-0.249	-0.307	0.168	0.609	-0.111	0.215	-0.079	0.031	0.019	0.754	
slr0967		hypothetical protein	1.625	2.634	3.15	2.859	1.84	0.969	0.91	error	error	error	error	error	error	
slr0969	cobJ	precorrin methylase	-0.481	error	-0.202	-0.339	-0.004	-0.236	0.059	-0.298	-0.075	0.026	0.007	0.074	0.557	
slr0971		hypothetical protein	0.116	0.125	-0.243	-0.455	0.186	0.028	0.128	-0.221	0.183	-0.318	0.269	-0.223	0.241	
slr0974	infC	initiation factor IF-3infC	0.49	1.255	1.95	2.006	1.188	0.272	0.839	0.812	1.996	1.495	1.065	1.907	-0.077	
slr0975		hypothetical protein	error	error	error	error	error	error	error	0.619	1.304	0.688	1.138	1.035	0.337	
slr0976		hypothetical protein	0.063	0.094	0.326	0.194	0.21	0.367	1.026	0.259	0.19	-0.01	0.584	0.363	0.366	
slr0977		ABC transporter, permease	0.413	0.073	0.46	0.704	0.022	-0.375	0.1	0.449	0.533	0.203	0.331	0.471	0.848	
slr0978		hypothetical protein	error	error	error	error	error	error	error	0.373	0.446	-0.167	0.269	0.072	0.645	
slr0980		hypothetical protein	1.322	error	0.357	-1.244	error	0.642	error	-0.102	0.29	-0.096	-0.02	-0.018	5.734	
slr0981		hypothetical protein	error	error	error	error	error	1.22	error	1.114	1.08	0.377	0.438	0.815	0.509	
slr0982		probable polysaccharide A	0.032	-0.34	-0.181	-0.192	-0.343	0.147	-0.267	error	error	error	error	error	error	
slr0983	rfbF	glucose-1-phosphate cytidy	0.211	-0.126	-0.162	error	-0.33	0.009	0.467	-0.274	-0.301	-0.345	-0.921	-0.578	0.474	
slr0984	rfbG	GDP-glucose 4,6-dehydrata	0.844	error	-0.215	-1.421	-1.137	-0.221	-	-0.139	0.017	-0.092	-0.49	0.008	1.162	
slr0985	rfbC	dTDP-4-dehydrorhamnose	0.532	0.561	1.286	0.785	0.865	0.562	0.634	0.12	0.412	-0.044	-0.18	0.204	0.939	
slr0989		hypothetical protein	0.085	error	0.673	-0.209	0.002	0.139	0.189	-0.022	0.409	0.973	-0.219	0.404	0.23	
slr0990		hypothetical protein	0.011	-0.1	0.113	0.766	0.019	-0.114	-0.424	-0.043	0.215	error	0.235	-0.063	0.49	
slr0992		probable tRNA/rRNA methy	0.788	0.989	error	-0.223	0.774	0.431	error	error	error	error	error	error	error	
slr0993		putative peptidase	-0.219	-0.446	-0.446	0.742	0.161	0.083	0.172	-0.147	-0.031	-0.165	0.457	-0.287	1.002	
slr0994		lipote-protein ligase B	0.692	0.766	0.165	-0.215	0.113	0.067	-0.162	0.073	0.144	0.058	-0.039	0.249	0.55	
slr1019		phenazine biosynthetic prot	-0.299	-0.002	0.423	error	0.364	0.141	error	-0.319	0.358	0.573	-0.109	0.153	-0.494	
slr1020		sulfolipid biosynthesis prote	-0.493	-0.565	-1.075	-0.093	-0.66	-0.783	-0.455	0.094	-0.575	-0.723	-0.073	-0.55	-0.538	
slr1022	argD	N-acetylmethionine aminotran	error	error	error	error	error	error	error	-0.231	-0.168	-0.674	-0.37	-0.215	0.422	
slr1023		unknown protein	0.357	0.123	0.357	-0.756	error	-0.139	error	-0.383	-0.19	0.901	-0.338	-0.16	0.593	
slr1024		fibrillin	-0.144	error	0.043	-0.48	-0.166	0.016	0.082	-0.278	-0.074	2.796	-0.545	-0.152	-0.21	
slr1025		hypothetical protein	0.266	0.524	0.072	-0.339	0.364	0.752	1.096	0.27	0.315	0.106	0.174	error	-0.213	
slr1028		unknown protein	-0.425	-0.205	0.017	0.284	-0.137	-0.044	0.101	-0.569	-0.186	-0.152	-0.433	-0.029	-0.998	
slr1030	chlI	magnesium-chelatase subu	-0.584	-0.346	0.069	0.534	-0.01	0.213	-0.211	-0.193	0.19	0.237	0.435	0.208	-0.497	
slr1031	tyrS	tyrosyl tRNA synthetase	0.029	-0.392	-0.245	0.426	0.465	0.087	0.196	-0.382	-0.163	-0.522	-0.002	-0.389	0.668	
slr1032		unknown protein	error	error	-0.084	-0.354	0.349	0.227	error	0.083	0.269	error	0.323	0.304	0.101	
slr1033		unknown protein	error	error	error	error	error	error	error	-0.501	-0.064	-0.296	-0.219	-0.397	0.756	
slr1034	ycf41	hypothetical protein YCF41	0.369	0.59	0.779	error	0.262	0.314	0.304	-0.124	0.953	0.352	0.001	0.555	1.323	
slr1035		hypothetical protein	error	error	error	error	error	error	error	-0.345	-0.123	error	-0.342	-0.063	0.274	
slr1037		two-component response re	-0.315	-0.443	-0.923	-0.446	-1.117	-0.344	-0.82	0.179	-0.094	0.179	-0.273	-0.213	-0.707	
slr1039		hypothetical protein	error	0.669	error	error	0.028	0.094	error	-0.148	0.167	-0.055	0.111	-0.229	0.791	
slr1041		two-component response re	-0.191	-0.335	-0.24	-0.582	-0.136	0.051	0.829	-0.039	0.016	0.617	0.152	0.178	-0.518	
slr1042		two-component response re	-0.17	-0.295	-0.709	-0.582	-0.748	-0.12	-0.133	-0.109	0.119	0.209	-0.154	-0.237	0.098	
slr1043	cheW	similar to chemotaxis protei	-0.145	-0.244	-0.13	0.155	-0.199	-0.026	-0.175	error	error	error	error	error	error	
slr1044		methyl-accepting chemotax	0.114	-0.381	-1.078	-0.756	-0.716	-0.427	-0.461	0.049	-0.239	0.159	-0.201	-0.146	-0.501	
slr1045	ycf63	hypothetical protein YCF63	error	error	error	error	error	error	error	-0.03	0.149	1.018	-0.071	0.141	0.746	
slr1046		hypothetical protein	0.322	0.274	-0.859	-0.265	error	0.092	0.147	0.022	-0.001	-0.503	-0.07	-0.397	0.2	
slr1047		hypothetical protein	-0.026	-0.062	-0.295	-0.854	-0.539	0.3	0.688	-0.272	0.209	-0.022	-0.398	error	-0.116	
slr1048		hypothetical protein	0.279	0.02	0.376	error	-0.016	0.301	error	-0.171	0.061	0.14	-0.055	-0.086	0.215	
slr1050		hypothetical protein	error	0.412	1.209	0.51	0.501	0.073	0.52	0.473	0.787	0.338	0.528	0.487	0.444	
slr1051		enoyl-[acyl-carrier-protein]	-0.257	-0.081	-0.617	-0.771	-0.521	-0.321	0.072	-0.284	0.103	0.627	-0.362	-0.072	-0.671	

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sir1052		hypothetical protein	0.1	-0.269	-0.157	-0.612	-0.547	0.048	error	-0.136	0.129	0.098	-0.358	-0.194	0.074
sir1053		unknown protein	-0.088	-0.432	-0.35	-0.72	-0.595	-0.395	-0.104	0.072	0.058	-0.215	-0.137	0.155	0.302
sir1055	chlH	magnesium-protoporphyrin	-0.583	-0.955	-1.908	error	-0.798	-0.797	-0.673	-0.06	-0.988	-0.389	-0.264	-0.943	-0.713
sir1056		unknown protein	0.434	-0.104	error	error	-0.119	0.002	error	-0.25	0.084	0.033	-0.276	-0.362	1.124
sir1062		unknown protein	0.466	error	-0.483	-0.905	error	0.44	0.19	0.163	0.138	-0.278	0.116	-0.07	-0.021
sir1063		plobable glycosyltransferas	-0.494	0.021	0.492	0.172	0.337	0.419	0.845	-0.336	1.085	-	-0.159	1.089	-0.111
sir1064		plobable glycosyltransferas	-0.456	-0.559	-1.487	-0.933	-1.496	-0.923	-0.652	-0.451	-0.698	-0.715	-0.947	-0.975	-0.832
sir1065		plobable glycosyltransferas	-0.225	-0.671	-0.597	-0.209	-0.333	-0.23	0.047	-0.541	-0.579	-0.36	-0.695	-0.822	-0.291
sir1066		unknown protein	0.015	error	-0.961	error	-0.421	0.105	0.357	-0.688	-0.456	-0.404	-0.745	-0.729	-0.305
sir1067		UDP-glucose 4-epimerase	-0.222	error	-0.227	0.125	-0.353	0.315	0.595	-0.755	-0.683	-1.215	-1.078	-1.053	0.384
sir1068		hypothetical protein	error	error	-0.317	-0.761	error	0.322	error	0.011	0.127	error	0.508	-0.057	0.334
sir1069		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sir1070		unknown protein	error	error	-0.618	error	error	0.826	error	0.389	-0.386	-0.14	-0.358	-0.511	-0.646
sir1071		unknown protein	error	error	error	error	error	error	error	0.171	-0.261	-0.406	-0.345	-0.515	-0.083
sir1072		GDP-D-mannose dehydrata	0.361	0.294	0.984	-0.06	0.276	-0.117	0.259	-0.352	-0.49	-0.302	-0.94	-0.624	0.232
sir1073		unknown protein	error	error	error	error	error	0.436	error	0.441	0.747	0.544	0.548	0.599	0.258
sir1074		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sir1075		putative transposase [ISY1	-0.37	-0.52	-0.437	0.184	-0.632	-0.605	-0.478	-1.09	-0.328	0.374	-0.697	-0.262	-1.249
sir1076		plobable glycosyltransferas	error	error	error	error	error	error	error	1.909	1.541	0.96	0.796	1.63	0.555
sir1077		plobable glycosyltransferas	error	error	error	error	error	error	error	-0.307	-0.091	-0.179	-0.287	-0.506	-0.354
sir1078		similar to UDP-glucose 4-ep	error	error	error	error	error	error	error	0.207	0.486	-0.058	0.451	0.104	0.221
sir1079		unknown protein	0.365	-0.269	0.245	0.101	0.792	0.358	0.558	-0.375	-0.092	0.163	0.88	-0.545	1.018
sir1081		hypothetical protein	0.804	0.332	error	-0.597	error	0.458	0.886	-0.009	0.18	0.22	0.528	-0.428	0.437
sir1082		unknown protein	-0.024	-0.408	-0.233	0.303	0.545	0.27	0.055	-0.61	-0.17	-0.082	0.673	-0.551	0.434
sir1083		hypothetical protein	0.23	0.336	0.233	error	0.209	0.488	error	-0.385	0.263	error	0.233	-0.39	0.731
sir1084		unknown protein	0.262	error	-0.367	-0.837	-0.746	-0.014	error	-0.209	-0.211	-0.486	-0.747	-0.377	0.51
sir1085		plobable glycosyltransferas	0.068	error	0.263	0.048	error	0.157	0.189	0.603	0.642	0.58	0.237	0.23	-0.293
sir1087		hypothetical protein	error	error	error	error	error	-0.421	error	0.014	0.116	0.06	-0.681	-0.33	-0.117
sir1090		GTP-binding protein	-0.078	-0.116	0.06	-1.275	-0.318	-0.363	-0.091	-0.615	-0.463	-0.416	-0.561	-0.494	5.218
sir1093	folK	2-amino-4-hydroxy-6-hydro	-0.062	-0.216	-0.246	-0.404	-0.247	-0.028	-0.061	-0.141	0.079	-0.492	-0.381	-0.027	0.671
sir1094		hypothetical protein	error	error	error	error	error	error	error	0.049	0.122	error	-0.142	0.051	0.139
sir1095		hypothetical protein	0.196	-0.091	0.358	error	0.432	0.216	-0.029	error	error	error	error	error	error
sir1096		dihydroilpoamide dehydrog	-0.666	-0.74	-0.999	-0.03	-0.771	-0.69	-0.622	error	error	error	error	error	error
sir1097		hypothetical protein	-0.188	error	-0.543	-1.065	-0.771	-0.08	-0.352	0.228	-0.039	-0.527	-0.266	-0.276	0.911
sir1098		hypothetical protein	-0.206	-0.311	-0.135	0.21	-0.311	-0.392	-0.676	error	error	error	error	error	error
sir1099	ubiX	3-octaprenyl-4-hydroxybenz	error	error	error	error	error	error	error	0.189	0.189	error	-0.522	-0.306	-0.306
sir1100		hypothetical protein	1.13	error	0.664	-0.126	1.018	0.344	-	0.257	0.812	error	0.569	0.46	1.724
sir1101		hypothetical protein	0.186	0.251	0.253	-0.177	-0.032	0.255	-0.157	error	error	error	error	error	error
sir1102		hypothetical protein	-0.037	0.291	0.472	0.746	0.054	-0.276	-0.18	error	error	error	error	error	error
sir1103		hypothetical protein	0.065	error	error	-0.902	error	-0.21	-0.414	-0.394	error	-0.499	-0.713	error	0.502
sir1104		hypothetical protein	-0.049	-0.493	-0.939	0.107	-0.541	-0.529	-0.358	-0.195	-0.148	0.114	-0.271	-0.604	0.033
sir1105		GTP-binding protein TypA	-0.277	-0.589	0.448	1.219	0.136	-0.231	-0.062	0.183	0.758	0.017	0.963	0.677	0.875
sir1106		prohibitin	-0.666	-0.631	-0.26	0.196	-0.053	-0.234	-0.098	0	0.464	0.126	0.275	0.353	-0.489
sir1107		unknown protein	0.953	0.058	error	-0.731	-0.431	0.232	error	-0.11	-0.238	-0.344	-0.248	-0.4	-0.905
sir1109		similar to ankyrin	0.014	0.514	0.071	0.149	-0.294	-0.272	-0.22	0.129	0.184	-0.34	-0.622	0.069	-0.638
sir1110		hypothetical protein	0.166	0.819	1.423	0.944	1.115	0.906	1.067	-0.069	0.816	0.588	0.283	0.602	-0.484
sir1113		ATP-binding protein of ABC	0.316	0.052	0.676	1.228	-0.015	-0.423	-0.298	0.084	0.922	0.846	0.343	0.738	0.751
sir1114		hypothetical protein	-0.232	-0.159	-0.24	0.26	-0.043	-0.122	-0.3	-0.206	-0.003	0.05	0.212	-0.019	-1.148
sir1115		probable methyltransferase	-0.328	-0.529	-0.086	-0.098	-0.618	0.121	-0.15	-0.183	0.182	0.134	-0.232	-0.192	-1.196
sir1116		hypothetical protein	-0.022	-0.481	-0.28	0.191	-0.179	0.026	-0.047	-0.096	-0.156	-0.395	-0.228	-0.312	-0.888
sir1117		hypothetical protein	0.04	0.153	-0.225	-0.468	-0.347	0.489	0.43	-0.034	-0.268	-0.461	-0.188	-0.444	-0.914
sir1118		probable UDP-N-acetyl-D-r	-0.31	-0.566	-0.494	-0.382	-0.592	0.087	0.043	0.007	error	-0.164	-0.693	error	-0.976
sir1119		hypothetical protein	0.376	0.464	0.85	1.175	1.445	0.872	1.354	0.338	1.115	1.064	1.327	0.616	0.969
sir1120		type 4 prepilin-like proteins	-0.176	-0.247	-0.537	0.097	error	-0.169	0.056	0.037	-0.049	0.052	0.255	0.065	-0.803
sir1122		hypothetical protein	-0.531	-0.361	-0.274	0.091	-0.678	-0.15	-0.734	-0.149	-0.173	-0.155	-0.164	-0.357	-0.944
sir1123		guanylate kinase	-0.658	-0.44	-0.166	-0.685	-0.351	0.2	0.079	-0.226	0.063	-0.615	-0.273	-0.174	-0.577
sir1124		phosphoglycerate mutase	-0.407	-0.33	-0.454	-0.468	-0.647	-0.123	-0.151	-0.035	-0.074	-0.282	-0.218	-0.308	-0.838
sir1125		probable glucosyl transfera	error	error	error	error	error	error	error	0.008	0.135	-0.682	-0.157	-0.035	0.167
sir1127		unknown protein	-0.485	-0.427	0.808	1.942	1.329	0.838	0.684	error	error	error	error	error	error
sir1128		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sir1129	me	ribonuclease Erne	0.76	0.81	1.249	1.562	0.666	0.235	0.294	0.833	1.351	0.66	0.951	1.067	0.597
sir1130	rhnB	ribonuclease HllrhnB	0.158	0.204	0.326	-0.428	-0.436	0.228	0.414	0.066	0.193	-0.041	-0.229	0.057	0.17
sir1133	argH	L-argininosuccinate lyasear	-0.491	-0.073	-0.338	-0.096	-0.618	-0.241	-0.776	-0.334	-1.29	-1.556	-1.416	-1.255	0.238
sir1134		mutator MutT homolog	-0.478	-0.571	-0.371	-0.379	error	-0.104	-0.31	0.045	-0.128	0.089	-0.449	-0.418	-0.502
sir1135		unknown protein	0.303	error	1.17	0.153	0.617	0.852	0.96	-0.135	0.531	-0.048	0.318	0.194	0.868
sir1136	ctaC	cytochrome c oxidase subu	-0.408	-0.93	-0.493	-0.058	0.235	0.262	0.432	-0.385	-0.568	-0.822	-0.192	-0.639	1.173
sir1137	ctaD	cytochrome c oxidase subu	-0.813	-0.946	-1.562	error	-1.207	-0.879	-0.727	-0.387	-0.865	-1.041	-0.813	-0.566	-0.304
sir1138	ctaE	cytochrome c oxidase subu	-0.432	-0.143	-0.993	-0.64	-0.351	0.04	0.598	-0.129	-0.218	-0.457	0.062	-0.079	0.094
sir1139	trxA	thioredoxintrxA	0.084	0.223	0.616	error	-0.094	-0.034	-0.233	0.07	0.224	-0.175	0.1	0.425	0.69
sir1140		DegT/DnrJ/EryC1/StrS fam	0.216	0.613	0.255	0.432	0.073	-0.426	-0.281	0.453	0.395	-0.143	0.155	0.454	-0.513
sir1142		hypothetical protein	error	error	-0.016	-0.398	-0.195	0.02	error	-0.431	-0.428	-0.366	-0.453	-0.425	-1.031
sir1143		hypothetical protein	error	error	error	error	error	error	error	-0.231	-0.172	1.042	-0.392	-0.311	0.105
sir1145	gltS	Monocomponent sodium-de	0.664	0.394	0.029	-0.09	-0.306	-0.129	-0.326	error	error	error	error	error	error
sir1147		two-component sensor hist	0.062	0.086	0.243	-0.401	-0.362	-0.35	0.366	-0.355	0.002	-0.304	-0.641	-0.13	0.859
sir1148		unknown protein	-0.484	error	-0.136	error	0.043	error	-0.354	-0.21	0.081	error	-0.448	-0.463	-0.582

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by Synechocytis PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1149		ATP-binding protein of ABC	error	-0.273	-0.443	0.344	-0.461	-0.266	-0.218	-0.072	-0.213	0.275	-0.044	-0.047	error
slr1150		unknown protein	0.02	-0.003	-0.347	0.125	0.067	-0.043	0.294	0.303	0.341	0.613	0.247	0.179	0.602
slr1152		hypothetical protein	-0.626	-0.539	0.046	0.61	-0.412	-0.154	-0.176	error	0.864	error	error	error	error
slr1159	purD	glycinamide ribonucleotide	-0.05	0.024	0.409	0.729	0.125	0.428	-0.083	0.182	0.649	0.499	0.381	0.482	-0.569
slr1160		hypothetical protein	0.031	-0.323	0.175	1.186	-0.075	-0.142	-0.387	0.828	error	error	0.523	error	error
slr1161		hypothetical protein	error	-0.238	-0.434	-0.579	-1.022	-0.265	-0.215	-0.224	-0.402	-0.932	-0.963	-0.573	0.516
slr1162		unknown protein	-0.238	error	-0.978	-0.977	-0.849	-0.228	-0.232	-0.499	-0.544	0.204	-0.611	-1.014	0.136
slr1163		unknown protein	-0.529	-0.15	0.121	0.763	0.062	-0.048	-0.346	-0.255	-0.035	0.267	0.33	-0.52	error
slr1164		ribonucleotide reductase su	-0.311	-0.466	-0.416	0.114	-0.563	-0.079	-0.031	-0.443	-0.18	0.293	-0.408	-0.14	-0.911
slr1165		sulfate adenyltransferase	-0.481	-0.457	-0.594	-0.259	-0.551	-0.344	-0.734	-0.228	-0.391	-0.423	-0.197	-0.402	1.011
slr1166		UDP-glucose:tetrahydrobio	0.018	-0.5	-1.152	-0.386	-0.765	-0.125	0.067	0.103	-0.237	0.83	-0.26	-0.358	-1.04
slr1167	gldA	glycerol dehydrogenasegld	-0.589	-0.832	-0.757	0.072	0.301	-0.367	-0.149	error	error	error	error	error	error
slr1168		unknown protein	-0.159	0.05	0.095	0.084	-0.292	0.149	-0.361	0.06	0.391	-0.005	0.193	-0.177	0.887
slr1169		unknown protein	0.452	error	error	error	0.406	0.01	error	0.076	0.283	0.088	0.503	0.052	1.143
slr1170		hypothetical protein	0.354	-0.096	0.169	0.072	-0.081	-0.11	-0.03	-0.371	-0.17	-0.014	-0.478	-0.187	0.228
slr1171	gpx1	glutathione peroxidase-like	-0.19	error	-0.16	0.941	2.226	0.725	1.912	error	error	error	error	error	error
slr1173		hypothetical protein	0.002	0.105	-0.611	-0.849	-0.998	-0.435	0.284	-0.728	-0.575	-0.339	-0.631	-0.48	0.042
slr1174		hypothetical protein	0.439	0.181	0.83	-0.098	0.837	0.097	error	0.267	0.951	0.674	1.807	0.596	1.96
slr1176		glucose-1-phosphate adeny	-0.656	-1.299	-1.747	-0.096	-0.385	-0.067	-0.128	-0.278	-0.922	-0.353	-0.162	-0.875	0.476
slr1177		hypothetical protein	error	error	-0.687	error	-0.097	-0.083	0.542	0.156	0.216	-0.284	0.149	-0.002	1.675
slr1178		hypothetical protein	0.469	error	error	error	-0.503	-0.116	error	-0.138	0.073	0.331	-0.075	-0.039	1.488
slr1179		hypothetical protein	-0.252	error	-0.15	0.005	-0.212	-0.264	-0.361	0.439	0.519	0.613	0.078	0.259	-0.595
slr1181	psbA1	photosystem II D1 proteinps	-0.697	-0.378	0.37	0.859	-0.387	-0.719	-0.381	0.696	1.689	1.391	0.503	1.692	-0.198
slr1182		hypothetical protein	-0.557	error	-0.422	-0.862	-0.573	-0.164	-0.142	0.044	0.21	0.633	0.067	0.094	-0.675
slr1183		hypothetical protein	error	error	-0.318	-0.992	error	0.413	error	0.452	0.175	0.439	-0.167	-0.271	error
slr1184		hypothetical protein	0.072	-0.217	0.067	-0.972	-0.682	0.287	error	-0.214	0.291	-0.294	-0.274	-0.351	0.171
slr1185		Rieske iron-sulfur protein w	-0.333	-0.325	-0.317	error	-0.204	-0.282	-0.004	error	error	error	error	error	error
slr1186		hypothetical protein	-0.438	-0.377	-0.699	error	error	0.296	0.108	0.046	-0.025	0.362	0.256	-0.136	-0.205
slr1187		unknown protein	-0.489	-0.783	-1.599	-1.03	-1.731	-1.276	-1.346	0.334	-0.56	0.021	-0.386	-0.453	-0.61
slr1188		hypothetical protein	0.449	0.152	0.04	-0.16	-0.401	0.457	-0.22	0.339	0.12	0.333	0.141	0.464	-0.035
slr1189		unknown protein	0.593	error	1.55	1.173	0.496	0.505	0.18	0.736	1.562	1.191	0.521	1.266	-0.659
slr1192		probable alcohol dehydroge	0.383	1.299	1.733	1.398	1.287	0.763	0.72	0.294	2.031	1.465	1.446	1.948	0.973
slr1194		hypothetical protein	-0.411	-0.035	-0.162	-0.229	0.307	0.087	0.366	-0.316	0.422	0.318	0.033	0.276	1.253
slr1195		hypothetical protein	-0.198	-0.059	-0.097	0.48	0.121	0.121	0.171	-0.146	-0.13	0.104	0.041	-0.169	-1.087
slr1196		hypothetical protein	-0.143	-0.344	-0.351	-0.055	-0.187	-0.183	-0.22	error	error	error	error	error	error
slr1197		SMF protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slr1198		antioxidant protein	-0.571	-0.496	-1.123	-0.46	-0.586	-0.585	-0.671	-0.215	-1.205	-1.612	-0.651	-1.387	-0.313
slr1199	mutL	DNA mismatch repair prote	1.272	0.526	0.767	-0.508	0.321	0.022	error	0.048	0.092	0.357	-0.247	-0.272	0.234
slr1200		permease protein of branch	-0.014	error	0.685	0.924	1.365	0.801	1.603	error	error	error	error	error	error
slr1201		permease protein of branch	0.113	-0.049	-0.372	-0.109	0.205	0.084	0.249	-0.319	-0.315	0.493	-0.029	-0.266	-0.67
slr1202		permease protein of sugar	0.294	0.96	0.978	0.409	0.944	0.77	0.706	error	error	error	error	error	error
slr1203		hypothetical protein	0.383	0.357	0.405	0.43	0.625	0.178	-0.031	error	error	error	error	error	error
slr1204		protease	0.757	2.127	2.265	2.292	2.77	1.876	2.004	1.418	1.604	0.758	1.703	1.47	2.191
slr1205		similar to chlorobenzene di	-0.454	-0.169	0.361	0.895	0.358	0.434	0.383	error	error	error	error	error	error
slr1206		hypothetical protein	0.114	0.352	0.591	0.312	0.486	0.854	0.503	0.065	0.277	0.21	0.053	0.063	-0.308
slr1207		hypothetical protein	-0.066	0.26	0.275	-0.004	0.191	0.035	0.222	-0.173	0.327	0.031	0.132	-0.068	0.566
slr1208		probable oxidoreductase	error	-0.132	-0.623	-0.438	-0.948	-0.839	-0.798	-0.287	0.166	-0.381	-0.66	0.188	-0.532
slr1209		hypothetical protein	0.776	1.043	1.553	0.708	0.469	0.353	0.268	0.71	1.472	0.773	0.333	1.026	0.805
slr1210		unknown protein	error	3.644	3.346	2.566	2.341	1.457	1.069	1.344	1.584	0.689	1.306	1.046	-0.009
slr1211	cobN	cobalamin biosynthetic prot	-0.532	-0.232	-1.248	-0.705	-1.601	-0.505	-0.743	-0.755	-0.85	error	-0.889	-0.551	-1.528
slr1212		similar to two-component se	-0.776	-0.554	-0.143	0.27	-0.194	0.019	0.123	-0.595	0.186	-0.096	-0.293	-0.062	-1.381
slr1213		two-component response re	0.148	-0.001	-0.505	-0.789	-0.325	0.413	0.739	-0.327	-0.035	-0.013	-0.376	-0.111	-0.623
slr1214		two-component response re	-0.417	-0.415	-0.99	-0.546	-1.328	-0.855	-0.728	0.12	-0.541	0.063	-0.703	-0.609	-1.124
slr1215		hypothetical protein	0.749	0.333	0.534	error	0.538	0.326	0.243	error	error	error	error	error	error
slr1216		Mg2+ transport protein	error	error	error	error	error	error	error	-0.643	-0.49	-0.024	-0.506	-0.412	0.097
slr1218	ycf39	hypothetical protein YCF39	-0.624	-0.055	-0.068	0.25	-0.08	0.248	0.283	-0.189	-0.053	-0.571	-0.417	-0.255	-1.088
slr1219	ureE	urease accessory protein E	error	error	-0.338	-0.984	-0.049	0.206	error	-0.051	-0.03	0.342	-0.209	-0.442	-0.822
slr1220		hypothetical protein	-0.445	-0.387	0.168	1.091	0.659	0.232	0.094	0.257	0.506	1.212	1.18	0.427	-0.017
slr1222		unknown protein	-0.247	-0.261	-0.04	0.37	-0.254	0.279	0.175	error	error	error	error	error	error
slr1223		hypothetical protein	-0.038	-0.033	0.2	0.299	-0.037	-0.187	-0.19	0.155	0.39	0.214	0.252	0.278	0.574
slr1224		ATP-binding protein of suga	-0.248	-0.128	-0.472	-0.331	-0.517	0.094	-0.098	-0.002	-0.066	0.419	-0.092	-0.129	-1.089
slr1225		serine/threonine kinase	0.114	0.217	0.347	0.108	0.121	0.147	0.066	-0.249	-0.016	-0.123	-0.176	-0.301	0.355
slr1226	purC	phosphoribosyl aminidazo	-0.271	-0.226	0.071	1.179	-0.296	-0.469	-0.57	0.143	0.223	-0.344	0.187	0.102	-0.69
slr1227		chloroplastic outer envelop	-0.166	-0.362	-0.006	0.637	-0.278	0.106	0.125	-0.152	-0.016	0.925	-0.123	0.07	-0.869
slr1228		peptide-chain-release facto	0.506	0.399	1.016	0.87	0.302	0.121	0.275	0.202	0.657	-0.232	0.218	0.771	0.716
slr1229		sulfate permease	error	error	0.366	-0.095	-0.022	0.004	-0.816	-0.311	0.139	-0.346	-0.352	-0.008	-0.29
slr1230		hypothetical protein	-0.211	-0.049	0.202	0.72	-0.055	0.288	0.077	error	error	error	error	error	error
slr1232		unknown protein	0.029	-0.105	-0.212	-0.478	-0.291	0.137	0.123	-0.321	0.358	-0.813	-0.693	-0.11	0.038
slr1233		succinate dehydrogenase f	0.082	-0.203	-0.416	-0.405	-0.244	0.26	0.761	error	error	error	error	error	error
slr1234		protein kinase C inhibitor	-0.039	-0.179	0.364	-0.13	0.16	0.18	0.423	-0.023	0.591	0.944	0.387	0.412	1.167
slr1235		hypothetical protein	0.176	0.385	0.756	0.824	0.36	0.157	0.449	0.365	0.87	0.166	0.639	0.648	0.637
slr1236		hypothetical protein	-0.128	-0.049	0.05	-0.045	0.25	-0.116	error	-0.443	-0.121	-0.433	-0.191	-0.458	0.961
slr1237		cytosine deaminase	-0.21	-0.56	-1.002	-0.398	-0.875	-0.655	-0.147	0.266	0.009	-0.524	-0.029	-0.005	-1.086
slr1238	gshB	glutathione synthetasegshB	0.135	0.249	1.007	0.472	0.638	0.198	0.736	0.491	0.357	error	0.604	0.023	0.834
slr1239	pntA	pyridine nucleotide transhy	-0.528	-0.789	-1.881	-1.427	-1.592	-1.452	-0.897	-0.393	-1.116	-1.547	-1.61	-1.09	0.113



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1240		unknown protein	-0.305	-0.182	-0.257	0.269	-0.143	0.359	0.05	-0.415	-0.303	-0.685	-0.673	-0.504	-1.089
slr1241		hypothetical protein	-0.276	error	0.359	0.332	-0.226	-0.088	-0.301	error	error	error	error	error	error
slr1243		unknown protein	-0.374	-0.261	-0.364	-0.946	-0.343	-0.35	-0.264	error	error	error	error	error	error
slr1245		transcriptional regulator	-0.253	-0.314	-1.13	-1.513	-1.349	-0.741	-0.761	-0.064	-0.406	-0.873	-1.099	-0.716	5.041
slr1246		putative transposase [ISY8]	0.283	0.446	0.481	error	0.073	error	0.088	0.283	0.513	0.547	-0.162	0.278	0.385
slr1247		phosphate-binding periplasm	-0.4	-0.073	-0.264	error	-0.504	-0.205	0.125	-0.285	-0.231	-0.168	-0.418	-0.337	-0.91
slr1248		phosphate transport system	error	error	error	error	error	error	error	-0.161	0.357	0.177	-0.074	0.221	0.245
slr1249		phosphate transport system	error	error	-0.382	-1.127	error	0.395	error	error	error	error	error	error	error
slr1250		phosphate transport ATP-b	0.424	error	0.877	-0.419	0.137	0.623	0.212	-0.644	0.114	-0.062	-0.443	-0.261	0.907
slr1251		peptidyl-prolyl cis-trans isom	0.093	0.306	0.498	1.101	0.38	0.126	0.325	0.353	0.653	-0.177	0.647	0.386	1.059
slr1253		unknown protein	-0.151	-0.271	0.007	-0.122	-0.207	-0.493	0.233	0.264	0.471	0.041	-0.131	0.161	-0.483
slr1254	pds, crtD,	phytoene dehydrogenase (p	-0.039	0.035	0.474	0.789	0.414	-0.057	0.415	error	error	error	error	error	error
slr1255	pys, crtB	phytoene synthasepys, crtB	-0.436	-0.476	-0.632	error	-0.615	-0.352	-0.347	-0.355	-0.062	-0.017	-0.455	-0.069	-0.298
slr1256	ureA	urease gamma subunitureA	-0.032	error	-0.753	-0.16	0.124	0.276	error	0.08	-0.116	-0.2	0.044	-0.288	0.128
slr1257		unknown protein	0.201	-0.062	-0.026	-0.26	0.418	0.339	0.575	-0.217	-0.05	0.538	-0.03	0.157	0.715
slr1258		unknown protein	-0.598	-0.343	-0.683	-0.721	-0.151	0.028	-0.163	error	error	error	error	error	error
slr1259		hypothetical protein	-0.278	-0.509	0.328	0.884	0.186	-0.047	0.113	-0.183	-0.021	-0.022	0.145	0.005	0.251
slr1260		hypothetical protein	-0.829	error	-0.274	-0.069	-0.019	0.37	0.511	0.276	0.245	0.828	0.514	0.137	0.181
slr1261		hypothetical protein	-0.106	-0.417	0.063	0.519	-0.149	-0.229	-0.412	-0.407	0.194	0.508	-0.035	-0.16	0.475
slr1262		hypothetical protein	error	error	-0.819	-0.579	-0.493	0.229	-0.309	-0.131	-0.117	0.434	-0.121	0.17	-0.48
slr1263		hypothetical protein	-0.209	0.241	-0.502	-0.385	-0.341	0.482	0.02	error	error	error	error	error	error
slr1265	rpoC1	RNA polymerase gamma-sub	-0.28	0.028	0.249	1.485	-0.115	-0.346	-0.555	0.417	0.269	0.056	0.346	-0.039	-0.556
slr1266		hypothetical protein	0.428	0.275	0.409	-0.026	0.082	0.102	0.309	0.196	0.617	-0.193	-0.03	0.159	0.405
slr1267	ftsW	cell division protein FtsWfts	-0.127	-0.345	-0.832	-0.014	-0.413	0.099	-0.154	-0.115	-0.458	-0.417	-0.148	-0.208	0.266
slr1269	ggt	gamma-glutamyltranspeptid	-0.515	-0.566	-0.56	0.048	-0.692	-0.67	-0.716	-0.089	-0.164	-0.194	-0.111	-0.349	0.027
slr1270		hypothetical protein	0.154	-0.39	0.046	0.342	0.25	-0.054	-0.015	0.219	0.267	0.907	0.879	0.351	1.692
slr1271		probable UDP-N-acetyl-D-m	0.669	0.488	-0.204	-0.704	-0.042	0.108	0.462	0.214	-0.054	0.485	-0.007	0.109	error
slr1272		probable porin, major outer	-0.438	-0.142	-0.387	0.124	-0.601	-0.308	-0.41	-0.159	-0.269	-0.142	-0.246	-0.415	-0.7
slr1273		hypothetical protein	0.113	0.229	0.402	1.057	-0.085	-0.101	-0.282	0.412	0.353	0.815	0.118	0.111	-0.807
slr1274	pilM	probable fimbrial assembly	error	error	error	error	error	error	error	0.388	1.197	0.861	0.586	0.776	1.471
slr1275		hypothetical protein	-0.246	-0.018	-0.054	-0.193	-0.785	-0.333	-0.544	error	error	error	error	error	error
slr1276		hypothetical protein	0.499	0.169	0.285	0.875	-0.257	-0.022	-0.49	0.302	0.127	0.582	-0.52	0.275	-0.289
slr1277		general secretion pathway	error	error	error	error	error	error	error	-0.207	-0.995	-1.198	-0.933	-1.043	-1.216
slr1278	ycf62	hypothetical protein YCF62	0.469	0.365	error	-1.092	error	0.548	error	0.186	-0.08	0.441	-0.085	-0.073	0.746
slr1279	ndhC	NADH dehydrogenase subu	0.072	0.284	0.371	-0.682	0.062	0.102	-0.09	0.196	0.27	1.115	0.006	-0.039	0.768
slr1280	ndhK	NADH dehydrogenase subu	-0.632	-0.839	-1.24	-0.34	-0.318	-0.322	-0.405	-0.177	-0.469	-0.75	0.102	-0.615	0.95
slr1281	ndhJ	NADH dehydrogenase subu	-0.302	-0.595	-0.693	0.085	-0.274	-0.231	0.023	0.191	-0.111	-0.542	0.286	-0.199	1.385
slr1282		putative transposase [ISY5]	0.806	0.576	0.161	0.346	0.501	0.396	1.228	0.019	0.44	0.64	0.214	0.306	0.021
slr1283		putative transposase [ISY5]	-0.279	error	0.017	0.203	-0.46	-0.509	-0.604	-0.119	0.314	-0.066	-0.007	-0.092	0.836
slr1285		two-component sensor hist	error	error	-0.419	error	error	0.87	error	0.065	0.344	-0.516	0.492	-0.291	-0.273
slr1287		hypothetical protein	error	0.562	0.589	error	0.614	0.251	error	0.086	0.213	0.863	0.103	-0.08	1.619
slr1288		hypothetical protein	error	error	error	error	0.076	0.362	error	-0.299	0.249	0.177	-0.112	-0.07	1.537
slr1289	icd	isocitrate dehydrogenase (h	-0.329	-0.253	-0.29	0.161	-0.071	-0.166	0.215	0.132	0.63	0.347	0.312	0.534	-0.281
slr1290		hypothetical protein	error	error	error	error	error	error	error	0.342	0.665	0.118	0.273	0.146	0.23
slr1291	ndhD2	NADH dehydrogenase subu	-0.619	-0.394	0.049	-0.001	0.288	0.036	0.253	-0.045	0.361	0.594	0.514	0.54	-0.324
slr1293		similar to phytoene dehy	-0.005	0.409	0.302	-0.029	0.002	0.143	error	error	error	error	error	error	error
slr1295	futA1	iron transport system subst	0.136	-0.081	-0.013	0.306	-0.01	-0.058	0.289	-0.267	-0.095	0.207	0.219	-0.214	0.506
slr1298		unknown protein	-0.388	error	-0.403	-1.281	error	0.145	error	-0.316	-0.393	0.199	-0.279	-0.423	0.027
slr1299		UDP-glucose dehydrogenas	0.173	error	-0.295	-0.132	0.467	0.222	0.71	error	error	error	error	error	error
slr1300		similar to 2-octaprenyl-6-me	error	error	error	error	error	error	error	-0.223	-0.381	0.871	-0.229	-0.368	-0.777
slr1301		hypothetical protein	error	error	error	error	error	error	error	2.686	2.289	-1.786	1.856	2.439	1.476
slr1302	cupB	protein involved in constitut	error	error	error	error	error	error	error	0.207	-0.283	-0.048	-0.043	-0.39	0.583
slr1303		hypothetical protein	0.826	0.53	0.694	error	error	1.112	1.575	0.538	0.319	0.671	0.193	0.242	-0.083
slr1305		two-component response re	error	0.396	0.583	-1.168	error	0.427	0.366	-0.548	-0.27	-0.417	-0.609	-0.099	-0.201
slr1306		hypothetical protein	-0.462	-0.576	-0.64	-0.368	-0.745	error	-0.527	0.258	-0.04	0.758	0.262	-0.29	1.405
slr1307		hypothetical protein	2.152	2.815	1.5	0.615	1.741	1.176	-	1.05	1.001	-0.079	0.319	0.57	-0.224
slr1311	psbA2	photosystem II D1 proteinps	-0.528	-0.116	error	error	error	-0.836	error	0.834	1.862	0.801	0.665	1.539	-0.102
slr1312		arginine decarboxylase	0.391	-0.132	-0.069	-0.176	-0.482	0.118	0.153	-0.725	-0.369	-0.442	-0.825	-0.552	0.285
slr1315		hypothetical protein	-0.23	-0.215	0.033	0.574	0.033	0.237	0.138	-0.076	0.148	0.037	0.315	-0.336	-0.724
slr1316		iron-uptake system permea	0.049	0.031	-0.059	-0.284	0.079	0.052	0.067	-0.438	-0.191	-0.091	-0.385	-0.014	5.267
slr1317		iron-uptake system permea	0	0.297	-0.214	-1.349	error	0.209	error	error	error	error	error	error	error
slr1318		iron-uptake system ATP-bir	-0.59	0.504	0.524	-0.185	-0.055	0.248	0.761	-0.093	0.164	0.177	-0.667	0.099	-0.43
slr1319		iron-uptake system binding	-0.165	-0.28	0.459	0.974	-0.044	-0.332	-0.552	-0.123	0.152	-0.515	-0.185	-0.703	0.359
slr1322	lldD	putative modulator of DNA	-0.406	-0.488	-0.076	error	0.062	-0.208	-0.525	-0.067	0.545	0.17	0.583	0.08	0.269
slr1324		two-component hybrid sens	-0.061	-0.138	-0.166	0.352	-0.15	-0.112	-0.063	-0.225	0.08	0.475	-0.154	0.336	-1.007
slr1325		GTP pyrophosphokinase	-0.106	-0.267	-0.407	-0.403	0.041	0.457	0.459	-0.227	-0.319	-0.651	0.128	-0.301	0.852
slr1327		hypothetical protein	1.054	error	1.161	-0.347	0.815	0.924	error	-0.079	error	error	0.371	error	error
slr1329	atpB	ATP synthase beta subunit	-0.57	-1.034	-1.554	-0.318	-1.041	-0.966	-0.889	-0.151	-0.72	-1.211	-0.505	-0.427	0.464
slr1330	atpE	ATP synthase epsilon subu	-0.472	-0.723	-0.958	-0.074	-0.863	-0.859	-0.634	0.051	-0.415	-1.008	-0.402	-0.461	-0.234
slr1331		processing protease	error	error	error	error	error	error	error	0.4	0.221	-0.014	-0.066	0.102	-0.406
slr1332		beta ketoacyl-acyl carrier p	1.037	0.93	0.54	-0.24	-0.152	0.322	0.628	0.342	0.092	-0.074	-0.032	-0.017	0.495
slr1334		phosphoglucosyltransferase	-0.154	error	0.333	error	-0.457	-0.086	-0.315	0.342	0.314	0.655	0.124	0.365	0.025
slr1336		H+/Ca2+ exchanger	0.233	-0.14	error	0.103	-0.008	0.176	1.802	0.351	0.478	1.44	0.312	0.376	0.856
slr1338		hypothetical protein	0.157	0.821	-0.172	-0.787	0.408	0.48	-	-0.078	0.144	0.074	0.241	-0.247	0.734
slr1339		hypothetical protein	-0.121	error	-0.164	error	-0.297	0.256	0.303	-0.737	-0.777	error	-0.652	-1.2	1.062

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1340		unknown protein	-0.203	error	error	0.434	-0.313	0.042	error	error	error	error	error	error	error
slr1342		hypothetical protein	error	error	error	error	error	error	error	-0.448	-0.337	-0.305	-0.592	-0.836	0.506
slr1343		hypothetical protein	0.196	-0.3	0.055	-0.59	-0.618	0.206	0.488	-0.621	error	0.153	-0.625	error	0.793
slr1344		hypothetical protein	-0.173	-0.556	-0.121	0.502	-0.242	0.084	-0.484	-0.278	-0.493	-0.334	-0.457	-0.408	-1.231
slr1347	icfA	carbonic anhydrase icfA	-0.179	-0.264	-0.253	0.299	-0.719	-0.572	-0.711	0.14	0.127	-0.308	-0.136	0.066	0.401
slr1348	cysE	serine acetyltransferase cysE	0.378	0.363	0.291	0.21	0.188	0.059	0.107	-0.11	-0.062	error	-0.458	-0.453	-0.212
slr1349		glucose-6-phosphate isomerase	-0.072	0.074	-0.376	0.1	0.143	0.172	0.301	error	error	error	error	error	error
slr1350	desA	fatty acid desaturase desA	-0.605	-0.698	-0.807	0.147	-0.712	-0.789	-0.687	-0.055	0.005	0.538	0.298	-0.108	0.383
slr1351	murF	UDP-N-acetylmuramoylalanine C-5 pyrophosphatase	0.118	0.135	0.477	0.785	-0.06	0.529	0.283	0.107	0.291	0.096	-0.047	0.099	-0.471
slr1353		hypothetical protein	0.602	error	0.995	0.909	0.828	0.493	0.739	0.17	0.782	1.081	0.901	0.575	1.628
slr1356	rps1a	30S ribosomal protein S19	-0.089	-0.342	0.177	1.332	-0.135	-0.53	-0.699	0.702	0.997	0.906	0.558	1.087	0.33
slr1357		putative transposase [ISY109]	-0.606	-0.532	-0.338	0.317	-0.608	-0.519	-0.733	-1.067	-0.343	0.478	-0.773	-0.352	-1.049
slr1362		hypothetical protein	error	error	error	error	error	error	error	0.139	-0.012	0.428	0.095	-0.035	-0.537
slr1363		hypothetical protein	0.163	error	-0.324	-0.847	-0.486	0.168	error	-0.555	-0.25	error	-0.687	-0.301	0.469
slr1364	bioB	biotin synthetase bioB	-0.427	-0.235	-0.042	0.024	-0.436	-0.122	-0.737	-0.209	0.041	-0.46	-0.194	0.004	1.708
slr1365		hypothetical protein	0.197	0.087	0.159	0.164	-0.13	-0.209	-0.349	0.156	0.139	-0.555	0.003	error	0.411
slr1366		lipoprotein signal peptidase	1.377	0.813	0.593	-1.291	0.532	0.075	error	0.334	0.452	0.483	0.404	0.203	1.272
slr1367		glycogen phosphorylase	error	-0.411	error	-0.84	0.307	0.409	0.731	-0.225	-0.395	0.155	0.17	-0.407	0.917
slr1368	cobL	precorrin decarboxylase cobL	0.925	1.213	0.755	error	0.644	0.603	1.146	0.5	0.653	-0.448	0.087	0.474	1.132
slr1369	cdsA	phosphatidate cytidyltransferase	-0.689	-0.793	-0.633	-0.323	-0.607	-0.425	-0.355	-0.127	0.098	-0.235	-0.197	-0.13	-0.768
slr1376		hypothetical protein	error	-0.483	0.382	-1.233	0.052	0.904	error	-0.158	0.372	0.353	0.438	-0.444	1.14
slr1377		signal peptidase I	0.324	0.394	1.742	1.533	1.077	0.436	0.808	0.186	1.291	0.971	0.928	0.957	1.023
slr1378		hypothetical protein	-0.048	error	-0.178	-0.579	0.278	0.168	-0.23	-0.014	-0.073	-0.116	-0.013	-0.405	-0.541
slr1379	cydA	cytochrome oxidase d subunit	-0.543	-0.666	-1.468	-0.759	-0.856	-0.394	-0.131	-0.097	-0.746	-0.699	-1.097	-0.845	-1.255
slr1380	cydB	cytochrome oxidase d subunit	-0.472	-0.888	-0.725	-0.714	-0.595	-0.107	0.176	-0.184	-0.214	-0.33	-0.675	-0.261	-0.56
slr1383		unknown protein	error	0.127	0.392	0.102	0.007	0.117	0.032	0.04	0.339	-0.102	0.147	0.284	-0.306
slr1384		hypothetical protein	error	error	error	error	error	error	error	-0.329	0.139	-0.297	-0.513	-0.287	0.119
slr1385		unknown protein	0.295	-0.741	0.128	error	-0.25	0.148	0.173	-0.401	-0.324	-0.319	-0.662	-0.713	0.248
slr1390	ftsH	cell division protein FtsH	-0.119	error	0.613	0.915	0.835	0.675	0.58	-0.009	0.513	2.278	1.214	0.624	0.3
slr1391		unknown protein	error	error	error	error	error	error	error	0.161	0.655	-0.88	0.346	-0.019	0.273
slr1392	feoB	ferrous iron transport protein	-0.162	0.435	0.936	1.026	0.781	0.294	0.742	0.5	1.159	1.17	1	1.219	0.63
slr1393		two-component sensor histidine kinase	0.115	error	0.331	-0.203	0.061	0.223	1.185	-0.338	-0.265	-0.53	-0.633	-0.251	0.482
slr1394		hypothetical protein	-0.268	-0.16	0.026	0.073	-0.028	-0.057	0.075	-0.173	0.117	0.082	-0.217	-0.13	-0.518
slr1395		hypothetical protein	-0.307	error	0.1	error	-0.169	0.361	error	-0.463	-0.297	-0.587	-0.66	-0.513	-0.161
slr1396		unknown protein	0.468	0.944	0.569	-0.573	0.613	0.574	0.607	-0.032	0.47	0.467	-0.014	-0.038	1.669
slr1397		unknown protein	0.47	1.041	1.269	0.671	0.643	0.364	0.37	0.506	1.224	0.286	0.372	1.167	0.528
slr1398		unknown protein	error	0.96	0.291	-0.283	0.839	0.362	0.564	0.244	0.474	error	0.305	0.176	0.657
slr1400		two-component hybrid sensor kinase	0.466	0	0.097	error	0.024	0.074	0.644	0.018	0.194	1.269	-0.084	0.07	0.044
slr1403		unknown protein	-0.206	-0.473	-0.646	-0.503	-1.009	-0.629	-0.88	error	error	error	error	error	error
slr1406		hypothetical protein	-0.7	-0.317	-0.764	-0.85	-0.921	-0.498	-0.644	-0.252	-0.565	-0.564	-0.854	-0.552	-0.85
slr1407		unknown protein	-0.231	error	-0.601	-1.598	-1.579	-0.341	-0.406	0.047	-0.305	-0.396	-1.055	-0.459	-0.272
slr1409		WD-repeat protein	-0.488	-0.376	0.142	error	-0.642	-0.368	-0.679	-0.23	-0.277	0.143	-0.519	-0.594	-1.233
slr1410		WD-repeat protein	error	error	error	error	error	error	error	-0.217	-0.966	-0.651	-1.693	-1.57	-1.295
slr1411		hypothetical protein	error	error	error	error	error	error	error	0.637	0.417	0.725	0.137	0.156	-0.154
slr1413		hypothetical protein	0.664	1.416	2.815	2.081	2.781	1.509	2.659	error	error	error	error	error	error
slr1414		two-component sensor histidine kinase	0.308	0.752	0.977	0.763	0.989	0.541	0.843	-0.066	0.291	0.059	0.106	0.28	0.987
slr1415		hypothetical protein	error	error	error	error	error	error	error	-0.047	0.26	error	-0.226	0.066	-0.113
slr1416		similar to MorR protein	0.51	error	-0.121	-0.566	-0.623	0.039	0.49	-0.216	0.287	-0.035	-0.12	0.196	1.251
slr1417	ycf57	hypothetical protein YCF57	0.088	0.352	0.716	1.282	1.049	0.174	0.258	error	error	error	error	error	error
slr1418	pyrD	dihydroorotate dehydrogenase	-0.259	-0.183	-0.081	0.412	-0.383	0.101	-0.292	-0.14	-0.15	-0.214	-0.132	-0.05	-0.606
slr1419		hypothetical protein	error	-0.092	error	-0.76	0.298	-0.033	error	-0.326	-0.154	-0.039	0.073	-0.619	0.614
slr1420		probable sugar kinase	0.781	0.269	0.39	error	error	0.252	error	-0.231	-0.237	-0.13	0.007	-0.242	-0.032
slr1421		unknown protein	0.178	0.533	0.475	0.143	0.114	0.09	-0.081	0.133	0.143	0.063	0.255	0.333	0.813
slr1423	murC	UDP-N-acetylmuramate-6-phosphate lyase	-0.632	-0.83	-0.918	-0.15	-0.515	-0.381	-0.456	-0.186	-0.553	-0.698	-0.644	-0.539	-0.953
slr1424		UDP-N-acetylenolpyruvoylglutamate decarboxylase	0.262	-0.246	-0.152	-1.028	-0.616	-0.376	-0.088	0.183	-0.184	-0.496	-0.504	-0.267	-0.101
slr1425		hypothetical protein	-0.207	error	0.155	-0.083	-0.185	-0.16	0.105	0.126	0.021	-0.313	-0.14	-0.361	0.409
slr1426	recR	recombination protein RecR	-0.177	0.195	0.095	-0.073	-0.47	-0.14	-0.296	-0.157	-0.075	-0.258	-0.171	-0.094	-0.33
slr1428		hypothetical protein	error	0.456	0.106	-0.818	-0.238	0.117	0.452	0.025	0.057	0.665	0.025	0.089	-0.015
slr1429		hypothetical protein	error	error	-1.055	error	error	error	0.017	0.464	0.347	0.541	0.313	0.379	0.079
slr1431		hypothetical protein	error	error	error	error	0.092	error	-0.16	-0.109	0.021	0.45	0.417	0.085	0.702
slr1434	pntB	pyridine nucleotide transhydrogenase	-0.475	-0.547	-1.061	-0.671	-1.6	-1.472	-0.985	-0.367	-0.104	0.328	-0.393	0.053	-1.215
slr1435		PmbA protein homolog	-0.035	-0.057	0.324	0.063	error	error	-0.246	-0.189	0.309	error	-0.038	0.174	0.754
slr1436		unknown protein	0.521	0.134	-0.611	-0.291	0	0.013	error	-0.171	-0.376	0.502	-0.181	-0.653	-0.367
slr1437		unknown protein	-0.399	-0.347	-0.065	0.589	-0.152	-0.041	-0.216	error	error	error	error	error	error
slr1438		hypothetical protein	-0.124	-0.001	-0.066	error	error	0.01	-0.003	error	error	error	error	error	error
slr1440		hypothetical protein	0.302	-0.205	0.037	-0.491	0.03	0.063	0.791	-0.45	-0.305	0.486	-0.279	-0.546	0.659
slr1441		hypothetical protein	0.159	0.276	0.252	0.407	0.243	0.246	error	-0.022	0.157	0.387	0.142	0.017	-0.194
slr1442		hypothetical protein	-0.429	-0.469	-0.651	-1.18	-0.268	-0.324	0.11	0.014	0.073	0.291	-0.028	-0.412	1.216
slr1443		serine/threonine kinase	0.774	0.682	0.388	-0.422	0.137	0.434	-	-0.181	0.117	-0.002	-0.236	0.377	0.911
slr1444		hypothetical protein	0.323	0.399	0.079	0.142	-0.143	-0.203	-0.173	0.384	0.38	-0.027	-0.108	0.163	-0.131
slr1448		fructokinase	0.393	0.439	0.84	0.745	0.518	0.48	1.498	-0.226	0.256	-0.454	0.117	0.111	0.66
slr1449		hypothetical protein	-0.465	-0.859	-0.795	-0.19	error	0.296	0.297	-0.248	-0.873	-0.455	-0.035	-0.947	0.425
slr1450		unknown protein	-0.071	-0.032	0.04	0.185	0.142	0.237	0.27	-0.048	0.123	-0.34	-0.23	-0.175	-0.732
slr1451		hypothetical protein	0.064	0.223	0.158	0.087	-0.004	0.112	0.297	-0.115	0.59	0.438	0.246	0.543	-0.24
slr1452	sbpA	sulfate transport system subunit	1.057	1.334	1.46	1.842	1.101	0.231	0.88	error	error	error	error	error	error

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
sir1453	cysT	sulfate transport system per	0.497	0.634	0.803	0.319	0.474	0.244	1.036	error	error	error	error	error	error
sir1454	cysW	sulfate transport system per	-0.361	-0.5	-0.113	-0.205	-0.188	-0.438	-0.679	-0.375	-0.425	-0.51	-0.376	-0.609	0.103
sir1455	cysA	sulfate transport system AT	-0.181	0.223	0.611	0.225	0.323	0.657	0.219	-0.458	0.006	0.616	-0.097	-0.054	1.073
sir1456		unknown protein	-0.401	-0.456	1.183	0.113	1.296	0.086	0.233	-0.038	0.493	1.458	0.637	1.169	-0.448
sir1457		chromate transport protein	0.426	0.905	0.79	0.401	0.635	0.443	0.259	0.09	0.3	0.749	-0.25	0.194	-0.523
sir1459	apcF	phycobilisome core compon	-0.804	-0.976	-1.996	-1.463	-1.725	-1.545	-1.214	-0.369	-0.842	-0.73	-1.177	-0.532	-1.537
sir1461		hypothetical protein	-0.387	-0.38	-0.774	0.077	-0.386	-0.585	-0.525	-0.487	-0.37	-0.512	-0.409	-0.591	0.531
sir1462		hypothetical protein	0.204	0.965	1.879	error	1.43	1.049	1.229	-0.257	0.53	0.395	0.431	0.614	1.526
sir1463	fus	elongation factor EF-Gfus	-0.558	-0.408	-0.42	0.171	-0.126	-0.486	-0.601	0.101	0.098	0.421	0.747	0.164	0.873
sir1464		hypothetical protein	0.092	-0.014	0.218	error	0.279	-0.306	-0.072	0.049	0.491	0.419	0.205	0.273	0.729
sir1467		precorrin isomerase	-0.232	0.333	0.355	0.681	0.057	0.168	0.429	-0.166	0.282	0.013	0.044	0.223	-0.46
sir1468		hypothetical protein	error	0.606	0.814	0.243	0.308	0.434	error	0.2	0.658	0.392	0.366	0.539	0.571
sir1469	mpA	protein subunit of ribonucle	0.293	0.958	1.628	1.825	1.167	0.54	1.143	error	error	error	error	error	error
sir1470		hypothetical protein	-0.608	-0.324	0.156	0.804	-0.163	-0.389	-0.558	0.007	0.54	0.314	0.333	0.326	-0.767
sir1471		hypothetical protein	-0.591	-0.381	-0.142	0.435	0.03	-0.434	-0.596	0.016	0.196	0.805	0.223	0.068	0.661
sir1472		hypothetical protein	0.731	0.698	1.03	0.779	0.487	0.296	0.702	0.741	0.945	0.948	0.306	0.825	0.085
sir1474		hypothetical protein	0.439	0.426	0.393	0.496	0.171	0.033	0.076	0.571	0.443	1.144	0.25	0.622	-0.385
sir1475		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
sir1476	pyrB	aspartate carbamoyltransfe	0.127	0.155	0.852	1.021	-0.06	-0.244	-0.214	0.6	0.988	0.537	0.499	1.059	-0.584
sir1478		hypothetical protein	-0.119	0.097	-0.198	error	-0.499	-0.301	-0.617	-0.118	0.264	-0.108	-0.287	-0.089	0.105
sir1484		unknown protein	-0.946	-0.491	0.694	0.603	0.325	0.699	1.072	-0.566	-0.358	-0.332	-0.883	-0.338	-0.467
sir1485		unknown protein	0.301	error	-0.245	-0.153	0.533	-0.142	0.878	-0.112	-0.198	0.05	-0.56	-0.415	-1.226
sir1488		ATP-binding protein of ABC	error	0.715	error	error	0.282	-0.043	0.393	-0.028	-0.107	0.271	-0.474	-0.44	-0.54
sir1489		transcriptional regulator	0.063	0.714	error	-0.754	0.384	0.662	error	0.149	0.447	error	-0.439	0.238	1.051
sir1490		ferrichrome-iron receptor	-0.442	-0.535	-0.722	-0.299	-1.023	-0.568	-0.713	error	error	error	error	error	error
sir1491		iron(III) dicitrate-binding pro	-0.114	0.326	0.344	-0.525	-0.328	0.313	0.386	error	error	error	error	error	error
sir1492		iron(III) dicitrate-binding pro	0.81	1.187	1.114	1.735	0.911	0.227	0.472	1.154	1.235	1.064	0.975	1.332	0.161
sir1493		hypothetical protein	-0.296	-0.83	-0.152	0.11	-0.644	-0.14	-0.531	-0.127	0.219	-0.107	-0.319	0.032	-0.408
sir1494		ATP-binding protein of ABC	0.137	0.006	0.473	0.809	0.06	-0.131	-0.025	0.258	0.388	0.308	0.012	0.336	0.227
sir1495		hypothetical protein	0.05	error	error	0.384	-0.455	0.119	error	0.069	0.66	0.13	-0.123	0.782	-0.679
sir1496		putative transposase	error	error	error	error	error	error	error	error	error	error	error	error	error
sir1498	hypD	hydrogenase isoenzymes fo	0.525	-0.215	-0.033	-0.301	0.68	0.244	0.704	-0.321	0.334	0.471	0.518	-0.123	0.742
sir1501		probable acetyltransferase	error	1.865	3.616	1.581	1.748	0.889	1.103	0.969	3.264	2.293	1.222	3.095	0.007
sir1503		hypothetical protein	error	0.396	-0.191	error	-0.404	0.074	-0.147	error	error	error	error	error	error
sir1505		unknown protein	-0.406	-1.085	-1.108	-0.823	-0.766	-0.199	error	-0.253	-0.18	-0.747	-0.26	-0.84	0.596
sir1506		hypothetical protein	-0.041	-0.561	-0.299	0.246	-0.371	-0.468	-0.455	error	error	error	error	error	error
sir1507		hypothetical protein	-0.236	-0.394	-0.636	-0.597	-0.84	-0.507	-0.557	error	error	error	error	error	error
sir1508		probable glycosyltransferas	-0.512	-0.245	0.721	0.833	0.475	0.366	0.23	error	error	error	error	error	error
sir1509		V-type sodium ATP synthas	0.106	0.114	0.191	0.282	0.148	0.054	0.094	-0.032	0.399	0.692	0.212	0.39	-1.142
sir1510	pisX	fatty acid/phospholipid synt	-0.462	-0.05	0.236	-0.229	-0.341	-0.277	-0.23	-0.03	0.382	error	-0.06	0.228	-0.038
sir1511	fabH	3-oxoacyl-[acyl-carrier-prote	-0.043	error	-0.679	-0.947	-0.818	-0.566	-0.309	error	error	error	error	error	error
sir1512		hypothetical protein	0.143	-0.151	-0.164	error	-0.319	0.102	0.192	error	error	error	error	error	error
sir1513		hypothetical protein	error	error	error	error	error	error	error	-0.262	-0.141	-0.337	-0.09	-0.065	0.558
sir1515		hypothetical protein	error	-0.068	0.078	-0.062	-0.089	-0.209	-0.187	0.033	0.365	-0.034	0.127	0.437	0.78
sir1516	sodB	superoxide dismutasesodB	1.361	2.133	3.423	3.991	3.052	1.733	1.898	2.874	4.268	3.185	3.92	3.855	3.25
sir1517	leuB	3-isopropylmalate dehydrog	error	error	error	error	error	error	error	0.756	1.106	0.683	0.591	0.826	-0.442
sir1518	menA	1,4-dihydroxy-2-naphtoic ac	-0.249	error	-0.241	-0.076	-0.547	-0.426	-0.636	0.11	0.004	-0.56	-0.181	-0.298	0.089
sir1519		hypothetical protein	-0.41	-0.012	-0.546	-0.278	-0.036	-0.402	-0.445	0.228	0.156	0.251	0.061	-0.027	-0.705
sir1520		oxidoreductase, aldo/keto r	error	1.109	0.688	-0.052	0.838	0.571	error	0.23	0.556	0.413	0.009	0.227	0.135
sir1521		GTP-binding protein	-0.398	-0.391	-0.608	-0.046	-0.517	-0.585	-0.352	-0.006	-0.342	-0.412	-0.425	-0.44	-0.97
sir1522		putative transposase [ISY3	-0.838	-0.752	-0.691	0.469	-0.358	0.011	0.03	-0.814	-0.244	0.698	-0.328	-0.484	-0.229
sir1523		putative transposase	-0.051	error	-0.049	0.591	-0.072	-0.005	-0.038	-0.098	0.316	0.273	-0.368	-0.209	0.141
sir1524		putative transposase [ISY1	error	-0.419	-0.145	0.574	-0.076	-0.534	-0.408	-0.942	0.012	0.255	-0.365	-0.085	-0.934
sir1529		nitrogen assimilation regula	-0.487	-0.887	-0.33	0.699	-0.936	-1.027	-0.69	-0.04	0.665	0.375	0.16	0.686	0.764
sir1530		hypothetical protein	-0.183	0.159	0.518	-0.596	0.456	0.439	0.24	0.066	0.932	0.011	0.265	0.513	1.079
sir1531	fhf	signal recognition particle p	-0.491	-0.471	-0.925	-0.265	-0.312	-0.105	-0.246	-0.788	-0.613	-0.117	-0.208	-0.484	-1.02
sir1533		hypothetical protein	0.524	0.485	0.54	-0.044	0.361	0.206	1.165	0.117	0.546	error	0.107	0.119	1.3
sir1534		hypothetical protein	error	error	error	error	error	0.198	error	0.042	0.456	-0.095	0.87	-0.295	-0.217
sir1535		hypothetical protein	-0.325	-0.301	0.366	0.997	0.702	0.484	1.144	-0.437	-0.229	-0.021	0.179	-0.28	-0.968
sir1536	recQ	ATP-dependent DNA helica	0.202	0.218	0.055	0.182	0.207	0.067	0.537	-0.194	-0.108	-0.37	-0.135	-0.352	1.216
sir1537		unknown protein	-0.473	-0.143	-0.539	-0.574	-0.708	0.098	-0.028	-0.272	-0.189	0.229	-0.426	-0.358	-1.25
sir1538		cobalamin biosynthesis pro	-0.263	0.413	0.247	0.056	-0.066	-0.03	-0.443	0.213	-0.287	-0.556	-0.401	-0.089	0.369
sir1540		mRNA-binding protein	-0.453	-0.435	-0.37	0.437	-0.297	0.087	-0.325	-0.049	0.041	0.035	-0.138	-0.054	-0.724
sir1541		hypothetical protein	0.086	error	-0.172	-0.518	-0.028	-0.07	-0.342	-0.154	-0.528	-0.684	-0.384	-0.722	-1.139
sir1542		2-C-methyl-D-erythritol 2,4-	-0.295	0.201	0.121	-0.513	0.025	0.158	0.717	-0.045	0.42	0.792	-0.02	0.275	0.022
sir1543		DNA-damage-inducible pro	error	error	error	error	error	error	error	0.192	0.307	0.618	0.06	0.281	0.178
sir1544		unknown protein	1.977	4.307	5.465	5.284	4.678	3.046	3.024	2.67	4.837	5.481	3.803	4.816	3.277
sir1545	sigG	group3 RNA polymerase sig	-0.764	-0.885	-0.601	-0.158	-0.73	-0.046	-0.317	-0.129	-0.066	-1.271	-1.073	-0.056	0.6
sir1546		hypothetical protein	-0.049	-0.237	-0.099	0.134	-0.246	0.114	0.049	0.379	0.692	-0.477	-0.441	0.265	0.426
sir1547		hypothetical protein	error	error	0.788	error	error	1.166	0.048	0.654	0.875	0.819	0.835	0.908	0.022
sir1549		polypeptide deformylase	-0.095	-0.159	0.692	0.931	0.837	error	0.045	0.158	1.02	1.712	1.317	1.053	1.74
sir1550	lysS	lysyl-tRNA synthetaseslysS	-0.314	-0.452	-0.392	0.105	-0.402	-0.295	-0.412	-0.001	0.006	-0.562	-0.458	-0.02	0.448
sir1552		unknown protein	-0.291	-0.634	-1.309	-1.596	-1.158	-1.337	-0.921	-0.464	-0.705	-0.623	-1.162	-0.915	0.04
sir1556		2-hydroxyacid dehydrogena	0.198	0.076	0.395	-0.126	0.065	0.433	0.999	-0.342	error	0.179	-0.005	error	0.954
sir1557		hypothetical protein	0.015	-0.016	0.431	0.73	-0.06	-0.178	-0.074	0.136	0.609	1.337	0.35	0.628	-0.306

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1559	aroE	shikimate 5-dehydrogenase	error	error	error	error	0.026	error	error	-0.213	-0.029	-0.275	-0.127	0.103	0.302
slr1560	hisS	histidyl tRNA synthetasehis	error	-0.564	-0.387	0.055	-0.48	-0.615	-0.925	-0.223	0.072	-0.19	-0.234	0.02	0.419
slr1562		glutaredoxin	error	error	error	error	error	error	error	0.255	0.056	-0.375	-0.042	0.209	0.318
slr1563		hypothetical protein	0.02	0.371	-0.038	-0.391	-0.362	0.444	error	-0.079	0.245	1.079	-0.082	-0.192	-0.345
slr1564	sigF	group3 RNA polymerase sig	0.347	0.055	0.586	-0.318	error	-0.047	0.413	-0.289	-0.082	-0.687	-0.583	-0.216	0.287
slr1565		hypothetical protein	-0.444	-0.654	-0.23	0.376	-0.366	-0.021	-0.178	-0.04	-0.047	-0.044	-0.286	-0.188	-0.887
slr1566		hypothetical protein	error	error	error	error	error	error	error	0.39	0.366	0.889	0.255	0.126	0.952
slr1567		unknown protein	0.103	0.283	0.273	error	-0.095	-0.359	-0.006	-0.501	0.018	0.089	-0.521	0.091	0.686
slr1568		hypothetical protein	0.177	error	-0.131	-0.413	-0.477	0.296	error	-0.106	0.249	1.088	0.432	0.268	0.898
slr1570		hypothetical protein	-0.541	-0.402	-0.248	-0.19	-0.22	0.04	1.209	-0.229	-0.263	-0.337	-0.307	-0.258	0.411
slr1571		unknown protein	error	error	0.315	error	-0.43	error	error	-0.024	0.112	0.843	-0.259	0.009	0.954
slr1572		hypothetical protein	-0.172	-0.312	-0.339	0.071	-0.453	-0.239	-0.36	-0.097	-0.05	0.023	-0.323	-0.056	-0.757
slr1573		hypothetical protein	0.198	0.254	0.031	0.861	0.099	0.204	0.062	-0.009	0.241	0.686	0.217	0.362	-0.033
slr1575		probable potassium efflux s	-0.173	-0.158	-0.186	0.367	0.136	0.367	0.167	-0.066	-0.123	0.355	-0.094	0.023	-0.729
slr1576		unknown protein	1.146	error	-0.011	-0.102	-0.236	0.474	0.242	0.442	0.6	0.599	0.112	0.154	0.092
slr1577		hypothetical protein	-0.455	-0.336	-0.732	-0.312	-0.648	-0.603	-0.341	-0.141	-0.187	-0.141	-0.382	-0.147	-1.175
slr1579		hypothetical protein	-0.735	-0.801	-0.71	error	-0.029	0.462	0.28	0.325	-0.115	0.297	-0.07	-0.097	-0.431
slr1583		hypothetical protein	-0.415	error	0.261	1.056	0.509	0.538	0.476	-0.014	0.419	error	0.939	0.218	5.871
slr1584		two-component transcription	-0.273	-0.418	-0.49	-0.702	-1.186	-0.596	-0.105	-0.609	-0.302	0.249	-0.68	-0.581	-0.234
slr1585		putative transposase [ISY5	1.234	error	1.257	-0.393	1.172	0.95	error	0.234	0.788	0.348	0.747	0.132	1.633
slr1586		putative transposase [ISY5	-0.101	0.108	0.35	-0.599	error	-0.397	error	-0.085	0.632	error	-0.152	0.232	0.788
slr1588		two-component transcrip	error	error	0.3	error	error	error	1.007	-0.003	0.607	0.704	0.327	0.3	1.457
slr1590		hypothetical protein	0.124	-0.357	error	0.135	-0.348	-0.215	-0.346	0.112	0.224	0.408	0.095	-0.047	1.328
slr1591		hypothetical protein	0.443	0.259	-0.221	-0.294	-0.238	0.282	error	-0.285	-0.169	-0.11	-0.554	-0.454	-0.911
slr1592		probable pseudouridine syn	error	error	error	error	error	error	error	-0.296	0.006	0.639	-0.187	-0.219	0.14
slr1593		hypothetical protein	-0.037	-0.318	1.052	0.372	1.069	0.592	1.825	-0.264	0.497	0.612	0.521	0.408	0.27
slr1594		two-component response re	-0.319	-0.35	0.653	0.283	0.69	0.784	1.659	-0.253	0.436	0.459	0.446	0.876	0.044
slr1595	nhaS4	Na <sup>+</sup> /H <sup>+</sup> antiporter nhaS4	error	error	error	error	error	error	error	-0.271	-0.109	-0.307	-0.383	-0.26	-0.494
slr1596	pxcA	a protein in the cytoplasmic	0.581	0.374	0.298	-0.643	-0.052	-0.359	-0.026	-0.038	-0.179	-0.248	-0.447	-0.008	5.499
slr1597		chromosome partitioning A	error	error	error	error	error	error	error	0.257	1.564	1.711	1.224	1.311	0.262
slr1598		lipoic acid synthetase	0.003	-0.353	-0.518	-0.445	-0.163	-0.375	0.05	-0.448	-0.169	0.068	-0.063	-0.118	error
slr1599		hypothetical protein	0.115	error	0.241	error	-0.436	-0.042	0.095	-0.06	0.28	-0.423	-0.279	-0.073	0.459
slr1600		hypothetical protein	error	-0.582	0.044	-0.554	-0.271	-0.29	0.042	-0.028	0.165	-0.032	0.015	-0.163	1.368
slr1601		hypothetical protein	-0.025	-0.478	-0.624	-0.509	-0.563	0.018	0.02	0.084	error	-0.604	-0.336	error	0.401
slr1603		hypothetical protein	0.168	0.572	2.304	1.817	2.133	0.839	1.095	0.39	2.467	1.727	2.065	2.145	1.067
slr1604	ftsH	cell division protein FtsHfts	-0.653	-0.407	0.731	1.98	0.431	-0.283	-0.554	0.318	1.625	2.794	1.904	error	0.256
slr1608		hypothetical protein	error	error	error	error	error	error	error	-0.22	-0.047	-0.397	0.133	-0.261	0.132
slr1609		long-chain-fatty-acid CoA li	-0.641	error	-0.105	-0.032	-0.394	-0.193	-0.405	-0.818	-0.786	-0.399	-0.791	-0.717	0.538
slr1610		putative C-3 methyl transfer	-0.087	0.028	0.717	0.288	0.152	0.15	-0.037	error	error	error	error	error	error
slr1611		hypothetical protein	-0.024	0.436	0.723	0.249	1.258	0.564	0.453	-0.188	0.565	0.778	1.315	0.392	1.676
slr1612		hypothetical protein	0.124	-0.281	-0.573	0.089	0.788	0.424	0.803	-0.053	-0.086	error	0.415	-0.358	error
slr1613		hypothetical protein	error	error	0.679	error	0.329	error	error	-0.246	0.251	error	0.491	-0.512	2.137
slr1614		hypothetical protein	error	error	error	error	error	error	error	0.263	0.468	error	0.627	0.452	0.357
slr1615	rfbE	perosamine synthetaserfbE	0.247	0.303	1.224	-0.171	0.703	0.31	0.713	-0.202	0.055	0.012	0.234	-0.302	0.654
slr1616		unknown protein	1.496	1.741	2.172	0.946	1.501	1.122	1.149	0.758	1.46	error	0.349	0.927	error
slr1617		similar to UDP-glucose 4-ep	error	error	error	error	error	error	error	-0.999	-0.823	error	-0.667	-1.37	0.641
slr1618		unknown protein	error	error	error	error	error	error	error	0.224	0.718	0.932	1.039	-0.205	-0.195
slr1619		hypothetical protein	error	-0.055	-0.53	-	-0.598	-0.222	-0.165	-0.128	-0.654	-0.283	-0.493	-0.73	-0.769
slr1622	ppa	soluble inorganic pyrophos	-0.28	-0.421	-0.562	-1.07	-0.565	-0.219	-0.116	0.269	-0.552	-0.399	-0.296	-0.837	0.633
slr1623		hypothetical protein	0.114	0.084	0.563	0.027	0.429	0.248	0.588	0.655	2.301	1.552	1.521	1.919	1.53
slr1624		hypothetical protein	0.039	-0.19	-0.487	-0.41	-0.304	-0.2	-0.171	-0.244	-0.256	0.092	-0.21	-0.055	0.648
slr1626		dihydroneopterin aldolase	0.637	0.172	-0.275	-0.052	0.204	0.422	0.491	error	0.423	error	error	error	error
slr1627		unknown protein	-0.496	error	-0.428	-0.408	-0.568	-0.186	-0.346	0.174	-0.171	0.567	0.174	-0.122	-0.176
slr1628		hypothetical protein	0.919	0.129	-0.122	-0.872	0.155	-0.006	1.066	-0.001	0.24	0.408	-0.099	-0.129	0.568
slr1629		ribosomal large subunit pse	1.277	0.324	-0.492	-0.179	-0.646	-0.372	-0.658	1.317	0.4	error	0.028	0.437	error
slr1634		hypothetical protein	-0.397	-0.575	-0.84	-1.016	-2.039	-1.18	-1.752	-0.059	-0.211	-1.839	-1.333	-0.325	-1.132
slr1635		putative transposase [ISY2	-0.798	-0.542	-0.749	-0.137	-0.385	0.258	0.51	-0.791	0.022	0.613	-0.227	-0.169	0.206
slr1636		unknown protein	-0.494	-0.69	-0.886	0.028	-1.214	-1.278	-1.447	-0.08	-0.702	-1.543	-1.055	-0.688	-2.162
slr1638		hypothetical protein	0.975	1.34	1.882	1.299	1.105	0.42	1.281	1.009	1.836	2.104	1.174	1.557	0.67
slr1639		SsrA-binding protein	1.089	1.209	1.344	0.732	0.507	0.317	0.906	0.773	0.977	0.665	0.605	0.661	-0.434
slr1641		ClpB protein	error	error	error	error	error	error	error	-0.032	0.523	0.402	0.432	0.514	-0.196
slr1643	petH	ferredoxin-NADP oxidoredu	-0.411	-0.628	-0.648	0.934	-0.225	-0.586	-0.259	-0.189	-0.208	0.496	0.112	-0.185	-0.444
slr1644		hypothetical protein	-0.547	-0.404	-0.023	0.22	-0.06	0.168	-0.191	0.069	0.221	-0.387	0.013	0.046	0.275
slr1645	psbZ	photosystem II 11 kD protei	-0.502	-0.607	-0.597	0.452	-0.376	-0.488	-0.227	0.028	-0.127	-0.322	0.049	-0.005	-0.683
slr1646	nc	ribonuclease III nc	0.172	-0.027	0.103	0.449	-0.277	-0.282	-0.197	0.338	0.522	-0.18	0.205	0.201	0.396
slr1647		hypothetical protein	0.87	error	0.664	0.023	0.293	0.513	0.213	0.164	0.587	0.085	-0.222	0.446	1.041
slr1648		hypothetical protein	-0.787	-0.55	-0.659	-0.287	-1.249	-0.921	-1.23	-0.701	-0.669	-0.873	-0.975	-0.701	-0.352
slr1649		hypothetical protein	-1.057	-1.128	-1.002	-0.527	-0.575	-0.723	-0.252	-1.218	-1.338	-0.912	-0.699	-1.603	0.032
slr1651		ABC transporter ATP-bindin	error	error	0.408	0.131	0.765	0.221	0.829	0.148	0.695	0.138	0.938	-0.486	-0.565
slr1652		hypothetical protein	-0.118	-0.458	-0.726	-0.32	-0.806	-0.215	-0.795	-0.361	-0.297	-0.257	-0.733	-0.665	-0.74
slr1653		N-acyl-L-amino acid amidof	-0.597	-0.317	-0.293	0.063	-0.103	-0.693	-0.354	-0.017	0.063	0.36	0.055	0.01	0.431
slr1655	psaL	photosystem I subunit Xlps	error	error	error	error	error	-1.078	error	-0.374	-0.677	-2.149	-1.386	-1.746	-1.364
slr1656	murG	UDP-N-acetylglucosamine	0.229	0.455	1.185	1.141	0.842	0.688	0.683	0.168	0.468	0.826	0.011	0.125	0.847
slr1657		hypothetical protein	-0.04	-0.222	-0.577	-0.837	0.405	0.331	0.98	-0.235	-0.081	0.784	0.05	-0.039	-0.247
slr1658		unknown protein	-0.425	-0.471	-0.973	-0.189	-0.27	0.205	0.161	-0.096	-0.708	0.275	0.26	-0.776	0.821

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1								Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	
sir1659		hypothetical protein	0.257	error	0.518	error	error	0.518	0.252	0.383	0.016	0.472	0.205	-0.096	0.18	
sir1660		hypothetical protein	-0.326	-0.314	-0.373	0.027	-0.241	-0.206	0.122	-0.055	0.19	0.551	0.006	0.458	-0.519	
sir1661		hypothetical protein	0.001	error	-0.186	-0.224	error	0.215	error	0.14	0.449	0.297	0.2	0.315	0.068	
sir1664		hypothetical protein	-0.437	-0.058	-0.234	-0.056	-0.287	-0.186	-0.434	-0.422	-0.574	0.178	-0.442	-0.722	-1.094	
sir1665	dapF	diaminopimelate epimerase	-0.478	-0.618	-0.646	-0.329	-0.835	-0.482	-0.084	-0.101	0.006	0.563	-0.197	-0.068	-0.558	
sir1666		pleiotropic regulatory protein	-0.461	-0.293	-0.577	-0.514	-0.805	-0.294	-0.277	0.035	0.523	-0.086	0.08	error	-0.148	
sir1667		hypothetical protein (target)	error	0.495	0.361	-1.533	-0.289	0.689	error	-0.05	0.443	0.185	-0.15	0.032	-0.389	
sir1668		hypothetical protein (target)	0.064	0.33	0.094	error	0.022	0.038	1.229	0.033	0.564	0.885	0.301	0.61	0.965	
sir1670		unknown protein	-0.468	0.245	0.548	0.837	0.521	0.051	0.374	-0.102	0.718	0.674	0.671	0.519	-0.604	
sir1672	glpK	glycerol kinase/glpK	-0.521	-0.785	-1.14	-0.169	-1.382	-1.062	-0.968	0.192	0.027	0.423	0.504	-0.249	-0.47	
sir1673		probable tRNA/rRNA methyltransferase	error	error	0.286	0.208	0.749	0.257	0.288	-0.036	0.07	0.787	0.75	-0.108	-0.1	
sir1674		hypothetical protein	1.122	2.83	4.319	4.227	4.11	2.476	2.863	1.833	3.745	3.508	3.017	3.668	1.379	
sir1675	hypA	hydrogenase expression factor	0.996	1.687	2.357	3.06	2.649	1.088	1.089	1.316	2.91	2.912	2.903	2.756	2.562	
sir1676		hypothetical protein	error	0.478	1.38	2.322	1.274	0.526	0.431	error	error	error	error	error	error	
sir1677		hypothetical protein	0.23	1.388	1.556	1.835	1.193	0.798	1.044	0.421	1.529	2.018	1.059	1.536	-0.085	
sir1678	rpl21	50S ribosomal protein L21/rpl21	0.064	0.391	1.262	2.146	-0.28	-0.895	-0.73	0.294	0.886	0.924	0.239	0.881	-1.525	
sir1679		hypothetical protein	-0.226	0.055	0.216	0.081	-0.338	0.009	-0.278	0.333	0.333	0.199	0.024	-0.183	-1.103	
sir1681		unknown protein	-0.182	0.151	0.428	-0.076	0.062	0.26	0.096	-0.295	-0.02	-0.343	-0.036	-0.17	0.927	
sir1682		putative transposase [ISY3]	-0.798	-0.662	-0.379	-0.299	-0.73	-0.307	-0.227	-0.442	-0.149	0.337	-0.576	-0.222	-1.179	
sir1683		putative transposase [ISY3]	-0.075	-0.332	0.444	-0.442	-0.233	-0.048	-0.033	-0.51	0.367	-0.301	-0.255	-0.09	0.162	
sir1684		putative transposase [ISY3]	-0.128	error	-0.724	error	error	error	-0.228	-0.439	-0.27	0.107	-0.434	-0.459	-0.944	
sir1686		hypothetical protein	0.232	1.517	2.146	1.379	1.809	0.061	error	1.142	2.707	1.773	2.231	2.56	2.078	
sir1687		hypothetical protein	1.17	2.725	3.66	3.163	3.462	1.862	2.699	2.054	5.092	4.02	3.955	5.024	3.088	
sir1689	fpg	formamidopyrimidine-DNA glycosylase	-0.125	0.016	-1.382	-0.495	-1.187	-0.705	-0.727	0.34	-0.668	-1.752	-1.43	-0.911	-1.273	
sir1690		hypothetical protein	error	error	error	-1.074	-0.281	0.078	error	-0.321	0.109	-0.415	-0.611	-0.352	-0.234	
sir1691		glutamine-dependent NADH dehydrogenase	-0.196	-0.704	-0.659	-0.058	-0.612	-0.293	-0.425	-0.806	-0.789	-0.278	-1.178	-0.878	0.007	
sir1692		hypothetical protein	error	error	error	-0.884	-0.38	0.213	error	-0.324	-0.232	error	-0.065	-0.461	0.947	
sir1693		two-component response regulator	0.232	-0.197	-1.277	-1.371	-1.036	-0.111	error	-0.538	-0.365	0.111	-0.53	-1.085	0.052	
sir1694		expression activator appA	-0.548	-0.731	-1.179	error	-1.429	-1.003	-1.49	-0.018	-0.576	-1.861	-1.154	-1.362	-1.927	
sir1697		serine/threonine kinase	0.045	0.465	0.215	0.163	0.219	0.179	-0.089	0.254	0.489	-0.834	-2.081	0.399	0.939	
sir1699		hypothetical protein	error	error	-0.3	-0.638	-0.033	0.378	error	-0.006	0.322	0.357	0.179	0.139	-0.479	
sir1702		hypothetical protein	error	error	error	-0.474	-0.295	0.154	error	-0.445	-0.118	-0.453	-0.428	-0.595	0.632	
sir1703	serS	seryl-tRNA synthetase/serS	0.259	-0.318	-0.232	0.88	-0.869	-0.768	-0.821	0.26	-0.261	-0.567	-0.471	-0.397	-1.416	
sir1704		hypothetical protein	0.126	2.034	3.383	3.399	3.216	2.275	2.091	error	error	error	error	error	error	
sir1705		aspartoacylase	-0.433	-0.245	-0.106	-0.124	-0.104	-0.685	-0.523	-0.032	-0.233	0.483	-0.082	-0.364	-0.775	
sir1706		dihydroflavonol 4-reductase	0.345	0.398	0.933	-0.082	0.569	0.169	0.485	-0.078	0.458	0.154	0.098	0.418	0.397	
sir1708		probable peptidase	-0.544	-1.219	-1.555	0.032	-0.488	-0.347	-0.508	-0.303	-0.72	-0.204	-0.073	-0.552	0.266	
sir1710		penicillin-binding protein	error	-0.194	-0.36	0.601	-0.214	0.238	-0.214	-0.195	-0.395	0.043	-0.538	-0.467	-1.149	
sir1712		hypothetical protein	0.214	0.159	-0.205	0.314	-0.052	0.284	0.252	-0.152	-0.03	0.302	-0.221	-0.003	-0.073	
sir1715		putative transposase [ISY10]	-0.105	-0.323	0.095	-0.025	-0.538	-0.405	-0.224	-0.683	0.028	0.301	-0.349	-0.126	-0.103	
sir1716		putative transposase [ISY10]	0.183	-0.386	-0.481	-0.416	-0.827	-0.379	error	-0.869	-0.033	0.694	-0.737	-0.476	0.666	
sir1717		hypothetical protein	0.803	0.054	0.202	-0.01	0.27	0.124	error	0.064	-0.024	0.298	0.179	-0.27	1.485	
sir1718		hypothetical protein	-0.129	-0.55	0.124	-0.212	-0.2	-0.021	0.137	-0.081	0.229	0.315	0.271	0.034	0.322	
sir1719		DrgA protein homolog	-0.251	error	-0.579	error	-0.497	-0.66	-0.046	0.104	-0.111	-0.394	-0.323	-0.402	1.08	
sir1720	aspS	aspartyl-tRNA synthetase/aspS	error	error	error	error	error	error	error	0.28	-0.177	0.735	0.002	-0.262	-0.233	
sir1721		hypothetical protein	0.018	-0.12	-0.328	error	-0.08	-0.112	0.121	0.079	0.236	0.209	0.031	0.345	0.409	
sir1722		inosine-5'-monophosphatase	-0.498	-0.56	-0.664	0.336	-0.737	-0.509	-0.369	0.019	-0.06	error	0.069	-0.018	-0.661	
sir1723		permease protein of sugar	error	error	error	error	error	0.709	error	-0.029	0.124	0.528	0.176	-0.216	0.488	
sir1724		hypothetical protein	-0.287	-0.343	-0.034	-0.007	-0.01	-0.231	-0.383	0.219	0.272	0.151	0.211	-0.07	0.762	
sir1726		unknown protein	0.194	0.767	0.853	-0.52	-0.407	0.142	-0.078	0.423	0.95	error	0.187	0.412	-0.145	
sir1727		Na <sup>+</sup> /H <sup>+</sup> antiporter	error	error	error	error	error	error	error	-0.233	-0.187	-0.443	-0.4	-0.372	0.1	
sir1728	kdpA	potassium-transporting ATPase	-0.074	0.482	1.547	2.937	4.263	3.021	3.599	0.103	0.463	2.091	3.865	0.404	error	
sir1729	kdpB	potassium-transporting ATPase	-0.281	-0.107	0.188	1.007	1.776	0.657	1.217	-0.274	0.178	0.653	2.731	0.122	2.134	
sir1730	kdpC	potassium-transporting ATPase	0.453	1.07	1.191	0.568	2.024	1.411	2.255	0.311	0.83	error	1.073	0.751	2.564	
sir1731	kdpD	potassium-transporting ATPase	error	error	error	error	error	error	error	0.015	0.249	error	0.48	0.159	0.58	
sir1732		hypothetical protein	-0.029	-0.165	0.189	0.02	0.146	-0.19	0.071	0.726	1.19	0.536	1.215	0.945	1.708	
sir1734	opcA	putative OxPPCycle protein	error	error	error	error	error	error	error	-0.208	0.033	-0.76	-0.22	-0.029	-0.04	
sir1735	bgtA	ATP-binding subunit of the	-0.015	error	0.091	0.833	0.371	0.201	error	0.098	0.398	0.609	0.547	0.578	-0.077	
sir1736		homogenisate phytoltransferase	-0.149	error	0.14	-0.246	0.558	0.486	0.203	-0.516	0.334	-0.193	0.183	0.296	0.83	
sir1737		hypothetical protein	-0.083	0.178	0.41	0.433	0.099	-0.104	-0.359	0.154	1.17	-0.086	-0.144	1.102	0.24	
sir1738		transcription regulator Fur	0.179	0.685	1.537	0.638	0.93	0.346	0.657	0.436	2.037	1.062	1.043	1.741	2.177	
sir1739	psbW	photosystem II reaction center protein	0.807	error	1.258	0.141	1.511	0.849	error	0.376	0.955	1.162	0.864	0.695	1.789	
sir1740		oligopeptide binding protein	1.755	1.736	1.255	1.675	1.471	0.488	0.967	2.1	1.434	1.404	1.489	1.655	1.428	
sir1742		probable cobyrinic acid synthase	error	error	-0.448	error	0.547	0.12	1.099	0.236	0.449	0.869	0.328	0.491	error	
sir1743	ndbB	type 2 NADH dehydrogenase	-0.548	-0.427	-0.403	0.241	-0.374	-0.732	-0.631	0.043	0.166	-0.344	0.289	0.216	0.164	
sir1744		N-acetylmuramoyl-L-alanine aminotransferase	error	0.188	0.686	1.397	0.611	0.361	0.386	-0.042	0.097	0.8	0.141	-0.021	0.594	
sir1746		glutamate racemase	-0.413	-0.502	-1.042	-0.636	-0.768	-0.662	-0.964	0.132	-0.359	-0.367	-0.418	-0.469	1.131	
sir1747		cell death suppressor protein	-0.201	0.205	0.68	0.833	1.23	0.327	1.632	error	error	error	error	error	error	
sir1748		probable phosphoglycerate kinase	1.293	1.454	1.734	1.812	1.826	0.97	1.24	0.761	1.957	1.646	2.008	1.705	2.493	
sir1751		carboxyl-terminal protease	error	error	error	error	error	error	error	0.05	0.617	1.303	1.666	0.52	0.349	
sir1752		hypothetical protein	0.112	-0.217	0.064	1.214	1.194	0.679	0.435	0.135	-0.081	0	0.824	-0.056	0.032	
sir1753		hypothetical protein	-0.123	0.483	-0.187	-0.554	error	0.337	error	-0.473	-0.056	0.003	-0.546	-0.311	-0.855	
sir1755		NAD <sup>+</sup> dependent glycerol-3-phosphate dehydrogenase	error	error	error	error	error	error	error	-0.388	0.039	-0.241	0.07	-0.144	0.293	
sir1756	glnA	glutamate-ammonia ligase	error	error	error	error	error	error	error	-0.161	0.165	0.47	0.398	0.217	0.27	
sir1759		two-component hybrid sensor	-0.507	-0.506	-1.024	-0.281	-1.458	-0.889	-1.248	-0.25	-0.025	-0.303	-0.449	-0.029	-1.18	

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1760		two-component response re	-0.416	-0.402	-0.669	-0.633	-1.5	-0.703	-0.723	0.095	-0.257	-0.603	-0.864	-0.16	-1.044
slr1761		FK506-binding protein	-0.837	-1.067	-1.293	-0.861	-1.56	-1.042	-0.538	-0.148	-0.519	-1.1	-0.863	-0.65	-0.852
slr1762		hypothetical protein	error	-0.363	0.362	0.852	0.223	0.182	0.178	error	error	error	error	error	error
slr1763		probable methyltransferase	-0.403	-0.615	0.026	0.044	error	0.125	0.022	-0.041	0.408	error	0.173	0.232	1.231
slr1764	terE	similar to tellurium resistanc	-0.354	-0.282	-0.538	-0.509	-0.175	-0.28	-0.307	-0.443	-0.538	0.131	-0.369	-0.499	-0.964
slr1767		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slr1768		unknown protein	error	0.005	0.609	-1.344	error	0.299	error	-0.288	0.193	-0.478	-0.532	-0.369	0.283
slr1770		hypothetical protein	1.516	0.456	0.694	error	0.52	0.386	error	-0.108	0.548	-0.057	0.246	-0.152	1.112
slr1771		unknown protein	0.541	0.212	0.021	-0.72	0.058	0.131	error	-0.165	0.119	0.467	-0.147	-0.221	0.487
slr1772		probable hydrolase	error	error	-0.106	-0.358	1.074	1.032	0.82	-0.161	-0.289	-0.403	-0.003	-0.496	0.099
slr1773		unknown protein	error	error	error	error	error	error	error	0.178	0.099	error	-0.518	-0.15	0.359
slr1774		unknown protein	-0.441	-0.306	-0.497	0.072	-0.458	-0.124	-0.069	-0.165	0.015	0.016	-0.522	0.286	-1.05
slr1776		high affinity sulfate transpor	-0.477	-0.394	-0.61	-0.234	-0.476	-0.589	-0.465	-0.034	-0.366	-0.665	0.044	-0.309	error
slr1777	chlD	magnesium-chelatase subu	-0.632	-0.594	-0.718	0.062	-1.063	-0.783	-0.659	-0.186	0.011	0.083	-0.141	0.014	-0.933
slr1778		unknown protein	error	error	0.233	0.003	error	0.203	-0.136	0.29	0.379	0.498	0.26	0.157	-0.044
slr1779	pdxJ	pyridoxal phosphate biosyn	0.528	1.086	0.385	-1.168	-0.755	-0.431	-0.782	0.002	-0.297	-0.293	-0.506	-0.143	-0.852
slr1780	ycf54	hypothetical protein YCF54	error	error	error	error	error	error	error	-0.016	-0.01	error	-0.669	-0.997	-0.824
slr1783	ycf29	two-component response re	-0.6	-0.548	-0.786	-0.246	-0.627	-0.53	-0.431	0.094	-0.157	-0.446	-0.402	-0.146	-0.31
slr1784	bvdR	biliverdin reductasebvdR	0.586	-0.256	-1.102	error	error	-0.812	0.187	-0.07	-0.031	-0.263	-0.345	-0.216	0.036
slr1787		thiamine-monophosphate k	-0.709	-0.197	-0.128	-0.14	-0.298	0.04	0.955	-0.641	-0.048	0.385	-0.19	-0.038	0.34
slr1788		unknown protein	0.42	error	-0.721	error	-0.597	-0.168	error	-0.296	0.165	-0.091	-0.64	-0.055	0.892
slr1789		unknown protein	-0.008	-0.177	0.318	0.008	0.016	-0.042	-0.341	error	error	error	error	error	error
slr1790		hypothetical protein	error	error	error	error	error	error	error	0.36	1.208	1.099	0.776	1.229	-0.215
slr1791	cysH	phosphoadenosine phosph	error	error	error	error	error	error	error	0.401	0.255	0.355	0.167	-0.126	0.288
slr1793		transaldolase	-0.255	-0.395	-0.449	error	-0.254	-0.162	-0.329	-0.26	-0.526	-0.793	-0.339	-0.511	0.367
slr1794		probable anion transporting	-0.235	-0.306	-0.678	-0.429	-0.792	-0.627	-0.713	-0.112	-0.158	-0.558	-0.157	-0.352	0.002
slr1795		peptide methionine sulfoxid	0.511	error	-0.571	-1.362	-0.039	-0.403	-0.813	0.155	0.06	-0.304	-0.104	-0.152	0.764
slr1796		hypothetical protein	-0.021	0.038	0.063	0.018	-0.006	0.199	-0.091	error	error	error	error	error	error
slr1798		unknown protein	0.076	-0.031	-0.32	error	error	-0.223	-0.263	-0.297	-0.273	-0.374	-0.507	-0.122	0.295
slr1799		hypothetical protein	0.265	0.484	1.044	1.194	1.078	0.665	0.776	0.179	0.701	0.745	0.729	0.74	-0.127
slr1800		hypothetical protein	error	error	error	error	error	error	error	0.388	0.786	0.445	0.545	0.702	-0.246
slr1803		adenine-specific DNA mety	0.178	0.144	0.025	0.151	-0.172	0.353	-0.138	0.13	0.564	-0.007	0.114	-0.073	1.25
slr1804		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
slr1805		two-component sensor histi	0.007	0.334	0.669	1.2	0.514	0.217	0.362	0.333	1.011	1.081	0.372	1.222	-0.526
slr1807		hypothetical protein	0.136	-0.207	-0.174	0.311	-0.091	-0.064	-0.053	0.099	0.195	-0.176	-0.069	0.043	2.062
slr1808	hemA	transfer RNA-Gln reductase	-0.871	-1.355	-1.977	error	-1.667	-1.133	-0.966	-0.811	-1.46	-1.311	-1.365	-1.447	error
slr1809		unknown protein	0.797	error	0.517	-0.138	0.494	0.385	1.302	0.371	0.655	0.454	0.599	0.413	0.798
slr1811		hypothetical protein	-0.153	error	0.968	error	error	0.668	error	-0.153	0.083	0.859	1.034	0.106	2.03
slr1812		hypothetical protein	0.687	0.384	0.522	0.604	1.221	0.667	1.273	-0.282	0.02	-0.082	0.811	-0.197	1.358
slr1813		hypothetical protein	0.583	error	0.14	error	1.276	0.674	0.893	-0.699	-0.07	1.286	0.875	-0.652	2.23
slr1814		hypothetical protein	0.254	-0.292	0.399	0.625	0.382	-0.144	0.563	-0.345	-0.298	0.713	0.73	-0.434	0.084
slr1815		hypothetical protein	-0.107	error	-0.147	-0.568	-0.401	0.138	-0.778	-0.427	-0.356	-0.519	-0.471	-0.646	-0.332
slr1816		hypothetical protein	0.347	0.667	1.458	0.923	1.18	0.931	0.55	0.098	0.008	-0.057	0.311	-0.165	0.109
slr1818		hypothetical protein	error	error	error	error	error	error	error	0.208	-0.092	0.592	0.24	-0.188	0.087
slr1819		hypothetical protein	-0.001	error	-0.401	error	-0.253	-0.524	-0.606	-0.32	-0.046	0.095	-0.298	-0.201	1.001
slr1820		hypothetical protein	-0.034	0.204	0.09	-0.59	0.232	0.399	0.918	error	0.008	error	error	error	error
slr1821		hypothetical protein	-0.06	-0.303	-0.695	-0.065	-0.216	-0.215	-0.2	-0.063	-0.093	-0.454	-0.052	-0.352	0.887
slr1822		endonuclease III	-0.163	0.129	-0.072	-0.785	-0.407	-0.043	0.074	0.225	0.349	0.418	-0.272	-0.119	-0.79
slr1826		hypothetical protein	-0.256	0.15	0.313	0.379	-0.048	0.629	0.488	error	error	error	error	error	error
slr1827		hypothetical protein	0.882	0.691	0.515	0.191	0.646	0.624	error	0.081	0.043	0.635	0.3	-0.023	-0.213
slr1828		ferredoxin, peIF-like protein	-0.408	-0.683	-1.69	-0.758	-1.695	-1.446	-0.934	0.143	-0.379	-0.556	-1.031	-0.442	-1.32
slr1829		unknown protein	0.091	0.126	0.179	0.261	0.158	0.517	0.389	-0.046	0.023	0.138	-0.004	-0.007	-0.505
slr1830		poly-beta-hydroxybutyrate p	0.73	0.166	error	-0.723	0.246	0.498	error	0.005	error	0.012	-0.04	error	0.501
slr1834	psaA	P700 apoprotein subunit la	-0.743	-1.115	error	error	-2.19	-1.464	error	0.006	-1.049	-2.543	-1.904	-0.86	-0.891
slr1835	psaB	P700 apoprotein subunit lb	-0.991	-1.176	-2.25	-1.571	-1.957	-1.646	-1.326	-0.008	-0.523	-2.691	-2.075	-0.628	-0.695
slr1837		two-component system resp	0.102	-0.083	-0.467	-0.181	-0.549	0.036	-0.128	0.182	-0.233	-0.637	-0.27	0.01	-0.603
slr1838	ccmK	carbon dioxide concentrati	-0.057	0.719	-0.465	-0.129	-0.287	-0.378	-0.13	0.044	-0.031	-0.375	-0.078	-0.14	-0.761
slr1839	ccmK	carbon dioxide concentrati	-0.28	-0.564	-0.943	-0.133	-0.917	-0.7	-0.595	-0.142	-0.306	-0.435	-0.367	0.029	-0.906
slr1840		hypothetical protein	error	error	error	error	error	error	error	0.814	1.773	1.927	1.09	1.855	1.043
slr1841		probable porin; major outer	-0.882	-0.936	-1.493	0.305	-0.396	-0.757	-0.84	-0.48	-0.962	-1.074	0.049	error	0.606
slr1842	cysK	cysteine synthasecysK	-0.014	-0.393	-0.927	-0.777	-0.735	-0.383	error	-0.477	-0.412	-0.707	-0.684	-0.557	0.698
slr1843	zwf	glucose 6-phosphate dehyd	-0.134	-0.476	-0.788	-0.163	-0.055	0.053	0.131	-0.533	-1.018	-1.403	-0.916	-1.16	0.353
slr1844	uvrA	excinuclease ABC subunit A	-0.24	-0.465	-0.543	-0.348	-0.431	-0.136	-0.087	-0.349	-0.2	0.166	-0.645	-0.367	-1.758
slr1846	ycf64	hypothetical protein YCF64	-0.344	error	0.102	0.23	0.38	-0.069	-0.524	0.051	0.737	0.991	0.85	0.973	1.536
slr1847		hypothetical protein	error	0.091	error	error	1.084	error	0.398	error	error	error	error	error	error
slr1848	hisD	histidinol dehydrogenasehis	0.005	0.028	-0.48	0.213	-0.277	-0.236	-0.525	0.089	-0.028	-0.141	0.36	-0.045	0.067
slr1849		probable mercuric reductas	-0.359	-0.67	-1.02	-0.416	-1.405	-0.939	-0.828	-0.073	-0.044	0.985	0.017	-0.413	-1.402
slr1851		hypothetical protein	error	error	0.414	error	error	0.32	error	-0.207	0.87	error	-0.031	0.79	1.62
slr1852		unknown protein	-0.593	-0.74	-1.67	-1.611	-2.011	-0.886	-1.119	-0.459	-1.336	-2.308	-2.466	-1.438	-1.115
slr1853		carboxymuconolactone dec	-0.302	-0.292	-0.567	-0.702	-0.712	-0.291	-0.531	-0.138	-0.385	-1.062	-0.753	-0.442	-0.038
slr1854		unknown protein	-0.163	-0.612	-1.932	-2.163	-2.372	-1.293	-1.474	-0.227	-1.289	-2.187	-3.219	-1.768	-0.58
slr1855		unknown protein	0.046	-0.407	-0.69	-0.082	-0.697	-0.166	-0.947	-0.088	-0.758	-1.462	-1.256	-0.777	-0.313
slr1856		anti-sigma B factor antagon	-0.078	error	-1.089	-1.677	-2.28	-0.788	-1.444	0.032	-0.317	error	-0.71	-0.917	-0.026
slr1857		isoamylase	-0.215	-0.313	-0.976	-0.748	-0.931	-0.813	-0.761	0.249	-0.512	-0.836	-1.199	-0.491	-0.387
slr1859		anti-sigma I factor antagoni	0.032	-0.262	-0.291	-0.109	-0.386	-0.079	-0.263	-0.26	-0.073	error	-0.489	-0.447	0.29

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1860	icfG	carbon metabolisms regula	-0.256	error	-0.218	error	-1.968	-0.437	-0.983	-0.903	-1.187	-1.574	-1.788	-1.454	-0.024
slr1861		probable sigma regulatory f	error	error	0.548	-1.85	error	0.217	error	-0.59	-0.13	-0.671	-0.71	-0.435	0.293
slr1862		unknown protein	0.267	-0.157	-0.215	-0.506	-0.367	0.387	0.033	-0.362	-0.239	0.267	-0.462	-0.051	0.45
slr1863		unknown protein	error	error	error	error	error	error	error	-0.222	-0.467	-0.296	-1.081	-0.834	-0.996
slr1864		hypothetical protein	-0.238	-0.317	-0.706	-0.446	-0.657	-0.108	-0.133	-0.342	-0.411	-0.18	-0.564	-0.394	-0.742
slr1865		unknown protein	-0.63	-0.436	-1.006	error	-1.735	-0.535	error	-0.045	-0.555	-0.129	-0.694	-0.747	-0.201
slr1866		unknown protein	-0.058	-0.16	-0.548	-1.083	-1.281	-0.053	-0.372	-0.703	-0.222	-0.187	-0.87	-0.466	-1.067
slr1867	trpD	anthranilate phosphoribosy	0.329	-0.216	error	-0.751	-0.363	0.226	error	-0.12	0.164	-0.055	-0.148	0.282	1.164
slr1869		unknown protein	error	-0.397	-0.561	0.725	0.774	0.595	0.36	-0.484	-0.926	-0.096	-0.491	-0.993	-0.256
slr1870		hypothetical protein	-0.288	0.041	-0.8	error	-0.85	-0.598	-0.885	-0.531	-0.216	error	-1.066	-0.446	0.655
slr1871		transcriptional regulator	-0.378	-0.524	-0.466	0.033	-0.753	-0.501	-0.201	-0.196	0.101	error	-0.184	0.139	-0.993
slr1874		D-alanine--D-alanine ligase	0.689	error	0.164	-1.009	error	0.108	0.959	0.285	0.733	1.385	0.636	0.737	1.282
slr1875		hypothetical protein	error	0.119	0.308	-0.054	0.267	0.24	1.403	0.297	error	0.442	0.179	error	0.267
slr1876		hypothetical protein	-0.027	error	-0.191	0.071	-0.666	-0.957	-0.728	0.208	0.434	0.136	0.071	0.303	0.705
slr1877		2-hydroxyhepta-2,4-diene-1	-0.705	-0.878	-0.861	-0.035	-0.569	-0.363	-0.141	error	error	error	error	error	error
slr1878	cpcE	phycocyanin alpha-subunit	-0.017	-0.109	-0.684	-0.648	-0.753	-0.255	-0.145	-0.168	-0.367	-0.19	-0.594	-0.229	-0.611
slr1879	cobI	precorrin-2 methyltransfera	-0.114	0.061	-0.035	0.01	-0.187	-0.042	-0.476	-0.251	0.104	0.009	-0.079	-0.069	error
slr1880		hypothetical protein	error	error	error	error	error	error	error	0.276	-0.338	0.593	-0.333	-0.54	-0.321
slr1881	natE	ATP-binding subunit of the	0.333	0.86	0.515	-0.177	0.729	0.674	error	error	error	error	error	error	error
slr1882	ribF	riboflavin biosynthesis prote	0.328	0.828	0.775	1.069	1.006	0.607	0.896	error	error	error	1.636	error	error
slr1884	trpS	tryptophanyl-tRNA syntheta	-0.139	0.253	0.749	1.148	0.681	0.492	0.215	0.265	0.528	-0.175	0.567	0.43	1.026
slr1885		hypothetical protein	1.04	1.626	1.758	1.321	1.539	0.634	0.9	1.459	2.128	1.139	1.772	2.028	1.888
slr1886		hypothetical protein	0.077	0.66	0.621	-0.101	error	0.47	0.381	0.293	0.649	error	0.969	0.802	1.319
slr1887	hemC	porphobilinogen deaminase	-0.612	-0.886	-0.805	-0.098	-0.364	-0.468	-0.162	-0.798	-0.364	-0.819	-0.121	-0.513	0.888
slr1888		4-hydroxybutyrate coenzym	0.675	0.273	-0.106	error	-0.002	0.207	error	-0.095	0.064	-0.094	-0.128	-0.158	1.138
slr1890		bacterioferritin	-0.103	0.087	0.118	0.47	-0.211	-0.344	-0.594	-0.319	-0.117	-0.069	-0.562	-0.058	-0.45
slr1894		probable DNA-binding stres	0.254	1.029	2.555	3.19	2.376	1.652	1.7	1.391	3.308	3.109	3.117	3.184	1.561
slr1895		hypothetical protein	0.07	0.731	1.422	0.872	1.65	0.591	0.855	0.608	1.879	1.127	1.883	1.57	1.928
slr1896		hypothetical protein	error	error	-0.064	error	error	0.716	-	0.372	1.231	1.994	0.552	0.865	1.567
slr1897		periplasmic sugar-binding p	-0.006	error	0.372	0.573	0.486	-0.035	0.365	0.373	0.48	0.551	0.074	0.589	-0.182
slr1898	argB	N-acetylglutamate kinase ar	-0.534	-0.442	-0.562	-0.039	-0.764	-0.376	-0.776	-0.536	-0.22	0.002	-0.185	-0.453	0.391
slr1899	ureF	urease accessory protein F	error	error	1.183	error	error	1.183	error	0.469	0.845	error	0.298	0.183	-0.446
slr1900		hypothetical protein	-0.237	-0.206	-0.006	error	-0.107	0.038	-0.138	error	error	error	error	error	error
slr1901		ATP-binding protein of ABC	-0.165	-0.138	0.336	1.396	-0.225	-0.381	-0.444	0.253	0.033	0.203	0.299	0.131	-0.653
slr1902		putative transposase [ISY1	0.423	0.474	0.377	error	0	-0.133	0.262	0.047	0.543	0.255	0.34	0.08	1.324
slr1903		putative transposase [ISY1	0.225	0.185	0.448	error	error	error	error	-0.085	0.558	0.647	0.296	0.374	0.512
slr1906		hypothetical protein	0.296	-0.094	error	-1.31	-0.155	0.125	error	-0.004	-0.026	-0.193	-0.145	-0.13	0.048
slr1907		hypothetical protein	-0.139	-0.042	0.007	0.666	-0.101	-0.089	-0.348	error	error	error	-0.304	error	error
slr1908		probable porin; major outer	-0.884	-1.336	-1.066	error	-0.861	-1.001	-0.92	0.035	-0.461	-0.207	-0.263	-0.304	-0.3
slr1909		two-component response re	-0.059	error	-1.144	-0.838	error	-0.232	-0.684	0.183	-0.18	0.526	-0.356	-0.251	-0.751
slr1910		probable N-acetylmuramoyl	-0.103	-0.03	-0.508	-0.266	-0.495	0.118	-0.195	0.247	-0.024	-0.475	-0.263	-0.2	-1.252
slr1911		hypothetical protein	-0.362	-0.148	-0.442	error	-0.639	0.292	-0.351	error	error	error	0.05	error	error
slr1912		anti-sigma F factor antagon	-0.23	-0.39	0.185	0.16	0.214	0.08	0.102	error	error	error	error	error	error
slr1913		hypothetical protein	error	error	-1.225	error	error	error	error	error	error	error	error	error	error
slr1914		hypothetical protein	0.717	0.424	0.149	0.234	-0.113	0.173	0.364	error	error	error	error	error	error
slr1915		hypothetical protein	1.99	2.902	3.036	2.783	2.727	1.312	error	2.577	3.258	3.093	2.204	2.958	2.021
slr1916		probable esterase	0.76	1.915	2.549	2.014	1.658	1.238	1.281	0.879	2.108	1.538	1.306	1.724	0.829
slr1917		hypothetical protein	error	error	error	error	error	error	error	0.081	0.059	-0.412	0.26	-0.217	0.091
slr1918		hypothetical protein	-0.152	-0.422	0.066	0.377	0.447	0.603	0.384	error	error	error	error	error	error
slr1919		hypothetical protein	-0.078	0.249	-0.14	0.526	0.31	0.114	0.453	-0.04	0.359	0.529	0.381	0.077	-0.182
slr1920		unknown protein	error	error	error	error	error	error	error	-0.172	-0.598	-0.903	-0.784	-0.86	0.069
slr1923		hypothetical protein	-0.494	-0.359	-0.084	0.229	0.186	0.042	-0.03	-0.284	0.003	-0.072	0.234	-0.183	0.165
slr1924		D-alanyl-D-alanine carboxy	-0.428	-0.504	-0.558	-0.139	-0.282	-0.146	-0.344	-0.69	-1.013	-0.413	-0.401	-1.036	-1.278
slr1925	cobD	cobalamin biosynthesis pro	0.434	0.138	-0.382	-0.323	0.394	0.192	0.038	0.124	0.169	-0.111	0.01	-0.252	-0.627
slr1926		hypothetical protein	-0.258	0.398	0.811	0.687	0.638	0.949	0.625	0.118	0.899	0.69	0.956	0.787	2.16
slr1927		hypothetical protein	error	error	0.637	error	0.656	0.599	1.055	0.168	0.731	0.811	0.673	0.691	0.683
slr1928		unknown protein	error	error	error	error	error	error	1.193	0.301	0.373	0.742	0.836	0.235	1.351
slr1929	pilin	type 4 pilin pilin	error	-0.531	-0.678	-0.168	-0.015	-0.128	0.527	-0.2	-0.077	0.201	0.314	-0.164	0.1
slr1930		unknown protein	error	error	error	error	error	error	error	0.708	0.789	1.479	1.228	0.211	1.68
slr1931		unknown protein	0.356	0.16	0.431	0.575	0.935	0.901	1.618	0.471	0.971	0.913	1.156	0.832	0.591
slr1932		unknown protein	error	error	error	error	error	error	error	2.027	3.193	3.454	2.753	3.008	2.682
slr1933	rfbC	dTDP-4-dehydrothamnose	-0.169	-0.174	-0.343	-0.659	-0.515	-0.473	-0.484	0.319	0.588	0.148	0.256	0.362	1.637
slr1934		pyruvate dehydrogenase E	-0.402	-0.446	-0.52	-0.002	-0.483	-0.245	-0.226	0.081	-0.037	-0.643	0.024	-0.041	0.089
slr1935		hypothetical protein	error	error	0.081	-1.532	error	0.233	0.447	-0.061	0.178	-0.125	-0.136	0.19	1.323
slr1936		putative transposase [ISY1	0.29	-0.354	-0.24	0.046	-0.399	-0.364	0.659	-1	-0.071	0.453	-0.564	-0.266	0.938
slr1937		putative transposase [ISY1	-0.343	-0.242	-0.057	-0.147	0.212	-0.348	-0.243	-0.616	-0.267	1.045	-0.414	-0.236	0.138
slr1938		putative translation initiatio	-0.078	0.015	0.069	0.109	0.087	0.283	error	error	error	error	error	error	error
slr1939		unknown protein	-0.31	-0.331	-0.047	error	-0.321	0.086	-0.092	-0.061	-0.13	-0.043	-0.482	-0.144	-0.102
slr1940		hypothetical protein	-0.303	error	0.503	0.159	0.591	0.633	0.495	0.096	0.583	-0.022	0.343	0.534	1.15
slr1942	kaiC3	circadian clock protein KaiC	-0.566	-0.659	-0.758	-0.247	-1.105	-0.563	-0.433	-0.459	-0.415	0.593	-0.834	-0.738	-1.095
slr1943		probable glycosyltransferas	-0.071	-0.497	-0.342	-0.057	-0.417	-0.151	-0.209	0.329	0.181	0.089	-0.252	-0.328	-0.175
slr1944		hypothetical protein	-0.303	-0.484	-1.099	-0.641	-0.595	0.192	0.942	-0.291	0.004	0.005	-0.383	-0.254	-0.968
slr1945		2,3-bisphosphoglycerate-in	-0.604	-0.724	-0.828	0.292	-0.292	-0.179	-0.046	0.134	-0.202	-0.303	0.163	-0.299	-0.423
slr1946		hypothetical protein	error	error	error	error	error	error	error	0.969	1.492	2.148	1.204	1.444	0.962
slr1949		hypothetical protein	1.798	2.726	2.882	2.98	2.573	2.236	2.714	1.748	2.705	-	2.193	2.476	3.094

Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocystis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr1950	ctaA	copper-transporting CPx-ty	0.473	0.318	0.292	0.913	0.317	-0.084	-0.006	0.256	0.788	0.426	0.36	0.797	0.207
slr1951		hypothetical protein	error	error	error	error	error	error	error	3.135	3.519	3.918	3.452	3.279	3.584
slr1956		unknown protein	error	error	error	-1.186	error	0.638	error	-0.242	-0.025	0.005	-0.065	-0.203	0.422
slr1957		hypothetical protein	-0.861	-0.429	-0.47	error	-0.949	-0.401	error	-0.624	-0.441	-0.14	-1.034	-0.872	-1.384
slr1958		unknown protein	0.12	0.187	-0.924	-0.947	-1.054	-0.168	0.586	-0.216	-0.848	0.113	-0.93	-0.794	-0.342
slr1959		unknown protein	-0.255	-0.422	-1.164	-0.935	-0.936	0.082	-0.034	error	error	error	error	error	error
slr1960		putative transposase	error	error	error	error	error	error	error	error	error	error	error	error	error
slr1962		probable extracellular solut	error	error	error	error	error	error	error	-0.589	-0.066	-0.04	-0.254	-0.443	0.827
slr1963		water-soluble carotenoid pr	-0.095	1.009	3.395	3.967	2.827	1.454	1.439	0.965	3.745	3.769	3.313	3.721	2.779
slr1964		hypothetical protein	error	error	error	error	error	error	error	-0.376	0.233	1.1	-0.082	-0.181	0.625
slr1966		hypothetical protein	0.079	error	-0.309	error	-0.674	-0.001	error	-0.476	error	-0.047	-0.521	error	0.797
slr1968		unknown protein	0.585	0.232	-0.177	-0.04	0.221	0.182	error	0.066	-0.176	-1.455	0.277	-0.287	0.573
slr1969		two-component sensor histi	error	-0.36	-0.649	-0.061	-0.981	-0.432	-0.52	-0.112	-0.362	-0.67	-0.838	-0.307	-1.064
slr1970		hypothetical protein	-0.528	error	-0.249	-0.84	-0.648	-0.075	-0.086	0.298	0.339	0.201	-0.118	0.01	0.258
slr1971		hypothetical protein	0.866	0.867	0.465	0.16	1.119	0.676	1.286	0.408	0.62	0.125	0.589	0.48	1.066
slr1972	ycf81	hypothetical protein YCF81	error	0.237	0.438	0.768	0.379	-0.098	0.184	error	error	error	error	error	error
slr1974		GTP binding protein	0.262	0.398	0.844	-0.047	0.287	0.012	error	0.432	0.813	1.18	0.461	0.533	0.932
slr1975		N-acetylglucosamine 2-epime	-0.353	-0.64	-0.844	0.096	-0.595	-0.465	-0.006	-0.12	-0.318	-0.13	-0.234	-0.313	-1.238
slr1977		hypothetical protein	-0.064	0.295	0.358	-0.505	0.145	0.462	error	0.01	0.484	0.858	-0.137	0.138	0.125
slr1978		hypothetical protein	0.237	0.442	0.524	-0.29	0.205	0.192	0.552	-0.058	0.278	-0.325	-0.073	0.063	0.801
slr1979	tpE	anthranilate synthase comp	0.342	-0.264	-0.079	-1.177	-0.478	0.109	error	-0.452	-0.366	-0.275	-0.712	-0.129	0.279
slr1980		unknown protein	error	error	error	-1.381	error	0.258	error	-0.684	-0.054	-0.499	-0.566	-0.503	0.356
slr1982		two-component response re	-0.372	-0.041	-0.168	-0.799	-0.57	-0.164	-0.316	-0.145	-0.298	-0.95	-0.316	0.211	-0.516
slr1983		two-component hybrid sens	-0.175	-0.242	-1.365	-1.381	-1.5	-1.283	-0.677	-0.532	-0.985	-1.269	-1.341	-1.225	-0.244
slr1984	nbp1,rps1t	nucleic acid-binding protein	-0.297	-0.192	0.413	1.434	-0.21	-0.439	-0.228	-0.015	-0.039	-0.045	0.03	-0.052	-0.577
slr1986	apcB	allophycocyanin beta subun	-0.644	-0.825	-2.136	-1.397	-2.408	-2.038	-1.761	0.335	-1.062	-2.496	-2.216	-1.348	-0.758
slr1990		hypothetical protein	0.337	0.033	1.01	0.873	error	0.424	0.517	0.311	0.691	1.704	1.037	0.552	1.175
slr1991	cya1	adenylate cyclasecya1	0.687	0.515	0.623	0.532	1.551	0.969	1.321	0.265	0.345	1.246	1.008	0.56	1.144
slr1992	gpx2	glutathione peroxidase-like	-0.29	0.299	0.583	0.55	0.888	0.413	0.632	0.365	0.817	0.795	1.211	0.95	0.058
slr1993	phaA	PHA-specific beta-ketothiol	error	0.023	-0.127	0.216	0.092	0.19	0.253	0.066	0.463	0.041	0.173	0.481	-0.464
slr1994	phaB	PHA-specific acetoacetyl-C	-0.05	-0.198	-0.058	-0.345	-0.019	-0.06	-0.51	-0.143	0.083	error	-0.279	-0.171	0.48
slr1998		hypothetical protein	-0.024	0.62	-0.083	-0.506	-0.325	1.148	-0.343	error	error	error	error	error	error
slr1999		hypothetical protein	error	error	1.129	0.153	0.916	0.718	error	-0.139	0.843	error	0.854	0.294	2.045
slr2000		hypothetical protein	-0.244	-0.31	-0.492	-0.208	-0.275	-0.331	-0.153	-0.551	-0.413	0.082	-0.57	-0.733	-1.254
slr2001		cyanophycinase	-0.065	-0.132	0.109	0.172	-0.263	0.084	0.095	error	error	error	error	error	error
slr2002		cyanophycin synthetase	-0.449	error	0.248	0.523	-0.352	-0.288	-0.431	error	error	error	error	error	error
slr2003		hypothetical protein	-0.091	-0.271	-0.431	-0.534	error	-0.156	-0.091	error	error	error	error	error	error
slr2004		unknown protein	0.113	0.288	-0.402	-0.422	-0.035	0.086	0.322	error	error	error	error	error	error
slr2005		hypothetical protein	0.081	0.185	0.544	0.215	0.1	0.132	0.085	-0.017	0.185	0.087	0.223	0.068	-0.213
slr2006		hypothetical protein	0.129	0.423	0.555	-0.197	0.276	0.256	0.809	-0.109	0.285	0.431	0.072	0.26	-0.458
slr2007	ndhD5	NADH dehydrogenase subu	-0.498	0.087	-0.035	-0.558	-1.031	-0.159	-0.053	-0.237	0.012	-0.273	-0.364	0.087	-0.538
slr2008		hypothetical protein	error	error	-0.084	-0.635	0.253	0.449	error	-0.177	0.331	0.338	0.229	0.117	-0.588
slr2009	ndhD6	NADH dehydrogenase subu	-0.523	error	-0.383	-0.262	-0.29	-0.237	0.052	-0.321	-0.121	-0.245	-0.077	0.135	error
slr2010		hypothetical protein	error	error	error	error	error	error	error	-0.073	0.242	error	-0.261	-0.172	error
slr2011		hypothetical protein	0.074	error	0.296	error	-0.254	0.167	0.155	-0.608	0.445	-0.51	-0.336	-0.108	0.554
slr2012		hypothetical protein	error	error	error	error	error	error	error	-0.532	-0.113	-0.719	-0.78	-0.38	0.132
slr2013		hypothetical protein	-0.031	0.714	1.792	1.623	1.395	1.275	1.297	0.168	1.129	1.13	0.512	1.156	1.935
slr2015		unknown protein	0.363	-0.355	error	error	-1.225	-0.091	error	-0.562	-0.198	-0.328	-1.138	-0.339	-0.143
slr2016		unknown protein	error	error	error	-1.798	error	0.243	error	-0.373	-0.131	0.327	-0.836	-0.594	0.271
slr2017		unknown protein	-0.389	-0.329	-0.413	-0.047	-0.16	0.446	0.236	-0.71	-0.364	-0.552	-0.469	-0.331	-1.121
slr2018		unknown protein	0.786	-0.153	-0.237	-1.099	error	error	error	-0.232	-0.323	0.305	-0.401	-0.666	0.475
slr2019		ATP-binding protein of ABC	-0.084	0.026	0.887	1.967	-0.292	-0.511	-0.687	0.415	0.619	0.27	0.461	0.412	-0.989
slr2023	fabD	malonyl coenzyme A-acyl c	0.042	0.271	0.267	-0.149	-0.247	-0.163	-0.229	error	error	error	error	error	error
slr2024		two-component response re	-0.194	-0.383	-0.84	-0.541	-0.488	-0.605	-0.435	-0.158	-0.22	-0.626	-0.186	-0.67	0.476
slr2025		hypothetical protein	-0.396	0.045	-0.7	-0.895	-0.349	-0.135	0.122	-0.047	-0.072	-0.174	-0.179	-0.367	0.868
slr2026	folP	dihydropteroate synthasefo	-0.123	-0.311	-0.21	0.137	-0.206	-0.246	-0.214	-0.425	-0.187	0.02	-0.323	-0.231	0.551
slr2027		unknown protein	-0.146	-0.169	0.063	-0.213	-0.182	0.138	-0.001	-0.502	-0.107	error	-0.308	-0.071	-0.929
slr2030		hypothetical protein	0.731	error	1.175	error	0.264	0.529	1.632	-0.267	0.213	-0.072	-0.189	-0.183	0.643
slr2031		hypothetical protein	-0.365	-0.457	-1.203	-0.88	-1.395	-0.991	-0.957	-0.094	-0.563	-0.863	-1.196	-0.477	-0.586
slr2032	ycf23	hypothetical protein YCF23	-0.614	-0.621	-0.713	0.277	-0.499	-0.626	-0.425	0.142	0.179	-0.008	-0.064	0.11	-0.794
slr2033	rub	rubredoxinrub	-0.934	-1.229	-1.454	-0.539	-0.901	-0.568	-0.114	error	error	error	error	error	error
slr2034	ycf48	photosystem II stability/ass	-0.41	-0.647	-0.124	-0.203	-0.881	-0.738	-0.807	error	error	error	error	error	error
slr2035	proB	glutamate 5-kinaseproB	-0.312	-0.39	-0.969	-1.14	-1.442	-1.076	-1.087	-0.121	-0.405	-1.243	-1.003	-0.713	-0.723
slr2036		putative transposase [ISY2	0.284	0.005	-0.004	0.685	-0.123	-0.412	-0.058	-0.004	0.242	0.417	0.05	0.169	0.285
slr2037		unknown protein	-0.173	-0.126	0.026	error	-0.118	1.016	0.02	error	error	error	-0.017	error	error
slr2038		hypothetical protein	0.308	-0.435	-0.91	-0.554	-0.673	0.191	0.105	0.233	-0.123	error	-0.263	-0.29	-0.095
slr2041		probable two-component re	-0.48	-0.565	-1.258	error	-2.111	-1.64	-1.391	0.158	0.451	0.585	-0.125	0.491	-0.272
slr2042		hypothetical protein	0.161	-0.075	0.24	0.183	-0.033	0.141	-0.083	error	error	error	error	error	error
slr2043		periplasmic solute binding p	0.137	error	error	error	-0.467	-0.091	error	0.005	0.088	-0.058	-0.485	-0.746	1.161
slr2044		ABC transporter ATP-bindin	0.654	0.238	0.342	0.156	-0.175	-0.066	0.324	0.296	0.311	0.356	0.202	0.303	0.312
slr2045		permease protein of ABC tr	0.049	error	error	-0.548	error	0.07	-0.002	-0.7	-0.153	error	-0.635	-0.126	0.905
slr2046		unknown protein	-0.383	-0.416	-0.697	error	-0.784	-0.105	0.262	-0.41	-0.795	-0.212	-0.436	-0.683	-0.098
slr2047		PhoH like protein	-0.091	-0.255	0.044	0.766	0.112	0.082	0.273	-0.04	0.3	0.842	0.452	0.394	-0.187
slr2048		unknown protein	0.041	-0.142	0.328	error	1.312	error	1.909	-0.137	0.437	0.59	0.914	0.297	0.733
slr2049	ycf58	hypothetical protein YCF58	error	error	error	error	error	error	error	0.309	0.509	0.961	0.492	0.02	0.643



Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1							Data set 2					
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
slr2051	cpcG1	phycobilisome rod-core link	-0.651	-0.833	-2.263	-1.63	-2.045	-1.695	-1.211	-0.232	-1.778	-2.612	-2.356	-1.595	-0.589
slr2052		hypothetical protein	-0.672	-1.022	-1.453	-1.356	-1.642	-0.88	-0.728	-0.437	-0.918	-1.335	-1.774	-1.052	-0.483
slr2053		putative hydrolase	0.737	error	0.585	-0.178	-0.197	-0.176	-0.704	0.302	0.474	-0.233	-0.401	-0.153	0.246
slr2057		water channel protein	-0.737	-0.645	-1.236	-0.605	-1.511	-1.029	-0.949	0.016	-0.037	error	-0.572	-0.179	-0.626
slr2058	topA	DNA topoisomerase I topA	-0.44	-0.489	-0.094	0.577	-0.079	-0.006	-0.176	-0.029	-0.367	-0.541	-0.17	-0.513	-0.998
slr2059		iron-sulfur cluster binding p	0.419	0.182	0.76	0.625	0.977	0.106	0.707	0.209	0.297	0.806	0.433	0.182	0.838
slr2060		hypothetical protein	0.644	0.248	-0.116	-0.542	-0.004	0.117	1.364	-0.531	error	0.335	-0.273	error	0.473
slr2062		putative transposase [ISY0	-0.37	-0.606	-0.273	-0.052	-0.285	-0.35	-0.313	-0.306	-0.168	-0.728	-0.232	0.13	0.992
slr2067	apcA	allophycocyanin alpha subu	-0.681	-0.867	-1.918	-1.496	-2.48	-1.132	-1.357	0.207	-0.829	-1.808	-1.786	-0.803	-1.597
slr2070		hypothetical protein	-0.42	-0.473	-0.14	0.31	-0.334	-0.049	-0.626	-0.28	0.042	0.202	0.001	-0.236	0.757
slr2071		unknown protein	0.362	0.144	0.506	0.082	0.584	0.289	-0.007	0.327	1.291	1.047	1.117	0.87	1.068
slr2072	ilvA	L-threonine deaminase ilvA	-0.104	-0.157	-0.104	-0.709	0.024	0.199	error	0.319	0.416	0.284	0.189	0.37	0.464
slr2073	ycf50	hypothetical protein YCF50	-0.611	-0.943	-1.499	-0.269	-1.03	-0.344	-0.542	-0.322	-1.113	-1.476	-1.405	-1.088	-0.62
slr2074		similar to mannose-1-phosp	0.372	error	0.698	error	0.136	-0.095	error	error	error	error	error	error	error
slr2075	groES	10kD chaperoningroES	0.271	0.848	2.288	3.29	1.787	0.403	0.143	0.871	2.72	2.516	2.632	2.619	1.674
slr2076	groEL	60kD chaperoningroEL	-0.165	0.411	2.05	2.697	1.293	-0.021	-0.066	0.752	2.817	2.821	2.415	2.756	1.049
slr2077		probable ABC transporter, p	-0.108	-0.398	-0.646	-0.346	-0.251	-0.312	-0.004	-0.238	0.146	0.02	-0.256	-0.195	-0.474
slr2078		hypothetical protein	error	error	error	error	error	error	error	0.138	0.473	0.002	0.043	-0.383	-0.128
slr2079		putative glutaminase	-0.184	-0.639	0.097	-	-0.388	-0.214	0.066	0.13	0.279	0.144	-0.105	-0.238	1.223
slr2080		hypothetical protein	error	0.912	error	error	error	error	error	0.116	0.407	error	0.05	0.034	1.544
slr2081	tyrA	phenenate dehydrogenase	-0.228	0.058	0.136	-0.357	-0.541	0.154	-0.039	0.154	-0.319	0.225	-0.157	-0.215	-1.019
slr2082	ctaDII	cytochrome c oxidase subu	-0.733	-0.62	-0.943	-0.855	-0.819	-0.504	-0.166	-0.2	-0.099	-0.234	-0.179	0.162	-0.55
slr2083	ctaEII	cytochrome c oxidase subu	-0.224	-0.227	-0.568	-0.64	-0.343	0.005	0.319	-0.08	-0.059	-0.07	-0.094	0.229	-0.572
slr2084		hypothetical protein	0.283	-0.1	0.32	error	-0.065	0.064	0.304	-0.082	0.138	-0.393	-0.138	-0.13	1.029
slr2087	ccs1, ycf44	c-type cytochrome biogene	-0.568	-0.818	-0.561	0.616	-0.663	-0.452	-0.321	-0.219	-0.363	-0.56	-0.009	-0.478	-0.565
slr2088	ilvG	acetohydroxy acid synthase	-0.577	-0.859	-0.516	0.489	-0.547	-0.656	-0.616	0.057	-0.282	-0.298	0.071	-0.598	-0.463
slr2089	shc	squalene-hopene-cyclasesI	0.412	-0.082	1.082	1.582	0.829	0.446	0.843	0.377	1.188	1.284	1.4	0.307	-0.582
slr2092		hypothetical protein	1.148	error	1.216	-0.447	1.356	1.18	error	0.393	0.762	error	0.939	0.298	1.68
slr2094	fbpI	fructose-1,6-/sedoheptulose	-0.931	-0.852	-1.393	-0.467	-1.455	-1.513	-1.319	-0.29	-0.865	-1.287	-1.023	-1.085	-1.071
slr2095		putative transposase [ISY1	-0.294	0.083	0.156	error	0.14	-0.172	-0.149	error	error	error	error	error	error
slr2096		putative transposase [ISY1	0.355	0.332	0.495	1.192	0.559	0.545	0.318	0.001	0.387	0.769	0.28	0.424	-0.095
slr2097	glnB	cyanogloblnB	-0.095	error	-0.156	error	0.024	-0.193	0.26	0.126	0.17	0.372	0.154	-0.137	0.429
slr2098		two-component hybrid sens	0.189	-0.263	-0.93	-0.654	-0.692	-0.558	0.1	-0.38	-0.282	0.209	-0.609	-0.525	-0.007
slr2099		two-component hybrid sens	-0.467	-0.481	-1.273	-0.961	-1.401	-1.032	-1.186	-0.231	-0.664	-0.926	-1.134	-0.705	-0.738
slr2100		two-component response re	0.261	0.292	0.122	-0.497	-0.793	-0.102	0.785	-0.392	-0.097	-0.486	-0.924	-0.185	0.753
slr2101		hypothetical protein	0.186	0.068	0.087	-0.547	-0.343	0.004	0.39	error	error	error	error	error	error
slr2102	ftsY	cell division protein FtsYfts	-0.399	-0.181	-0.459	-0.032	-0.031	-0.228	-0.253	-0.291	-0.119	0.207	-0.07	0.154	0.041
slr2103		hypothetical protein	0.532	error	-0.05	-0.438	0.351	0.416	0.708	0.685	error	error	0.478	error	0.148
slr2104		two-component hybrid sens	-0.322	-0.424	-0.765	-0.892	-1.215	-0.414	-0.76	-0.269	-0.515	error	-0.765	-0.401	-1.59
slr2105		hypothetical protein	-0.386	-0.531	-0.467	0.252	-0.021	-0.053	-0.134	error	error	error	error	error	error
slr2107		probable polysaccharide A	0.703	1.054	1.333	1.532	0.771	0.113	0.313	error	error	error	error	error	error
slr2108		probable polysaccharide A	error	error	error	error	error	error	error	0.281	0.574	0.152	0.394	0.405	0.586
slr2110		unknown protein	0.194	0.388	-0.399	-0.769	0.134	0.153	error	-0.001	0.305	0.298	1.36	-0.14	0.765
slr2111		unknown protein	-0.238	0.329	-0.356	-0.547	-0.449	-0.008	-0.604	-0.064	0.197	-0.265	-0.332	0.085	-0.674
slr2112		putative transposase [ISY1	0.356	0.014	-0.217	0.05	-0.399	-0.385	-	-0.868	0.091	0.636	-0.209	0.258	0.949
slr2113		putative transposase [ISY1	-0.435	-0.485	-0.385	-0.356	-1.018	-0.411	-0.585	-0.997	-0.253	1.153	-0.845	-0.487	-0.15
slr2114		perosamine synthetase	error	error	-0.885	-1.105	-0.326	0.279	error	-0.598	-0.53	-0.163	-1.163	-0.635	-0.492
slr2115		unknown protein	error	error	error	error	error	error	error	-0.91	-0.713	-0.734	-0.836	-1.029	0.693
slr2116		probable glycosyltransferas	-0.555	-0.614	-0.704	-0.29	-0.439	0.031	-0.281	-0.108	-0.316	-0.72	-0.434	-0.856	-0.786
slr2117		hypothetical protein	error	error	-0.64	-0.101	0.044	0.162	error	0.094	-0.169	0.067	0.386	-0.668	-0.084
slr2118		unknown protein	0.171	0.117	-0.024	-0.46	-0.143	error	0.577	-0.211	0.089	-0.386	-0.153	-0.475	-0.023
slr2119		unknown protein	0.244	error	0.062	-0.627	0.052	0.136	0.655	error	error	error	error	error	error
slr2120		hypothetical protein	error	error	error	error	error	error	error	-0.475	-0.297	-0.583	-0.249	-0.494	0.6
slr2121		hypothetical protein	0.616	1.478	1.165	0.148	0.039	0.35	0.093	0.221	0.623	0.251	0.024	0.325	1.05
slr2122		hypothetical protein	-0.371	-0.035	0.132	error	-0.038	0.005	0.054	0.006	-0.133	-0.358	-0.335	-0.252	0.098
slr2123		similar to D-3-phosphoglyc	0.363	0.1	-0.257	error	-0.481	-0.31	0.252	-0.335	-0.14	-0.348	-0.559	-0.143	0.585
slr2124		3-oxoacyl-acyl-carrier prote	0.387	1.108	1.328	1.43	0.987	0.797	0.978	0.259	0.546	0.218	0.005	0.435	-0.094
slr2125		hypothetical protein	error	error	error	-1.022	0.492	0.459	error	-0.406	-0.103	0.159	0.561	-0.894	1.183
slr2126		probable glycosyltransferas	-0.53	-0.227	-0.199	-0.555	-0.237	0.086	0.331	-0.487	-0.014	0.112	-0.092	-0.028	-0.331
slr2127		hypothetical protein	error	0.269	0.205	-0.43	error	0.339	error	-0.094	0.092	0.427	-0.003	0.253	-0.632
slr2128		hypothetical protein	error	-0.264	-0.212	-0.454	error	0.008	0.088	0.043	0.287	-0.003	0.213	-0.127	1.053
slr2130	aroB	3-dehydroquinate synthase	-0.259	-0.465	-0.53	-0.329	-0.352	-0.303	-0.376	-0.37	-0.509	-0.13	-0.55	-0.549	-1.145
slr2131		RND multidrug efflux transp	0.02	0.41	0.494	1.023	0.475	0.237	0.521	error	error	error	error	error	error
slr2132		phosphotransacetylase	-0.078	0.457	-0.03	-0.198	-0.009	0.577	0.593	-0.466	-0.295	-0.351	-0.242	-0.32	-1.117
slr2135		hydrogenase accessory pro	-0.163	0.046	0.297	0.054	-0.046	0.061	0.068	-0.454	-0.011	-0.372	0.009	-0.225	0.537
slr2136		GcpE protein homolog	-0.43	error	-0.454	-0.295	-0.294	-0.66	-0.584	0.305	0.438	0.214	-0.026	0.322	-0.553
slr2141		hypothetical protein	0.04	0.311	0.605	0.386	0.592	0.079	0.37	-0.446	0.204	error	0.006	0.163	0.939
slr2143		L-cysteine/cystine lyase	error	-0.031	1.125	-0.472	0.416	0.019	error	-0.574	-0.148	-0.387	-0.798	-0.543	-0.059
slr2144		hypothetical protein	-0.37	-0.501	-0.664	0.305	-0.063	-0.276	-0.427	-0.626	-0.247	error	-0.178	-0.471	0.677
smI0001	psbI	photosystem II reaction cen	-0.487	-0.621	-0.824	error	-0.486	-0.352	0.048	-0.258	-0.331	-0.113	0.019	-0.074	-0.081
smI0002	psbX	photosystem II PsbX protei	-0.18	-0.817	-1.101	-0.305	-0.969	-0.681	-0.371	-0.388	-0.928	-1.711	-0.699	-0.83	5.103
smI0003	psbM	photosystem II reaction cen	0.206	0.063	-0.821	-0.251	-0.418	-0.14	0.3	-0.46	-0.634	-0.517	-0.793	-0.484	-0.33
smI0004	petN	cytochrome b6-f complex su	error	error	error	error	error	error	error	0.528	error	error	0.586	error	-1.006
smI0005	psbK	photosystem II PsbK protei	-0.441	-0.681	-1.133	0.005	-0.815	-0.833	-0.473	-0.311	-0.746	-0.635	-0.881	-0.628	-0.675
smI0006	rpI36	50S ribosomal protein L36r	0.478	error	0.354	error	0.145	-0.669	error	0.402	0.852	1.137	0.67	0.704	0.282







Table A-2 Gene expression profiles in response to 650 mM NaCl shock treatment by *Synechocytis* PCC6803

Salt shock log <sub>2</sub> expression ratios			Data set 1						Data set 2						
Orf	Symbol	Product	30 min	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr	1 hr	3 hr	6 hr	12 hr	18 hr	24 hr
ssr1375		hypothetical protein	error	-0.537	-1.475	-0.854	-1.117	-0.757	error	-0.618	-0.836	-0.859	-1.317	-1.088	-1.088
ssr1386	ndhL	NADH dehydrogenase subu	-0.242	-0.228	0.554	1.164	-0.08	-0.663	-0.617	0.075	0.642	1.193	0.628	0.604	-0.736
ssr1391		hypothetical protein	-0.438	-0.105	error	0.625	-0.225	-0.353	-0.412	error	error	error	error	error	error
ssr1398	rpl33	50S ribosomal protein L33r	0.099	0.372	0.821	1.195	0.094	-0.538	-0.114	0.329	0.861	1.106	0.674	0.566	0.263
ssr1399	rps18	30S ribosomal protein S18r	0.219	0.498	0.71	1.071	0.256	-0.279	-0.18	0.152	0.572	-0.087	0.416	0.315	0.085
ssr1407		hypothetical protein	0.388	0.367	0.591	0.236	0.713	0.547	error	-0.08	0.459	0.001	0.423	0.086	0.657
ssr1425	ycf34	hypothetical protein YCF34	0.228	0.417	-0.079	0.124	0.314	0.973	1.044	-0.109	0.059	0.06	0.879	0.072	-0.007
ssr1473		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr1480		RNA-binding protein	0.055	0.659	-0.005	0.308	0.067	0.141	0.447	0.09	0.077	0.162	0.493	0.188	0.046
ssr1499		hypothetical protein	-0.516	-0.172	error	0.073	0.729	0.215	0.22	-0.349	-0.107	0.114	0.242	0.02	1.092
ssr1513		hypothetical protein	-0.18	error	0.048	-0.811	-0.014	0.53	error	error	error	error	error	error	error
ssr1527		probable molybdopterin [mp	error	error	error	error	error	error	error	-0.029	0.342	0.27	0.277	-0.077	0.418
ssr1528		hypothetical protein	error	error	error	error	error	0.115	error	0.464	error	error	0.58	error	0.378
ssr1552		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr1558		hypothetical protein	0.349	0.47	0.83	0.528	0.308	0.588	0.359	0.567	1.33	0.474	0.547	0.699	-0.04
ssr1562		hypothetical protein	error	error	-1.612	error	0.116	0.073	-0.621	0.007	-0.036	0.013	0.419	-0.216	0.076
ssr1600		similar to anti-sigma f factor	-0.187	0.387	-0.444	0.869	-0.159	-0.307	-0.438	0.381	0.059	0.218	0.306	0.026	-0.243
ssr1604	rpl28	50S ribosomal protein L28r	0.288	0.207	0.699	1.393	0.261	-0.022	0.177	0.181	0.426	0.461	0.412	0.36	-0.791
ssr1698		hypothetical protein	error	error	0.476	error	0.534	0.437	error	0.47	0.97	0.006	0.364	0.242	-0.39
ssr1720		similar to tyrosyl tRNA synt	0.061	0.328	0.275	-0.634	-0.071	0.155	0.157	0.104	0.379	-0.367	-0.03	0.03	0.133
ssr1736	rps32	50S ribosomal protein L32r	0.238	error	0.438	1.109	0.045	-0.124	error	0.605	0.941	0.02	0.206	0.607	-0.11
ssr1765		hypothetical protein	error	error	error	error	error	error	error	0.686	1.328	1.397	1.205	0.923	1.22
ssr1766		hypothetical protein	error	0.708	-0.158	error	0.59	0.599	0.78	0.621	1.042	1.258	0.661	0.771	0.858
ssr1768		unknown protein	error	error	error	error	error	-0.447	error	0.666	0.449	-1.169	-0.497	-0.126	-0.064
ssr1789	hiID	CAB/ELIP/HLIP-related pro	0.476	0.42	0.273	0.171	0.155	0.233	0.317	0.35	0.572	0.044	0.217	0.779	-0.308
ssr1853		unknown protein	0.428	error	0.469	1.381	1.285	0.406	1.351	0.118	0.519	0.477	1.316	0.227	5.866
ssr1880		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr1951		hypothetical protein	0.231	0.471	0.858	0.222	0.071	0.156	0.176	0.375	0.692	0.125	0.204	0.504	0.944
ssr1966		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2009		hypothetical protein	-0.344	-0.027	0.121	-0.152	0.026	0.32	0.115	error	error	error	error	error	-0.763
ssr2016		hypothetical protein	error	error	error	error	error	-0.233	error	0.034	-0.163	0.1	0.101	-0.279	-0.413
ssr2047		hypothetical protein	-0.084	0.027	-0.001	0.284	0.27	-0.143	0.465	-0.017	0.576	0.511	0.419	0.387	0.385
ssr2049		unknown protein	0.022	-0.085	-0.382	-0.623	0.245	0.233	0.018	0.041	0.444	0.291	0.278	0.038	0.984
ssr2060		unknown protein	-0.278	0.057	0.125	0.515	-0.027	0.297	-0.134	0.011	0.122	0.094	-0.058	-0.315	-1.029
ssr2061		glutaredoxin	-0.06	0.24	0.543	error	0.845	0.376	0.357	0.07	0.401	0.298	0.936	0.244	1.758
ssr2062		hypothetical protein	-0.459	-0.638	-0.744	0.407	error	0.011	-0.774	error	error	error	error	error	error
ssr2066		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2067		putative transposase	0.796	error	0.44	-1.819	error	0.357	error	-0.082	0.411	error	-0.079	0.218	1.033
ssr2078		putative transposase [ISY8	-0.123	0.504	0.177	-0.528	-0.035	0.209	1.603	-0.212	0.269	0.83	-0.237	0.61	-0.497
ssr2087		hypothetical protein	-0.43	-0.383	-0.459	-0.485	-0.161	0.276	-0.054	error	error	error	error	error	error
ssr2130		hypothetical protein	0.032	-0.158	0.032	error	-0.309	-0.165	-0.482	0.037	0.333	-0.16	0.35	0.18	0.748
ssr2142	ycf19	hypothetical protein YCF19	-0.459	-0.492	-0.103	1.03	1.105	0.339	0.608	-0.041	0.154	0.339	1.492	0.073	1.223
ssr2153		unknown protein	1.507	3.076	3.733	2.908	3.322	2.593	2.788	2.466	3.557	2.029	2.561	3.002	3.773
ssr2194		unknown protein	error	error	error	error	error	error	error	-0.032	0.421	-0.223	0.225	0.008	1.223
ssr2201		unknown protein	error	error	error	error	error	error	error	-0.351	0.338	0.329	0.062	-0.193	0.79
ssr2227		putative transposase	error	error	0.632	-0.526	error	0.119	error	-0.127	0.436	0.466	-0.481	0.343	1.331
ssr2254		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2317		unknown protein	error	error	error	-0.944	error	error	error	0.617	0.872	error	0.231	0.167	error
ssr2318		unknown protein	error	error	error	error	error	error	error	-0.127	-0.075	-0.821	0.083	-0.166	0.384
ssr2333		unknown protein	0.826	error	0.839	-0.222	1.524	1.027	1.482	0.278	1.093	-0.245	0.821	0.389	1.548
ssr2340		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2377		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2406		unknown protein	-0.08	0.048	-0.181	error	-0.053	0.298	-0.032	-0.061	0.091	-0.455	-0.466	-0.351	-0.058
ssr2422		unknown protein	-0.055	0.128	0.12	error	-0.167	-0.112	-0.002	error	error	error	error	error	error
ssr2439		hypothetical protein	0.093	-0.228	0.257	-0.615	-0.526	-0.077	0.299	-0.027	0.459	-0.389	0.077	-0.093	-0.13
ssr2549		unknown protein	1.057	1.536	1.57	1.38	0.83	0.376	0.336	1.121	1.352	0.461	0.901	1.208	1.52
ssr2551		hypothetical protein	0.393	0.617	error	error	-1.32	0.088	error	0.088	0.797	0.677	0.179	0.566	1.062
ssr2553		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2554		hypothetical protein	error	error	-0.201	-0.742	-0.644	-0.053	-0.471	0.23	0.398	-0.124	0.175	0.35	0.148
ssr2595	hiIB	high light-inducible polypep	0.332	-0.003	0.33	1.377	1.861	0.752	0.625	-0.089	0.192	1.214	1.928	0.353	2.032
ssr2611		hypothetical protein	0.99	error	1.278	-0.635	error	0.771	error	0.36	0.951	error	0.554	0.392	1.924
ssr2615		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2699		putative transposase [ISY5	0.41	0.28	0.574	-0.127	0.466	0.232	0.48	-0.308	0.267	0.488	0.105	0.289	5.447
ssr2708		hypothetical protein	0.274	0.567	0.05	0.272	-0.083	0.564	-0.177	0.119	0.188	0.55	0.138	0.275	-0.039
ssr2710		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2711		hypothetical protein	-0.333	-0.272	0.228	1.035	0.39	-0.087	0.16	error	error	error	error	error	error
ssr2723		hypothetical protein	-0.027	0.251	0.842	1	1.024	0.412	error	-0.049	0.566	0.757	0.79	0.468	1.361
ssr2754		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2755		hypothetical protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2781		hypothetical protein	0.138	0.333	0.26	0.43	0.27	0.381	error	0.453	1.356	1.646	0.826	0.879	-0.075
ssr2784		antitoxin ChpI homolog	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2787		unknown protein	error	error	error	error	error	error	error	error	error	error	error	error	error
ssr2799	rpl27	50S ribosomal protein L27r	-0.258	-0.058	0.673	1.606	0.106	-0.208	-0.216	0.427	0.582	0.557	0.471	0.355	-0.798
ssr2802		hypothetical protein	error	error	error	error	error	-0.269	error	-0.36	0.767	error	0.293	-0.471	-0.501
ssr2803		hypothetical protein	error	0.733	0.967	-0.592	0.907	0.279	error	0.169	0.82	error	-0.022	0.164	2.064



VITA



Bradley L. Postier

Candidate for the degree of

Doctor of Philosophy

**Thesis:** STUDIES ON THE PHOTOSYNTHETIC MICROORGANISM  
*SYNECHOCYSTIS PCC6803* AND HOW IT RESPONDS TO THE EFFECTS OF SALT  
STRESS

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