ABSTRACT

Title of Dissertation: ADAPTIVE MECHANISMS OF AN ESTUARINE *SYNECHOCOCCUS* BASED ON GENOMICS, TRANSCRIPTOMICS, AND PROTEOMICS

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Picocyanobacteria are important phytoplankton and primary producers in the ocean. Although extensive work has been conducted for picocyanobacteria (i.e. *Synechococcus* and *Prochlorococcus*) in coastal and oceanic waters, little is known about those found in estuaries like the Chesapeake Bay. *Synechococcus* CB0101, an estuarine isolate, is more tolerant to shifts in temperature, salinity, and metal toxicity than coastal and oceanic *Synechococcus* strains, WH7803 and WH7805. Further, CB0101 has a greater sensitivity to high light intensity, likely due to its adaptation to low light environments. A complete and annotated genome sequence of CB0101 was completed to explore its genetic capacity and to serve as a basis for further molecular analysis. Comparative genomics between CB0101, WH7803, and WH7805 show that CB0101 contains more genes involved in regulation, sensing, and stress response. At the transcript and protein level, CB0101 regulates its metabolic pathways, transport systems, and sensing mechanisms when nitrate and phosphate are limited. Zinc toxicity led to oxidative stress and a global down regulation of photosystems and the translation

machinery. From the stress response studies seven chromosomal toxin-antitoxin (TA) genes, were identified in CB0101, which led to the discovery of TA genes in several marine *Synechococcus* strains. The activation of the $relB^{2}/relE^{1}$ TA system allows CB0101 to arrest its growth under stressful conditions, but the growth arrest is reversible, once the stressful environment dissipates. The genome of CB0101 contains a relatively large number of genomic island (GI) genes compared to known marine *Synechococcus* genomes. Interestingly, a massive shutdown (255 out of 343) of GI genes occurred after CB0101 was infected by a lytic phage. On the other hand, phage-encoded host-like proteins (*hli, psbA, ThyX*) were highly expressed upon phage infection. This research provides new evidence that estuarine *Synechococcus* like CB0101 have inherited unique genetic machinery, which allows them to be versatile in the estuarine environment.

ADAPTIVE MECHANISMS OF AN ESTUARINE *SYNECHOCOCCUS* BASED ON GENOMICS, TRANSCRIPTOMICS, AND PROTEOMICS

by

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Dedication

To Emily and my family for their unconditional love and support

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Table of Contents

2.5 D

List of Tables

List of Figures

Chapter 1: Introduction

1.1 Ecological significance of Picocyanobacteria

Bacteria living in diverse habitats must sense, respond, and adapt to versatile environmental conditions. No other oxygenic photosynthetic organism has survived for longer and adapted to such diverse environments as cyanobacteria (1). As one of the oldest living phyla on Earth with fossil records dating back more than ~2.15 Gyr (2), cyanobacteria are credited with producing our present atmospheric oxygen. Cyanobacteria are a fascinating and adaptive group that are widely distributed in habitats ranging from aquatic to terrestrial systems, tropical to polar regions, and hot springs to hypersaline ponds with immense biogeochemical influence (3). Among cyanobacteria, picocyanobacteria, whose abundance and global significance was only discovered thirty-seven years ago (4–7), exemplifies this adaptive heritage and plays a significant ecological role.

Small unicellular cyanobacteria less than 2-3µm are usually called picocyanobacteria (8, 9). Marine picocyanobacteria contribute to roughly half of the global net primary production and play a key role in regulating global biogeochemical cycles (10) (Fig 1.1). The biological fixation of carbon dioxide by picocyanobacteria (as small phytoplankton in Fig 1.1) is the major driving force of the ocean's carbon cycling. Further, picocyanobacteria are the backbone of the marine food web due to not only supplying energy up the trophic levels but also being a major component of detritus to the deep ocean. It has recently been reported that marine picocyanobacteria can make up 40-60% of the digestible gut content of copepods from the Baltic Sea. This could have major implications on food web models and economic cost analysis for other fisheries as

copepods makeup important food sources for oysters, Blue Crabs, and Stripped Bass with a combined economic value of $622 million per year.

Marine picocyanobacteria contain two major genera, *Prochlorococcus* and *Synechococcus* (8, 9). *Prochlorococcus* are small photosynthetic prokaryotes (diameter, 0.5-0.8 μm) that are ubiquitous in the euphotic zone from the surface to a depth of ~150m in the open ocean between 40°N and 40°S. Within this range, the abundance of *Prochlorococcus* in warm surface waters is typically greater than 10^5 cells ml^{-1}, while the abundance declines beyond these latitudinal limits. *Prochlorococcus* are thought to be absent when the temperature of seawater is below 15 °C (11). Furthermore, the *Prochlorococcus* lineage is believed to be outcompeted by other phytoplankton in high-nutrient waters (12, 13). *Synechococcus*, another major genus of picocyanobacteria, is also abundant in the ocean. Compared to its sister genus *Prochlorococcus*, *Synechococcus* is more ancient, diverse, and adaptive to environments ranging from freshwater, estuarine, coastal, and oceanic waters (14–20). Although concentrations of *Synechococcus* are typically an order of magnitude lower than those of *Prochlorococcus*, its larger average cell size (0.6-2.1 μm), coupled with a larger range, makes it approximately equal in terms of global photosynthetic biomass, thus allowing them to fix an order of magnitude more carbon (21). *Synechococcus* is usually limited to the upper 100 m of the water column (13), but have a broader latitudinal distribution, withstanding temperatures as low as 2°C (22, 23).

As a key component of picophytoplankton, *Synechococcus* can greatly influence the global cycling of carbon (10) (Fig. 1.1). *Synechococcus* supplies photosynthetically fixed carbon to higher trophic levels, plays a central role in dictating the elemental

composition of seawater over evolutionary time (24), and influences the dynamics and availability of nitrogen, phosphorus, and other potentially limited nutrients in the oceans (25). Although nutrients and trace metals play an important role in *Synechococcus* abundance and distribution, key ecological determinants such as light, temperature, and the degree of physical perturbations also influence the biogeographic distribution of *Synechococcus* (20). Annual mean averages of *Synechococcus* cells are 7.0×10^{26}, which account for 16.7% of total net global primary production. Projections of future global niche models suggest that oceanic *Synechococcus* communities will experience an increase in abundance of at least 14 % by the end of the 21st century, assuming current levels of warming continue. These increases in cell abundance and large shifts in communities will likely occur both in current regions and result in an overall expansion over the next 50 to 100 years (26). Considering the high abundance and productivity of *Synechococcus* in the ocean, it becomes imperative to fully understand how they respond to environmental changes.

1.2 Current understanding of subcluster 5.2 and estuarine *Synechococcus*

Currently, marine *Synechococcus* are divided into three subclusters, 5.1, 5.2, and 5.3 (Fig. 1.2) (16, 18, 27–29), illustrated in Figure 1.2. These include at least 20 clades (23, 27, 30). *Synechococcus* displays geographic niche adaptation (20). More specifically, clade II *Synechococcus* is common in tropical open ocean waters, whereas clades I and IV are largely found in coastal and higher latitude regions (14, 20, 31). The *Synechococcus* found in the estuarine or coastal bays often contain unique genotypes distinct from those in the open oceans. For example, *Synechococcus* isolated from the Chesapeake Bay and East Sea is predominantly from subcluster 5.2 and clade CB4 or

CB5 (32, 33). CB4 and CB5 clade strains lack PUB and some are motile found in temperature coastal waters while, CB5 is unique in that they are prevalent in polar/subpolar waters. However, much less is known about the biogeography of subclusters 5.2 and 5.3 *Synechococcus* compared with subcluster 5.1. The responses of subcluster 5.1 *Synechococcus* to changing environments such as wavelengths of light (27, 29, 34), nitrate (NO_3^-) concentrations (27, 35, 36), and organic phosphorus sources (30, 37) have been studied. Further, due to their ecological significance and functional divergence, 31 genomes of marine *Synechococcus* have been sequenced (38, 39). Of these 31 genomes, only three belong to subcluster 5.2. While 16 clades have been characterized for subcluster 5.1 *Synechococcus*, only clades CB4 and CB5 have been identified for subcluster 5.2 (23, 40).

Compared to coastal and oceanic *Synechococcus*, much less is known about the ecological function and genomic evolution of estuarine *Synechococcus.* Estuaries are highly productive ecosystems at the precipice of anthropogenic influences. These *Synechococcus* thrive in a highly dynamic environment with constantly changing conditions in which open ocean cyanobacteria would fail. In 2004, 13 strains of *Synechococcus* were isolated from the Chesapeake Bay (Chen et al. 2004). The phylogenetic analyses based on the partial RuBisCO gene sequences and internal transcribed spacer (ITS) sequences show that most of these Chesapeake Bay *Synechococcus* isolates are different from coastal and oceanic strains (19, 32). The clone library analyses based on the environmental *rbcL* and ITS sequences both showed that subcluster 5.2 are the dominant *Synechococcus* in the Chesapeake Bay (19, 32). Microscopic counting shows that picocyanobacteria (mostly *Synechococcus*) make up 20-

40 % of phytoplankton chlorophyll-a in the Chesapeake Bay during the summer (41). Phycoerythrin (PE) containing estuarine subcluster 5.2 *Synechococcus* contain a novel phycobilisome (PBS) gene cluster not seen in other subclusters (42). Nowadays, more subcluster 5.2 *Synechococcus* strains or sequences have been reported in other estuarine or bay environments such as the East Sea, Gulf of Mexico, Bering Sea, Chuckhi Sea, and Baltic Sea (23, 33, 42). Subcluster 5.2 lineages, although generally found in estuarine or coastal environments, have also been identified in Arctic and subarctic oceans. The potential niche adaptation of this *Synechococcus* sub-cluster requires further research.

Synechococcus strain CB0101, a well-referenced strain of subcluster 5.2, represents the most common and abundant *Synechococcus* in the upper Chesapeake Bay (40, 43). As the largest estuarine ecosystem in the U.S., the Chesapeake Bay is known for its strong environmental gradients and seasonality. It has distinct upper and lower sections; its upper part above the Potomac (38^{o} 1'11.8 N; 76^{o} 20'8.7 W) is a deep drowned river channel sided by clay cliffs which have the tendency to become sub-anoxic at depth during the summer time. The lower section is heavily influenced by tides. This hydrology, as well as chemical and physical influences, plays a hefty role in determining *Synechococcus* communities. Microorganisms living in estuaries need to cope with rapid changes to salinity, temperature, light intensity, nutrients, and trace elements. From previous studies it was found that CB0101 could grow under a wide range of salinities (0-35 ppt) and temperatures (4-30 °C), reflecting its adaption to the strong hydrodynamics in the Bay (44). Nutrients in the Chesapeake Bay vary greatly over time and space (45). During the winter and spring, concentrations of nitrate, ammonium, and phosphate are high due to large amounts of precipitation and river runoff. These

nutrients can be used up quickly in the summer and fall when phytoplankton biomass increases dramatically (45–48), then causing seasonal nutrient limitation that suppresses excess algal and cyanobacterial growth (45, 49, 50). Cyanobacteria are heavily influenced in this environment across gradients of light, nutrients, and salinity. Considering the dynamic nature of estuarine ecosystems, *Synechococcus* species living in the Chesapeake Bay experience rapid environmental changes over a short period of time. CB0101 is often used as a phylogenetic reference for subcluster 5.2 (6, 15, 17, 42). Therefore, CB0101 represents a good model strain for studying the ecology and molecular functional capability of estuarine or subcluster 5.2 *Synechococcus*.

Cyanobacterial viruses or cyanophages can influence the abundance, diversity, and productivity of *Synechococcus spp.* in the ocean. Further, it has been predicted that 20-40% of all marine picocyanobacteria killed each day are due to viral lysis (51–53). All known marine cyanophages are tailed double-stranded DNA viruses, belonging to three well-defined bacteriophage families: *Myoviridae*, *Podoviridae*, and *Siphoviridae*. Cyanomyovirus infects a broad range of hosts, while cyanopodoviruses and cyanosiphoviruses are host specific (41, 52–54). Many viruses that infect coastal and open-ocean *Synechococcus* have been isolated from various marine environments. The isolation of subcluster 5.2 *Synechococcus* from Chesapeake Bay allows the further isolation of different viruses, which infect Chesapeake Bay *Synechococcus* (55). Unlike the widely present myoviruses (broad host range) infecting open-ocean *Synechococcus*, viruses infecting estuarine *Synechococcus* are predominantly host-specific podoviruses and siphoviruses (55). The predominance of cyanopodoviruses in the estuarine environment is evident based on the metagenomic recruitments (56). Cyanopodoviruses

are grouped into two phylogenetic clusters (MPP-A and MPP-B) and based on the DNA *pol* gene phylogeny (55, 56).

Recent studies suggest that MPP-B podoviruses are more abundant than MPP-A podoviruses (55–59), but few (12) of their genomes have been completed. Of the cyanopodovirus genomes sequenced, five were isolated using *Synechococcus* CB0101. CB0101's susceptibility to phage infection could have consequences for the cyanobacteria's ecological role due to its relative abundance and similarity to a number of other *Synechococcus spp.* found in the Chesapeake Bay. One of these podoviruses is S-CBP1, which is phylogenetically clustered in MPP-B. S-CBP1 is a podovirus with a capsid size of 52 ± 3, 48 kb genome, burst size of 86, and a fast latent period of just 6-8 h (55). Another unique characteristic of S-CBP1 is the presence of the cyanobacterial photosynthetic core gene (*psbA*), which has been a point of interest for over a decade (56, 60–62). With the available host (CB0101) and phage (S-CBP1) cultures and their respective genome sequences, we can apply transcriptomics and proteomics to study the gene regulation of both host and phage by following the infection cycle of phage.

1.3 Genomics, Transcriptomics, and Proteomics: what it all means

In recent years, genomic approaches have been used to study questions of ecological importance ranging from adaptation of organisms in changing environments to evolution of complex phenotypes (63, 64). High-throughput sequencing, lowers costs, and methodological advancements have allowed next generation sequencing (NGS) to proliferate. Consequently, omic approaches have now been used to study *Synechococcus* genetic adaptation in rapidly evolving systems and variation among populations and

species. The advent of molecular biology and DNA sequencing methodologies has greatly extended our knowledge on microbial diversity in nature.

Since the first report of a completed genome sequence of marine *Synechococcus* in 2003 (65), a considerable number of partial or complete cyanobacterial genome sequences (100 cyanobacteria, of which 35 are *Synechococcus*) are now publicly available (66). This increasing number of sequenced genomes provides new opportunities for understanding microbial diversity, genomic evolution, metabolic organization, and ecological adaptation in diverse environments. For example, genome sequences of a coastal *Synechococcus* shows greater capacity to sense and respond to environmental stresses compared to an open ocean *Synechococcus* (67). The genomes of marine *Synechococcus* range in size from 2.2 to 2.9 Mbp with 52-67 % of their genes (~1570) common to all strains (38, 40). Extensive work has been done comparing *Synechococcus* gene pigment types and associated phycobilisome structures, leading to ecotype models for adaptation to various light niches (40, 68–70). There are at least 30 genome sequences of coastal and open ocean *Synechococcus* strains in the database (39). However, only two *Synechococcus* genomes (CB0101 and CB0205) come from the estuarine environment. *Synechococcus* WH5701 comes from a mud flat, and its genome sequence has been suggested to be a contaminated sequence which contains partial genome sequences from two different strains (40). In this dissertation, I used three complementary sequencing tools to gain a better understanding of how the estuarine *Synechococcus* CB0101 adapts to its highly variable environment.

Genomics studies the entire set of genes as a dynamic system over time to determine how they interact and influence biological pathways, networks, and physiology

within an organism. There are numerous sequencing platforms (454 pyrosequencing, PacBio, Illumina Hi-Seq, Illumina Mi-Seq, and Ion torrent), each with advantages and disadvantages. In my study, the genome of CB0101 was sequenced using two types of sequencers: 454 GS-FLX and PacBio. The advantages of these sequencing methods have been compared (71). Genomics is the bedrock upon which further functional studies into the transcriptome and proteome can be built (72).

The transcriptome is the complete set of transcripts in a cell and their quantity for a specific developmental stage or physiological condition (73). Understanding the transcriptome is essential for interpreting the functional elements of the genome and revealing the molecular constituents of cells (74). The key aims of transcriptomics are: to catalogue all species of transcript, including mRNAs, non-coding RNAs, and small RNAs; to determine the transcriptional structure of genes, in terms of their start sites, 5' and 3' ends, splicing patterns and other post-transcriptional modifications; and to quantify the changing expression levels of each transcript during development and under different conditions (73). Transcriptomics of *Synechococcus* has cataloged their responses to environmentally relevant stresses (75, 76), confirm putative non-coding transcripts (77), identify adaptation responses (78), explore cyanophage-host interactions (79), and explore time-variable synchronous patterns of gene expression (80). In this dissertation, I applied RNA-Seq to explore the transcriptional response of CB0101 to various environmental stresses and phage infection.

The term proteome was first coined to describe the set of proteins encoded by the genome (81). The study of the proteome, called proteomics, now evokes not only the proteins in any given cell, but also the set of all protein isoforms and modifications, the

interaction between them, the structural description of proteins, and their higher-order complexes (72, 82, 83). Proteomics complements other functional genomic approaches, including RNA-Seq based expression profiles and systematic genetics. Integration of these datasets through bioinformatics serves as a powerful reference of protein properties and functions (72, 82). Proteome work on *Synechococcus* is not as prevalent as genomics or transcriptomics, but recent studies have identified posttranslational modifications, response to nutrient stress (84), daily rhythms of cyanobacteria (85), cell division studies (86), and *Synechococcus-Roseobacter* interactions (87).

Physiological studies of *Synechococcus spp.* are important in understanding how a strain responds to specific growth conditions. However, by themselves, such studies do not provide information on biological control and regulation at the molecular level. The integration of molecular techniques and physiological tests is a powerful approach to predict function, interaction, competition for nutrients, symbioses, and other processes that determine the overall roles of the distinct marine organisms. Towards this goal, I combined physiological data derived from 'model strain' isolates with functional responses via omics (genomic, transcriptomic, proteomic, and metabolomics analyses) to explore how *Synechococcus* regulatory networks underpin marine ecological distinctness in estuarine environments.

1.4 Scope of this dissertation

Current knowledge of *Synechococcus spp*. is largely built upon open-ocean and coastal ecosystems studies. Little effort has been made to understand the physiological and ecological traits associated with estuarine *Synechococcus*, specifically those of subcluster 5.2. Being at the precipice of anthropogenic influence and its ability to thrive

in the dynamic estuarine ecosystem, *Synechococcus* CB0101 presents a perfect opportunity to explore adaptive mechanisms of this poorly understood group. Coupled with the immense depth and vast data produced using the latest techniques in NGS, further exploration will allow for an unprecedented examination of molecular functions of estuarine picocyanobacteria. This dissertation has helped bring into focus the poorly understood *Synechococcus* subcluster 5.2 and opened the door to understanding novel molecular drivers of *Synechococcus* adaptation.

The dissertation is divided into 6 chapters, all addressing the ecological adaptation of *Synechococcus* CB0101. The term adaptation, by its general nature, encompasses a wide range of mechanisms and evolutionary processes that lead to enhanced fitness and survival of individuals. My research integrates physiology, comparative genomics, and gene expression at the mRNA and protein levels. The work will focus on the following questions: 1) Does estuarine *Synechococcus* strain CB0101 respond to environmental stresses differently compared to coastal and oceanic *Synechococcus* strains? 2) Do CB0101 gene regulatory networks underpin estuarine ecological distinctness? 3) What differences in regulatory gene and protein expression for stress responses are present for CB0101? 4) How does CB0101 respond to phage infection at the omics level?
The three major findings in my dissertation include:

1) Estuarine Synechococcus *CB0101 is highly adaptable*

When compared with coastal and open ocean *Synechococcus* (WH7803 and WH7805), estuarine *Synechococcus* CB0101 demonstrated its higher adaptability to changing environments, such as heavy metals, salinity, and temperature. Comparative genomics between CB0101, WH7803, and WH7805 also showed that CB0101 has an

increased genetic capacity to sense, respond, and adapt to variable environments compared to its coastal and oceanic counterparts (Chapter 3).

2) Toxin-antitoxin systems aid Synechococcus *in responding to variable environments*

Toxin-antitoxin (TA) systems have been found in many bacteria but not previously in marine picocyanobacteria. TAs are stress response systems that allow microbial cells to survive under harsh environmental conditions. We demonstrated that TA systems, specifically *relB/relE* in marine *Synechococcus*, respond to environmental stresses and play an active role in conferring niche adaptation. This growth modulator induces a reversible persister state to enhance fitness and competiveness. As a result, picocyanobacteria can persist during prolonged stress conditions and revive when suitable conditions arise. Further, eight other *Synechococcus* strains were found to contain TA systems, suggesting the role they play in the diversity and function of picocyanobacteria is still unknown.

3) Genomic-Island genes play a major role during phage infection

Synechococcus spp. are abundant in the marine estuarine ecosystem and subjected to frequent viral infection. What interactions occur at the molecular level during infection are not well defined. Thus, we investigated the whole transcriptome and proteome expression of the estuarine *Synechococcus* (CB0101) upon infection of podovirus S-CBP1. Strikingly, most expression occurred within genomic islands (GI), which were massively shutdown within 30 min post phage infection. Throughout the infection, phage-encoded host-like proteins (*hli, psbA, ThyX*) were highly expressed. Such a strong response in the GI system was not observed when CB0101 was exposed to nutrient or heavy metal stresses. Podovirus S-CBP1 seems to shut down the host GI system promptly

to prevent the development of host resistance, meanwhile promoting the activities of some "shared genes" between phage and host. The global shutdown of GI genes in estuarine *Synechococcus* could be an important phage-regulated process for a successful lytic infection.

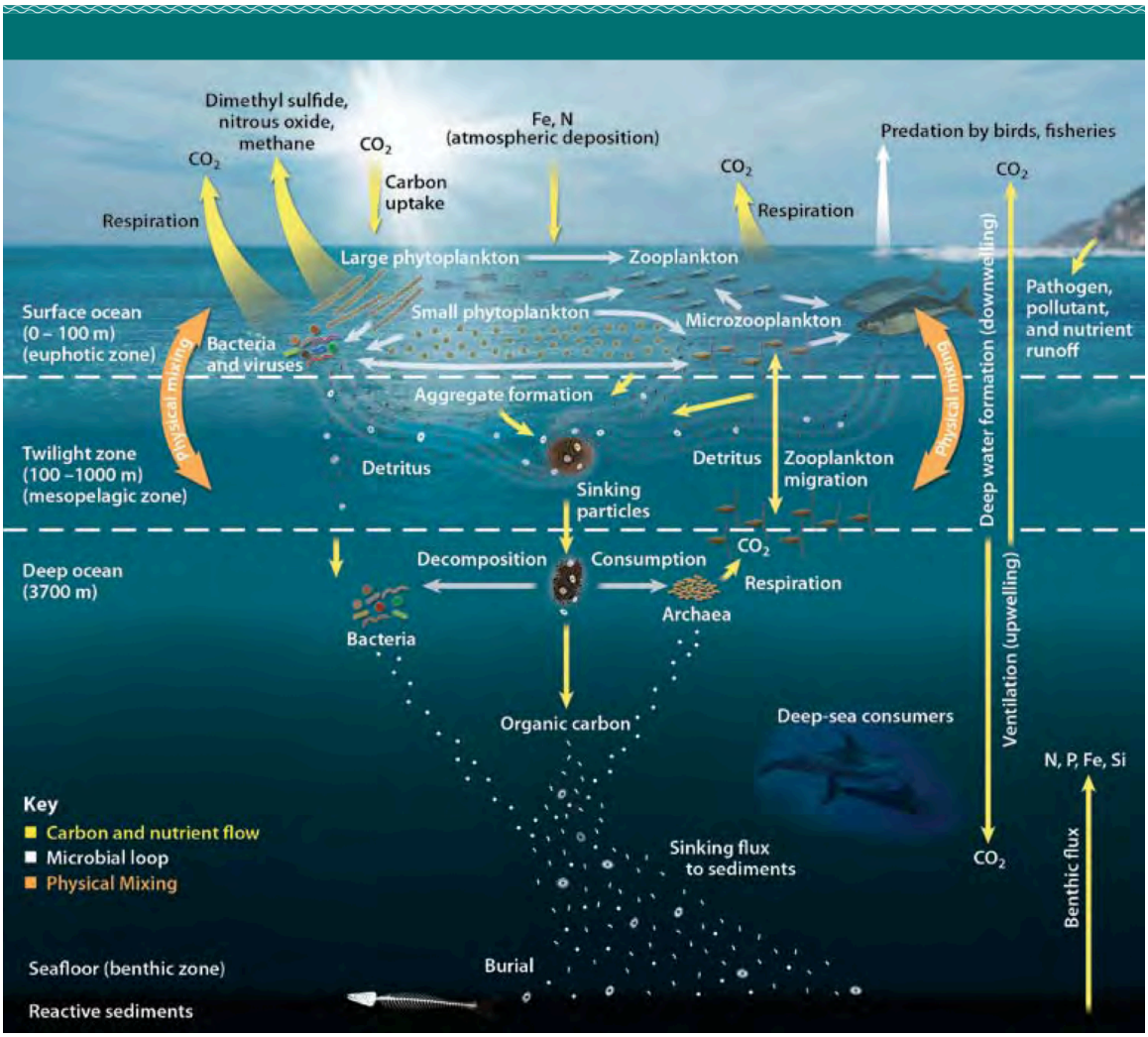

Fig. 1.1. Marine Food Web and the Carbon Cycle: Small photosynthetic organisms, including picocyanobacteria (i.e. *Synechococcus*) lie at the heart of the marine carbon cycle. Sunlit surface waters teem with picocyanobacteria that convert inorganic carbon dissolved in surface waters to organic carbon – which forms the basis of the marine food web – and accounts for about half of all primary production on earth. CO_2 fixed during photosynthesis in the upper ocean can be transferred to the depths via three major processes: passive sinking of particles, physical mixing of particulates and dissolved organic matter through currents, and active transport by zooplankton migrating to deeper

water. Climate change and ocean acidification significantly alter marine ecosystems functions, the efficiency of this biologically mediated ocean carbon export may change, leading to an effect on the net annual uptake of carbon.

Phytoplankton, such as those described above, are grazed upon by marine heterotrophs known as zooplankton. Viruses, which act as predators in oceanic food chains by infecting and lysing marine bacteria, also play an important but still poorly understood role in marine carbon turnover. The overall efficiency with which organic carbon is exported to the deep ocean depends on the type of phototrophic cells that create the organic material and the efficacy with which heterotrophic organisms respire it.

Carbon fixed in small phytoplankton (i.e. *Synechococcus*) eventually enter the water column as either particulate or dissolved organic carbon through directed exudation, consumption by grazing zooplankton, viral lysis, or cell death. Subsequently, most of this carbon material is degraded by heterotrophic bacteria, resulting in particulate solubilization and conversion of organic carbon back to CO_2. CO2 fixed during photosynthesis by small phytoplankton (i.e. *Synechococcus*) in the upper ocean can be transferred to the depths via three major processes: passive sinking of particles, physical mixing, and active transport by zooplankton. However, if climate change and ocean acidification significantly alter marine ecosystems' functions, the efficiency of this biologically mediated ocean carbon export may change, leading to an indirect effect on the net annual uptake of carbon. For full description see; (88), adapted with permission from authors and publisher.

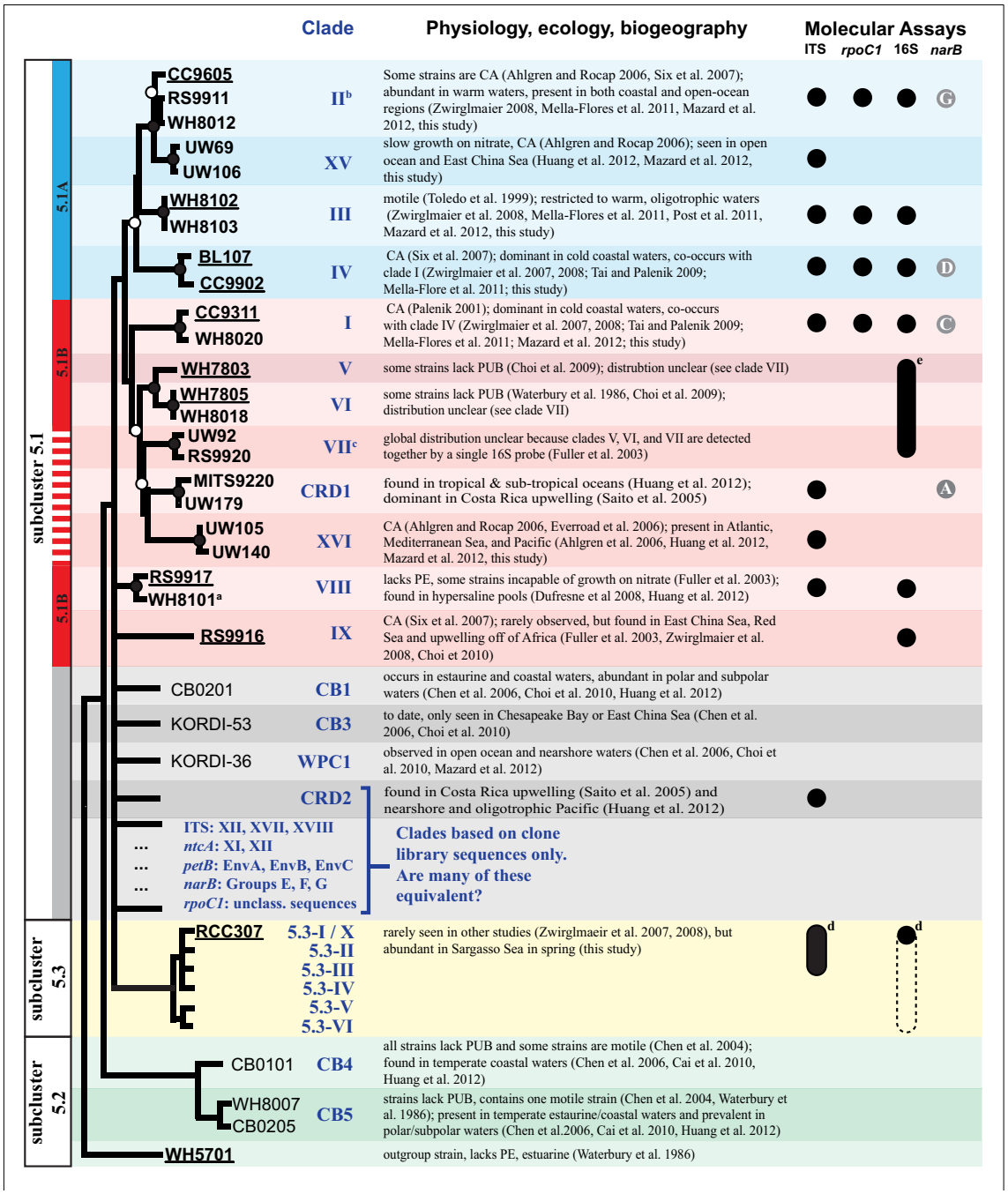

Fig. 1.2 Schematic phylogenetic tree summarizing the genetic and ecological diversity of marine *Synechococcus* and molecular assays that have been developed to measure particular clades in the oceans. The depicted tree is approximately based on a four loci concatenated tree. Examples of commonly studied strains in each clade are shown. Strains in bold were selected for multiple gene loci analysis, and strains with

sequenced genomes are underlined. Branch tips without taxa names indicated clades that are only represented by environmental sequences. Nodes with bootstrap support of >55% with circles. Polytomies indicate cases where the placement of clades is uncertain because of low bootstrap support of the absence of sequences available for multiple loci. Marine Synechococcus are classified into three subclusters 5.1, 5.2, and 5.3. Chromatic adaptation (CA) is the ability to shift the ratio of accessory pigments phycourobilin (PUB) and phycoerythrobilin (PEB) according to the spectral quality of light. Circles indicate clades for which quantitative molecular assays have been designed to measure their abundance in the environment. See original article for detailed description (17), adapted with permission from authors and publishers.

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Chapter 2: Estuarine *Synechococcus* are more tolerant to changing environments compared to coastal and open ocean *Synechococcus*

Estuarine *Synechococcus* are more tolerant to changing environments compared to coastal and open ocean *Synechococcus*

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Keywords: *Synechococcus*, stress response, estuary, comparison, subcluster 5.2

2.1 Abstract

Estuaries are among the most productive and dynamic aquatic ecosystems. Mixing of fresh and marine waters provide strong environmental gradients to the cyanobacteria living in these ecosystems. *Synechococcus* are the dominant picocyanobacteria in the estuarine environment; however, little is known about their niche adaptation in relevance to their coastal and open ocean counterparts. In this study, we compared the growth performance of representative estuarine, coastal, and oceanic *Synechococcus* strains (CB0101, WH7803, and WH7805) under different chemical and physical conditions, such as varied nutrients (nitrate, urea, ammonium, cyanate, and phosphate), metals (copper, zinc, and iron), salinity, temperature, and light intensity. We found that, estuarine *Synechococcus* CB0101 has a broader salt and temperature tolerance. In addition, CB0101 is less sensitive to metal toxicity but more sensitive to high light as compared to WH7803 and WH7805. Nitrogen and phosphate utilization was statistically the same throughout the three strains. Our results suggest that estuarine *Synechococcus* grow in a much wider range of environmental gradients compared to the coastal and open ocean strains represented by WH7803 and WH7805, respectively. This physiological comparison based on CB0101 is the first step towards predicting functions, interaction, competition for nutrients, and other processes that determine the overall roles of estuarine *Synechococcus*.

2.2 Introduction

Synechococcus are widely distributed and abundant picocyanobacteria which contribute to primary production in the surface waters of global oceans (1). Marine *Synechococcus* are phylogenetically and phenotypically diverse (2) and are divided into 3 subclusters: 5.1, 5.2 and 5.3 (3, 4). Of these, subcluster 5.1 (predominantly found in open ocean environments) represents a well-studied group of marine *Synechococcus*. Subcluster 5.1 contains many *Synechococcus* cultures isolated from coastal and open ocean, which can be divided into at least 20 clades (2). Extensive studies have been done to understand the physiology, diversity, genomics and evolution of subcluster 5.1 *Synechococcus* (2, 5–10). In contrast, our knowledge on subcluster 5.2 and 5.3 *Synechococcus* is limited (11–13).

Subcluster 5.2 strains are phycocyanin-enriched (PC-type) euryhaline strains widely distributed in coastal and estuarine waters (2, 12, 14). The establishment of subcluster 5.2 began with the isolation and characterization of many *Synechococcus* from the Chesapeake Bay (14, 11). As the largest estuarine ecosystem in the U.S., the Chesapeake Bay is known for its strong environmental gradients and being seasonally influenced. Two major clades (CB4 and CB5) within subcluster 5.2 have been identified in the Chesapeake Bay (11, 12, 15). Subcluster 5.2 *Synechococcus* dominates the upper Chesapeake Bay where the salinity is relatively low, while subcluster 5.1 becomes more abundant in the lower bay where tidal influences bring high salinity waters of the Atlantic Ocean (11, 15). The composition of subcluster 5.2 *Synechococcus* varies seasonally in the bay (16). Subcluster 5.2 *Synechococcus* are prevalent in summer, decreases in the winter,

but clade CB4 is still present even during lows of 4°C (15). Recently, the presence of subcluster 5.2 *Synechococcus* was reported in other coastal estuaries, such as East Sea (17), Gulf of Mexico, Bering Sea, Chuckhi Sea(12), and Baltic Sea(13).

Despite the wide presence of subcluster 5.2 *Synechococcus* in coastal estuaries, little is known on their environmental tolerance, particularly in comparison with coastal and open ocean *Synechococcus*. Numerous studies have been conducted to compare the growth of coastal and open ocean *Synechococcus* under different nutrient, light, temperature, and salinity conditions (6, 10, 18–22). Considering that *Synechococcus* living in estuaries need to cope with rapid changes to salinity, temperature, light intensity, nutrients, and trace elements, we hypothesize that estuarine *Synechococcus* can handle variable environmental conditions compared to coastal and oceanic *Synechococcus*.

Synechococcus strain CB0101, a well-referenced estuarine strain of subcluster 5.2, represents the most common and abundant *Synechococcus* in the upper Chesapeake Bay (2, 23). CB0101-like *Synechococcus* have been found throughout the Chesapeake Bay under a wide range of salinities (0 to 35 ppt) and temperatures (4 to 30 °C), reflecting its adaption to the hydrodynamics in the Bay (11). Nutrients in the Chesapeake Bay vary greatly over time (seasonally) and space (upper to lower Bay) (24). In the winter-spring time, concentrations of nitrate, ammonium, and phosphate are usually high due to large amounts of precipitation and river runoff. Consequently, these nutrients are used up more quickly in summer-fall seasons when phytoplankton biomass increases dramatically (24–27). The concentrations of nitrogen and phosphorus in the Chesapeake Bay, water can be low enough to seasonally limit excess algal and cyanobacterial growth (24, 28, 29). Considering the dynamic nature of estuarine ecosystems, *Synechococcus*

species living in the Chesapeake Bay experience rapid environmental changes over a short period of time, within a small spatial distance.

In order to fully understand the niche adaptation of estuarine *Synechococcus*, we propose to compare the growth performance of representative strains of estuarine, coastal, and oceanic *Synechococcus* in response to different chemical and physical settings. In this study, we compared the growth of three representative *Synechococcus* strains, CB0101 (estuarine), WH7803 (coastal), and WH7805 (open ocean), under various growth conditions, which include salinity, temperature, nutrient, light, and trace metals.

2.3 Methods

2.3.1 Growth conditions of Synechococcus *CB0101, WH7803, and WH7805*

CB0101 was cultivated in SN medium (30), with 15 ppt and vitamin B12 (10μg/L) (referred as SN15 hereafter). WH7803 and WH7805 were grown in accordance to previously published optimal conditions (A+ and SN30 media) (31, 32). In the laboratory, all cultures were grown at 23°C temperature with 15 μE m^{-2} s^{-1} continuous light. Filtered (0.2 μm pore size) air was bubbled into individual 500 mL cell culture flasks. From these main cultures, exponentially growing cells, at an optical density (OD) of 0.6, were separated into triplicate 25 mL cell culture flasks and subjected to the various conditions for at least 72 hours.

To compare the stress responses between estuarine, coastal and oceanic *Synechococcus*, estuarine strain CB0101, coastal strain WH7803, and open-ocean strain WH7805 were used in this study. WH7803 and WH7805 were selected because they have been used for extensive physiological and molecular work and are well represented

as coastal and oceanic ecotype strains (2, 4, 9, 31). The growth rates of CB0101, WH7803, and WH7805 under different concentrations and sources of nutrients and metals were compared. Cell counts were collected for each strain under a range of salinity (0-35 ppt), temperature (4-35 °C), and light intensity (15-400 μE m^{-2} s^{-1}) with their growth rates calculated (Fig. 2.2). For the nutrient test, triplicate cultures were subjected to near 0, 0, 1 nM, 1 μM, 1 mM, and 1 M of nitrate, urea, cyanate, ammonium, and phosphate, respectively (Fig. 2.3). For the metal tolerance experiment, CB0101, WH7803, and WH7805 were cultivated at near 0, 1 nM, 1 μM, 1 mM, and 1 M of zinc, copper, and iron, respectively (Fig. 2.4). Triplicate samples for every treatment were taken at each time point. The growth of cultures was monitored by counting cells using an Accuri C6 flow cytometer. The specific growth rate was calculated from the logarithmic change $\mu = \frac{lnX2 - lnX1}{t2 - t1}$ where X1 and X2 are densities at times t1 and t2.

2.4 Results

2.4.1 Growth comparison of estuarine, coastal, and open-ocean Synechococcus *in different conditions*

CB0101 was able to grow in salinities of near 0, 10, 15, 20, 25, 30, and 35 ppt, with the optimal growth at 15 ppt (Fig. 2.1A). WH7803 and WH7805 maintained high growth rates when salinity was higher than 20 ppt. However, WH7803 and WH7805 growth decreased dramatically when the salinity dropped from 20 to 10 ppt (Fig. 2.1A) and nearly ceased to grow below 10 ppt. When cultivated at 7 different temperatures (4, 10, 17, 20, 25, 30, and 35 °C), CB0101 showed optimal growth at 25 °C, while WH7803 and WH7805 reached optimal growth at 30 °C (Fig. 2.1B). All three strains were greatly inhibited when temperatures were above 35 °C or below 15 °C; however, CB0101 was

able to maintain a relatively high growth rate compared to WH7803 and WH7805. It is noteworthy that CB0101 was able to grow slowly at 4 °C (with a specific growth rate ~0.22 d^{-1}), while the growth of WH7803 and WH7805 were completely inhibited at 4 °C (Fig. 2.2B). CB0101 responded to light changes differently from WH7803 and WH7805 (Fig. 2.2C). The growth rate of CB0101 decreased with increasing light intensity (15 to 400 μE $m^{-2}s^{-1}$), but the growth rates of WH7803 and WH7805 increased with increasing light intensity. WH7805 grew slightly faster than WH7803 under the high light conditions (200-400 μE $m^{-2}s^{-1}$). In general, CB0101 grew best at lower light intensities (15-100 μE $m^{-2}s^{-1}$), while WH7803 and WH7805 grew optimally at higher light intensities (>150 μE $m^{-2}s^{-1}$) (Fig. 2.1C).

Similar growth responses for CB0101, WH7803, and WH7805 were seen under all nitrogen sources and concentrations, except for WH7803, which was unable to grow with urea (Fig. 2.3A, B, C, D). CB0101 had the highest growth rate with 1 μM - 1 mM nitrate, or 1 nM urea, cyanate, or ammonium. WH7803 and WH7805 showed a similar growth pattern with these nitrogen sources and concentrations. WH7803 was not able to grow with urea (Fig. 2.2B) as a nitrogen source but was able to utilize cyanate, while WH7805 displayed the highest growth rate at 1 nM of urea and cyanate (Fig. 2.2B and 2.3D). CB0101 outperformed WH7803 and WH7805 at 1 mM ammonium (Fig. 2.2C).

When comparing growth under different phosphate concentrations, both CB0101 and WH7803 exhibited the highest growth rate at 1mM phosphate, while WH7805 grew best at 1 μM phosphate (Fig. 2.3A). CB0101 had a lower growth rate compared to WH7803 and WH7805 with phosphate concentrations less than 1 μM. This data shows

that CB0101 does not grow well in environments with lower concentration of phosphate and prefers to grow in phosphate rich environment.

Zinc, copper, and iron are essential micronutrients for cyanobacteria, but at higher concentrations they can be toxic to *Synechococcus.* CB0101 was able to maintain high growth rates (~0.95 d^{-1}) with zinc and copper at concentrations between 1 nM and 10 mM, while the growth of WH7803 and WH7805 were inhibited when zinc and copper concentrations were higher than 1 nM (Fig. 2.3B & 2.3C). The growth of CB0101 was inhibited when zinc and copper concentrations exceeded 1 μM. CB0101 showed the highest growth rate at 1 mM iron and proliferated in a wide range of iron concentrations (1 nM to 1 M) (Fig. 2.3D). However, the growth of WH7803 and WH7805 were inhibited when iron concentrations were higher than 1 mM. Taken together, our results show that CB0101 has a wider tolerance to metal toxicity than WH7803 and WH7805.

2.5 Discussion

2.5.1 Environmental tolerance of estuarine Synechococcus

Comparative physiology tests show that estuarine *Synechococcus* CB0101 is more flexible in response to changing nutrient and trace elements compared to coastal and oceanic *Synechococcus*, represented by WH7803 and WH7805, respectively. CB0101 was originally isolated from the Chesapeake Bay (15, 33). As the largest estuarine ecosystem in the U.S., the Chesapeake Bay is well known for its strong environmental gradients and seasonality. Microorganisms living in estuaries need to cope with rapid changes to salinity, temperature, light intensity, nutrients, and trace elements. CB0101 can grow in a wide range of salinities (0 to 35 ppt) and temperatures (4 to 30 °C), reflecting its adaption to the strong hydrodynamics in the Bay. In contrast, coastal and

oceanic strains WH7803 and WH7805 failed to grow in lower salinity (<10 ppt) and temperature (<10-15 °C). It is noteworthy that CB0101 is more sensitive to higher light intensity (> 150 μE m^{-2} s^{-1}) compared to coastal and oceanic *Synechococcus* (Fig. 2.1C). The upper Chesapeake Bay is dominated by high turbidity water that causes light to be attenuated quickly(27). CB0101 outperformed WH7803 and WH7805 in higher concentrations of phosphate (>1 mM) but is less competitive in the lower end (phosphate <1nm). We did not observe a significant difference in growth among CB0101, WH7803, and WH7805 under different concentrations of nitrate and cyanate. Marine *Synechococcus* seem to share a large portion of common metabolism capabilities for nitrogen and phosphate sources (2, 9). CB0101 grew faster than WH7803 and WH7805 at 1 mM of ammonium, but the growth of all three strains was inhibited at 1 M of ammonium. Nutrients in the Chesapeake Bay vary greatly over time and space (24). In the winter-spring time, concentrations of nitrate, ammonium, and phosphate are usually high due to increased precipitation and river runoff, while these nutrients can be used up quickly in summer-fall seasons when phytoplankton biomass increases dramatically(24–27). The concentrations of nitrogen and phosphorus in the Chesapeake water can be low enough to seasonally limit excess algal and cyanobacterial growth (24, 28, 29).

It is clear that CB0101 has a higher tolerance for metal toxicity such as zinc and copper compared to WH7803 and WH7805. In estuarine environments, a sharp spike or decline in concentrations of metals can occur after a heavy rain or strong tidal movement (25, 26). Considering the dynamic nature of estuarine ecosystem, *Synechococcus* species living in the Chesapeake Bay can experience rapid environmental changes over a short period of time or within a small spatial distance. It can be hypothesized that due to the

variability of the environment CB0101 has gained genes, which would aid in adapting to such conditions.

2.6 Conclusion

Our results show that *Synechococcus* CB0101 is more adapted to grow at low light, high concentrations of nutrients and metals, and wider salinity or temperature ranges relative to WH7803 and WH7805. The results here are the first step towards understanding the ecological adaptation of estuarine *Synechococcus*. Additional studies based on genomics and functional genomics could provide more insight into specific genes or pathways that are responsive to the changing environment.

Figures:

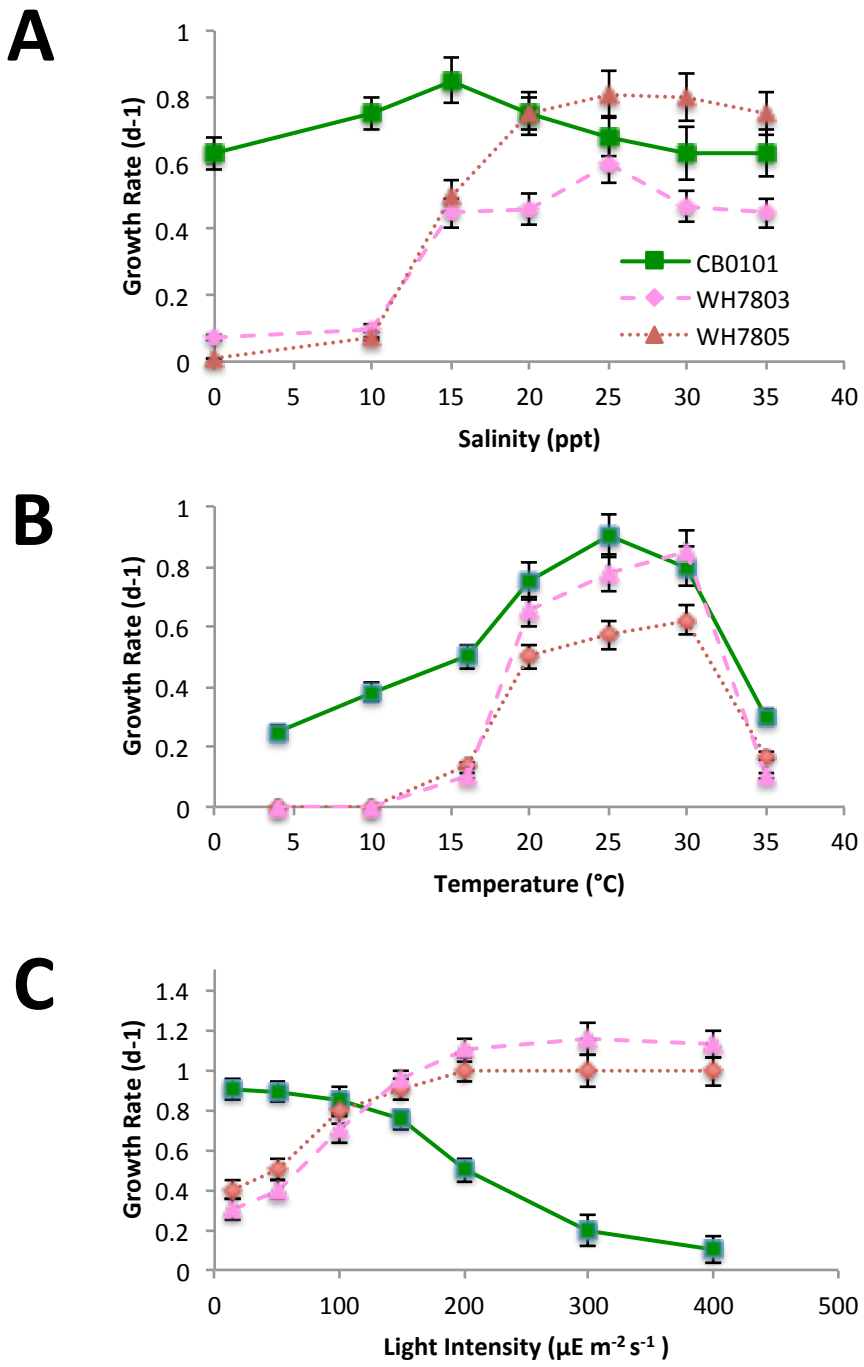

Figure 2.1. Comparison of specific growth rates between an estuarine (CB0101), coastal (WH7803), and open ocean (WH7805) *Synechococcus* under different A) salinities, B) temperatures, and C) light intensities.

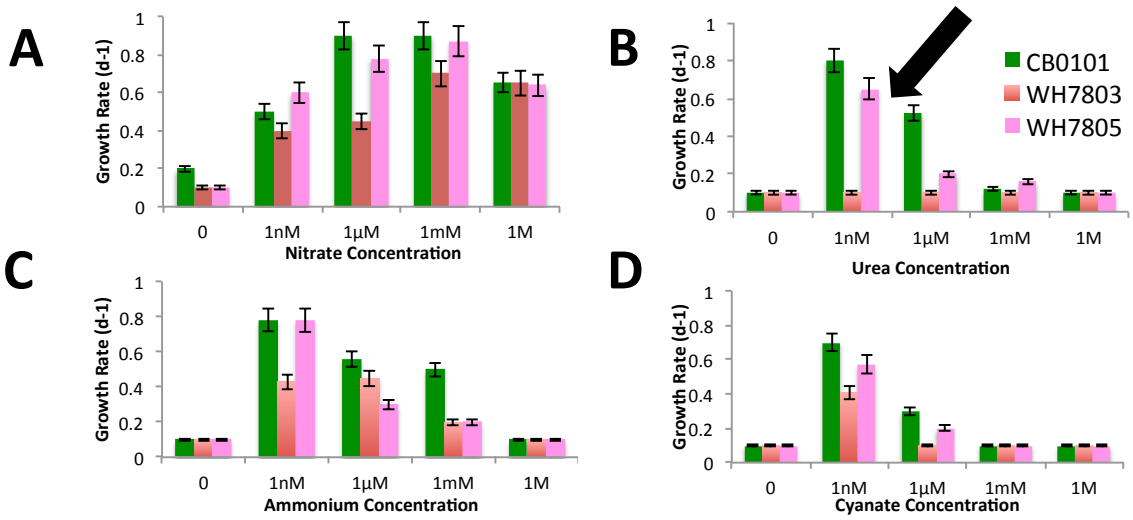

Figure 2.2. Comparison of specific growth rates between an estuarine (CB0101), coastal (WH7803), and open ocean (WH7805) *Synechococcus* under different concentrations of A) nitrate, B) urea, C) ammonium, D) and cyanate.

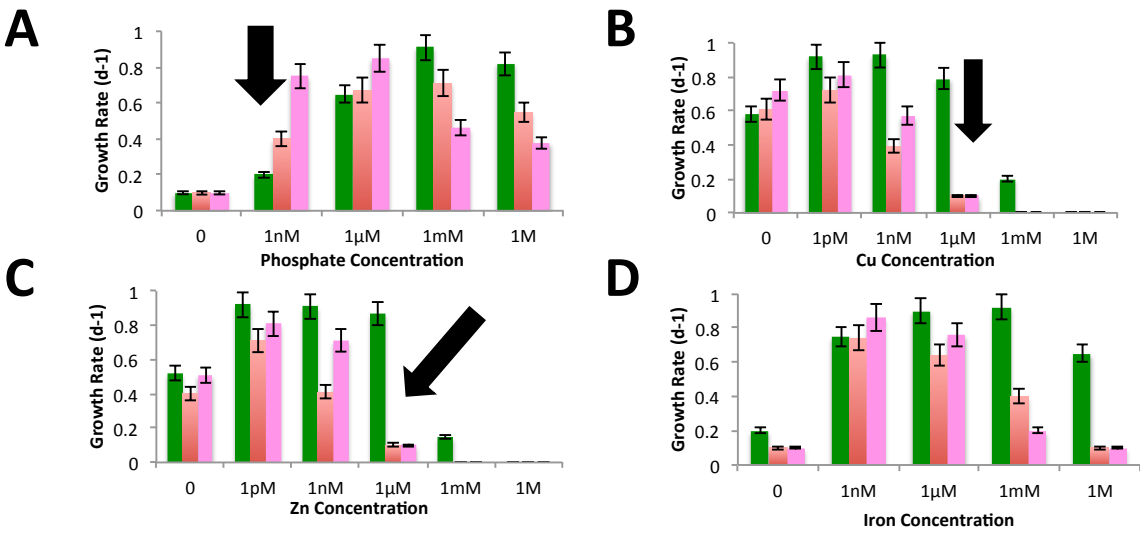

Figure 2.3. Comparison of specific growth rates between an estuarine (CB0101), coastal (WH7803), and open ocean (WH7805) *Synechococcus* under different concentrations of A) phosphate, B) zinc sulfate heptahydrate, C) copper sulfate, and D) iron.

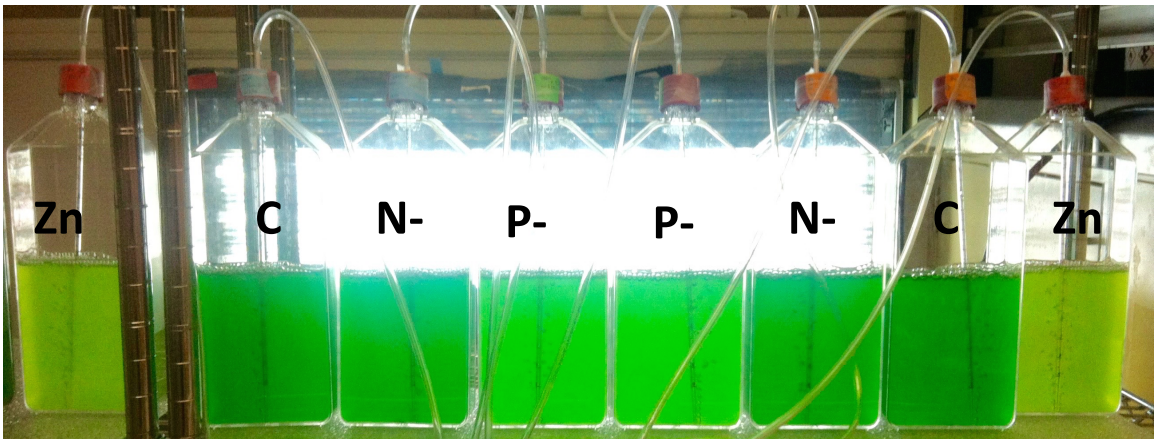

Figure 2.4. Cell culture growth apparatus for physiology experiments of *Synechococcus* CB0101. 'C' represents control, 'N-' nitrate limited, 'P-' phosphate deplete, and 'Zn' zinc toxic conditions. Cultures were grown under constant light with 15 $\mu E\ m^{-2}\ s^{-1}$ continuous light at 23°C temperature and SN15 growth medium.

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Chapter 3: Understanding the adaptive nature of estuarine *Synechococcus* using a multi-omics approach

Understanding the adaptive nature of estuarine *Synechococcus* using a multi-omics approach

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3.1 Abstract

Estuaries are among the most productive and dynamic marine environments. Estuarine *Synechococcus* are abundant and key drivers of carbon and nitrogen cycling, however little is known on how they thrive and adapt to such a dynamic system. The majority of estuarine *Synechococcus* belong to subcluster 5.2, which is poorly studied in terms of molecular mechanisms underlying their niche adaptation. *Synechococcus* CB0101, a member of subcluster 5.2, is commonly present in the Chesapeake estuary. In this study, we applied multi-omics (genomics, transcriptomics, and proteomics) analyses to investigate how CB0101 responds to selected environmental stressors. Our data shows that CB0101 seamlessly adjusts its metabolic pathways and transport systems when faced with nitrate and phosphate limitation. Oxidative stress caused by zinc toxicity resulted in down regulation of photosystems and translational machinery. CB0101 contains a suite of genes involved in toxin-antitoxin regulation (stress response), zinc excess sensors, phosphate starvation, polyphosphate utilization, and five different nitrogen metabolism pathways combined with multiple copies of transporter systems, which enables it to respond quickly to the dynamic estuarine environments.

3.2 Introduction

Cyanobacteria are an ancient and diverse group of prokaryotes found in many different habitats, which reflects their ability to adapt to variable or extreme environments (1). In the marine environment, unicellular cyanobacteria *Prochlorococcus* and *Synechococcus* are the two major prokaryotic primary producers. Compared to their sister genus *Prochlorococcus*, *Synechococcus* are more ancient and diverse in varying geographic environments ranging from estuarine, coastal and oceanic waters (2–8). *Synechococcus* can be temporally or regionally important to carbon fixation (9) and their larger cell size allows them to fix an order of magnitude more carbon than *Prochlorococcus* cells (10). Currently, marine *Synechococcus* are divided into three subclusters, 5.1, 5.2, and 5.3 (4, 6, 11–13) which include at least 20 clades (11, 14, 15). The vast majority of coastal and oceanic *Synechococcus* belong to subcluster 5.1. The adaptive potential of subcluster 5.1 *Synechococcus* to changing environments such as wavelengths of light (11, 13, 16), nitrate (NO_3^-) concentrations (11, 17, 18), and organic phosphorus sources (15, 19) is well defined.

Molecular functional analysis of subcluster 5.1 *Synechococcus* now allows for both *in situ* and *in vivo* studies providing valuable insights into their biogeochemical functions and factors controlling their distributions (8, 17, 20–22). A number of subcluster 5.1 *Synechococcus* genomes have provided insights into environmental adaptations (22–25). Specific gene differences have explained *in vivo* variations in pigment composition and nitrogen utilization (13, 24–26). In addition, strains have been shown to contain different complements of iron sensing and acquisition genes (24, 26). Transcriptomic studies of subcluster 5.1 *Synechococcus* have allowed researchers to

catalog responses to environmentally relevant stresses, confirm putative non-coding transcripts, and identify adaptation responses (22, 27–29).

Synechococcus strain CB0101, a well-referenced strain of subcluster 5.2, represents the most common and abundant *Synechococcus* in the upper Chesapeake Bay (24, 30). As the largest estuarine ecosystem in the U.S., Chesapeake Bay is well known for its strong environmental gradients and seasonality. Nutrients in the Chesapeake Bay vary greatly over time and space (31). In the winter-spring time, concentrations of nitrate, ammonium and phosphate are usually high due to high precipitation and river runoff, while these nutrients can be used up quickly in summer-fall seasons when phytoplankton biomass increases dramatically (31–34). The concentrations of nitrogen and phosphorus in the Chesapeake water can be low enough to seasonally limit excess algal and cyanobacterial growth (31, 35, 36). Considering the dynamic nature of estuarine ecosystems, *Synechococcus* species living in the Chesapeake Bay can experience rapid environmental changes over a short period of time or within a small spatial distance.

CB0101 is often used as a phylogenetic reference for subcluster 5.2 (3, 5, 37, 38), therefore, CB0101 is a good model strain for studying the ecology and molecular functional capability of estuarine or subcluster 5.2 *Synechococcus*. In this study, we applied a multi-omics approach (genomics, transcriptomics, and proteomics) to explore stress responses of the estuarine *Synechococcus* strain CB0101 under nitrate depletion, phosphate depletion, and zinc toxicity. The goal is to understand how *Synechococcus* adapt to the estuarine environment by studying their stress responses at the molecular level. Our study provides the first comprehensive analysis of molecular functions of

estuarine or subcluster 5.2 *Synechococcus* in response to different environmental conditions.

3.3 Results

3.3.1 Genome sequencing of Synechococcus *CB0101*

The complete genome sequence of CB0101 was determined using a hybrid approach combining 454 GS-FLX Titanium 8-kb paired-end and PacBio libraries. The genome sequence of CB0101 consists of 2,789,627 bp (63.4 % G+C content) with 3,176 genes and 46 tRNAs (Fig. 3.1A). Roughly 36 % (1,132 genes) of the genome can be assigned to a known functional cluster of orthologous groups (COG) while 64 % (1331 hypothetical and 710 known genes) were unable to be grouped. The assigned genes were filtered into 27 subsystem features. Those genes associated with an increased capacity to sense and respond to changes in the environment were 35 membrane transporters, 35 regulation and cell signaling, 58 stress response, 33 virulence, disease and defense and 3 dormancy.

Further, a genome comparison between CB0101 and other strains from the coastal and open ocean environments was conducted (Fig. 3.1B). Stress response related COGs were compared and found that the three strains share 36 genes while 6 were specific to CB0101. These six genes consisted of various oxidative stress sensing genes. Information gleaned from the complete genome showed an ability for CB0101 to sense and respond to environmental conditions such as nitrogen or phosphate depletion and zinc metal excess. Merely, identifying genes and pathways does little to understand the functional response of an organism. Thus, a genome wide profiling of the transcriptome and proteome expression under all three environmental stressors was conducted.

3.3.2 Transcriptomic responses of CB0101 to nutrient depletion and zinc toxicity

To understand how CB0101 adapts and responds to nutrient and metal stress at the molecular level three culture experiments were designed. CB0101was exposed to media with limited nutrients (nitrate or phosphate) or high concentrations of zinc 50 μm. We selected these conditions for two reasons 1) to obtain a strong response at the mRNA and protein level in order to clearly observe expression dynamics; 2) these conditions correspond to those found seasonally in the Chesapeake Bay, thus meaning CB0101 must be adapted to the potential stressors. The growth of CB0101 under each condition is shown in Fig. 3.S1. Without nitrate or phosphate, CB0101 grew much slower compared to the control (Fig. 3.S1where is this?). The growth inhibition of CB0101 with a lack of phosphate was more severe than that with a lack of nitrate. CB0101 growth was almost fully inhibited with 50 μM zinc in the culture medium. This experiment shows distinct growth responses of CB0101 to nutrient starvation (or stress) or metal toxicity can be seen after 2-3 days.

Transcriptional (mRNA) response of CB0101 exposed to three stress conditions for 72 h was shown in Fig. 3.2A. Transcriptional responses with nitrogen and phosphate stress displayed a similar global response of gene regulation as depicted in the heat map (Fig. 3.2A). The gene expression pattern for zinc toxicity was distinct from those of nitrogen and phosphorus limitation (Fig. 3.2A). Based on a 2-fold change of mRNA, 843 (27 %), 368 (12 %), and 1,195 (38 %) differentially expressed genes were identified from CB0101 (3,173 total genes) ($p<0.01$ and minimum 2-fold) for nitrogen, phosphate, and zinc treatments, respectively (Table 1). Based on a 4-fold change of mRNA, 108, 15, and 370 differentially expressed genes ($p<0.01$ and minimum 4 fold) were observed for

nitrogen, phosphate, and zinc treatments, respectively (Table 1). Transcript wide response of CB0101 treated with zinc greatly exceeded that of nitrogen or phosphorus depletion (Table 1).

When filtered into cluster of orthologous groups (COGs), an interesting response for each individual stressor was observed (Fig. 3.2B). Response to nitrogen depletion genes the urea cycle highly expressed. This is represented by the up-regulated COG categories of: amino acids (urea metabolism pathways), respiration and electron transport system (urea metabolism i.e. cytochrome/ferredoxin), co-factors (ATP and energy pathways), carbohydrates (TCA cycle and glycogen), nitrogen metabolism (ammonium metabolism), and stress response (protection from oxidative stress caused by using urea). In contrast, down-regulated genes involved nitrate metabolism including transporters, RNA metabolism and folate biosynthesis (gene transcript and protein fold differences for CB0101 under every experiment described in this dissertation is included in the Appendix). The major upregulated gene and protein expression included UreaABC, UreA, GlnA, and GltB.

Phosphate depletion resulted in less differentially expressed transcripts compared with the other treatments (Table 1). Of the differentially expressed genes in the phosphate treatment, the up-regulated responses consisted of pathways to extract phosphate from other molecules and sources (Fig. 3.2B). The highest represented COGs included respiration (cytochrome and electron carriers), phosphorous metabolism (ABC phosphate transporters, polyphosphate kinase, alkaline phosphatase (cleaves phosphate from other molecules i.e. nucleotides, proteins, and alkaloids), carbohydrate metabolism (pentose phosphate pathway), and nitrogen metabolism (ammonia and nitrite transporters, and

cyanate hydratase) (Fig. 3.2B). The major gene pathways included P-specific ABC transporters, PhoR, and PPX. Conversely, the down-regulated genes were dominated by RNA metabolism and protein metabolism.

Lastly, under zinc toxicity, mRNA expression at the 2-fold level displayed over 1,195 differentially expressed genes, among which 525 genes were up-regulated and another 670 were down-regulated (Table 1). Under a high concentration of zinc, the genes involved in photosynthesis, protein metabolism, carbohydrate metabolism, and respiration were down-regulated significantly (Fig. 3.2B). On the other hand, the genes responsible for cofactors/vitamin/prosthetic metabolisms, DNA, RNA, and protein metabolisms were up-regulated (Fig. 3.2B). The major upregulated genes and proteins included RND, ATPase, ZiaA, ZIP, ZnuABC, ZiaR, ZUR, COG0523 and SmtB.

3.3.3 Proteomic responses of CB0101 to nutrient depletion and zinc toxicity

At the protein level 522 total unique proteins with peptides that matched were identified over all treatments. A total of 103 and 63 differentially expressed proteins ($p<0.01$ and minimum 2-fold) were identified from CB0101 in nitrogen and phosphate treatments, respectively (Table 1). We were unable to obtain protein data from CB0101 in the zinc treatment due to potential translational inhibition caused by toxin-antitoxin. In general, proteomics detected fewer differentially expressed genes compared to transcriptomics.

The protein expression patterns of CB0101 under nitrate and phosphate depletion were displayed in the heat map (Fig. 3.3). The proteomic responses for both treatments were similar in the upper cluster, but distinct responses were seen in the lower clusters (Fig. 3.3A). CB0101 under phosphate depletion showed more protein down-regulation

compared to nitrogen depletion. These proteins participated in pathways for the metabolism of carbohydrates and amino acids, potentially to source phosphate. Cellular processes also slowed, represented by down-regulation of photosynthesis, cell division, and protein production (Fig. 3.3B). The number of down-regulated proteins was comparable for both treatments except that the respiration of CB0101 under phosphate depletion was more down regulated than that under nitrate depletion (Fig. 3.3B). However, only a fraction of all differentially expressed genes were detected by the proteomic analysis. This markedly different response between the transcriptomic and proteomic analyses could be caused by a delay in translation of protein, along with posttranslational regulation occurring. Another factor, and likely the main cause could be that the protein isoforms may be too lowly abundant to be detected, unlike the greater sequencing depth of the RNA-Seq work.

3.4 Discussion

3.4.1 Stress handling capability unveiled by comparative genomics

The genomic sequence of CB0101 represents the first complete genome for subcluster 5.2 *Synechococcus*. Based on the specific genes and gene clusters carried by CB0101, we hypothesized that CB0101 had an increased genetic capacity to sense and respond to changes in the estuarine environment. To test that hypothesis, we compared CB0101's genome content to that of two other well-understood coastal and oceanic *Synechococcus* strains (WH7803 and WH7805). It is not the intention of this study to conduct a comprehensive comparative genomics between all known *Synechococcus* genomes (see (24, 25) for comparative genomics of marine *Synechococcus*). These previous studies identified specific genome structures of *Synechococcus*, which included

core and variable gene content. Our work focuses on identifying ecologically significant genes in estuarine *Synechococcus* to understand how they respond to environmental stressors.

Insights from the comparative genomics (CB0101, WH7803 and WH7805) reveal nutrient adaptability and a metal-intensive ecological strategy, as indicated by the many more genes involved in metal homeostasis as well as metal enzymes, sensor kinases and various metabolic pathways for nitrogen, phosphate, and amino acid metabolism that were not present in oligotrophic strains WH7803 and WH7805. Unique genes within CB0101 (as compared to WH7803 and WH7805) were predominately found within the functional categories of amino acids and derivatives, stress response, membrane transport, virulence/defense, and regulation/cell signaling. A number of heavy metal ABC transporters (Ni, Co, Cu, Zn, Fe) and high affinity branched chain amino acid transport systems are present. CB0101 contains unique *phoH*, alkaline phosphatase, and an additional ammonium transporter not seen in the other strains. The *phoH* gene is from the phosphate starvation inducible family of proteins that responds under phosphate limited conditions and is thought to have a function in regulating the cellular response to phosphate limitation (21, 26). Alkaline phosphatase is used to obtain phosphate from other organic sources (23). The additional ammonium transporter (*amt*) likely allows for greater scavenging uptake of ammonium (39). These genes were up regulated in CB0101 and might play a key role during nitrate and phosphate deplete conditions (Fig. 3.2). Interestingly, CB0101 contains 15 toxin-antitoxin (TA) genes, was found to be associated with stress response; specifically the *relE/relB* pair regulates oxidative stress by arresting

translation (Chapter 4). This is likely one of many mechanisms that CB0101 has developed to adapt to the estuarine environment.

CB0101, WH7803, and WH7805 differ in aspects of their membrane transporter complement that may reflect alterations in the nutrients they are exposed to in different ecosystems. Interestingly, CB0101 has a unique set of 7 ABC transporters for branched chain-amino acid transport, arguably for metabolism of organic nutrients, but determining the actual activity will require future nutrient uptake studies. Unique to CB0101 metal enzymes, cofactors, and metal transporters suggests a greater capacity to store, move, and utilize metals. This is consistent with higher metal quotas for copper and zinc. Interestingly, it has been shown that *Synechococcus* WH8016, which contains similar transporters was more resistant to copper than oligotrophic strains(40).

Fifty-eight stress response genes were identified in CB0101, with COG systems of heat shock, oxidative stress, and detoxification being most numerous. Of these 58 genes, 8 were unique to CB0101 when compared to WH7803 and WH7805. Thirty-four genes are involved in virulence defense including resistance to antibiotics and toxic compounds, and 6 of them are related to Co-Zn-Cd resistance. Within stress response type genes CB0101 contains a unique set of 5 oxidative stress genes, but lacks 5 other oxidative stress genes contained in WH7803 and WH7805 (Table S2). Interestingly, CB0101 has manganese and iron superoxide dismutases (SOD), while WH7803 and WH7805 contain copper and zinc SOD. Cu and Zn-SOD have been found in many marine *Synechococcus*, but many freshwater and estuarine cyanobacteria have only Fe or Mn SOD. Marine *Prochlorococcus* possess only Ni-SOD (41). CB0101 does not contain 6 osmotic stress genes found in WH7803 and WH7805, suggesting that estuarine

Synechococcus may not suffer similar osmotic stress like their coastal and oceanic counterparts.

3.4.2 Responses of CB0101 to stresses at the omics level

CB0101 was inhibited the most with zinc toxicity, moderately with phosphate depletion, and the least with nitrogen depletion (Fig. 3.S1). The genetic capacities of CB0101 led us to hypothesize a greater ability to cope with metal stresses and nitrogen and phosphate. We now wanted to understand how CB0101 regulates its transcript and protein expression in response to these stresses.

When cells were grown with a depleted nitrogen-source, CB0101 adjusts metabolism pathways to the available N-source. Transcript and protein levels for genes associated with urea metabolism, urea transporters, cytochrome/ferredoxin, TCA cycle, glycogen, ammonium metabolism, and stress response protection from oxidative stress caused by metabolizing urea were all highly expressed. These pathways worked to transport urea in order to metabolize it to ammonium, then to Gln and Glu (Fig. 3.4). Using urea has the ill effect of oxidative stress, which causes stress response pathways to become active. At the same time nitrate metabolism pathways including transporters, RNA metabolism and folate biosynthesis were downregulated. These responses were in line with previous work showing that most cyanobacteria can use nitrate, nitrite, and ammonia as primary N-sources, although urea and organic N-compounds can also be used in some cases (42). CB0101 is capable of using all of those N sources, and when nitrate is removed from the medium it adjusts accordingly to scavenge urea (Fig. 3.4).

When starved of phosphorus, CB0101 cells significantly increased phosphate scavenging with a 3-fold increase of numerous ABC phosphate transport. Furthermore,

periplasmic alkaline phosphatases, for example *phoA*, release phosphate from various compounds, making it available for the transport systems. These enzymes may provide the ability to scavenge phosphate from a large variety of substrates, as suggested by its in vitro activity. Sensor kinase and response regulators comprising a two-component signal transduction pathway governs the response to phosphorus limitation. Transcripts of phosphate regulon (Pho regulon), three clusters of genes exhibited substantial induction upon phosphate starvation. One such cluster contains a periplasmic protein, *urtA,* which was highly repressed under phosphate-limited conditions (Fig. 3.4).

Strong transcriptional responses were evident when CB0101 was exposed to zinc. CB0101 contains numerous zinc related genes to cope with zinc toxicity or homeostasis, which are absent in WH7803 and WH7805. Some of these genes, which are upregulated during toxic conditions are *ZIP* (zinc transporter family protein), *ZnuB* (ABC transporter inner membrane), *ZnuC* (ABC transporter ATP-bind protein), *ZnuA* (two copies, ABC transporter periplasmic-binding protein), COG0523 (zinc homeostatsis GTPase family), *ZUR* (zinc uptake regulation protein), zinc finger SWIM domain, ATP-dependent zinc metalloprotease, and *czc* system (mediates low-level metal ion resistance). These genes in combination are thought to aid cyanobacteria in coping with metal induced stress and were all upregulated at the mRNA and protein level (Fig. 3.4).

In order to deal with excess zinc, *Synechocystis* sp. PCC6802 has a zinc specific efflux pump, *ZiaA* (43), which is similar to other P1-type ATPase metal ion transporters responsible for transporting Zn^{2+} from the cytoplasm to the periplasmic space. Expression of *ZiaA* is induced by zinc and is regulated by *ZiaR* (43), a zinc-specific repressor protein. CB0101 contains similar zinc efflux pumps, which are upregulated during zinc

toxicity (Fig. 3.4). Genes for zinc excess sensors, *smtB* and *ziaA*, found in CB0101 are absent in WH7803 and WH7805, both of which are upregulated. The *smt* locus of CB0101 contains a metal-regulated gene (*smtA*), which encodes a class II metallothionein, and a divergently transcribed gene, *smtB*, which encodes a repressor of *smtA* transcription (44). Together with at least one ZnuABC system and a putative ZIP transporter for uptake, as well as at least one zinc-related CO0523 protein, this strain utilizes the suite of genes to cope well with both zinc excess and scarcity. It has been suggested that metallothioneins in *Synechococcus* may be under the control of Zur, which is in line with the response of CB0101 in our experiments. It suggests that, metallothioneins are not just devices to combat metal toxicity, but may play a more central role in essential zinc homeostasis (Fig. 3.4). By integrating multi-omics molecular techniques to predict functions (i.e. response to nutrient depletion or metal toxicity) with ecological data derived from 'model strain' isolates we now have a better understanding of the distinct responses of CB0101 to the Chesapeake Bay environment. We believe similar mechanisms are at play with other estuarine subcluster 5.2 *Synechococcus* strains.

3.5 Conclusion

The adaptive nature of estuarine *Synechococcus* is reflected by additional stress responding genes in CB0101 and the expression of these genes and proteins. The omics studies highlighted the flexibility of different nitrogen metabolism sources, with CB0101 seamlessly switching from nitrate to urea. While under phosphate limiting conditions upregulation of additional transporters and breakdown of polyphosphate were confirmed at the mRNA and protein level. Finally, zinc toxicity caused almost total shutdown of mRNA and protein expression, however genes associated with zinc sensing and

transporters were active. The combination of multi-omics analyses provides a deeper understanding on the niche adaptation of *Synechococcus* in the estuarine environment. Omics studies based on other environmental settings or other members of subcluster 5.2 *Synechococcus* can be developed in the future to explore broader environmental responses of estuarine picocyanobacteria.

3.6 Experimental Procedures

3.6.1 Culture conditions for growth of CB0101

For the multi-omics experiments, CB0101 was cultivated in SN medium with 15 ppt salinity and vitamin B12 (10 μg/L) (referred to as SN15 medium hereafter), and duplicate cultures were subjected to 4 different conditions for 72 h: (1) Control, where the culture was grown in SN15 medium; (2) Nitrogen-deplete condition, where the culture was cultivated in the SN15 medium that did not contain sodium nitrate; (3) Phosphate-deplete condition, where the culture was grown in the SN15 medium that lacked dipotassium phosphate; (4) Zinc toxic condition, where the culture was grown in the SN15 medium amended with 50 μM of zinc sulfate heptahydrate. Triplicate samples for every treatment were taken at each time point. The growth of cultures was monitored by counting cells using an Accuri C6 flow cytometer. Samples for mRNA and protein analysis were immediately extracted at 0 h and after 72 h. The specific growth rate was calculated from the logarithmic change $\mu = \frac{\ln X2 - \ln X1}{t2 - t1}$ where X1 and X2 are densities at times t1 and t2.

3.6.2 Genome sequencing of CB0101

The partial genome of CB0101 was previously described and sequenced using 454 (45). To span difficult repeat regions, we obtained long Pacific Biosciences sequences. Cells were collected by centrifugation (10,000 x g, 10 min), the pellet transferred into a 2 ml tube and immediately processed. We obtained DNA from 25 ml cultures using the Epicentre Masterpure kit (Epicentre) and sequenced the genome at the Institute of Genome Sciences (IGS). Total reads resulted in 121,716 with an average read

length of 6,295 bp, resulting in ~40X coverage. Low quality regions of sequencing data were removed from the raw PacBio data using the HGAP assembly program. Contigs were ordered into putative scaffolds based on their similarity to closely related closed *Synechococcus* genomes, as determined by Mauve (46). As the cultures sequenced were known to contain heterotrophs, we identified the most '*Synechococcus*-like' contigs from non-axenic cultures by searching each resulting contig against a custom database of sequenced marine microbial genomes using BLAST (47). Contigs with a best match to a non-*Synechococcus* genome were removed from the assembly.

3.6.3 Genome annotation and comparisons

The assembled complete genome for CB0101 was annotated using the RAST server (48) and MANATEE (49) programs. Subsequently, the annotations of each were compared and any discrepancies were manually explored and assigned. Clusters of orthologous groups of proteins (COGs) were computed, as described in each program. To facilitate comparisons among other picocyanobacteria genomes, we re-annotated *Synechococcus* WH7803 and WH7805 with the RAST and MANATEE pipelines as described above; this ensured that a uniform methodology for gene calling and functional annotation was used. For genome analysis, a combination of three gene modeling programs- CLC, Manatee, and RAST were used in the determination of potential coding sequences. These assignments were further checked manually. A revised gene/protein set was searched against the KEGG genes, Pfam, PROSITE, PRINTS, ProDom and COGs databases, in addition to BLASTP against the NCBI non-redundant database. From these results, categorizations were developed using the KEGG and COGs hierarchies. Transfer

RNAs were identified using CLC. To identify regions of atypical nucleotide composition, the trinucleotide composition was determined.

3.6.4 Extraction of mRNA

At the designated time points (0 and 72 h post media change) samples were collected and immediately processed for mRNA and protein analysis. RNA and protein were separated using Trizol extraction. mRNA was extracted from the total RNA using Ambion MICROBExpress kit (Life technologies, AM1905), modified with 4 specific oligo primers for rRNA depletion of CB0101 ribosome. rRNA removal evaluation was conducted using the Agilent 2100 Bioanalyzer resulting in 98 % removal of rRNA and confirmed the presence of high quality mRNA. The NEXTflex RNA-Seq kit (BIOO Scientific, #5129-01) was then used to prepare mRNA libraries for sequencing using the Illumina Hi-Seq. RNA libraries were created and barcodes assigned to each sample for multiplexing of a single Hi-Seq lane. Using a Hi-Seq with 100 bp read length, RNA-Seq sequencing was carried out by the IGS and resulted in 144,403,530 read sequences. RNA-Seq analyses were carried out using the CLC platform R, Bioconductor, top-hat/cufflinks (Table S1).

3.6.5 Protein extraction and mass spectrometry analysis

Proteins were extracted using the same sample for RNA extraction. The bottom layer containing proteins was transferred to a new tube and the extraction procedure followed the extraction procedure previous described (50). Protein quantification was carried out according to the instruction of 2D Quant kit (GE Healthcare, 80-6482-56). Equivalents of proteins (200 μg) in each sample were loaded on a prepared SDS-PAGE (manufactory) for in gel digestion (51). The tryptic peptides were extracted with solvent

containing 50% acetonitrile (ACN) and 0.1% trifluoroacetic acid, and then vacuum dried using a SpeedVac for further mass spectrometry (MS) analysis.

Samples were introduced into a Waters nanoACQUITY UPLC using a C18 trap column (1.7 μm particle size, 100 μm x 100 mm internal diameter) fitted with a C18 trap column. (5 μm particle size, 180 μm x 20 mm internal diameter). Peptides were eluted at a flow rate of 300 nl/min using an acidified (formic acid, 0.1 % v/v) water-acetonitrile gradient (2 %-35 % acetonitrile in 135 min, full-time 185 min). The peptides were subjected to nanoelectrospray ionization followed by tandem mass spectrometry (MS/MS) in a Q EXACTIVE (ThermoFisher Scientific, San Jose, CA) coupled online to the UPLC. Data-dependent scans were conducted by precursor ion selection in the Orbitrap followed by high-energy collision induced dissociation. One full m/z scan between 350 and 2,000 Da was followed by 15 MS/MS scans with a following Dynamic Exclusion duration of 15 s. The electrospray voltage applied was 1.6 kV and the heated capillary was at 280 ˚C. Automatic gain control (AGC) was used to optimize the spectra generated by the Orbitrap.

3.6.6 Protein identification

The instrument data files (.raw) were interpreted using Proteome Discoverer (ver. 1.4.0.288; ThermoFisher Scientific, San Jose, CA). MS/MS spectra were searched with SEQUEST engine against a protein database containing 15,527 translated protein-coding sequences predicted from genome of *Synechococcus* CB0101 and its phage genome as well as 6,774 contaminated bacterial sequences and 247 contaminant sequences such as keratin and trypsin. Database searching was restricted to tryptic peptides. For protein identification, a mass tolerance of 10 ppm was permitted for intact peptide masses and

0.05 Da for fragmented ions, with allowance for one missed cleavages in the trypsin digests and carbamidomethyl (C) as the fixed modification, oxidation (M) as the variable modification. Peptides having a Delta Cn better or equal to 0.05 were used for Percolator. Peptide spectral matches were further validated based on q-value of decoy database search at a level of 1% false discovery rate (FDR). Peptide identifications were grouped into proteins with Proteome Discoverer according to the law of parsimony and filtered to 1% FDR. Finally, proteins matched with at least two peptides were accepted as confident identifications for further bioinformatics analysis.

3.6.7 Functional annotation and semi-quantitative analysis

Functional annotations of proteins identified were derived from their annotations of RNA or DNA sequences. For semi-quantitative analysis(52), spectral counts were normalized by the total number of spectra identified in each sample as well as by the length of the matching protein. The resulting values were used for statistical significance test and represented as protein expression level.

Table 3.1. Differentially expressed (A) 2 fold p<0.01 and (B) 4 fold p<0.01 transcripts and proteins for three stress conditions, nitrogen and phosphate limited and zinc toxicity of the estuarine *Synechococcus* CB0101 (N/A= no data available). Differential expression was determined as each condition compared to the control expression. Percentages are based on the total number of coding genes found in *Synechococcus* CB0101 (3,173).

A

	Transcriptomics			Proteomics		
2 Fold change (p<0.01)	Nitrogen	Phosphate	Zinc	Nitrogen	Phosphate	Zinc
Total responsive genes/proteins	843 (27%)	368 (12%)	1195 (38%)	103 (3%)	63 (2%)	N/A
Total up-regulated genes/proteins	400	222	525	64	23	N/A
Total down-regulated genes/proteins	443	146	670	39	40	N/A

B

	Transcriptomics			Proteomics		
4 Fold change (p<0.01)	Nitrogen	Phosphate	Zinc	Nitrogen	Phosphate	Zinc
Total responsive genes/proteins	108	15	370	19	12	N/A
Total up-regulated genes/proteins	41	10	43	16	4	N/A
Total down-regulated genes/proteins	67	5	327	3	8	N/A

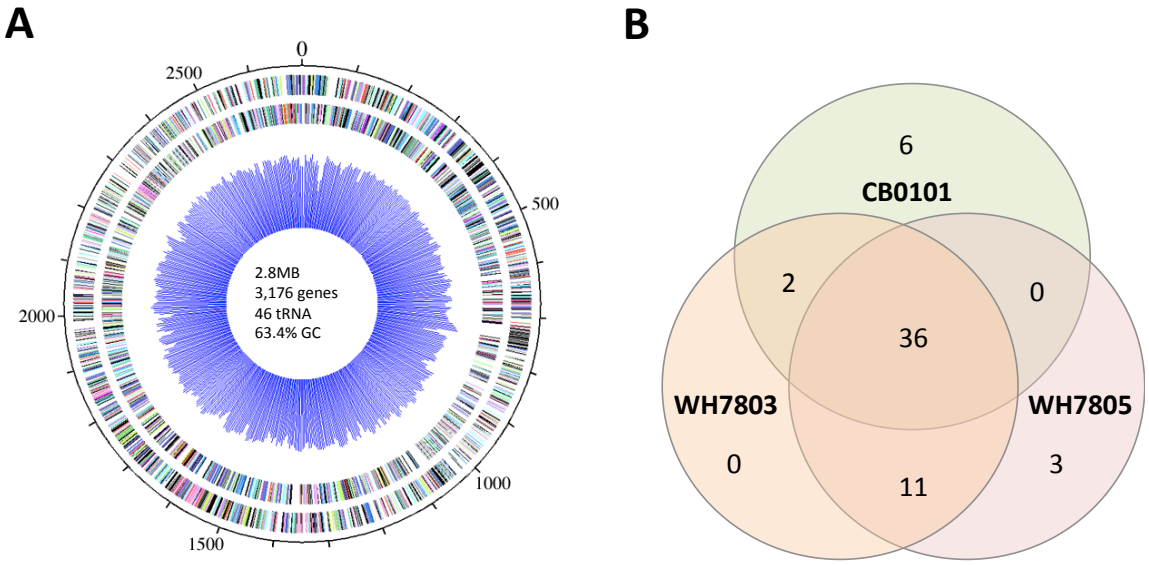

Figure 3.1. Genomic characteristics of estuarine *Synechococcus* CB0101. A) Circular representation of *Synechococcus* sp. CB0101 complete genome structure. Genome stats are: 2.8MB, 3,176 coding genes, 46tRNA, and a GC content of 63.4%. The outer scale designates coordinated in base pairs. The first circle shows predicted coding regions on the plus strand, color-coded by role categories. The second circle shows predicted coding regions on the minus strand color coded by role categories. The inner circle represents coverage of the genome, which averaged 40x. B) COG comparison between estuarine (CB0101), coastal (WH7803), and open ocean (WH7805) *Synechococcus* genomes. Gene categories related to stress response, sensing, transport, storage and export were compared. COG categories were determined using the RAST server.

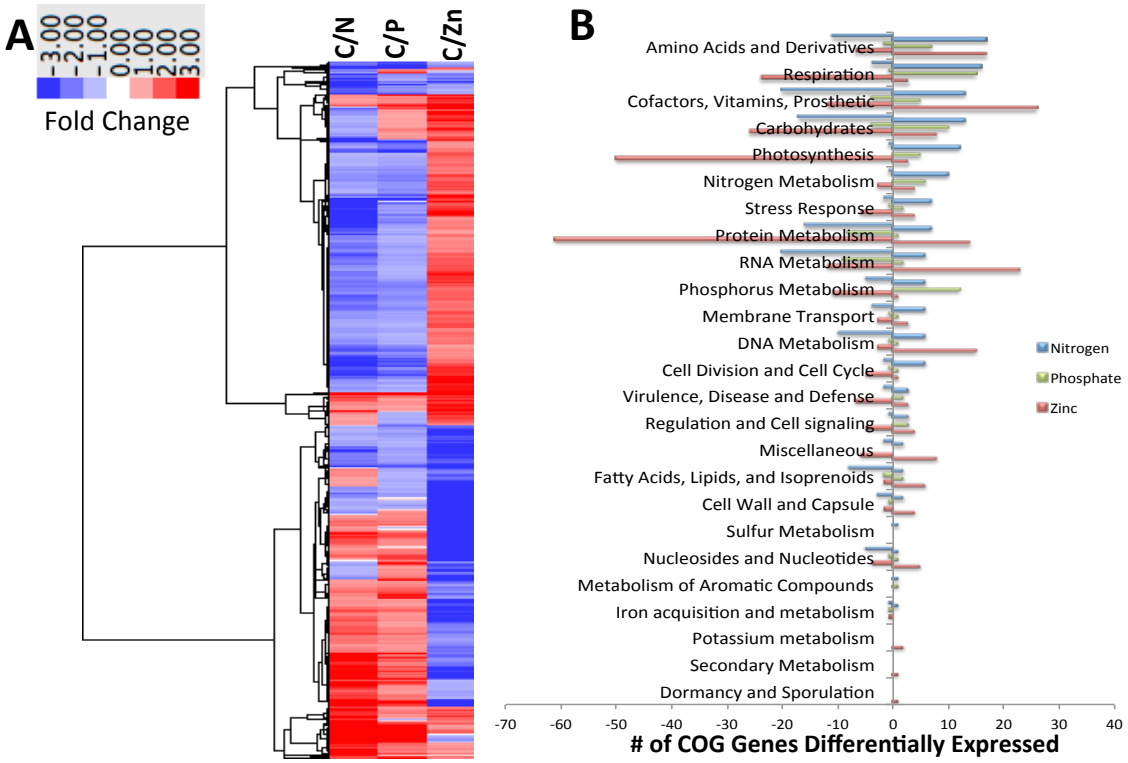

Figure 3.2. The transcript expression program to stress responses in the estuarine *Synechococcus* CB0101. A) Heat map and clustering of differentially expressed genes by their expression patterns. Stress conditions are all compared to Control, with C/N representing nitrogen depletion, C/P phosphate depletion, and C/Zn zinc toxicity. Dark red equates to a strong increase (>3 fold), while dark blue to a strong decrease (>3 fold) in gene expression. (B) Differentially expressed genes filtered into COGs for each of the three stress conditions. The left hand side denotes the number of downregulated genes differentially expressed while the right is the number of upregulated genes.

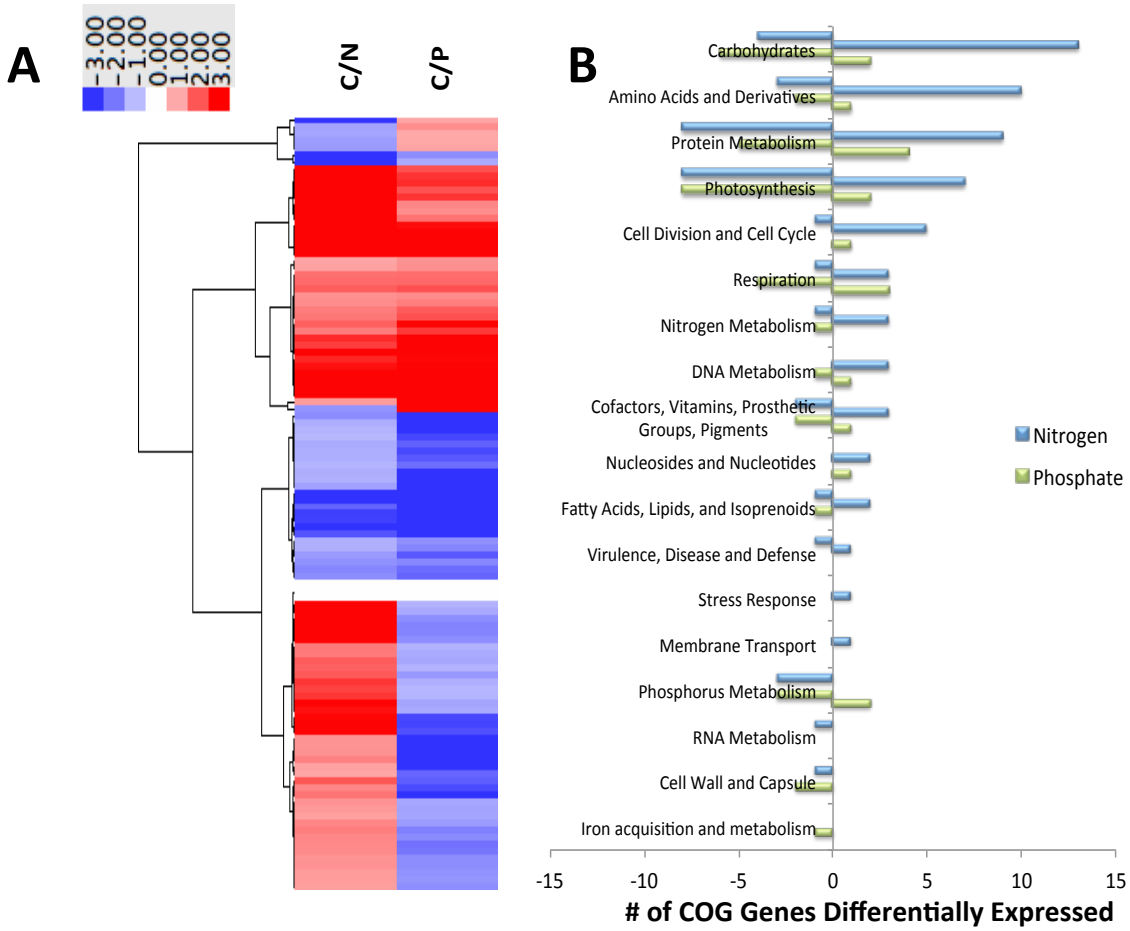

Figure 3.3. The protein expression program to stress responses in the estuarine *Synechococcus* CB0101. A) Heat map and clustering of differentially expressed proteins by their expression patterns. Stress conditions are all compared to Control, with C/N representing nitrogen depletion, C/P phosphate depletion. Protein was unable to be analyzed from the Zinc samples. Dark red equates to a strong increase (>3 fold), while dark blue to a strong decrease (>3 fold) in gene expression. (B) Differentially expressed genes filtered into COGs for each of the stress conditions. The left hand side denotes the number of downregulated genes differentially expressed while the right is the number of upregulated genes.

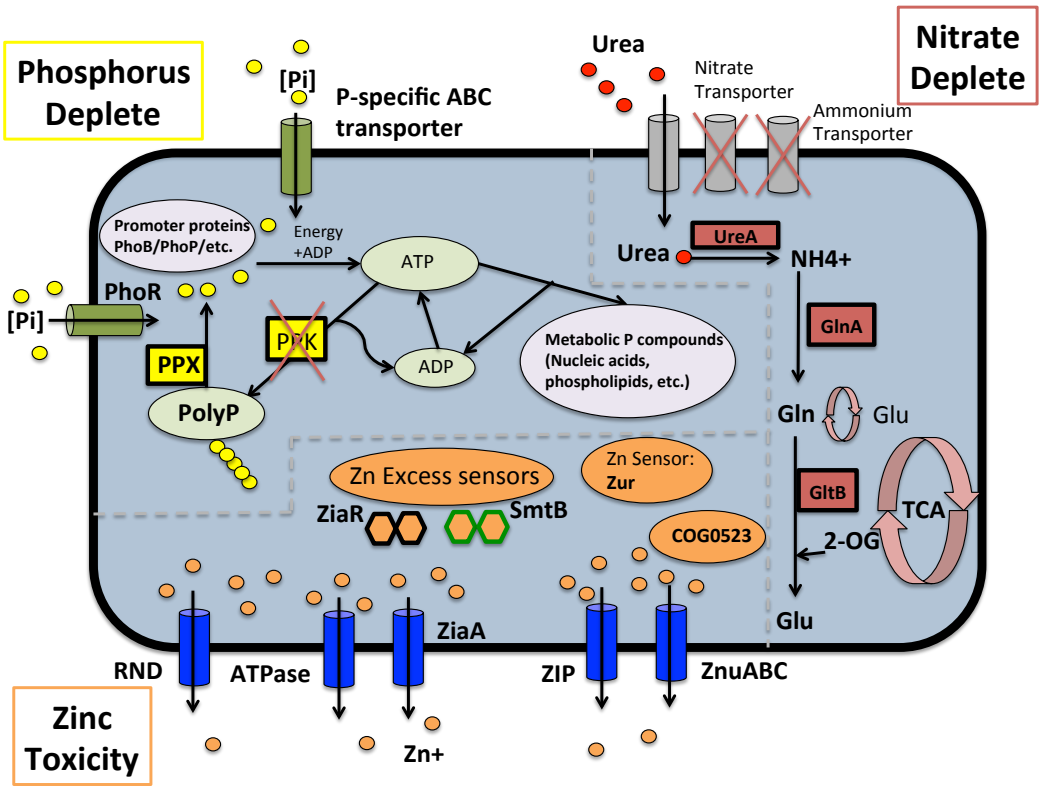

Figure 3.4. Molecular mechanisms of nitrogen or phosphate deplete and zinc toxic conditions of the estuarine *Synechococcus* CB0101. This diagram represents a composite of upregulated mRNA and protein (shown in bold text) and down regulated (red X) pathways. Black arrows indicate pathways by which each condition transported or metabolized the nutrient. Cylinders indicate transporter protein complexes, circles – specific nutrient pools, squares- protein or enzymes seen being differentially expressed, oval- promoters or sensors differentially expressed. Nitrogen depletion conditions causes nitrate and ammonium transporters to be down regulated which ureaABC transporters were upregulated. CB0101 transports urea into the cell, which is then metabolized to ammonium, by *ureA*. The pathway continues with GlnA+NH^{4+} producing Gln. The TCA cycle is upregulated and 2-OG along with Gln is used to produce Glu, all of which is

aided by GltB. Under phosphate deplete conditions, upregulation of P-specific ABC transporters and PhoR scavenge for any available phosphate. PPX is highly expressed, resulting in the metabolism of PolyP to create [Pi] in order to produce other metabolic P compounds (Nucleic acids, phospholipids). Zinc toxicity is dominated by efflux transporters (RND, ATPase, ZiaA, ZIP, ZnuABC), which are controlled by various zinc excess sensors (ZiaR, SmtB, Zur, and COG0523).

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Chapter 4: Surviving in a highly variable environment - the novel toxin-antitoxin systems in the estuarine *Synechococcus* strain CB0101

Surviving in a highly variable environment - the novel toxin-antitoxin systems in the estuarine *Synechococcus* strain CB0101

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Keywords: *Synechococcus*, Toxin-Antitoxin system, persister cell, stress response, *relB/relE*

Significance Statement

Toxin-antitoxin (TA) systems have been found in many bacteria, but not in marine picocyanobacteria. TAs are stress response systems that allow microbial cells to survive under harsh environmental conditions. We demonstrated that TA systems, especially *relB/relE* in marine *Synechococcus* respond to environmental stresses, and play an active role in conferring niche adaptation. This growth modulator induces a reversible persister state to enhance fitness and competiveness. As a result, picocyanobacteria can persist during long periods of time under stress conditions and revive when suitable conditions arise. Further, eight other *Synechococcus* strains were found to contain TA systems, suggesting the role they play in the diversity and function of picocyanobacteria is still unknown.

4.1 Abstract

Bacterial toxin-antitoxin (TA) systems are genetic elements composed of a toxin gene and its cognate antitoxin, with the ability to regulate growth. TA systems have not previously been reported in marine *Synechococcus* or *Prochlorococcus*. Here we report the finding of seven TA system pairs (Type II) in the estuarine *Synechococcus* CB0101, and their response to five different stressors; nitrogen and phosphate starvation, phage infection zinc toxicity, and photo-oxidative stress. Database searches discovered that 8 other marine *Synechococcus* strains also contain at least one TA pair but none in *Prochlorococcus*. We demonstrated that the *relB/relE* TA pair was active and arrested translation through RNA degradation when CB0101 was under oxidative stress caused by either zinc toxicity or high light intensities, but the arrest was reversible when the stress event was removed. We propose that having TA systems such as *relB/relE* allows for niche adaptation to the low light environments of the Chesapeake Bay enabling *Synechococcus* like CB0101 to thrive. Consequently, other picocyanobacteria should be able to utilize their TA systems to cope with rapidly changing environments (e.g. nutrient or oxidative stress) by regulating cell growth, thus conferring niche adaptation and enhancing fitness.

4.2 Introduction

Cyanobacteria are an ancient and diverse group of prokaryotes found in habitats worldwide, which reflects their considerable ability to adapt to variable and extreme environmental factors such as nutrient availability, light intensity, and metal toxicity [1]. Estuaries, which are among the most productive yet variable aquatic environments on Earth, are one such habitat. Mixing of fresh and marine waters provides strong environmental gradients to the cyanobacteria living in these ecosystems. Estuarine cyanobacteria (e.g. *Synechococcus*) contribute significantly to global primary production and are at the interface of direct anthropogenic affects [2–4]. In estuaries, the bioavailability of nutrients (e.g. N and P), light intensity, and trace metals (e.g. Fe and Zn) are highly variable. Due to the complex geochemistry of these compounds and physical dynamics, understanding cyanobacterial response to the estuarine environment is important towards understanding the function of ecosystems.

Indeed, in their long evolutionary history, cyanobacteria have developed highly refined response strategies shared with other prokaryotes under various stressors [5,6]. One common successful survival strategy is the ability to undergo reversible growth arrest [5,6] using chromosomal toxin-antitoxin (TA) systems. TA systems have been documented in many organisms, especially *Escherichia coli*, to cope with various stresses by reducing growth, inhibiting growth or killing a subpopulation of cells [7–9]. The freshwater filamentous cyanobacteria *Anabaena sp*. PCC7120 contains numerous chromosomal TA systems, some of which are predicted to promote survival under particular stresses [10].

TA systems, also referred to as addiction or suicide modules, typically consist of an auto-regulated operon encoding a stable toxin and a labile antitoxin [9,11,12]. Based on the antitoxin nature and mode of action, TA systems are grouped into type I, II, III, IV, and V classes [13–15]. Antitoxins of type II, the most abundant type of TA, are proteins that inactivate toxins by forming TA complexes [11]. The vast majority of type II toxins are mRNA specific endoribonucleases, also called mRNA interferases, such as *mazF*, *relE*, and *hicA* toxins [16]. Almost all described type II TA systems share this mode of regulation: tight expression auto-regulated by a TA complex binding to the promoter region and toxin neutralization by formation of a TA complex. All apparently result in translation inhibition.

Type II systems have been found in plasmids and chromosomes of free-living bacteria [17–19]. Type II TA system prevalence has led to the proposal that chromosomal TA systems are stress-response elements contributing to prokaryotes' adaptation to stressful environments [9,11]. According to this hypothesis, under unfavorable conditions antitoxins would be degraded by stress-induced proteases, which cause relief of transcriptional repression of TA operons and release of toxins from TA complexes [16]. As a consequence, the free toxins would induce reversible growth arrest or cell death by inhibiting an essential cellular process such as protein synthesis or DNA replication [16]. This hypothesis has been supported by a series of recent experimental findings [20–23]. For instance, in *E. coli*, activation of TA systems is triggered by various stresses, and ectopic expression of nearly all characterized chromosomal toxins could improve the ability to confer resistance to stress [20].

Despite the ubiquity of TA systems in other prokaryotic organisms, they have not previously been reported in marine picocyanobacteria such as *Synechococcus* or *Prochlorococcus*. Previous studies have hypothesized that a lack of TA systems in some prokaryotes is related to their small genome sizes (<3Mb) and relatively simple life style in stable environments [17]. Currently, more than 60 marine picocyanobacteria genomes have been sequenced (NCBI search as of Jan 2016). In general, genome sizes of marine *Synechococcus* and *Prochlorococcus* are smaller than 3Mb [24–26]. Recently, we identified seven putative chromosomal TA pairs in the genome (2.8Mb) of *Synechococcus* strain CB0101, which was isolated from the Chesapeake Bay [27].

Marine *Synechococcus* can be divided into three major subclusters, 5.1, 5.2 and 5.3 [24,25,28]. Subclusters 5.1 and 5.3 *Synechococcus* are present in coastal and oceanic waters, while subcluster 5.2 *Synechococcus* mainly occupies estuaries [29]. Compared to coastal and oceanic *Synechococcus*, much less is known about the ecological function and genomic evolution of estuarine *Synechococcus*. Subcluster 5.2 *Synechococcus* dominate the estuarine environment [30] making up 20-40 % of phytoplankton chlorophyll-a during the summer [31] and contain a novel pigment gene cluster not seen in other subclusters [29]. *Synechococcus* strain CB0101 (a member of subcluster 5.2) is able to grow in a wide range of salinities (0-30 ppt) and temperatures (4 to 32 °C), and is often subjected to viral infection [31–33]. The presence of TA systems in the genome of CB0101 leads to the hypothesis that estuarine cyanobacteria similar to CB0101 retain TA systems to aid in adaptation to strong environmental gradients in the estuary.

In this study, we identified and characterized the chromosomal TA systems found in *Synechococcus* strain CB0101 [27]. The expression of TA systems in CB0101 in

response to stressful environmental conditions (nutrient, metal toxicity, light intensity, and phage infection) were analyzed using RNA-Seq, confirmed through qPCR, and further confirmed through Western blotting of extracts. Time series experiments displayed the activation and shutdown of the toxin and antitoxin proteins when a stressful environment (i.e. Zn toxicity or photo-oxidative stress caused by high light intensity) was encountered and subsequently relieved. Our results suggest that by inducing a reversible growth arrest, TA toxins allow stressed cells to remain in a dormant or non-growing stress-tolerant state until more favorable environmental conditions return. Genomic searches led to the finding of TA systems in 8 other marine *Synechococcus*. This is the first identification, characterization, and functional confirmation of TA systems in marine picocyanobacteria.

4.3 Methods

4.3.1 Cyanobacterial strains and stress experiments

Cultures of CB0101 were grown in SN medium with 15 ppt salinity and vitamin B12 (10μg/L) (referred to as SN15 medium hereafter) at 23 °C under 15 μE m^{-2} s^{-1} continuous light. Filtered (0.2 μm pore size) air was bubbled into individual 500 mL cell culture flasks. For the RNA-Seq analysis, CB0101 cultures were initially grown under the above conditions and duplicates were subjected to 4 different conditions for 72 h: (1) Control, where the culture was grown in SN15 medium; (2) Nitrogen depleted condition, where the cultures were cultivated in the SN15 medium that did not contain sodium nitrate; (3) Phosphate deplete condition, where the cultures were grown in the SN15 medium that lacked dipotassium phosphate; (4) Zinc toxic condition, where the cultures were grown in the SN15 medium amended with 50 μM of zinc sulfate heptahydrate. The

growth of cultures was monitored by counting cells using an Accuri C6 flow cytometer. The specific growth rate was calculated from the logarithmic change $\mu = \frac{\ln X2 - \ln X1}{t2 - t1}$ where X1 and X2 are densities at times t1 and t2. Samples were taken at 0 min and after 72 h, and mRNA was extracted immediately after sampling.

For the phage infection experiment the length of the lytic cycle was determined by one-step growth curve**.** Once the lytic cycle was determined, three time points were identified to correlate with attachment (30 min), latent (5 h), and lysis (12 h). Triplicate cultures of CB0101 were grown to exponential phase (10^8 cells ml^{-1}), and then infected with S-CBP1 [33] podovirus (10^8 infective phage particles ml^{-1}) for a multiplicity of infection (MOI) of 1. Control cultures were amended with sterilized SN15 medium. At the designated time points mRNA was extracted (Supplemental Table 4.S2).

For the light intensity experiment, exponentially growing CB0101 culture (in SN15 medium) was split into five 25-ml cell culture flasks, which were exposed to five different light intensities (15, 50, 100, 150, and 200 μE m^{-2} s^{-1}). The entire culture was extracted and mRNA and protein were separated for qPCR and Western blot analysis, respectively.

4.3.2 Extraction of mRNA and qPCR reaction

Samples were collected and immediately processed for mRNA analysis. RNA was separated using Trizol extraction. mRNA was extracted from the total RNA using Ambion MICROBExpress kit (Life technologies, AM1905), modified with 4 specific oligo primers for rRNA depletion of CB0101 ribosomes. rRNA removal evaluation was conducted using the Agilent 2100 Bioanalzyer resulting in 98 % removal of rRNA and confirmed the presence of high quality RNA. The NEXTflex RNA-Seq kit (BIOO

Scientific, #5129-01) was then used to prepare mRNA libraries for sequencing using the Illumina Hi-Seq. RNA libraries were created and barcodes assigned to each sample for multiplexing of a single Hi-Seq lane. RNA-Seq was carried out by the Institute of Genome Sciences (IGS) using a Hi-Seq with 100 bp-paired end read length. As a further confirmation, qPCR was used to validate the expression of each TA pair transcript expression (Supplemental Table 4.S2).

4.3.3 TA system identification in CB0101 and completely sequenced Synechococcus *and* Prochlorococcus *genomes*

BLASTCLUST (-L 0.75 –S1.0) searches for all identified TA genes grouped by family and cluster was used to identify TA genes within *Synechococcus* CB0101. These TA systems were further validated using the RASTA-Bacteria and TA finder programs [34,35]. Further, this method was used with representatives of each cluster used as queries in a BLAST search (e-value 0.01) against ~60 completely sequenced *Synechococcus* and *Prochlorococcus* genomes available on the NCBI Microbial Genomes website at the time of this analysis (January 2016) [36]. Significant hits among proteins encoded in these genomes were classified as toxins or antitoxins; in the case of multiple matches to different TA families, the protein was assigned according to the highest-scoring match TA query. Co-directed genes with adjacent chromosome locations belonging to different toxin/antitoxin families were recorded as a TA pair.

4.3.4 Western Analysis

Western blot analysis was conducted using a procedure described by Mahmood and Yang [37]. Amino acid sequences for all 7 TA pairs were provided to GenScript for epitope analysis. Results were analyzed using their Optimum Antigen design tool and the

relB^{2}*/relE*^{1} pair was selected due to transcript expression under each stress and favorable antigen design. Antibodies were raised for one TA pair, relB^{2}/relE^{1} using GenScript service. The antibody epitope sequences used were TARLPDDLTAELDAC and CVLVVRVGHRKEVYR. Western blot analysis was performed against samples from the resulting cultures using a primary rabbit polyclonal anti-FLAG antibody and a goat anti-rabbit HRP conjugated secondary antibody as directed by the manufacturer. Constant whole cell equivalents (~2x10^{7} cells) mixed in running buffer were used for each Western. NuPAGE Novex gels with 4-12% Bis-tris gel with MES running buffer was used. Gels were further processed using ImageJ and image lab software for the Bio-Rad ChemiDoc imager. Pixel densities and predicted molecular weights were calculated for each gel.

4.4 Results

4.4.1 Annotated toxin/antitoxins in CB0101

Genome annotation revealed the presence of 7 chromosomal pairs of TAs, homologous to *E. coli* types II (Table 4.1 and Fig. 4.1). Each TA pair was analyzed using InterProScan 5 and ExPASy for motif, PI, and molecular weight prediction (Supplemental Table 4.S1). The type II TA pairs included *yefM*^{1}*/yoeB*^{1}, *mazE*^{1}*/mazF*^{1}, *relB*^{2}*/relE*^{1}, *vapB*^{1}*/vapC*^{1}, *relB*^{1}*/vapC*^{1}, *phd*^{1}*/doc*^{1}, and *phd*^{2}*/doc*^{2} all of which use protein-to-protein interactions and arrest translation.

The amino acid sequences of each TA pair from CB0101 were BLAST searched in GenBank to identify their closest homologs. The closest neighbors to the TA pairs of CB0101's are shown in Table 4.1. The DNA sequence identities of these closest hits varied from 50 to 93 % among the 7 TA pairs. Two-thirds of TA genes were related to

the TA genes in picocyanobacteria (mainly marine *Synechococcus* and *Cyanobium*), while one-third of CB0101 TA genes seem to arise from heterotrophic bacteria, i.e. *Collimonas fungivorans*, *Thioalkalivibrio sulfdiphilus*, and *Polaromonas glacialis* (Table 4.1). Interestingly, the TA systems were found in diverse ecotypes of marine *Synechococcus*, i.e. KORDI-49 (coastal), WH8103 (open ocean), WH5701 (estuarine), and CB0205 (estuarine). Also of note is the consistent presence of toxin and antitoxin pairs from the same organism i.e. TA pair #3 from *Cyanobium sp.* PCC7001 (Table 4.1). Most pairs exhibit highly basic or acidic PI values strengthening the case for their covalent binding with each other (Supplemental Table 4.S1). Many of the pairs contain 1-3 nucleotide overlaps suggesting transcriptional coupling (Fig. 4.1). For most of the TA pairs the coding regions on either side contain palindromic sequences (Fig. 4.1). The genome location of each TA pair falls within regions defined as genomic islands. Genomic islands (GIs) are large regions (more than eight kilobases long) of non-conserved, non-core genes that are sporadically distributed among the genome. Genomic islands were identified using the IslandViewer program.

4.4.2 Responses of Synechococcus *TA systems to the environmental stresses*

The growth rate of CB0101 under different stress conditions (nitrogen depletion, phosphorus depletion, and zinc toxicity) is shown in Fig. 4.2. CB0101 grew more slowly compared to the control under all conditions (Fig. 4.2). However, the growth of CB0101 under phosphate depletion and zinc toxicity was significantly slower than the growth of control ($p<0.05$). High zinc exposure nearly suppressed the growth of CB0101 completely (t-test value 2.7, $p=0.09$), which is significantly different than the control.

RNA-Seq analysis was conducted to determine the expression response of CB0101 to four stress conditions (nitrate depletion, phosphorous depletion, zinc toxicity, and phage infection) (Table 4.2 and Supplemental Table 4.S2). The transcripts of toxin *relE*^{1} were progressively upregulated 2.3, 3.1, and 10.5 fold ($p<0.01$ and minimum 2 fold) in nitrate depletion, phosphate depletion, and zinc toxicity, respectively (TA pair #5, Table 4.2). *relE*^{1} was also upregulated 2 fold at 30min post infection of phage S-CBP1. The antitoxin gene *relB*^{2} was downregulated by 2.5 fold when CB0101 was grown under nitrate depletion (TA pair #5, Table 4.2).

Other upregulated toxin genes included *doc*^{1} (2.7 fold in zinc toxicity) and another *yoeB*^{1} (2.2 and 2.1 fold in both nitrate depletion and zinc toxicity). The antitoxin *phd*^{1} was upregulated 2.5 fold only under nitrate deplete conditions. *relB*^{2} was only downregulated (2.5 fold) under nitrogen deplete conditions. While *relB*^{1} was downregulated 2.6-fold under zinc toxic conditions.

In order to confirm the RNA-Seq expression data, PCR primers were made for each TA pair and the quantity of specific TA gene transcripts was measured using qPCR (Supplemental Table 4.S3). The same samples were used from the RNA-Seq experiments to verify results ($p<0.01$ and minimum 2 fold). The qPCR further confirmed the RNA-Seq expression data that the TA systems were active under the different stress experiments (Table 4.2). To demonstrate the actual activity of TA systems at the protein level, we selected one TA pair (*relB*^{2}/*relE*^{1}) to further study the expression of their proteins based on the detection of specific antibodies. This TA pair was selected because the toxin was expressed at the transcript level, showed the largest expression difference and optimally designed antibodies could be made to both pairs. The degradation of the

tRNAs and ribosomal RNAs of CB0101 under high Zn conditions was observed, consistent with *relE* toxin translation inhibition (Supplemental Fig. 4.S1).

4.4.3 Production of relE^{1} *arrests the growth of CB0101*

The *relE*^{1} and *relB*^{2} genes on CB0101's chromosome encode RelE and RelB homologous to the *E. coli* RelE (24 % identity) and RelB (41 % identify), respectively. RelE is predicted to be an 84-residue sequence at 9.53 kDa, while RelB is predicted at 73 residues and 8.08 kDa (Supplemental Table 4.S1). The protein structures of *relE*^{1} and *relB*^{2} were predicted using Phyre2 (Supplemental Fig. 4.S2). Expression of mRNA for the *relB*^{2}*/relE*^{1} pair in response to nitrate depletion, phosphate depletion and zinc toxicity were shown in Fig. 4.3A. The mRNA expression of the *relB*^{2}*/relE*^{1} pair has been described above. The antibodies were used to confirm the presence of each protein (Fig. 4.3B-C). The expressed RelB^{2}/RelE^{1} proteins in all stress conditions were detected using specific antibodies loaded with constant cell equivalents (Fig. 4.3B-C). Under the normal growth condition (control) a dimer of RelB^{2}/RelE^{1} was detected at 18 kDa (Fig. 4.3C), while the toxin protein RelE^{1} was not detected at its predicted weight 9 kDa (Fig. 4.3B). When CB0101 became stressed in all three treatments, toxin protein RelE^{1} (band 9kDa) became more prevalent and the dimer of antitoxin/toxin protein RelB^{2}/RelE^{1} (band 18 kDa) declined (Fig. 4.3B-C).

4.4.4 Reversible relB^{2}/relE^{1} *expression when the stress is removed*

After confirming the presence of both toxin and antitoxin proteins (RelB^{2}/ RelE^{1}) in all stress treatments, a time series experiment was set up to determine the progression of the TA pair when CB0101 was exposed to zinc toxicity (Fig. 4.4). In some characterized TA systems, the toxin can be counteracted by subsequent production of

antitoxin. It would be interesting to know if the stress responses of toxin and antitoxin (*relB*^{2}*/relE*^{1}) are reversible when the stress level is reduced. In this experiment, CB0101 was exposed to the same zinc toxicity (as the previous experiment), and subsamples were collected at 9 different time points (0, 0.5, 3, 12, 24, 36, 38, 50, 62, and 72 h). CB0101 was grown in the presence of zinc for 36 h; the culture was then exposed to fresh non-toxic media and allowed to grow for another 36 h (Fig. 4.4). When the zinc was added to the culture the toxin (RelE^{1}) began to accumulate over time (Fig. 4.3A; 0-24 h). Upon removal of zinc at 36 h, toxin protein began to dissipate gradually over time (Fig. 4.4A; 36-72 h). The opposite trend was observed with the dimer of antitoxin/toxin. Upon exposure to zinc the RelB^{2}/RelE^{1} complex decreased gradually and was fully degraded within 24 h (Fig. 4.4B). When the culture was released from zinc toxicity at 36 h, the dimer of RelB^{2}/RelE^{1} recovered almost instantaneously (Fig. 4.4B). Pixel densities shows the inverse synchronization of the toxin and antitoxin proteins (Fig. 4.4C). The growth rate of CB0101 was inhibited with zinc exposure in the first 24 h, and recovered after the release of zinc stress (Fig. 4.4D).

4.4.5 Light response for relB^{2}/relE^{1}

Since zinc toxicity is inducing *relB*^{2}*/relE*^{1} and this type of stress induces oxidative stress, we believe a better representation of niche adaptation would be responses to photo-oxidative stress. A major source of oxidative stress which photosynthetic organisms deal with is the production of reactive oxygen species (ROS) [38] at high light intensities. CB0101 grew rapidly at low light intensities (15-50 μE m^{-2} s^{-1}) and the

growth was severely inhibited when light intensity exceeded 200 μE m^{-2} s^{-1} (Fig. 4.5A). The level of photo bleaching increased with increasing light intensity (Fig. 4.5B).

The upper Chesapeake Bay, in which CB0101 thrives in, is a low light environment due to increased particulate influxes. The qPCR analysis of each TA pair showed the expression of *relE*^{1} was upregulated (2.7, 3.9 and 5.6 fold) when CB0101 was exposed to light at 100, 150, and 200 μE m^{-2} s^{-1}, respectively (Fig. 4.5C). The transcripts of two other toxins, *yoeB*^{1} and *doc*$^{1, 2}$, were upregulated (2.4 and 2.6 fold, respectively) at the highest light intensity. Lastly, the mRNA of two antitoxins, *relB*^{1} and *phd*^{2} were downregulated at the highest light intensity. The Western blot of $RelB^{2}/RelE^{1}$ showed the presence of a dimer (18kDa), which progressively decreased as the light intensity increased (Fig. 4.5D). Conversely, the $RelE^{1}$ protein became visible at 100 μE m^{-2} s^{-1} and increased at 150 and 200 μE m^{-2} s^{-1}.

4.5 Discussion

4.5.1 Why do Synechococcus spp. *contain TA systems?*

The presence of 7 pairs of TA systems in the chromosome of CB0101 is the first description in marine cyanobacteria (Table 4.1 and Fig. 4.1). The number and type of TA systems in CB0101 are comparable to other prokaryotes [12]. TA systems have been found in prokaryotic plasmids and chromosomes. While the plasmid-encoded TAs are known to stabilize plasmids in cells, the chromosome TA systems have multiple functions [39]. Four possible mechanisms for the presence of TA systems in chromosomes have previously been identified: 1) TA systems on chromosomes may fulfill a similar function to plasmid types and mediate stabilization of important genetic regions [19]; 2) Protection against invading DNAs such as plasmids and phages [20,40]; 3) Formation of bacterial persister cells [41]; 4) Regulation of biofilm formation or global regulators of translation [7].

We believe that at least three of the four above-mentioned mechanisms are applicable to TA systems in CB0101. First, TA systems of CB0101 are in close proximity to important genes such as Type IV pilus, DNA repair, rod shape-determining proteins (*Mre*), SOS-response repressor and protease *LexA* (mechanism 1). All of which are involved in functions to boost niche ecotype or overall survival. Secondly, the up-regulation of the $relE^{1}$ toxin of the $relB^{2}/relE^{1}$ pair occurred within 30 min of cyanophage infection (Supplemental Table 4.S2). Expression of $relE^{1}$ may cause the cell to arrest translation, thus slowing or stopping the phage from replicating (mechanism 2). Thirdly, TA systems may allow CB0101 to develop dormancy or persister cells in response to environmental stresses (mechanism 3). This is reflected by the ability for CB0101 to

arrest translation and growth during stressful environmental conditions by regulating its TA systems such as *relB*^{2}/*relE*^{1} (Fig. 4.4). CB0101 was able to resume its growth when the stress was removed, likely undergoing a persister state (Fig. 4.4). A bacterial persister state is a quasidormancy state where the cells may recover and proliferate if enough antitoxin is produced to neutralize the toxin [40,41]. Formation of persister cells regulated by TA systems could be an important mechanism for *Synechococcus* species living in dynamic or unstable environments.

4.5.2 The relB/relE *system*

The expression of antitoxins and toxin genes, *relB*^{2}/*relE*^{1}, were tightly regulated by the various stress conditions (Fig. 4.4 & 4.5). The mechanisms behind how *relB*^{2}/*relE*^{1} respond to stress could be homologous to other prokaryotic systems such as *E. coli* [40]. Typically transcription of the TA operon is auto-regulated by binding of the antitoxin or by the TA system to the promoter [42]. Depending on the stoichiometric ratio of antitoxin to toxin, several types of complexes may be formed with distinct affinities to the promoter [43–46]. This coincides with the time-series experiment where the antitoxin RelB^{1} rapidly recovered after the stress was released (Fig. 4.4).

Our studies show that RelB^{2}/RelE^{1} growth inhibition of CB0101 could be completely eliminated by subsequently ending the stress condition allowing RelB^{2} to recover almost instantaneously (Fig. 4.4). The *relB*^{2}/*relE*^{1} TA pair was active and arrested translation when under zinc oxidative stress, and the arrest was reversible when the stress event was removed (Fig. 4.1 & 4.4). This result is in accordance with the previous demonstration that the overproduction of TA toxin caused reversible growth arrest [43,45]. Therefore, it is reasonable to propose that the chromosomal *relB*^{2}/*relE*^{1}

system of CB0101 represents a growth modulator that induces a persister state to enhance fitness and competiveness under particular stress conditions, such as metal or oxidative stress. As a result, cyanobacteria with this TA system can persist for a long period of time under stressful conditions and revive when suitable conditions arise.

4.5.3 Ecological significance and oxidative response of relB/relE

Oxidative stress caused by high light intensities is known to be one of the greatest forms of stress caused to photosynthetic organisms. The penetration of sunlight into water places constraints on the survival and spatial distribution of marine cyanobacteria. Light penetration through the water column is controlled by the amount and kinds of materials that are dissolved and suspended in the water [47,48]. Water turbidity in the Chesapeake Bay is highly variable with highly turbid conditions present in the upper bay. This turbidity creates a low light environment of (10-100 μE m^{-2} s^{-1} within 0.15 m and 1 m) [47]. Estuarine *Synechococcus* CB0101 is low light adapted relative to coastal and oceanic *Synechococcus* (Fig. 4.5). In the event of upwelling, lower turbidity, or clearing water, CB0101 becomes stressed due to higher light intensities. In order to limit that stress, CB0101 is able to induce *relB*^{2}*/relE*^{1} TA system, which arrests growth and translation (Fig. 4.5).

Irradiance has long been known to exert a major control on cyanobacteria proliferation; excessive light can cause photo-oxidative cell death and *Prochlorococcus* and *Synechococcus* have different strategies to minimize this potential light-induced death [49,50]. The phototrophic nature of these organisms means that they not only need to manage the oxidative stress generated by oxygen reduction in the same way as heterotrophic organisms, but also produce oxidative oxygen during photosynthetic

electron transport [38]. Reactive oxygen species (ROS) are byproducts of aerobic metabolism and potent agents that cause oxidative damage [38]. In oxygenic photosynthetic organism such as cyanobacteria, ROS are inevitably generated by photosynthetic electron transport. Photosynthetic organism are able to overcome photodamage by the rapid and efficient repair of PSII [38,51]. Based on these findings, along with the observation of persister state effect of the *relB*^{2}*/relE*^{1} system, it seems reasonable to propose that the activation of the *relB*^{2}*/relE*^{1} system might redirect the energy normally utilized for growth to aid in repair mechanisms caused by brief amounts of high light intensities. In this model, the *relB*^{2}*/relE*^{1} system is envisioned to delay programmed cell death and instead undergo a persister state. With TA systems found within GIs we can predict that they were acquired through horizontal gene transfer from other bacteria, perhaps from freshwater ecotypes where TA systems are common.

4.5.4 Presence of TA systems in broader picocyanobacteria

Based on a search of *Synechococcus* and *Prochlorococcus* genomes publically available on NCBI (described in methods). Eight *Synechococcus* strains ranging from estuarine, coastal, and open ocean (CB0205, WH5701, WH8102, WH8103, RS9916, RS9917, KORDI-49, and KORDI-51) with putative hits to at least one pair of TA were identified. Hits to current *Prochlorococcus* genomes were not found. Our results suggest that TA systems in marine *Synechococcus* are probably more widely dispersed than thought. Although it is not our focus here to conduct a thorough investigation of the distribution of TAs in marine picocyanobacteria the diversity and function of TA systems deserves further investigation.

It has been proposed that the absence of TA systems in prokaryotes with small genomes could be due to their relatively simple life style in stable environmental conditions [17]. Makarova et al., [18] argued that the lack of TAs in small genomes is a consequence of the general "laws" of scaling of differential functional categories of genes with genome size. Although it has been predicted (with 95 % confidence) that no TAs are present in microbial genomes, which contain less than 3,100 genes [18]. This is clearly not the case since TAs are present in marine *Synechococcus* strains CB0101, CB0205, WH5701, WH8102, WH8103, RS9916, RS9917, KORDI-49, and KORDI-51, whose genomes contain less than 3,100 genes. Further work is needed to understand the number, type, diversity, evolution and ecological significance of TAs in marine picocyanobacteria. It is clear that TA systems play a major role in regulation of *Synechococcus*.

4.6 Conclusion

Here we described the first TA systems in marine picocyanobacteria. *Synechococcus* strain CB0101, a member of marine *Synechococcus* subcluster 5.2, contains 7 chromosomal toxin-antitoxin gene pairs which were expressed in response to five different stressors; nitrogen or phosphate starvation, zinc toxicity, phage infection and photo-oxidative stress. Based on the TA pair $relB^{2}/relE^{1}$ we demonstrated that the TA system arrests the growth and translation under stress conditions, and revives growth when the adverse event is removed. Activation of the $relB^{2}/relE^{1}$ system allows *Synechococcus* like CB0101 to regulate growth in response to oxidative stress caused by variable light intensities in the Chesapeake Bay. Therefore, the presence of numerous TA systems in the chromosome of CB0101 may contribute to its ability to acclimate to

variable conditions in the estuarine ecosystem. The growth regulation of chromosomal type II TA systems may promote marine *Synechococcus* to cope with stressful environments.

The BLAST search on known marine *Synechococcus* and *Prochlorococcus* genomes led to the finding of TA pairs present in eight different marine *Synechococcus* strains isolated from estuarine, coastal, and open ocean environments. Intriguingly, none were found within *Prochlorococcus*. The presence of TA genes in diverse *Synechococcus spp*. suggests that we know very little about the diversity, evolution and ecological functions of TA genes in marine picocyanobacteria. Evaluating TA system-mediated growth regulation of marine picocyanobacteria in response to various environmental changes, i.e. temperature and salinity is important towards understanding the effect of climate change on ecosystem function.

Table 4.1. The outcome of protein BLAST search of the 7 *Synechococcus* CB0101 TA gene pairs. Toxin is represented by bold and antitoxin by italics. All matches represent a best fit to length (>90%).

TA Pair #	TA Family	Closest Neighbor	Identity	E value
1	*yefM*[1]	*Synechococcus* sp. KORDI-49	76%	3E-38
1	**yoeB**[1]	*Synechococcus* sp. WH8103	81%	1E-43
2	*phd*[1]	*Cyanobium* sp. CACIAM 14	87%	2E-36
2	**doc**[1]	*Collimonas fungivorans*	50%	4E-33
3	*vapB*[1]	*Cyanobium* sp. PCC7001	75%	2E-33
3	**vapC**[1]	*Cyanobium* sp. PCC7001	74%	7E-63
4	*relB*[1]	*Synechococcus* WH5701	72%	1E-14
4	**vapC**[2]	*Synechococcus* sp. WH5701	81%	4E-67
5	*relB*[2]	*Thioalkalivibrio sulfdiphilus*	55%	4E-19
5	**relE**[1]	*Thioalkalivibrio sulfdiphilus*	64%	5E-28
6	*mazE*[1]	*Thauera phenylacetica*	59%	2E-24
6	**mazF**[1]	*Polaromonas glacialis*	71%	5E-63
7	*phd*[2]	*Synechococcus* sp. CB0205	93%	0E+00
7	**doc**[2]	*Cyanobium* sp. CACIAM 14	67%	5E-32

Table 4.2. Expression of 7 *Synechococcus* CB0101 toxin/antitoxin pairs under various stress conditions detected by RNA-Seq and qPCR. Upregulation (red) or down regulation (blue) is based on expression of the control sample ($p<0.01$ and minimum 2 fold). Toxin is represented by bold and antitoxin by italics.

TA Pair #	TA Family	Toxin Activity	Nitrogen RNA-Seq	Nitrogen qPCR	Phosphate RNA-Seq	Phosphate qPCR	Zinc RNA-Seq	Zinc qPCR
1	*yefM*[1]	mRNA interferase or inhibitor of translation initiation	-1.6	-1.9	-1.4	-1.7	-1.3	-1.3
1	**yoeB**[1]		2.2	2.6	1.5	1.8	2.1	2.4
2	*phd*[1]	Binds to the 30S ribosomal subunit	2.5	2.8	1.3	1.5	-1.2	-1.7
2	**doc**[1]		1.8	2.0	1.2	1.5	2.7	2.6
3	*vapB*[1]	Cleavage of tRNA	1.8	2.0	1.6	1.6	-1.7	-1.7
3	**vapC**[1]		1.4	1.8	-1.2	-1.5	1.7	1.6
4	*relB*[1]	Cleavage of tRNA	-1.0	-1.5	-1.0	-1.3	-2.6	-2.9
4	**vapC**[2]		1.1	1.2	1.3	1.6	-1.1	-1.2
5	*relB*[2]	Cleavage of ribosome-bound mRNA	-2.5	-3.0	1.2	1.6	1.1	1.3
5	**relE**[1]		2.3	2.5	3.1	3.5	10.6	11.2
6	*mazE*[1]	Ribosome-independent mRNA cleavage and cleavage of 23S rRNA	-1.2	-1.6	-1.2	-1.3	1.4	1.3
6	**mazF**[1]		-1.1	-1.3	-1.4	-1.5	1.7	1.7
7	*phd*[2]	Binds to the 30S ribosomal subunit	1.4	1.5	1.2	1.5	-2.0	-2.2
7	**doc**[2]		-1.5	-1.7	-1.3	-1.6	1.1	1.3

TA pair:

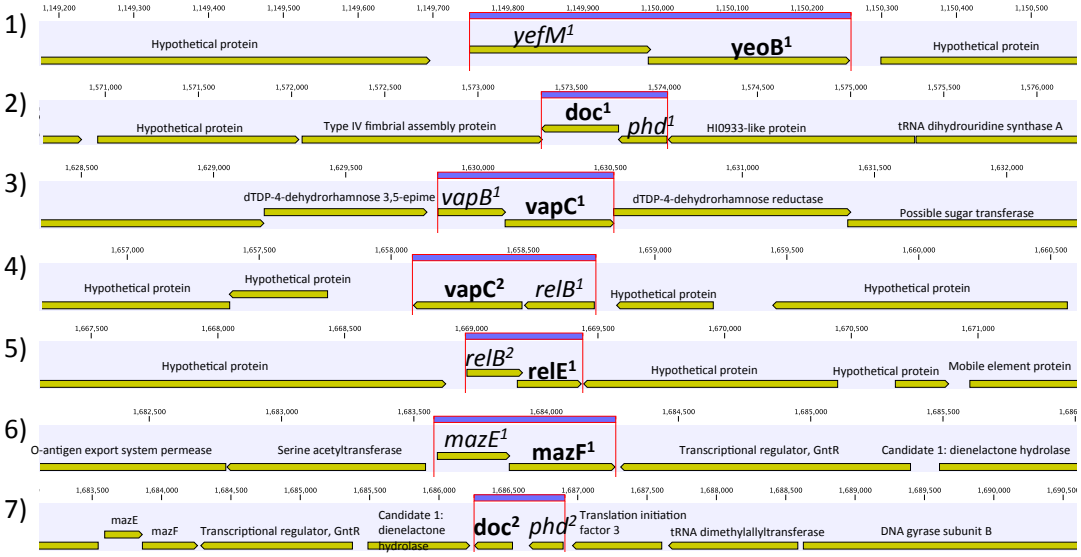


Figure 4.1. Genetic organization of the 7 TA systems of *Synechococcus* CB0101. Schematic representation of the 7 TA pairs (highlighted in purple) and associated genes. Toxin is represented by bold and antitoxin by italics.

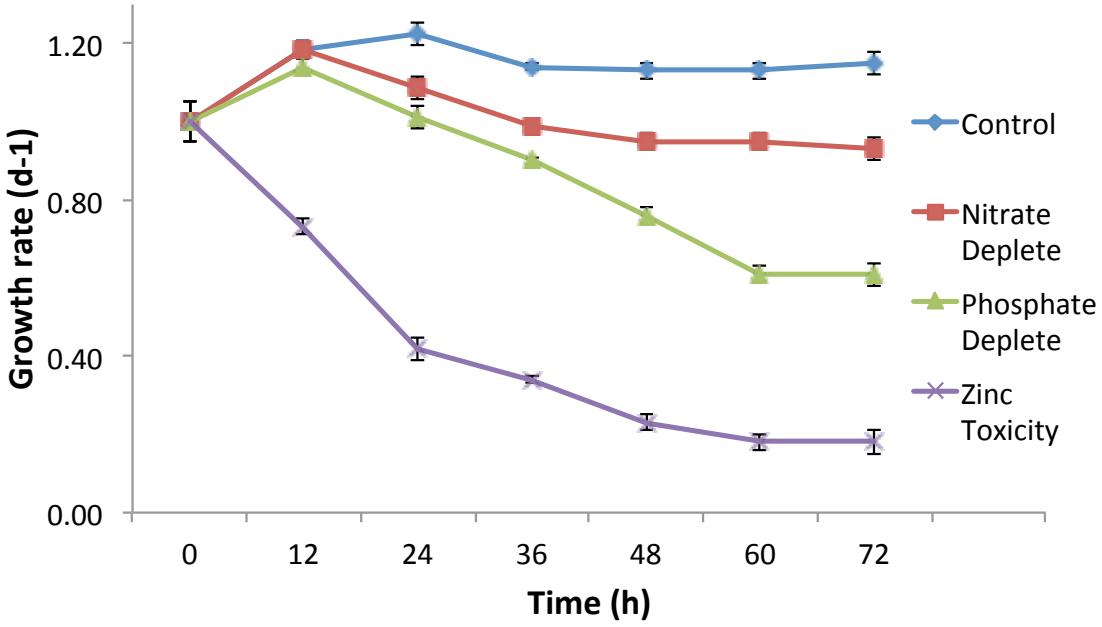


Figure 4.2. Growth rate of *Synechococcus* CB0101 during a 72 h period under different stress conditions: control medium, nitrogen limitation, phosphate limitation, and zinc toxicity (n=3). See Chapter 3 for detailed explanation on *Synechococcus* CB0101 response to these conditons.

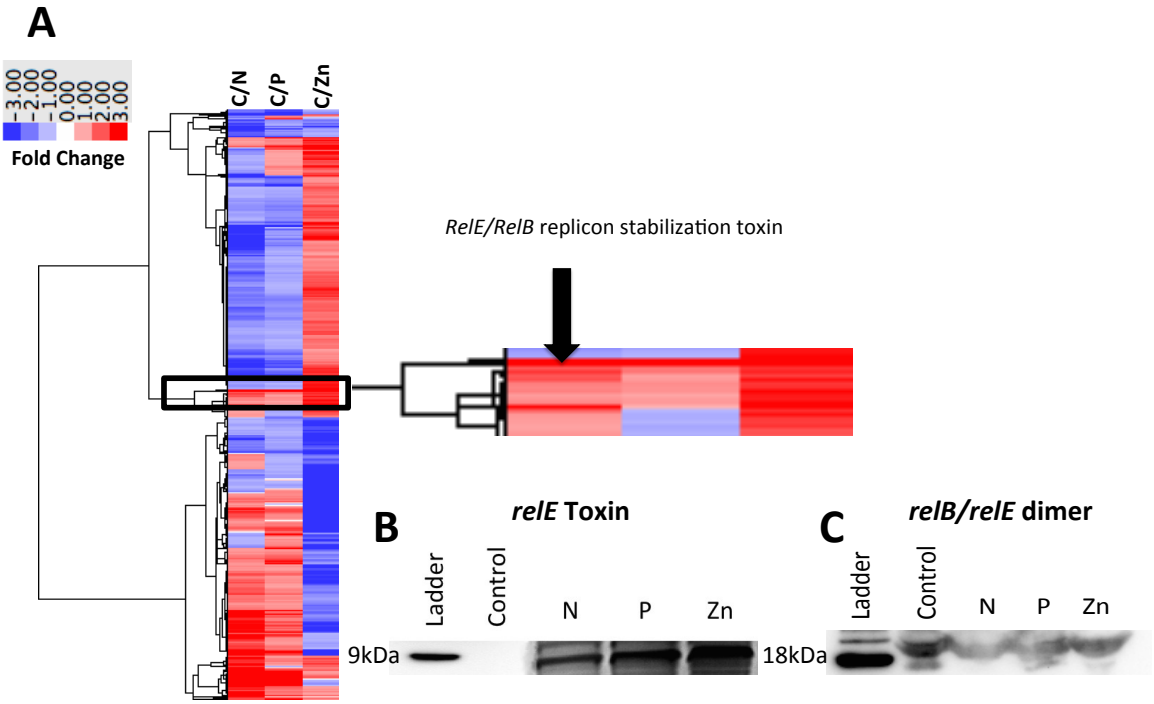


Figure 4.3. Global transcript expression of *Synechococcus* CB0101 to three stressors measured using RNA-Seq ($p<0.01$ and minimum 2 fold) and compared to a control expression. A) Heat map and clustering of differentially expressed genes. Stress conditions are all compared to Control, with C/N representing nitrogen depletion, C/P phosphate depletion, and C/Zn zinc toxicity representing 843 (27%), 368 (12%), and 1,195 (38%) differentially expressed genes identified from 3,173 total genes. Dark red equates to a strong increase (>3 fold), while dark blue to a strong decrease (>3 fold) in gene expression. Zoomed image of the expression from the toxin-antitoxin pair *relB*^{2}/*relE*^{1}. B) Detection of the toxin RelE^{1} and C) antitoxin/toxin dimer RelB^{2}/RelE^{1} proteins by Western blot analysis from each stress condition including nitrogen (N) and phosphate (P) depletion, and zinc toxicity (Zn). Constant cell equivalents were used.

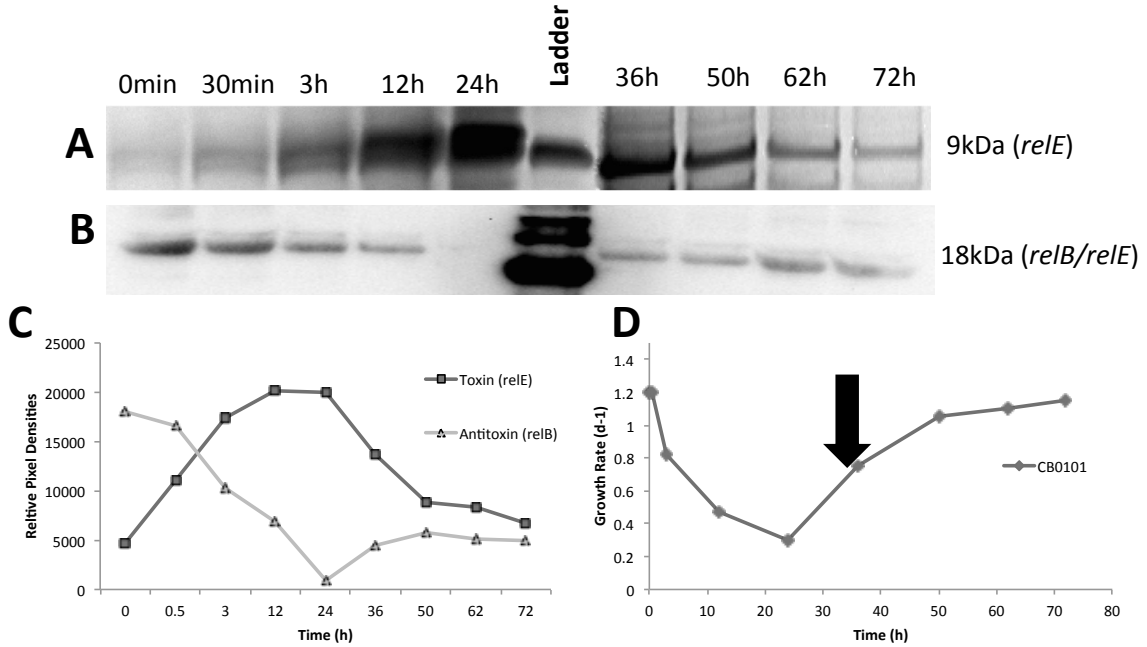
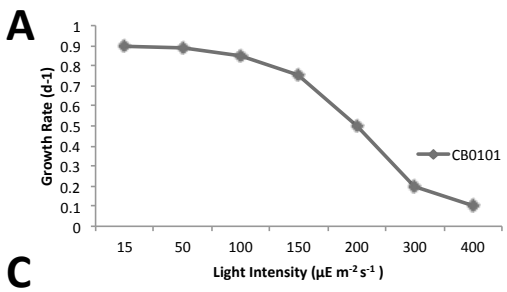
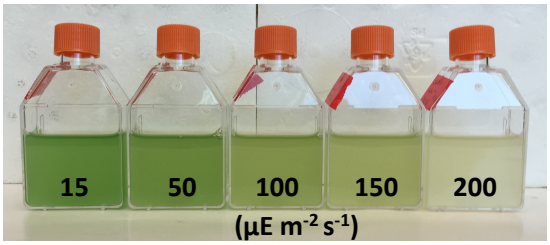


Figure 4.4. Time series detection of RelB[2]/RelE[1] proteins by Western blot analysis during zinc toxicity and subsequent releasing at 30 h using constant whole cell equivalents (~2x10[7] cells) mixed in running buffer. NuPAGE Novex gels with 4-12% Bis-tris gel with MES running buffer was used. A) Toxin RelE[1]; B) Antitoxin/toxin dimer RelB[2]/RelE[1]; C) Pixel density analysis to determine relative protein abundance; D) Growth rate of *Synechococcus* CB0101 during the time series with black arrow representing media change (release of zinc toxic conditions) at 35.5 h.





C

TA Pair #	TA Family	Toxin Activity	Light Intensity (μE m^{-2} s^{-1}) 15	50	100	150	200
1	*yefM*^{1}	mRNA interferase or inhibitor of translation initiation	1.1	1.1	1.0	1.2	1.1
1	**yoeB**^{1}		1.1	1.2	1.3	1.6	2.4
2	*phd*^{1}	Binds to the 30S ribosomal subunit	1.0	1.1	1.0	1.0	1.0
2	**doc**^{1}		1.3	1.1	1.5	1.8	2.6
3	*vapB*^{1}	Cleavage of tRNA	1.1	1.1	1.1	1.0	1.2
3	**vapC**^{1}		1.2	1.2	1.0	1.1	1.0
4	*relB*^{1}	Cleavage of tRNA	1.3	1.2	1.0	1.0	-2.0
4	**vapC**^{2}		1.1	1.2	1.1	1.0	1.1
5	*relB*^{2}	Cleavage of ribosome-bound mRNA	1.1	1.2	1.2	1.6	1.1
5	**relE**^{1}		1.2	1.5	2.7	3.9	5.6
6	*mazE*^{1}	Ribosome-independent mRNA cleavage and cleavage of 23S rRNA	1.0	1.0	1.1	1.1	1.0
6	**mazF**^{1}		1.6	1.0	1.2	1.0	1.0
7	*phd*^{2}	Binds to the 30S ribosomal subunit	1.0	1.4	1.0	1.1	-2.1
7	**doc**^{2}		1.3	1.0	1.2	1.0	1.0

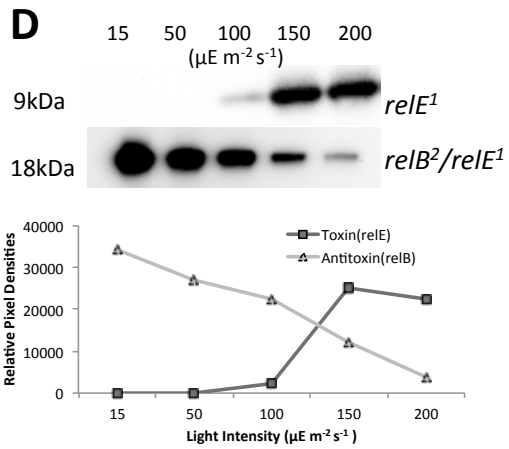


Figure 4.5. Photo-oxidative stress caused by different light intensities induces TA systems and arrests growth of CB0101. A) Growth rate of *Synechococcus* CB0101 under different light intensities; B) CB0101 cultures exposed to different light intensities 15, 50, 100, 150, and 200 μE m^{-2} s^{-1} for 48 h; C) Expression of each CB0101 TA system responding to different light intensities detected by qPCR; D) Western blot analysis of RelE^{1} toxin at 9kDa and RelB^{2}/RelE^{1} dimer at 18kDa under different light intensities with pixel densities measured.

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Chapter 5: Phage infection of *Synechococcus* leads to massive shutdown of genomic island genes

Phage infection of *Synechococcus* leads to massive shutdown of genomic island genes

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Key words: *Synechococcus*, phage-host, genomic islands, host-like metabolic genes

5.1 Abstract

Synechococcus spp. are abundant in the marine estuarine ecosystem and subjected to frequent viral infection. What interactions occur at the molecular level during infection is not well defined. Thus, we investigated the whole transcriptome and proteome expression of the estuarine *Synechococcus* (CB0101) upon infection of podovirus S-CBP1. Strikingly, most differential expression occurred within genomic islands (GI), which were massively shutdown within 30 min post phage infection. Throughout the infection, phage-encoded host-like proteins (*hli, psbA, ThyX*) were highly expressed. Such a strong response in the GI system was not observed when CB0101 was exposed to nutrient or heavy metal stresses. Podovirus S-CBP1 seems to shut down the host GI system promptly to prevent the development of host resistance, meanwhile promoting the activities of some "shared genes" between phage and host. The global shutdown of GI genes in estuarine *Synechococcus* could be an important phage-regulated process for a successful lytic infection.

5.2 Introduction

Picocyanobacteria of the genus *Synechococcus* are ubiquitous and abundant in the world's oceans (1, 2). As a major primary producer, *Synechococcus* contributes significantly to photosynthetic carbon fixation (3, 4). Marine *Synechococcus* are genetically diverse and exhibit geographic niche adaptation (5–14). Due to *Synechococcus spp.* ecological significant and genetic diversity, over 31 genomes have been sequenced (11, 15). Genomes range in size from 2.2 to 2.9 Mbp with 52-67% of their genes (~1570) common to all strains (11, 13). These core genes are often interrupted at discrete locations by genomic islands (GIs) - large regions (more than eight kilobases long) of non-conserved, non-core genes that are sporadically distributed among members of the genus (11, 13).

Hypervariable GI regions are often differentially expressed in response to environmental stressors (16, 17) and viral infection (18). GI genes are involved in niche differentiation, such as nutrient scavenging, stress response, and phage resistance (17, 19, 20). However, they are also characterized by large numbers of novel genes of unknown function, such as those annotated as phage-like genes. The number of GIs is strongly correlated with genome size, often representing 10-31% of the total genome sequence of *Synechococcus* (11).

Synechococcus in the marine environment are subjected to frequent viral infection (21–23). Many viruses infecting marine *Synechococcus* have been isolated, and all are known to belong to three major tailed phage families (*Myoviridae*, *Podoviridae* and *Siphoviridae*) (24–28). Several lines of evidence indicate that GIs are part of the co-evolutionary process between marine cyanobacteria and their phages. Previous work with

Prochlorococcus has identified important phage-resisting machinery (20) and the dominance of up-regulated genes within GIs during podovirus infection (29). Recently, Doran et al., (2015) explored the transcript response of three oceanic *Synechococcus* strains infected by a broad host cyanomyovirus. They found within all three hosts that the vast majority of expression was located in GIs. Will estuarine *Synechococcus* follow the same GI responding pattern found in oceanic *Synechococcus* upon phage infection?

In general, *Synechococcus* living in various marine environments can be subdivided into three major subclusters, 5.1, 5.2 and 5.3 (11, 13, 30). Subclusters 5.1 and 5.3 *Synechococcus* are present in coastal and oceanic waters, while subcluster 5.2 mainly occupies estuaries. Compared to oceanic *Synechococcus*, much less is known about the ecological function and genomic evolution of estuarine species. Subcluster 5.2 *Synechococcus* dominate the estuarine environment (10) making up 20-40 % of phytoplankton chlorophyll-a during the summer (31) and contain a novel pigment cluster (32). Viruses infecting subcluster 5.2 *Synechococcus* have been isolated from the Chesapeake Bay, one such is the podovirus S-CBP1 (28), which infects the well-studied subcluster 5.2 strain *Synechococcus* CB0101 (here-after CB0101). The genome of CB0101 has been sequenced with a genome size of 2.8Mbp and 3,176 genes, of which 343 are GI genes (33).

In this study, we analyzed the genome wide mRNA and protein expression of subcluster 5.2 strain CB0101 during the infection of a lytic phage, S-CBP1, in tandem. Surprisingly, massive down-regulation of host GI genes occurred upon phage infection. Among 129 differentially expressed GI genes, 83 % were down regulated 30 min post

phage infection. This type of rapid and extensive shutdown of host GI systems during infection has not been previously reported.

5.3 Materials and Methods

5.3.1 Synechococcus culture growth

Synechococcus CB0101 was grown at 23 °C under 15 μE m^{-2} s^{-1} continuous light in SN medium with 15 ppt salinity and vitamin B12 (referred to as SN15 medium hereafter). Filtered (0.2 μm pore size) air was bubbled into individual 500 mL cell culture flasks. Six liters of CB0101 culture were grown to exponential phase at a density of $1x10^8$ cells/mL as determined by counting use an Accuri C6 flow cytometer. The culture was then split into 500 mL cell culture flasks to begin the phage host experiments.

5.3.2 Sampling time point determination: One-step growth curve

S-CBP1 growth, burst size, and latent time has previously been characterized by (28), building upon this analysis a one-step growth curve was performed before the RNA-Seq and proteomic analysis to determine sampling points. The one-step growth curve was measured following the method described by Jiang and colleagues (34) with some modifications. In our modified protocol, flow cytometry counting of released viral particles, instead of conventional plaque assay method, was used to avoid plating and shorten the observation time. Phage lysates (approximately 10^9 PFU ml^{-1}) were inoculated into the exponentially growing host cultures (approximately $1x10^8$ cells ml^{-1}, with a doubling time of 24 h, as measured by cell counts) with a multiplicity of infection of 1.2-1.5 for 1 h at 25 °C. The control received the same amount of microwave-killed phage lysates. The mixture was then diluted in fresh SN15 media by 100-fold to

minimize the further adsorption of phage to host cells. After inoculation (taken as T0), a subsample of suspension was withdrawn from each culture periodically for up to 6 days. The released virus-like particles (VLPs) were counted using the Accuri C6 flow cytometer. The latent period was estimated by the time interval of first wave of significant increase in VLPs (3-fold increases as threshold) observed in the samples and found to be 8 h for S-CBP1. From these results the sampling time points of 0.5, 5, and 12 h were selected to roughly correlate to attachment, latent, and cell lysis.

From the one-step growth curve samples time points were determined to best capture the attachment, latent and rise period of infection. 25 mL was sampled at 0.5, 5, and 12 h to roughly correlate with our desired infection periods. Triplicate cultures of CB0101 were grown to exponential phase (10^8 cells ml^{-1}), and then infected with S-CBP1 podovirus (10^8 infective phage particles ml^{-1}) for a multiplicity of infection (MOI) of 1. Triplicate uninfected control cultures were amended with 50mL of microwaved killed S-CBP1 in SN15 medium and sampled at designated time points. Counting of Synechococcus cells and viruses were conducted using the above described flow cytometry method throughout the infection period 0 to 60 h.

5.3.3 RNA-Seq

At the designated time points 25 mL samples were collected and immediately processed for mRNA and protein analysis. Samples were centrifuged at 10,000 rpm then separated using Trizol extraction for RNA and protein. mRNA was extracted from the total RNA using Ambion MICROBExpress kit (Life technologies, AM1905), modified with specific primers for rRNA depletion of CB0101 ribosome. rRNA removal evaluation was conducted using the Agilent 2100 Bioanalyzer resulting in 98 % removal

of rRNA and confirmed the presence of high quality RNA. The NEXTflex RNA-Seq kit (BIOO Scientific, #5129-01) was then used to prepare mRNA libraries for sequencing using the Illumina Hi-Seq. RNA libraries were created and barcodes assigned to each sample for multiplexing of a single Hi-Seq lane. RNA-Seq sequencing was carried out by the Institute of Genome Sciences (IGS) using a Hi-seq with 100bp paired-end read length. Resulting in 144,403,530 read sequences. RNA-seq and exhaustive statistical analysis were carried out using the CLC platform, R, Bioconductor, top-hat/cufflinks, described in detail below (Supplemental Table 5.S1 and Fig. 5.S1-5.S3).

The 100bp reads were aligned separately for each sample to the reference genomes of CB0101 and S-CBP1, using bowtie2. Reads from the whole-transcriptome library were counted for each gene, normalized to uninfected control host transcript levels and to gene length. The normalized data were used for clustering the phage genes by their expression profile and are shown in the supplemental figures 5.S1-5.S11. A summary of the RNA-sequencing data (number of reads, number of mapped reads and so on) is presented in Supplementary Table 5.1.

5.3.4 Normalization of read counts, calculation of RPKM and heat map representation

Read counts of phage and host were normalized separately using the R software package *edgeR* in Bioconductor (35). The results matrices were used for calculating the RPKM values (36) for all genes and for differential expression analysis.

5.3.5 Sample Clustering

After normalization and calculation of RPKM, host-infected and control samples were hierarchically clustered via Pearson's correlation using the pvclust package (37) in R. Node support was calculated through multi-scale resampling (10,000 bootstraps).

5.3.6 Differential Expression Analyses

Differential expression was calculated between infected and control host smaples at every time point, between time points of host control samples and between time points of phage infected samples. Statitistcal package *edgeR* (35) was used and genes with a false discovery rate <0.01 were considered as differentially expressed. Further, genes were "up-regulated" if normalized RPKM >2 and "down-regulated" if <-2.

5.3.7 Functional group assignment to differentially expressed host genes

Host genes found differentially expressed between infected and control samples at every time point were placed into one of 14 functional categories based on MG-RAST (38) by grouping similar functions into the same category using R.

5.3.8 Protein extraction and mass spectrometry analysis

Proteins were extracted using the same sample for RNA extraction. The bottom layer containing proteins was transferred to a new tube and follow the extraction procedure previous described (39). Protein quantification was carried out according to the instruction of 2D Quant kit (GE Healthcare, 80-6482-56). Equivalents of proteins (200 μg) in each sample were loaded on a prepared SDS-PAGE for in gel digestion (40). The generated tryptic peptides were extracted with solvent containing 50 % acetonitrile (ACN) and 0.1 % trifluoroacetic acid, and then vacuum dried using a SpeedVac for further mass spectrometry (MS) analysis.

Samples were introduced into a Waters nanoACQUITY UPLC using a C18 trap column (1.7 μm particle size, 100 μm x 100 mm internal diameter) fitted with a C18 trap column. (5 μm particle size, 180 μm x 20 mm internal diameter). Peptides were eluted at a flow rate of 300 nl/min using an acidified (formic acid, 0.1 % v/v) water-acetonitrile

gradient (2%-35% acetonitrile in 135 min, full-time 185 min). The peptides were subjected to nanoelectrospray ionization followed by tandem mass spectrometry (MS/MS) in a Q EXACTIVE (ThermoFisher Scientific, San Jose, CA) coupled online to the UPLC. Data-dependent scans were conducted by precursor ion selection in the Orbitrap followed by high-energy collision induced dissociation. One full m/z scan between 350 and 2,000 Da was followed by 15 MS/MS scans with a following Dynamic Exclusion duration of 15 s. The electrospray voltage applied was 1.6 kV and the heated capillary was at 280 ˚C. Automatic gain control (AGC) was used to optimize the spectra generated by the Orbitrap.

5.3.9 Protein identification

The instrument data files (.raw) were interpreted using Proteome Discoverer (ver. 1.4.0.288; ThermoFisher Scientific, San Jose, CA). MS/MS spectra were searched with SEQUEST engine against a protein database containing 15,527 translated protein-coding sequences predicted from genome of *Synechococcus* CB0101 and its phage genome as well as 6,774 contaminated bacterial sequences and 247 contaminant sequences such as keratin and trypsin. Database searching was restricted to tryptic peptides. For protein identification, a mass tolerance of 10 ppm was permitted for intact peptide masses and 0.05 Da for fragmented ions, with allowance for one missed cleavages in the trypsin digests and carbamidomethyl (C) as the fixed modification, oxidation (M) as the variable modification. Peptides having a Delta Cn better or equal to 0.05 were using for Percolator. Peptide spectral matches were further validated based on q-value of decoy database search at a level of 1 % false discovery rate (FDR). Peptide identifications were grouped into proteins with Proteome Discoverer according to the law of parsimony and

filtered to 1 % FDR. Finally, proteins matched with at least two peptides were accepted as confident identifications for further bioinformatics analysis.

5.3.10 Functional annotation and semi-quantitative analysis

Functional annotations of identified proteins were derived from their annotations of RNA or DNA sequences. For semi-quantitative analysis (41), spectral counts were normalized by the total number of spectra identified in each sample as well as by the length of the matching protein. The result values were used for statistical significance test and represented as protein expression level.

5.3.11 Genomic Island type gene identification

Genomic island's and genes were identified using the IslandViewer 3 website and interface (42). Following the directions described by the developers CB0101 genome was uploaded for analysis. The resulting information identified 343 potential GI genes present in the genome, with at 4 GI regions confirmed.

5.4 Results

5.4.1 Infection Cycle

When CB0101 was challenged with podovirus S-CBP1, cell counts began declining 8 h after infection, ultimately reaching complete lysis at 48 h. Viral counts began to increase 8 h after infection with progeny first released (Fig 5.1). mRNA and protein samples were taken at 30 min, 5 h and 12 h, respectively, representing attachment, latent, and maturation of phage infection cycle. Statistical analysis confirmed that extensive coverage of both CB0101 and S-CBP1 mRNA were accomplished with 15 to 3 million (~7x coverage) reads mapping to CB0101 and 1.5 to 12 million (~240x

coverage) to S-CBP1. Reproducibility between duplicates were statistically significant (Supplemental Table 5.S1 and Fig. 5.S1-5.S3).

5.4.2 Host response to phage infection

CB0101 contains a total of 3,176 known genes including 2,833 core and 343 GI genes. At 30 min post infection, 5 % (131 genes) of core CB0101 genes were down-regulated, and 3 % (77 genes) were up-regulated as compared to the baseline uninfected control sample (Table 5.1). A continuation of down-regulation was observed 12 h post infection, 9 % (268 genes) of CB0101 core genes while, 2 % (67 genes) were up-regulated ($p<0.01$ and minimum 2 fold) (Table 5.1). The general trend over the infection is more genes being down-regulated while those that are up-regulated stay constant from 30 min to 12 h of infection (Fig 5.2A). 31 % (107 genes) of all GI genes were down-regulated at 30 min post infection, while just 6 % (22 genes) were up-regulated (Table 5.1, Fig. 5.2B). The GI genes were then progressively down-regulated as the infection continued to 12 h, accounting for 69% (235 of 343) of all differentially expressed genes (Table 5.1). When differentially expressed genes are filtered into clusters of orthologous groups (COG), the massive down-regulation of GI genes evident (Fig 5.2B). Interestingly, 20 of the GI genes were constantly up-regulated throughout the entire infection. Among these 20 GI genes, some can be identified and included those coding for high-light-inducible stress response (*hli*), transcription (*rpoC1, rpoA*), ribosome (*rplO*), translocase (*secF, secD*), DNA-binding (*stpA*), menaquinone (menB; electron transport), enolase (eno), accelerated folding of proteins associated with photosynthesis (*TLP40*), sulfide quinone reductase (SQRDL: electron acceptor), and transcriptional regulator (*vidC*).

For the core genes of CB0101, protein metabolism transcripts increased during the early (30 min) infection but gradually decreased (5 h and 12 h) (Fig 5.2B). These protein metabolism genes are almost exclusively ribosomal subunits responsible for translation. Other COG categories that were continuously up-regulated were associated with energy production (i.e. CO2 fixation, ATP synthesis) (Fig 5.2B). In contrast, a set of photosynthetic genes was progressively down-regulated (photosystem II associated genes p*sbL, psbD, psbZ, psbJ, psbL, psbK, psbI, psbY*, and *psbX*).

At the proteomic level, a total of 825 proteins (26% of all predicted) from CB0101 were identified (Fig. 5.3A). At 30 min, 435 proteins were identified, with 112 (4%) core proteins being differentially expressed (Table 5.1). At 5 h post infection, 397 proteins were found, and 60 (2%) were differentially expressed. At 12 h post infection, 362 proteins were identified, and 52 (14%) were differentially expressed. Overall, the downward trend in the number of identified proteins from 30 min to 12 h can also be seen in the COG data (Fig 5.3B). The GI proteins (Hli*,* RpoC1, RpoA, RplO, SecF, SecD, StpA, MenB, Eno, TLP40, SQRDL, and VidC) were up-regulated (by 2 fold) during the entire lytic cycle. Because large portions of GI genes were down-regulated at the mRNA level, proteins of these GI genes were not detectable due to low abundance or from rapid degradation.. Proteins associated with energy production and various forms of metabolism (i.e. CO2 fixation and ATP synthesis) dominated as the most abundant up-regulated protein categories, coinciding with the transcript response (Fig 5.2B and 5.3B).

5.4.3 Phage response during infection

Phage S-CBP1 was linearly transcribed resulting in a lack of differentially expressed transcripts ($p<0.01$ and minimum 2 fold). However, expression clusters can be determined, showing attachment, replication, and maturation stages of infection (Supplemental Fig 5.1-5.3). Nevertheless, differential expression at the protein level was observed, likely due to differences in folding speed (Fig 5.4A). We were able to detect proteins from 55% of the phage genome throughout the infection. Of the 28 phage proteins identified, 12 were differentially expressed (Fig 5.4A), while the remaining 16 were relatively constant over the infection. Three proteins, *hli*, hypothetical protein 15, and *psbA* ranked among the most abundant in the phage proteome (Fig 5.4B). These proteins clustered together in the genome of S-CBP1 at a location labeled "hot spot" (Fig 5.4C). Of the 2,265 phage protein counts, 68-78% belonged to the "hot spot" region proteins (Fig 5.4B & 5.4C). These proteins were constant throughout the entire infection. Moreover, the "hot spot" proteins including ssDNA and ThyX are host-like genes with homologues found in the genome of CB0101.

5.5 Discussion

5.5.1 Rapid shutdown of host GI system

This study is the first to explore the transcriptional and proteomic program of a subcluster 5.2 *Synechococcus* infected by a podovirus. Our findings indicate that GI genes in estuarine CB0101 are far more involved in lytic infection than the host core genes. At 30 min post infection, 129 of 337 differentially expressed transcripts were from GI regions. Among them, 83 % (107 out of 129 genes) were down regulated (Table 5.1). The transcript data is reinforced by the proteomic expression, where a lack of GI proteins is observed (Fig 5.3B), indicting that GI response could be similar to an on-off switch

rather than a gradual change at the protein level. The percentile (83 %) of down-regulated GI genes is much higher than those (35-51%) reported from the responses of marine *Synechococcus* WH7801, WH8102 and WH8109 to the infection of myovirus Syn9 (18). The marked difference in GI gene response to phage infection between estuarine and open ocean *Synechococcus* strains was unexpected. It is unclear why GI genes in estuarine CB0101 are massively shutdown in response to the infection of a podovirus. Such a dramatic response in the GI system was also not observed when marine *Prochlorococcus* MED4 was infected by podovirus P-SSP7 (29).

One potential explanation could be the genomic difference between estuarine (subcluster 5.2) and open ocean *Synechococcus* (subcluster 5.1). It has been known that the number of GI genes varies greatly among *Synechococcus* strains sequenced (11). Estuarine strains like CB0101, CB0205, and WH5701 have relatively large genomes and contain more GI genes than their open ocean counterparts. It is thought that the increased number of GI genes aids in sensing and adapting to the rapid changes for each specific ecotype. Rapid shutdown of GI genes in estuarine CB0101 could be a function that lytic podovirus S-CBP1 use to quickly turn off the GI system to reduce host resistance ability. Further study is needed to understand whether such a GI shutdown during infection is a common feature among estuarine *Synechococcus* or other subcluster 5.2 species.

Another explanation for the unexpected massive shutdown of GI genes could be the superior detection of low abundance transcripts and dynamic range of RNA-seq. This broader dynamic range allows for the detection of more differentially expressed genes (43). This means for RNA-seq, if you sequence deep enough, you can get the same dynamic range as the actual RNA molecules in the sample. While most research papers

have >10 million mapped reads/sample on average, RNA-seq should provide higher sensitivity than microarray, thus allowing for a much clearer picture of whole genome expression.

GI residing genes are often differentially expressed in response to environmental stresses (16, 17, 44). However, in a separate experiment when CB0101 was exposed to nutrient starvation or oxidative stress, only a few genes within the GI regions were differentially expressed (Table 5.2). These results suggest that the GI systems respond differently to phage infection and to these environmental stresses, at least for estuarine CB0101.

5.5.2 Up-regulation of GI genes and proteins

Despite the massive shutdown, 20 GI genes remained up-regulated at the transcriptomic and proteomic level throughout the infection period. These GI genes were coded for high-light-inducible stress response (*hli*), transcription (*rpoC1, rpoA*), ribosome (*rplO*), translocase (*secF, secD*), DNA-binding (*stpA*), menaquinone (menB; electron transport), enolase (*eno*), accelerated folding of proteins associated with photosynthesis (*TLP40*), sulfide quinone reductase (*SQRDL*: electron acceptor), transcriptional regulator (*vidC*). Of these up-regulated genes, similar homologues were also found expressed within *Prochlorococcus* and other *Synechococcus* GI regions (18, 29).

Perhaps the most compelling evidence for host GI genes being linked to a phage infection tactic is the numerous homologues of host-like genes found in the phage genome. The homologues of *hli, psbA, ssDNA*, and *ThyX* can be found within GI regions, which are expressed during infection of CB0101 (Fig 5.2 and 5.3). Furthermore, homologues of similar host genes are prevalent in phage genomes infecting

Synechococcus and *Prochlorococcus spp*. (16, 45). Thus, there seems to be a connection between genes up-regulated during infection, their position in the host genome, and the presence of homologues in phage for both *Synechococcus* and *Prochlorococcus*. Additionally, not only did these same patterns occur in two different host genera, but also in response to infection by phages belonging to two very different phage families, T7-like (29) and T4-like cyanophages (18). It is clear that GI genes play an important role during cyanophage infection(13, 18, 20, 29). We hypothesize that it is possible some of these host responses reflect an attempt at defense against infection, as inferred from the identity of some of the response genes. Alternatively, these genes may be induced by the phage to aid in the replication process, with the immediate response induced by phage proteins entering into the cell together with phage DNA.

5.5.3 Host core gene and protein response

Transcript and protein COG categories display how evidently the host metabolic processes shifted towards phage needs over time (Fig. 5.2B and 5.3B). Upon phage infection (30 min), we observed a much lower percentage of host core gene expression compared to the GI genes. However, the up-regulation of genes associated with phage reliance is evident by increased host ribosomal subunit expression within 30 min of infection. The expression of transcripts and proteins for ribosomal subunits peaked at 5 h and declined during the maturation phase at 12 h. Such a response pattern is consistent with the classical expression phases for other T7-like phage (46). Other transcripts and proteins up-regulated at all time points were associated to energy production (i.e. CO2 fixation, ATP synthesis). In contrast, a set of photosynthesis genes were progressively down-regulated over the time series, specifically photosystem II associated genes *psbL,*

psbD, psbZ, psbJ, psbL, psbK, psbI, psbY, and *psbX*. This is particularly of note because phage replication is a function of host growth rate, which has been linked with a dependence on photosynthesis(47). A decline in host photosystem II transcript and protein could caused by the slow shutdown owning to cell lysis or a factor of phage photosystem proteins replacing/supplementing host factors.

Until about a decade ago, it was generally thought that phage infection led to a complete shutdown of host transcription (48). However, the employment of whole-genome transcriptional analyses to assess responses to infection has shown this not to be the case, with a range of expression in different host-phage systems (18, 29, 49, 50) (this study). First, common across all systems is an immediate brief expression followed by a subsequent response to infection. Furthermore, some but not all bacteria experience a massive decline in host gene expression upon infection. However, our findings can be generalized across subcluster 5.2 *Synechococcus* (this study), marine *Synechococcus* (18), and *Prochlorococcus* (29), with both transient increases in transcript levels accompanied by an overall decline in host expression.

5.5.4 Phage responses

The transcriptomic data shows that the genome of phage S-CBP1 is linearly transcribed, resulting in no differential expression at the mRNA level. Rather, the proteomic data displays a robust response with a set of three highly expressed proteins. Interestingly, a cluster of three phage genes, the "hot spot" region (as described in this paper), made up of *hli*, *psbA*, and a hypothetical protein, were the most active proteins identified throughout the entire infection (Fig 5.4B). The "hot spot" region made up 68-78% of the total protein counts and was constant through the attachment, replication, and

maturation phases. These important phage genes are thought to be significant for continued host photosynthetic activity, production of ATP, and reducing equivalents needed for phage DNA replication and nucleotide biosynthesis (18, 29, 47, 51).

S-CBP1 protein abundance was highly skewed towards host-like genes, specifically Hli, PsbA, ssDNA, and ThyX (Fig 5.4B). The photosynthesis genes found in this cluster are thought to be involved in the production of energy, while ThyX is an alternative type of thymidylate synthase which synthesizes the essential DNA precursor, thymidylate (dTMP), from uridylate (dUMP) (52). Among the sequenced cyanophage genomes, *thyX* is only found in cyanopodoviruses, which infect *Synechococcus* (53). We hypothesize that the "hot spot" cluster and *thyX* in podovirus S-CBP1 are involved in redirection of host metabolism. Together, these findings suggest that these genes form a functional unit to produce energy and deoxynucleotide carbon substrates necessary for cyanophage DNA replication.

The genome content and architecture of the cyanophage S-CBP1 are similar to that of the *Escherichia coli*-infecting T7 podovirus. As in T7, the S-CBP1 genome was transcribed linearly (46) from left to right of the genome map (Fig 5.4C), with three distinct infection phases discerned (Supplemental Fig 5.1-5.7). The first phase includes the *marR* gene, which suggests a role in redirecting transcription from the host towards the phage. The second phase is the expression of genes participating in DNA metabolism and replication, which allow for RNA transcription and/or DNA replication. The third phase consists of genes involved in phage particle formation and DNA maturation. Thus, the three expression phases in S-CBP1 are analogous to T7 and T4-like phage including those infecting *Synechococcus's* sister genera, *Prochlorococcus* (18, 29).

Regardless of the mechanism of shutdown, we hypothesize that S-CBP1 has evolved to not only make use of host up-regulated proteins (such as RpoC1, RpoA, RplO, SecF, SecD, StpA, Eno, TLP40, SQRDL, and VidC*),* but also shutdown potential host defenses within GIs. Certainly, phages are known to exploit host stress-response proteins during infections (54, 55). As well, *Prochlorococcus* have shown phage resistance through shuffling of genes within GI regions (20). We believe that rapid response, within the first 30 mins, to phage infection is common among marine cyanobacteria ((18, 29); this study).

The presence and expression of host-like genes that are involved in the maintenance of photosynthesis, phosphate stress, and mobilization of carbon stores during infection is not a new observation (16–18, 29, 44, 45). However, a central question as to what type of benefit and why they are linked to host GI regions remains unknown. We do know that a statistically significant number of phage host-like genes have consistently been shown to be present in GI regions (16–18, 29, 44). It could be that phages have evolved to use these gene products to gain a fitness advantage. Incorporation of these genes into their own genomes would enable phage to regulate their expression, conferring a fitness advantage, and leading to preferential retention. This retention would increase the probability of transfer back to the host in genome islands, unsuccessful infection, and those genes beneficial to the host would remain in the host genome. Analysis of CB0101's GI regions provides an interesting illustration in support of this scenario. GI genes possibly associated with host defense are down-regulated, while GI gene homologues to phage "host-like" genes are up-regulated in response to phage

infection aiding the host metabolic shift towards phage production. Further work should be conducted to see how GI genes and host-like genes in phages could be linked.

5.6 Conclusion

Estuarine *Synechococcus* strain CB0101 (subcluster 5.2) exhibited a strong shutdown of GI genes in response to infection by podovirus S-CBP1. It is striking to see such a massive shutdown of host GI genes upon infection, compared to a relatively small portion of down-regulation in the non-GI genes. Although GIs are known to be involved in response to environmental stress, we did not observe such a dramatic down regulation when CB0101 was grown under nutrient starvation or exposed to heavy metal toxicity. It could be that podovirus S-CBP1 is able to prevent the development of host resistance by quickly shutting down the GI system as is seen in other T7-like phage.

At the transcriptional level, phage S-CBP1 was linearly transcribed, but three distinct expression clusters (attachment, replication, and maturation) were observed. Several phage-encoded 'host-like' genes (e.g. *hli*, *psbA*, and *thyX*) were highly expressed at the protein level. These "hot spot" phage genes are often found in the GI region, suggesting a mutual benefit for cyanophage and cyanobacteria to maintain ecologically important genes. Studying the role of GI genes in response to phage infection is an important step towards understanding the ecological interaction and co-evolution between cyanobacteria and cyanophage.

Table 5.1. Transcript and protein counts of differentially expressed total core (2,833 genes, core genes are any gene not contained in a genome island) and genomic islands (343 genes) ($p<0.01$ and minimum 2 fold). Identified proteins were 435, 397, and 362 for 30min, 5h, and 12h, respectively.

	Transcriptomics			Proteomics		
	0.5h	5h	12h	0.5h	5h	12h
Total core responsive genes/proteins	208 (7%)	340 (12%)	335 (12%)	112 (4%)	60 (2%)	52 (2%)
Core up-regulated genes/proteins	77 (3%)	132 (5%)	67 (2%)	106 (4%)	52 (2%)	49 (2%)
Core down-regulated genes/proteins	131 (5%)	208 (7%)	268 (9%)	6 (0.2%)	8 (0.2%)	3 (0.1%)
Total responsive GI genes/proteins	129 (38%)	236 (69%)	255 (74%)	21 (6%)	10 (3%)	9 (3%)
# of up-regulated GI genes/proteins	22 (6%)	54 (16%)	20 (6%)	18 (5%)	7 (2%)	8 (2%)
# of down-regulated GI genes/ proteins	107 (31%)	182 (53%)	235 (69%)	3 (1%)	3 (1%)	1 (1%)

Table 5.2. CB0101 Genomic island residing gene transcript and protein differentially expressed under different stressors ($p<0.01$ and minimum 2 fold).

	Viral Infection	Nitrogen Deplete	Phosphate Deplete	Zinc Toxicity
Total responsive GI transcripts	255	74	25	92
Total responsive GI proteins	21	20	10	N/A
# of up-regulated GI transcripts	54	35	15	43
# of up-regulated GI proteins	18	19	7	N/A
# of down-regulated GI genes	235	39	10	49
# of down-regulated GI proteins	3	1	-	N/A

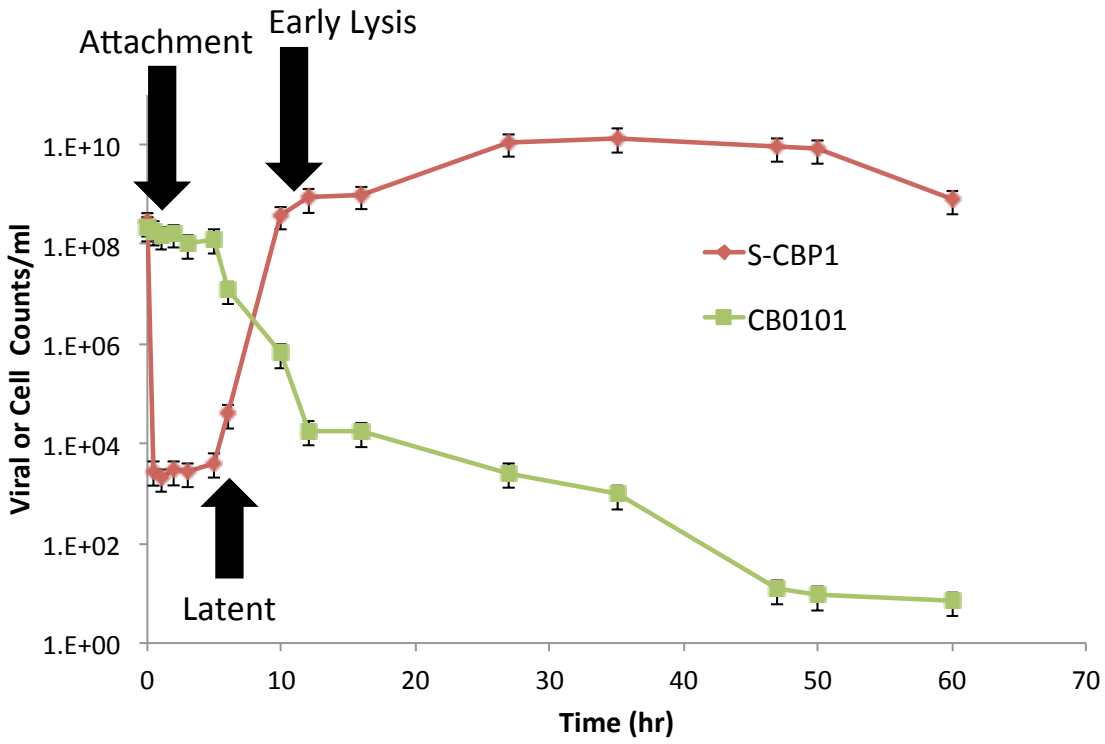

Figure 5.1. Infection dynamics of the S-CBP1 phage in an estuarine *Synechococcus* CB0101 host. Timing of phage replication was determined by one-step growth curve, cell and viral counts. mRNA and protein were measured at 0, 30 min, 5 h, and 12 h to correspond to attachment, latent, and early lysis phases. Total host lysis occurs within 48 h of infection.

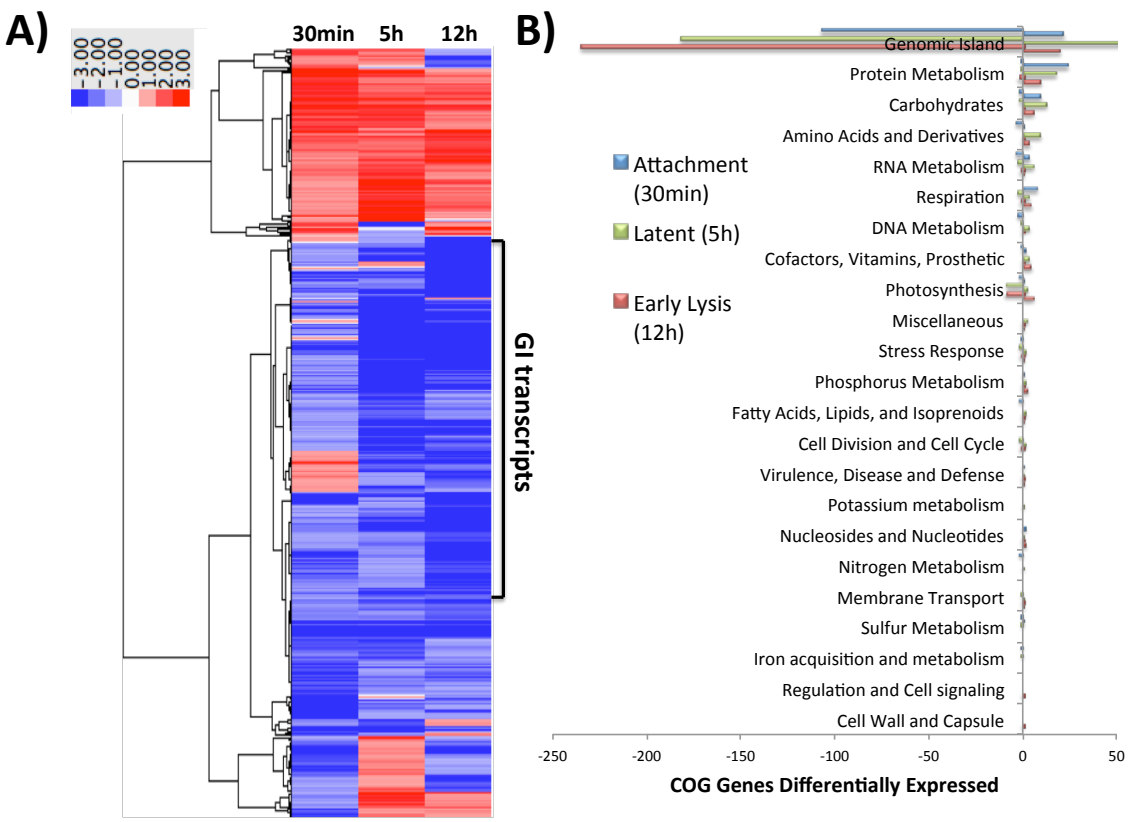

Figure 5.2. The transcript expression program of *Synechococcus* CB0101. (A) Heat map and clustering of the 590 unique differentially expressed genes by their expression patterns ($p<0.01$ and minimum 2 fold). Dark red equates to a strong increase (>3 fold), while dark blue to a strong decrease (<-3 fold) in gene expression. (B) Differentially expressed genes filtered into 23 COGs. X-axis denotes the number of unique genes that are either up-regulated (positive side of graph) or down-regulated (negative side of graph).

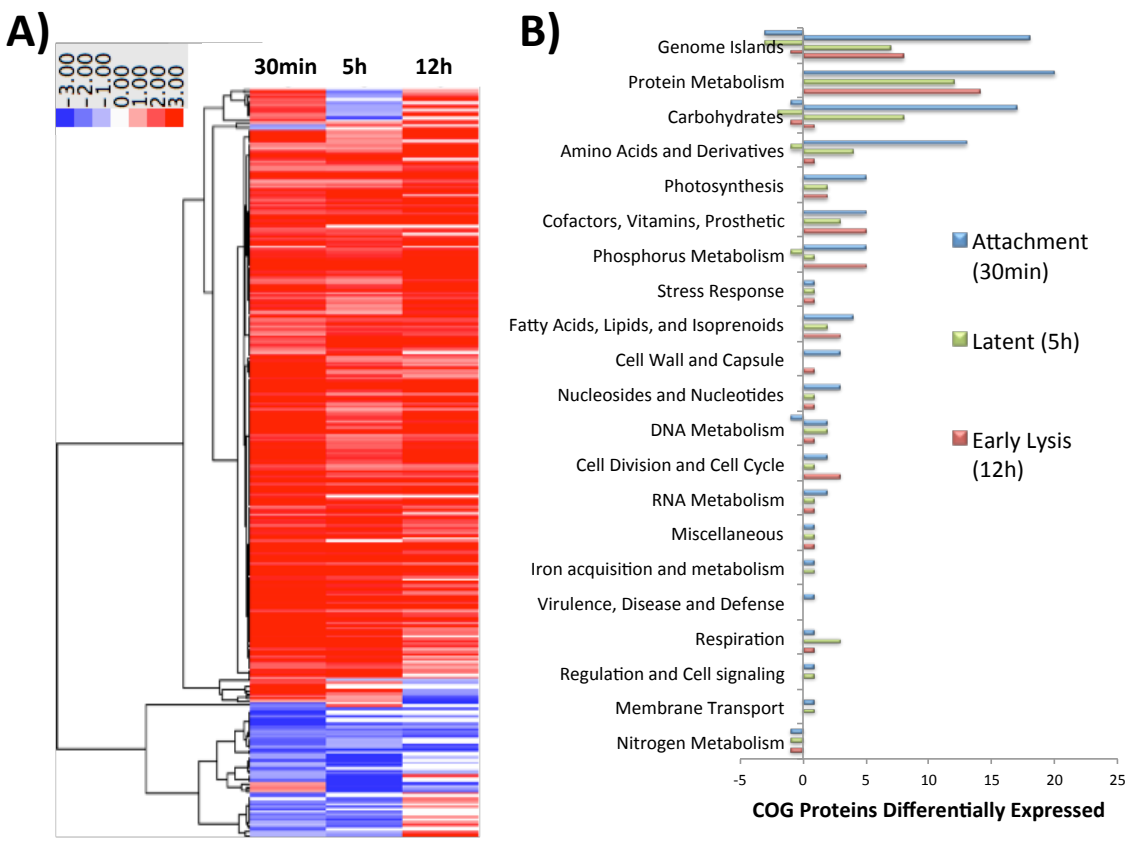

Figure 5.3. The protein expression program of *Synechococcus* CB0101: (A) Heat map and clustering of the 133 unique differentially expressed proteins by their expression patterns ($p<0.01$ and minimum 2 fold). Dark red equates to a strong increase (>3 fold), while dark blue to a strong decrease (<-3 fold) in protein expression. (B) Differentially expressed proteins filtered into 21 COGs. X-axis denotes the number of unique genes that are either up-regulated (positive side of graph) or down-regulated (negative side of graph).

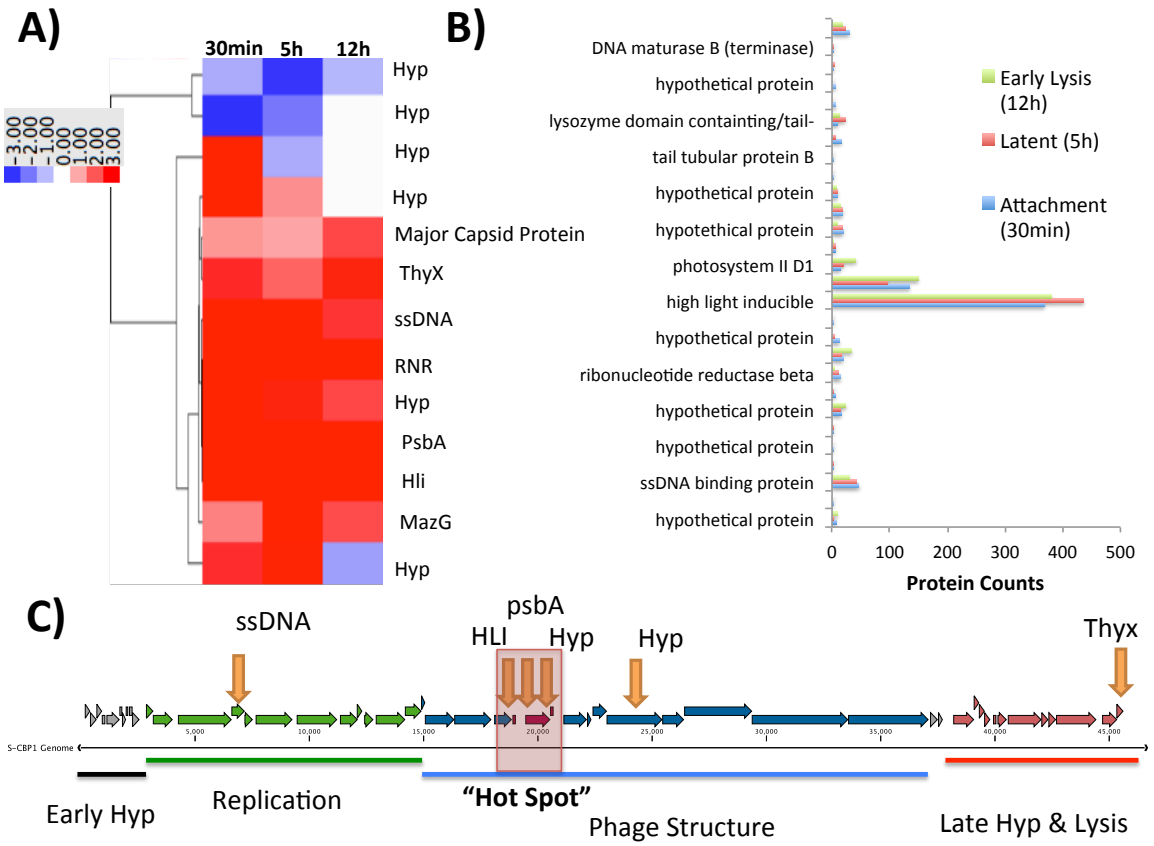

Figure 5.4. Temporal expression dynamics of S-CBP1 phage proteins during infection of *Synechococcus* CB0101. (A) Heat map and clustering of differentially expressed proteins by their expression patterns as compared to T0. (B) Protein counts mapping back to each individual phage protein over the three sampling points. (C) Genome map highlighting the location of the "hot spot" at the center of the genome and the other most expressed phage proteins.

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Chapter 6: Conclusions and Future Directions

6.1 Conclusions

As a representative strain of subcluster 5.2, estuarine *Synechococcus* CB0101 demonstrates its flexibility in response to strong environmental gradients. In comparison with coastal and oceanic *Synechococcus* strains (represented by WH7803 and WH7805, respectively), which are members of subcluster 5.1, estuarine strain CB0101 exhibits strong adaptive capability for handling chemical and physical changes. This is exemplified by the facts that: 1) CB0101 is able to grow in much wider range of salinity (0-35 ppt) compared to WH7803 and WH7805. CB0101 is not affected by salinity changes, while WH7803 and WH7805 are when salinity is lower than 20 ppt; 2) CB0101 can tolerate a wider temperature range (4-35 °C) compared to WH7803 and WH7805, especially when the temperature is below 15°C; 3) CB0101 can tolerate higher concentrations of heavy metals, such as copper and zinc, compared to WH7803 and WH7805. The high environmental tolerance of CB0101 is reflected by the strong seasonal and spatial variations in the Chesapeake estuary. My results show that CB0101 is more sensitive to higher light intensity compared to WH7803 and WH7805, suggesting that some subcluster 5.2 *Synechococcus* found in estuaries could be adapted to lower light availability in the turbid upper Chesapeake Bay. In general, no major difference was observed on the growth of CB0101, WH7803, and WH7805 in terms of nutrient utilization. This work was presented in Chapter 2.

The complete genome sequence of CB0101 was obtained by combining 454 and PacBio sequencing technologies. The genome size of CB0101 is 2.79 Mb, larger than that of WH7803 (2.37Mb) and WH7805 (2.65Mb). The GC content of CB0101 is 63.4%, higher than that of WH7803 (60.0 %) and WH7805 (57.0 %). Higher GC content is

known to increase tolerance and ability for organisms to grow under extreme conditions (1). CB0101 contains many genes involved in stress responses. For example, the chromosome of CB0101 contains 14 toxin-antitoxin genes, which are not found in WH7803 and WH7805. Chromosomal toxin-antitoxin systems are commonly found in prokaryotes and are involved in stress response by regulating the growth of cells or inducing cell death. The CB0101 genome contains 2,833 core genes of which 343 genes are found within genomic islands. The amount of genomic island genes in CB0101 is much higher than that found in coastal and open ocean *Synechococcus*. Genomic islands are known to be the locations where horizontal gene transfer occurs frequently. For example, acquisition of antibiotics or heavy metal resistant genes could enable microorganisms to be more competitive in stressful environments. In comparison with WH7803 and WH7805, CB0101 contains many more genes involved in metal homeostasis, sensor kinases, and various metabolic pathways for nitrogen and phosphorus metabolism. The genomic features of CB0101 suggest that estuarine subcluster 5.2 *Synechococcus* may inherit many stress responding systems, which allows them to thrive in the dynamic estuarine environment. This work was presented in Chapter 3.

In order to understand how CB0101 responds to changing environments at the genomic level, I applied transcriptomics and proteomics to study the expression of mRNA and proteins under different growth conditions. CB0101 was incubated under nitrate limitation, phosphate limitation, and high zinc exposure, respectively. The results show that CB0101 seamlessly adjusts its metabolic pathways, transport systems, and sensing mechanisms when faced with nitrate and phosphate limitation. Oxidative stress

caused by zinc toxicity resulted in a global down regulation of photosystems and translation machinery.

From this study a particularly intriguing translational regulator became apparent; the CB0101 genome contains seven pairs of toxin-antitoxin (TA) genes, which have not been found in known marine *Synechococcus* (and *Prochlorococcus*) genomes. Efforts were made to understand under stress conditions how the TA systems in CB0101 were regulated at the mRNA and protein level. Among the 14 identified TA genes, 2 toxin genes ($yoeB^1$ and $relE^1$) and 1 antitoxin gene ($relB^2$) were significantly up-regulated (> 2 fold) under nitrogen limitation. Three toxin genes ($yoeB^1$, doc^1 and $relE^1$) were up-regulated significantly (> 2 fold) under high zinc exposure. Under phosphate limitation only $relE^1$ was up-regulated. It appears that $relE^1$ is the most sensitive antitoxin gene among the 7 CB0101 toxin genes in response to nutrient and metal stresses as evidenced by high transcriptional fold change. One antitoxin gene $relB^2$ was down regulated (> 2 fold) under nitrogen limitation, and two antitoxin genes $relB^1$ and phd^2 were down regulated (> 2 fold) under high zinc condition. The expressions of these TA genes were comparable between RNA-Seq and qRT-PCR analyses. We developed specific antibodies for the $RelB^2/RelE^1$ TA pair in order to confirm the presence of these proteins. To understand the regulation of TA genes at the protein level, we applied Western blot analysis to observe protein expression of $RelB^2/RelE^1$ TA pair under heavy metal and photo-oxidative light stresses. Under normal growth conditions (control), a protein dimer of $RelB^2/RelE^1$ was detected, indicating strong binding between the inactivated toxin and antitoxin. When CB0101 became stressed by nutrient limitation or heavy metal exposure, the $RelB^2/RelE^1$ dimer decreased, resulting in more $RelE^1$ toxin protein. This inverse

relationship is the result of the antitoxin being degraded, thus allowing the $RelE^1$ toxin protein to act on its intended target, cleaving ribosome bound mRNA, and causing translational inhibition.

When CB0101 was exposed to high zinc concentration, the growth was inhibited with the dimer $RelB^2/RelE^1$ to declining within 24 hours and resulting $RelE^1$ toxin increasing. Upon the removal of zinc toxicity, the growth resumed and the yield of dimer $RelB^2/RelE^1$ increased, indicating that the arrest was reversible when the stress event was removed. A clear $RelB^2/RelE^1$ response was observed when CB0101 was cultivated under a wide range of light intensities (15-200 $\mu E\ m^{-2}\ s^{-1}$). The growth of CB0101 was inhibited and the yield of toxin protein $RelE^1$ began to increase when the light intensity exceeded 100 $\mu E\ m^{-2}\ s^{-1}$. We conceived that TA systems, such as *relB/relE*, allow for niche adaptation to the low light environments of the Chesapeake Bay, enabling *Synechococcus* like CB0101 to thrive. We demonstrate that TA genes in CB0101 are regulated under different manipulated growth conditions at both mRNA and protein level. This TA system is one such example for how CB0101 has an enhanced capability for niche adaptation in a highly variable environment. The actual ecological function of TA system of estuarine *Synechococcus* in the natural environment still remains to be explored. The TA genes of CB0101 appear to originate from genes in diverse bacteria. The finding of TA system in CB0101 led to the discovery of TA systems in eight other marine *Synechococcus* strains including two estuarine strains (WH5701 and CB0205), two coastal strains (KORDI-49 and KORDI-51), and four open ocean strains (RS9916, RS9917, WH8102, and WH8103). The relationship between TA genes among these

marine *Synechococcus* should be further investigated. This work was presented in Chapter 4.

Synechococcus CB0101 is infected by many phages isolated from the Chesapeake Bay. How does CB0101 respond to a phage infection at the molecular level? S-CBP1 is a podovirus, which infects CB0101, and whose complete genome has been sequenced in our lab. I monitored the global gene expression of host CB0101 and phage S-CBP1 simultaneously using transcriptomics and proteomics, following a viral infection cycle, which included attachment, latent, and early lysis stages. Surprisingly, a massive shutdown of genes located in the genomics islands (GI) of CB0101 was observed upon the attachment of phage S-CBP1 (within 30 minutes of phage addition). The down-regulation of GI genes continued to increase at the latent and early lysis stages. Many genes located in the GI regions aid in the development of phage resistance. It is unclear why the infection of a cyanophage results in such dramatic shutdown of GI genes of host. A possible explanation is that podovirus S-CBP1 prevents the development of host resistance by quickly turning off the host GI system.

Many cyanophages are known to contain host-like genes, especially the genes related to photosynthesis. Despite the rapid shutdown of host GI genes upon phage infection, several phage-encoded host-like genes (e.g. *hli*, *psbA*, and *thyX*) in phage S-CBP1 were highly expressed at the protein level. This result suggests that expression of these host-like genes is critical during the phage infection. This work was presented in Chapter 5.

In summary, my dissertation greatly deepens our understanding of the physiology and ecology of the member of subcluster 5.2 *Synechococcus* CB0101. The application of

multi-omics (genomics, transcriptomics, and proteomics) provides new insight into the specific molecular mechanisms used by subcluster 5.2 *Synechococcus* for its niche partitioning.

6.2 Future Directions

Picocyanobacteria are abundant and ubiquitous in the aquatic ecosystem. As a major group of picocyanobacteria, *Synechococcus* species exhibit great adaptive ability and genetic diversity throughout the marine environment. Estuaries are highly variable ecosystems where nutrient rich freshwater meets seawater. The overall understanding of how *Synechococcus* subcluster 5.2 live and adapt to the estuarine environment is still limited. However, my dissertation research offers the first biological and molecular evidence on how subcluster 5.2 *Synechococcus* strain CB0101 responds to potential environmental stresses, and this is the first step towards understanding ecological adaptation and molecular evolution of subcluster 5.2 or estuarine *Synechococcus*.

6.2.1 Still a lot to learn from Chesapeake Bay Synechococcus

The Chesapeake Bay is an ideal estuary to investigate the biographic distribution of subcluster 5.2 *Synechococcus*. It has been shown that the population structure of *Synechococcus* changes greatly with salinity and temperature (2–4). In order to gain a comprehensive understanding of genetic regulation in subcluster 5.2 *Synechococcus* and the underlying physiological response variations, additional cultures should be isolated from different times and locations. The strains from subcluster 5.2 could then be compared at the physiological and omics level to further define the adaptability of subcluster 5.2 *Synechococcus*.

The finding that CB0101 has low light adaptability is an interesting feature. CB0101 was isolated from the upper Chesapeake Bay; therefore, will other subcluster 5.2 *Synechococcus* isolated from the Chesapeake Bay also be sensitive to light? Or is this merely a factor of niche adaptation for CB0101? Further, is it possible to see light partitioning of *Synechococcus* along the salinity gradient of Chesapeake Bay?

Additional genome sequences from subcluster 5.2 *Synechococcus* are needed. Currently, only one complete genome sequence (CB0101) is available for estuarine subcluster 5.2 *Synechococcus*. The other two estuarine isolates, *Synechococcus* WH5701 and CB0205, contain uncompleted genome sequences. I would recommend fully sequencing additional subcluster 5.2 members, which represent different clades and niche habitats of the Chesapeake Bay.

With the additional genomes an extensive comparative genomics analysis could be conducted. I anticipate this comparative genomics analysis will first focus on subcluster 5.2 *Synechococcus,* identifying unique genes between different niches and the creation of a broad picture of the genetic capacity of each clade. Furthermore, comparative genomics between winter and summer Chesapeake Bay *Synechococcus* could provide a better understanding on cold adaptation of *Synechococcus*. From this analysis, a comparison of freshwater, estuarine, coastal, and open ocean *Synechococcus* could be conducted to identify genes unique to estuarine and subcluster 5.2 strains, which allow for their increased adaptability to variable environments.

Another dataset to study is the meta-genomic and meta-transcriptomic data we collected in the Chesapeake Bay and Delaware Bay between 2013 and 2015. This DOE-supported sequencing effort includes viral and bacterial samples in both bays over

temporal and spatial scale. Once the final sequence data is analyzed, we can focus the sequence data on the *Synechococcus* communities. This survey will allow us to investigate how different types of *Synechococcus* are distributed along the estuarine gradient; what *Synechococcus* genes are highly regulated *in situ*; and how *Synechococcus* gene expression is related to environmental variation. Moreover, the interaction between *Synechococcus* and phage can be explored by examining both viral and bacterial meta-omics data.

The above analyses not only hold scientific importance, but also economic. The Chesapeake Bay creates an economic value between $3.39 billion in sales and $890 million in income. In order to better predict future output and protect this valuable recourse a firm understanding throughout the entire food chain must be appreciated. Numerous studies have examined the importance of copepods to higher trophic level organism like oysters, Blue Crabs, and Stripped Bass. These organisms have an economic value in the Chesapeake Bay of $44 million, $78 million, and $500 million respectively. The collapse of copepods would cause irreparable harm to the major fisheries. In order to fully appreciate what copepods food source we need to fully understand the picocyanobacteria communities in the Chesapeake Bay, which they feed on.

Recent research has discovered that marine picocyanobacteria are an important food source for copepods, making up between 40-60% of their digested gut content. *Synechococcus* can contribute as much as 40% of primary production during the summer months of the Chesapeake Bay. Among metazooplankton, appendicularians, cladocerans, rotifers, and bivalve larvae are known to substantially feed on picocyanobacteria. It has recently been shown that copepods not only ingest but also assimilated *Synechococcus*.

Therefore, grazing on *Synechococcus*, like CB0101, by crustacean zooplankton should be more appreciated in food web and productivity assessments. The grazing on *Synechococcus* may be a common year-round phenomenon, in aquatic environments, like the Chesapeake Bay. If copepods are capable to directly and efficiently utilize *Synechococcus*, this would facilitate a direct energy transfer from microbial to metazooplankton, surpassing the microbial loop. Thus, a full study on Chesapeake Bay picocyanobacteria community structure, abundance, and analysis of copepod digested picocyanobacteria should be conducted in order to ensure sustainability of this invaluable fishery.

6.2.2 How large of a role do TA systems play in picocyanobacteria?

Our work with TA systems in CB0101 demonstrates an exciting regulatory mechanism within picocyanobacteria. The presence of at least one TA in other *Synechococcus* strains allows for a much wider and comprehensive exploration of their potential function. One such example would be TA system cross-talk within CB0101. It has been shown that other bacterial TA systems mutually affect each other's expression and activity (5). Most bacteria have many different TA systems like CB0101. Although their functions are debatable, many TA toxins have similar activity and an inhibitory effect on bacteria. Therefore, an important question is whether TA systems are redundant or not. Another intriguing issue is whether distinctive TA systems are functionally connected and cross-talk in *Synechococcus*, as seen in other prokaryotes (6, 7). It was found in *E. coli* that such cross-reaction occurs with the $relB^2/relE^1$-dependent transcriptional activation of *mazE/mazF* (5). As both TA systems are present in CB0101 it would be interesting for future work to see if such cross-reaction or cross-talk can

occur in *Synechococcus spp*. Examples of future studies that should be pursued include: 1) A comprehensive search of publically available partial and complete genomes from *Synechococcus* and *Prochlorococcus* for TA systems. This will allow us to identify the distribution of TA genes within picocyanobacteria and potentially understand the evolution of TA genes in picocyanobacteria. 2) *In situ* monitoring of the expression of *Synechococcus* TA genes is an important step for demonstrating the ecological relevance of TA system in the natural environment. For examples, we do not know how abundant TA genes are in the Chesapeake Bay. Further, if TAs are expressed, are there differences between the upper bay *Synechococcu*s compared to those of the lower bay? Additionally, are different types of TA genes more prevalent in different niche habitats? Although meta-transcriptomics is a powerful tool to address this question, other specific detection methods such as qRT-PCR or antibody analysis can be used to quantify the expression of specific genes or proteins over various biogeochemical gradients. The major challenge will be to identify the suitable gene markers that are conserved among a defined *Synechococcus* group.

6.2.3 GI response: A factor only in CB0101 infection or a wider trend?

With the increased appreciation of GI regions in picocyanobacteria, it has become clear that these areas play important parts, not only in niche adaptation, but also in phage infection. However, as stated in the above section, many of the genes found within GIs are hypothetical or poorly understood due to a lack of homology to known functional proteins. Earlier studies, together with this work, have shown that many GI genes respond to phage infection, often with over a 2-fold response as compared to control. In order to fully understand what is occurring, many of these genes need to be elucidated. It is

possible that there is a cross-talk system between GI regions, which would confirm why there is a global shutdown of almost every GI region. Further, it is clear that host-like genes in the phage genome are playing a part during infection. It has been suggested that they are used to increase phage fitness during infection, but this hypothesis has not been fully confirmed. Future questions that still need to be answered include: 1) Is this GI response common among *Synechococcus* strains, or is this a variation from this single system? A single study, which includes a large deal of sequencing depth using RNA-Seq to test results, can be found in (8, 9). 2) If the *hli*, *psbA*, and *ThyX* genes are knocked out from the phage, how is the infectivity affected, if at all? 3) Do other podoviruses that infect CB0101 cause the similar GI response? How do the GI regions of CB0101 react to the infection of myoviruses or siphoviruses?

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Appendices

Table 3.S1 Sequencing statistics from RNA-Seq experiments run on an Illumina Hi-Seq 100bp paired end reads.

Sample Name	Control		N Deplete		P Deplete		Zn Toxicity	
Replicate	1	2	1	2	1	2	1	2
Number of reads	16,475,981	15,255,472	21,253,553	17,331,616	20,081,184	12,868,239	25,707,352	15,430,133
Mapped reads	14,851,449	13,460,718	19,393,230	15,550,524	17,517,735	11,625,811	23,913,853	13,631,813
% mapped reads to CB0101	90%	88%	91%	90%	87%	90%	93%	88%

Table 2.S2 Stress response COG categories as compared between the genomes of *Synechococcus* CB0101, WH7803 and WH7805.

Category	Subcategory	Subsystem	Role	CB0101	WH7805	WH7803
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Chaperone protein DnaJ	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Chaperone protein DnaK	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Glutathione synthetase (EC 6.3.2.3)	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Heat shock protein GrpE	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Heat-inducible transcription repressor HrcA	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Hypothetical radical SAM family enzyme in heat shock gene cluster, similarity with CPO of BS HemN-type	x	x	-
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Nucleoside 5-triphosphatase RdgB (dHAPTP, dITP, XTP-specific) (EC 3.6.1.15)	x	x	-
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Ribonuclease PH (EC 2.7.7.56)	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	Translation elongation factor LepA	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	rRNA small subunit methyltransferase I	x	x	x
Stress Response	Heat shock	Heat shock dnaK gene cluster extended	tmRNA-binding protein SmpB	x	x	x
Stress Response	Osmotic stress	Betaine biosynthesis from glycine	Dimethylglycine N-methyltransferase	-	x	x
Stress Response	Osmotic stress	Betaine biosynthesis from glycine	Glycine N-methyltransferase (EC 2.1.1.20)	-	x	x
Stress Response	Osmotic stress	Betaine biosynthesis from glycine	Sarcosine N-methyltransferase	-	x	x
Stress Response	Osmotic stress	Choline and Betaine Uptake and Betaine Biosynthesis	L-proline glycine betaine ABC transport system permease protein ProV (TC 3.A.1.12.1)	-	x	x
Stress Response	Osmotic stress	Choline and Betaine Uptake and Betaine Biosynthesis	L-proline glycine betaine ABC transport system permease protein ProW (TC 3.A.1.12.1)	-	x	x
Stress Response	Osmotic stress	Choline and Betaine Uptake and Betaine Biosynthesis	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)	-	x	x
Stress Response	Oxidative stress	Glutaredoxins	Glutaredoxin 3 (Grx1)	x	x	x
Stress Response	Oxidative stress	Glutaredoxins	Uncharacterized monothiol glutaredoxin ycf64-like	x	x	x
Stress Response	Oxidative stress	Glutathione: Biosynthesis and gamma-glutamyl cycle	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	x	x	x
Stress Response	Oxidative stress	Glutathione: Biosynthesis and gamma-glutamyl cycle	Glutathione synthetase (EC 6.3.2.3)	x	x	x
Stress Response	Oxidative stress	Glutathione: Non-redox reactions	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	x	x	x
Stress Response	Oxidative stress	Glutathione: Non-redox reactions	Lactoylglutathione lyase (EC 4.4.1.5)	x	x	x
Stress Response	Oxidative stress	Glutathione: Redox cycle	Glutaredoxin 3 (Grx1)	x	x	x
Stress Response	Oxidative stress	Glutathione: Redox cycle	Glutathione peroxidase (EC 1.11.1.9)	x	x	x
Stress Response	Oxidative stress	Glutathione: Redox cycle	Glutathione reductase (EC 1.8.1.7)	x	x	x
Stress Response	Oxidative stress	Glutathione: Redox cycle	Uncharacterized monothiol glutaredoxin ycf64-like	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Alkyl hydroperoxide reductase subunit C-like protein	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Fe2+/Zn2+ uptake regulation proteins	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Ferric uptake regulation protein	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Ferric uptake regulation protein FUR	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Ferroxidase (EC 1.16.3.1)	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Iron-binding ferritin-like antioxidant protein	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Non-specific DNA-binding protein Dps	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Peroxide stress regulator	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Superoxide dismutase [Fe] (EC 1.15.1.1)	x	x	x
Stress Response	Oxidative stress	Oxidative stress	Zinc uptake regulation protein ZUR	x	x	x
Stress Response	Oxidative stress	Oxidative stress	transcriptional regulator, Crp/Fnr family	x	x	x
Stress Response	Oxidative stress	Protection from Reactive Oxygen Species	Superoxide dismutase [Fe] (EC 1.15.1.1)	x	x	x
Stress Response	Oxidative stress	Glutathione: Non-redox reactions	Distant similarity with leukotriene C4 synthase (microsomal glutathione S-transferase)	x	-	-
Stress Response	Oxidative stress	Glutathione: Non-redox reactions	Glutathione S-transferase (EC 2.5.1.18)	x	-	-
Stress Response	Oxidative stress	Glutathione: Non-redox reactions	Glutathione S-transferase family protein	x	-	-
Stress Response	Oxidative stress	Oxidative stress	Manganese superoxide dismutase (EC 1.15.1.1)	x	-	-
Stress Response	Oxidative stress	Oxidative stress	Rubrerythrin	x	-	-
Stress Response	Oxidative stress	Rubrerythrin	Rubredoxin	x	-	-
Stress Response	Oxidative stress	Cluster containing Glutathione synthetase	Putative Holliday junction resolvase YggF	-	x	x
Stress Response	Oxidative stress	Glutathione: Biosynthesis and gamma-glutamyl cycle	Similar to 5-oxoprolinase (EC 3.5.2.9) and Methylhydantoinases A, B (EC 3.5.2.14)	-	x	x
Stress Response	Oxidative stress	Oxidative stress	Catalase (EC 1.11.1.6)	-	x	x
Stress Response	Oxidative stress	Oxidative stress	Peroxidase (EC 1.11.1.7)	-	x	x
Stress Response	Oxidative stress	Oxidative stress	Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)	-	x	x
Stress Response	no subcategory	Hfl operon	GTP-binding protein HflX	x	x	x
Stress Response	no subcategory	SigmaB stress responce regulation	RNA polymerase sigma factor SigB	x	x	x
Stress Response	no subcategory	SigmaB stress responce regulation	Serine phosphatase RsbU, regulator of sigma subunit	x	x	x
Stress Response	Detoxification	Glutathione-dependent pathway of formaldehyde detoxification	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	-	-	x
Stress Response	Detoxification	Glutathione-dependent pathway of formaldehyde detoxification	S-formylglutathione hydrolase (EC 3.1.2.12)	-	-	x
Stress Response	Oxidative stress	Oxidative stress	Metallothionein	-	-	x

Table 4.S1 Protein description of the TA systems found within CB0101. Toxin represented by bold and anti-toxin by italics. *Bold amino acid sequences were used for peptide selection of antibodies.

TA Family	Amino Acid Sequences	PI	Mw
yefM[1]	MGSISASEARRRLFALIDEVRESHQPVEIHGKRGSAVLLAEQDWRAIQETLYLCAIPGMRESILEGLATPVEELSEDAGW	4.77	8891.07
yoeB[1]	MSWRVLFTRQAQKDARKLASSSPALKNKAQQLLELLAVDPFQQPPPFEALVGDLQGAYSRRINIQHRLVYAVDREAAVVK VLRLWSHYD	9.98	10215.81
phd[1]	MESSIGAFEAKAQLSRLLRAVEQGEHFTITVRGRPVADLVPHRSPSSEGVAAAIEALQAFPRIRGVSDADVTSFVAEGRR	4.95	14900.04
doc[1]	MTLVIDASMALAWVFERQQASDAQRASELLACCGQQAWWVPGLWHLEVANALLVAERRGVIAQDASDLFLVRLSSLPIC TDSDAGPEQQPRLIALARAHGLSSYDATYLDLAHRLGAALASFDRQLNQAAVAMGVPLT	6.92	9311.45
vapB[1]	MTASLPSRVFNNGNSQAVRIPAEFRLGTDQVQISRTPEGDLLIHPCPPQRGQALFNALAGFDADFAERLEQSRAEAQPIQ TREGL	5.21	9319.42
vapC[1]	MIYLLDTNILIYLIKQRPPEVAERIDQLPGTAQLAMSFITWAELLQGAVGSSRRDAVERQLDHLARQVEVLYPEDSQICRHYA EQATALRRAGTPIGANDLWIACHALAVDATLVTHNLREFTRMSGLSVVDWVQQP	5.48	15422.67
relB[1]	MHLLLDTHLLIWAMGSPQRLPNGLADMLEDPGNTPLFSVASLWELVIKQAPNKPDFNVQPALLRRALLECGWQELTITAN HALAVADLPPLHRDPFDRLLLAQAKADGLLLITADEQLARYPGPIRWMAPLRPSEES	5.22	15254.73
vapC[2]	MLLDTGMRQVNMHEAKTHLSRLVEEAAAGESFLICKAGKPMVRVTSIDQSDAPRPLPRRLGLLEGQCSVPDDFDRFGSE AIADLFEGA	5.02	9614.99
relB[2]	**MAQVTARLPDDLTAELDAVAQQLNRCRADVIRQAIEYYLDDIEDLRAGAASLRDPADPVLDWAEVRDVLLAAD**	4.06	8081.04
relE[1]	**MCCSLRIKRSAAKALAELPNADRLRLVAAIDKLCEVPAAGSALKGEFEGLRRLRVGRYRIVCEWQQQELVVLVVRVGH RKEVYR**	9.95	9533.32
mazE[1]	MTMRYDGEAVVRARLFMSGRSQALRLPARLRLRGPDVEIEPIGDGLWVQPCADPSEGLGDWLERFYADHPPLPVEFLED RQDQQPQERDWA	4.64	10520.84
mazF[1]	MRRTLDTNICSYVLRKRPVQVVERFRQLDRRQLWLSAIVAAELRFGAEKLGSSRFRGSVEAWLSGFELRDWPLAATHHY ARLRAQLEAKGTPVGNLDLMIAAHALAEDSVVITNNAREFHRIPGVAVEEWQLD	9.5	15208.44
phd[2]	MRTVNVHEAKTHFSRLIDAAHAGETIVVAKGGKPWARLVPLETPAPQRQPGVLAGQLQLPPPEILLEALPEDELRAFEIPL P	5.86	8944.4
doc[2]	MSAATAWELATKVRLGKLEIAEPLLSDLPCLLAAQGFELLSVDLRHGLRAGGYPHAHRDPFDRLLVAQAELESLTLVSINAA LRDFPCRLLW	5.84	10133.81

Table 4.S2 Toxin-antitoxin pairs as identified in the genome of the estuarine *Synechococcus* CB0101 during phage infection by S-CBP1. Toxin represented by bold and anti-toxin by italics.

TA Pair #	TA Family	Toxin Activity	Viral 30min RNA-Seq	Viral 30min qPCR	Viral 5hr RNA-Seq	Viral 5hr qPCR	Viral 12hr RNA-Seq	Viral 12hr qPCR
1	*yefM*[1]	mRNA interferase or inhibitor of translation initiation	-1.2	-1.1	-1.1	-1.1	-1.2	-1.1
1	**yoeB**[1]		-1.0	-1.0	-2.0	-1.8	-1.6	-1.4
2	*phd*[1]	Binds to the 30S ribosomal subunit	-1.8	-1.9	-2.0	-2.0	-2.9	-2.7
2	**doc**[1]		-1.8	-1.5	1.3	1.4	-1.3	-1.3
3	*vapB*[1]	Cleavage of tRNA	1.1	1.0	1.0	1.0	-1.2	-1.1
3	**vapC**[1]		-1.0	-1.0	1.4	1.4	-1.1	-1.1
4	*relB*[1]	Cleavage of tRNA	1.0	1.0	-1.0	-1.0	-2.1	-2.0
4	**vapC**[2]		-1.1	-1.0	-1.1	-1.0	1.0	1.0
5	*relB*[2]	Cleavage of ribosome-bound mRNA	-1.0	-1.0	-1.1	-1.1	-1.3	-1.2
5	**relE**[1]		2.5	2.6	-1.3	-1.2	1.7	1.7
6	*mazE*[1]	Ribosome-independent mRNA cleavage and cleavage of 23S rRNA	-1.1	-1.1	-1.5	-1.4	-2.3	-2.2
6	**mazF**[1]		-3.2	-3.1	1.3	1.2	-1.1	-1.3
7	*phd*[2]	Binds to the 30S ribosomal subunit	-1.0	-1.0	1.0	1.0	1.5	1.5
7	**doc**[2]		-1.4	-1.3	-1.4	-1.5	-1.3	-1.3

Table 4.S3 Primers developed for qPCR confirmation of RNA-Seq transcript expression. Toxin represented by bold and anti-toxin by italics.

TA Pair #	TA Family	**Forward Primer**	**Reverse Primer**
1	*yefM*[1]	cgttgagattcacggcaag	tcgctcagttcctccacag
1	**yoeB**[1]	caagctcgctagctcctcac	tcagtcgtagtggctccaga
2	*phd*[1]	gagtgagcttttggcttgct	cagataggtggcgtcgtagc
2	**doc**[1]	acggttactgagggctgttg	cacatctgcatccgaaacac
3	*vapB*[1]	gtcattgcctagccgtgtgt	gattgctccaaacgttcagc
3	**vapC**[1]	caggtggaggtgctgtatcc	acccaatccaccacagacag
4	*relB*[1]	ctggacacacacctgctgat	agttcttgccagccacactc
4	**vapC**[2]	acccacctctctcgcctagt	tacagaacattggccctcca
5	*relB*[2]	aatcgatgccgagctgac	ctcagcccaatccagaacag
5	**relE**[1]	acaagctttgcgaggttcc	gatacacctccttgcgatgc
6	*mazE*[1]	gatatgacggtgaggctgtg	gagggtgatcggcatagaag
6	**mazF**[1]	gctctccgggtttgagttg	caatccaactgccactcctc
7	*phd*[2]	ttccacattcagcaggacag	gttgatcgcgcacgtagat
7	**doc**[2]	tctgagtgatctgccgtgtc	agcgtgagtgattccagctc

Table 5.S1 Sequencing statistics from RNA-Seq experiment run on Illumina Hi-Seq 100bp paired end read.

Time point	0min		30min		5h		12h	
Replicate	1	2	1	2	1	2	1	2
Number of reads	16,475,981.00	15,255,472.00	15,763,839.00	13,632,482.00	10,767,144.00	30,896,516.00	16,248,159.00	11,845,502.00
Mapped reads	15,518,810	14,588,719	14,758,335	13,102,290	10,557,414	27,372,056	14,974,210	11,443,627
% mapped reads	94%	96%	94%	96%	98%	89%	92%	97%
Mapped to phage	-	-	1,566,536	2,829,025	3,588,045	12,932,785	11,081,136	8,351,591
Mapped to host (non-rRNA regions)	15,518,810	14,588,719	13,191,799	10,273,265	6,969,369	14,439,271	3,893,074	3,092,036
% mapped to phage/mapped to non-rRNA	0%	0%	10%	21%	33%	42%	68%	71%
% mapped to host/mapped to non-rRNA	94%	96%	84%	75%	65%	47%	24%	26%

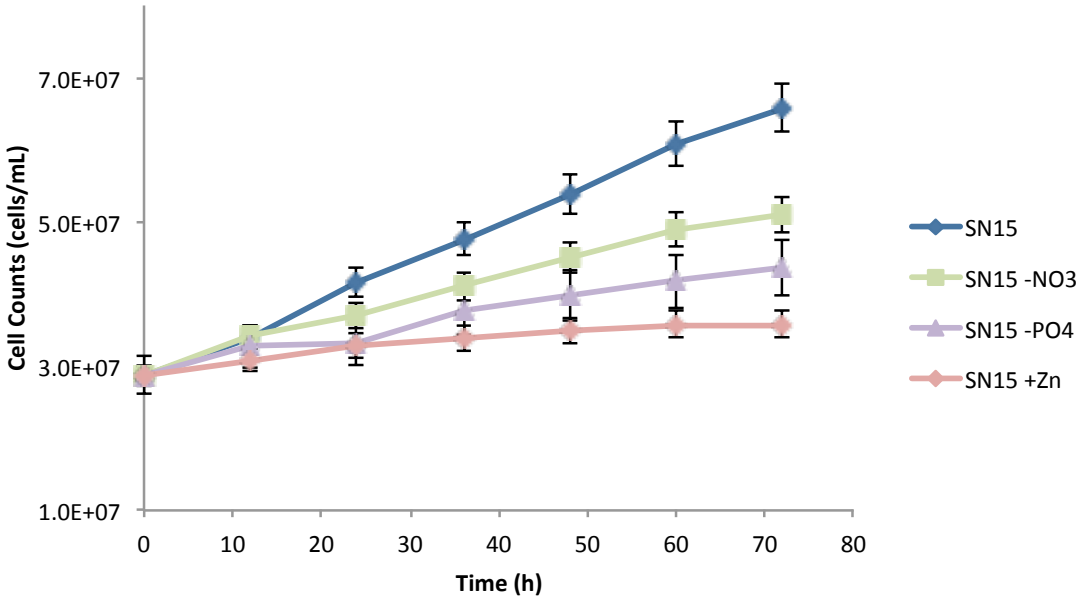


Figure 3.S1 Experimental setup for stress response of the estuarine *Synechococcus* CB0101 Depicts growth after 72 h under the different stress conditions with "C" control, "N-" nitrogen deplete, "P-" phosphate deplete, and "Zn" zinc toxicity.

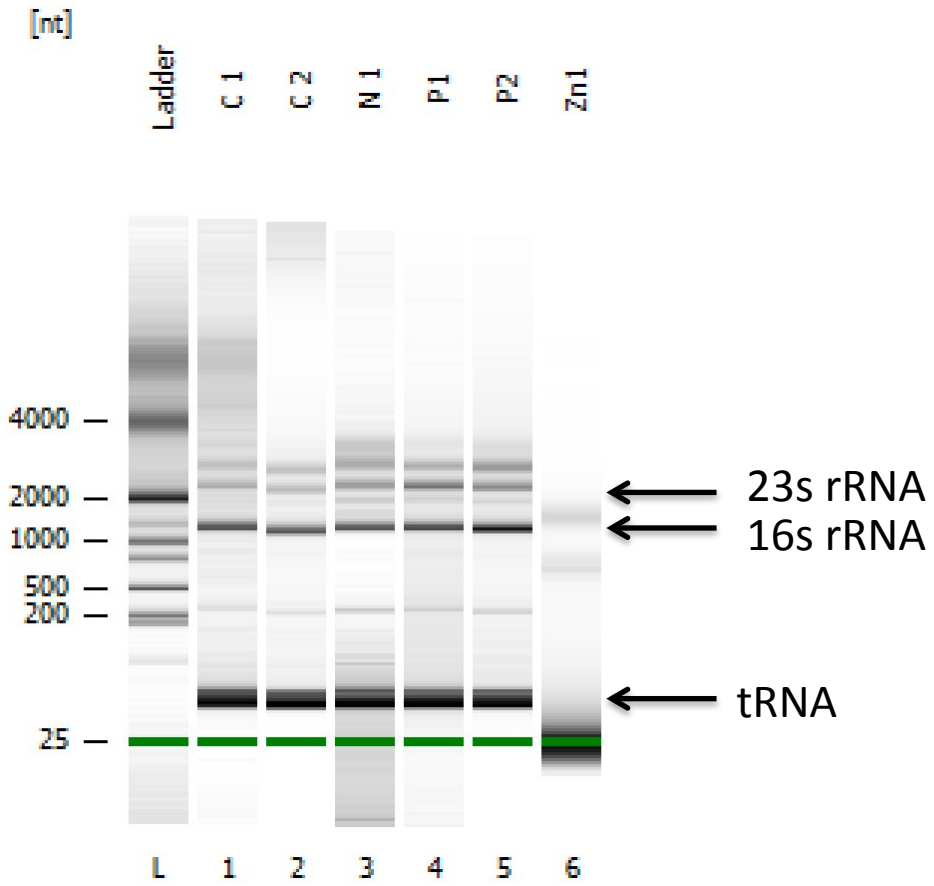


Figure 4.S1 Agilent 2100 Bioanalyzer analysis of total RNA controls and 5 treatments. Other lanes represent Control (C1 & C2), nitrogen deplete (N1 & N2), and phosphate deplete (P1 & P2) each with intact ribosomal subunits, while Zn is degraded.

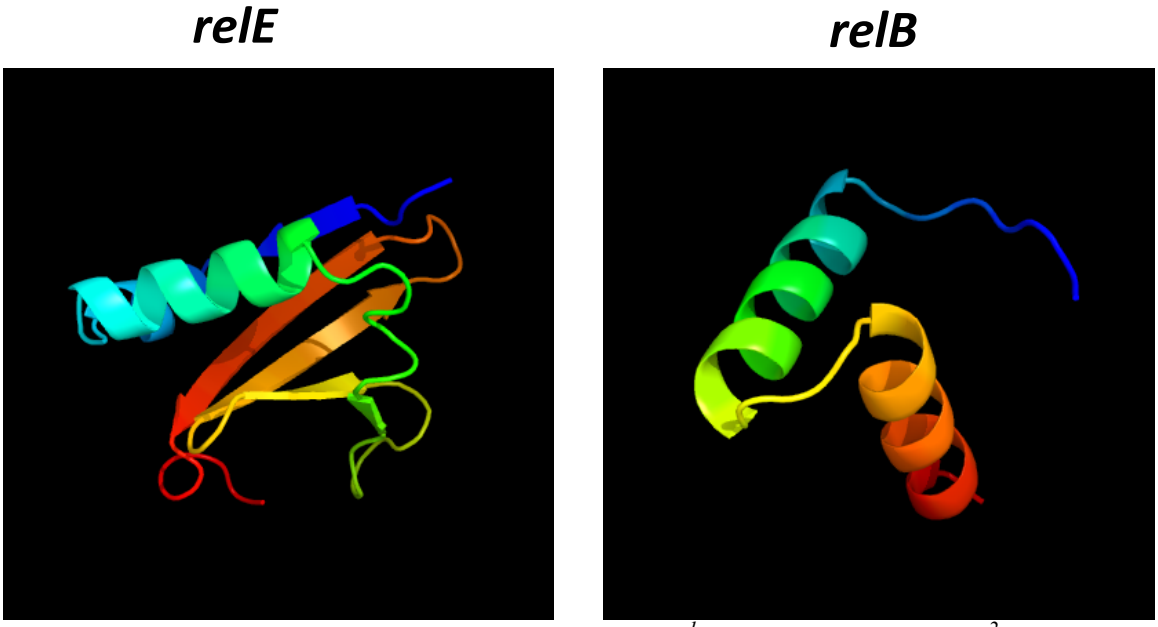


Figure 4.S2 Predicted protein structure of the *relE*[1] toxin protein and *relB*[2] antitoxin from CB0101 made using phyre2.

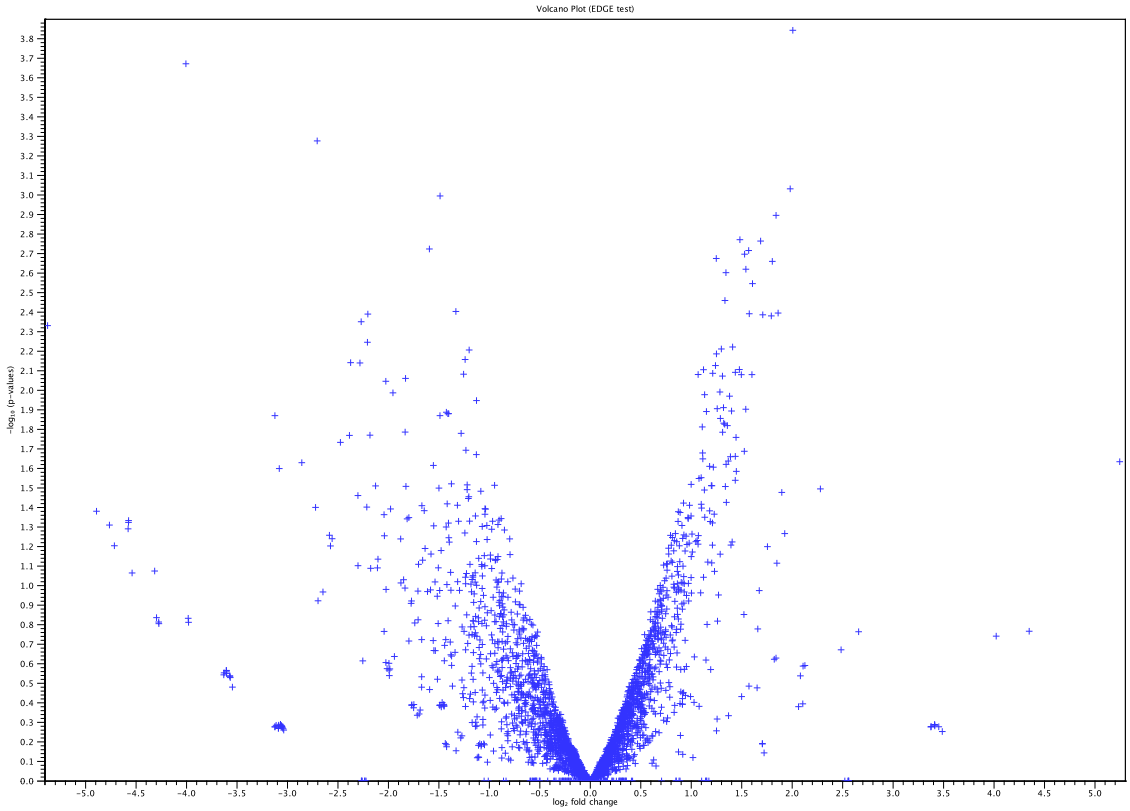


Figure 5.S1 CB0101 transcript statistical DGE test for 30 min post infection. Solid vertical lines indicate 2-fold change in gene expression compared to control sample. Each gene is represented with blue cross.

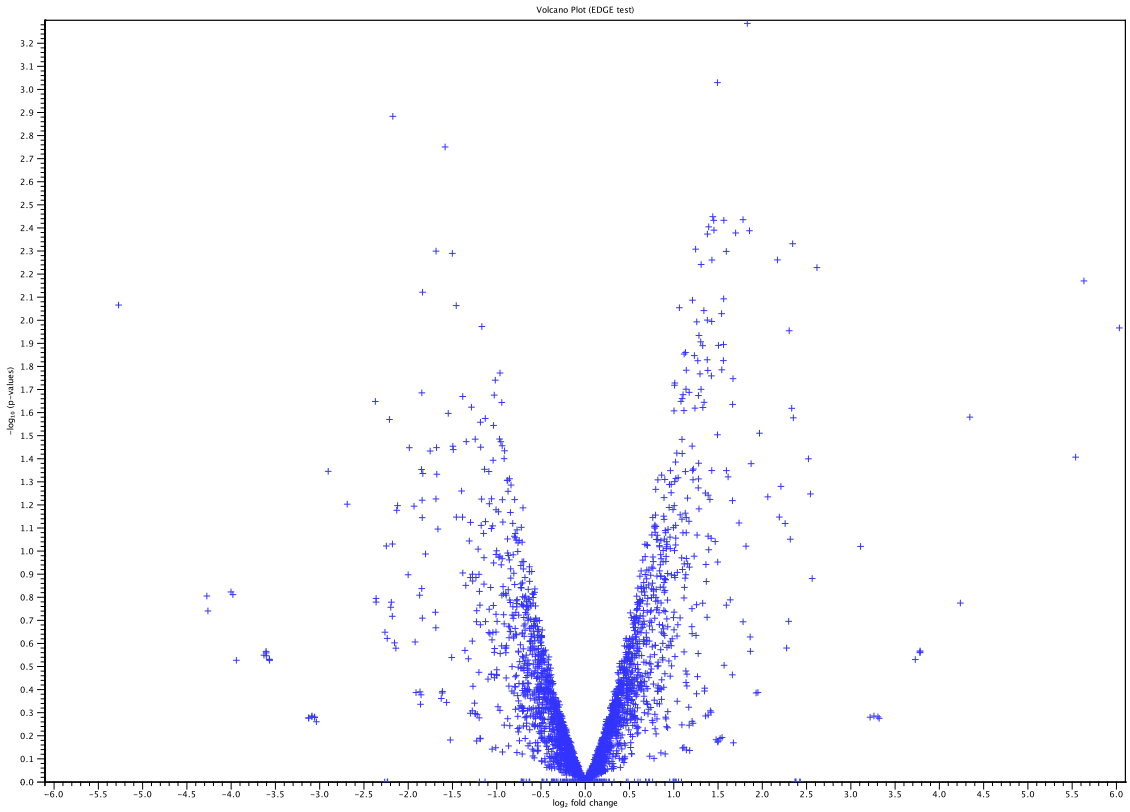


Figure 5.S2 CB0101 transcript statistical DGE test for 5 h post infection. Solid vertical lines indicate 2-fold change in gene expression compared to control sample. Each gene is represented with blue cross.

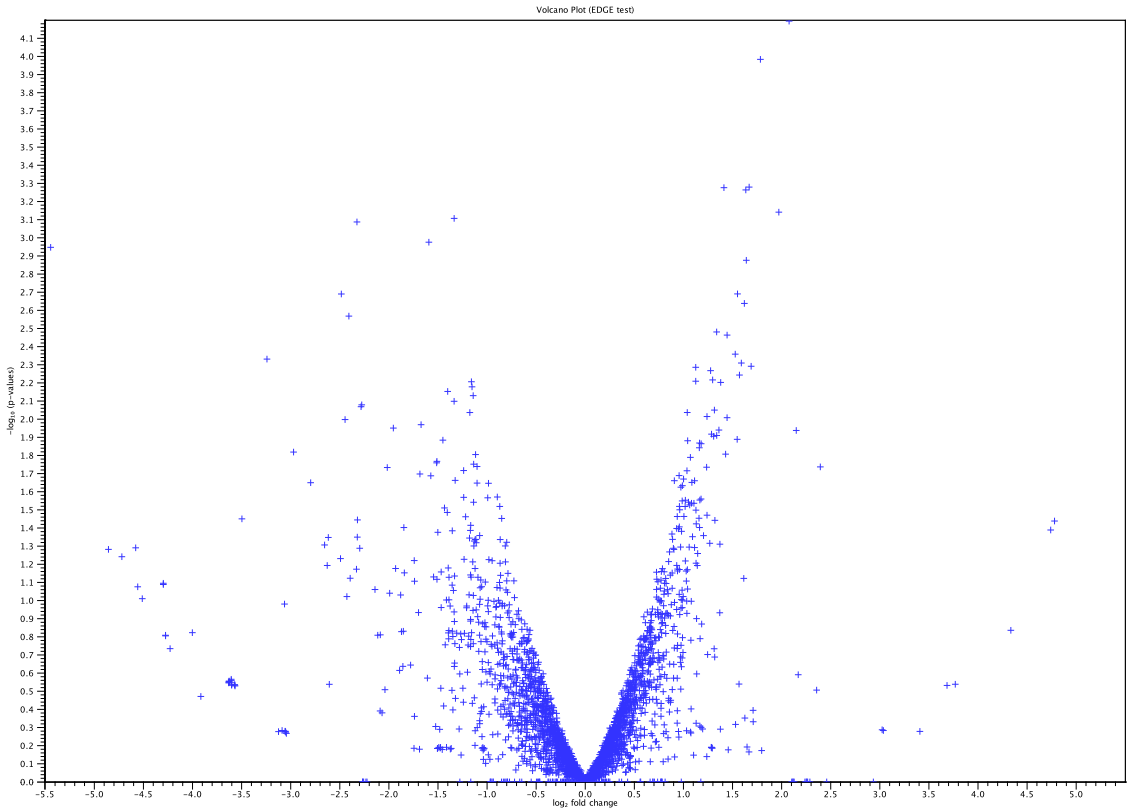


Figure 5.S3 CB0101 transcript statistical DGE test for 12 h post infection. Solid vertical lines indicate 2-fold change in gene expression compared to control sample. Each gene is represented with blue cross.

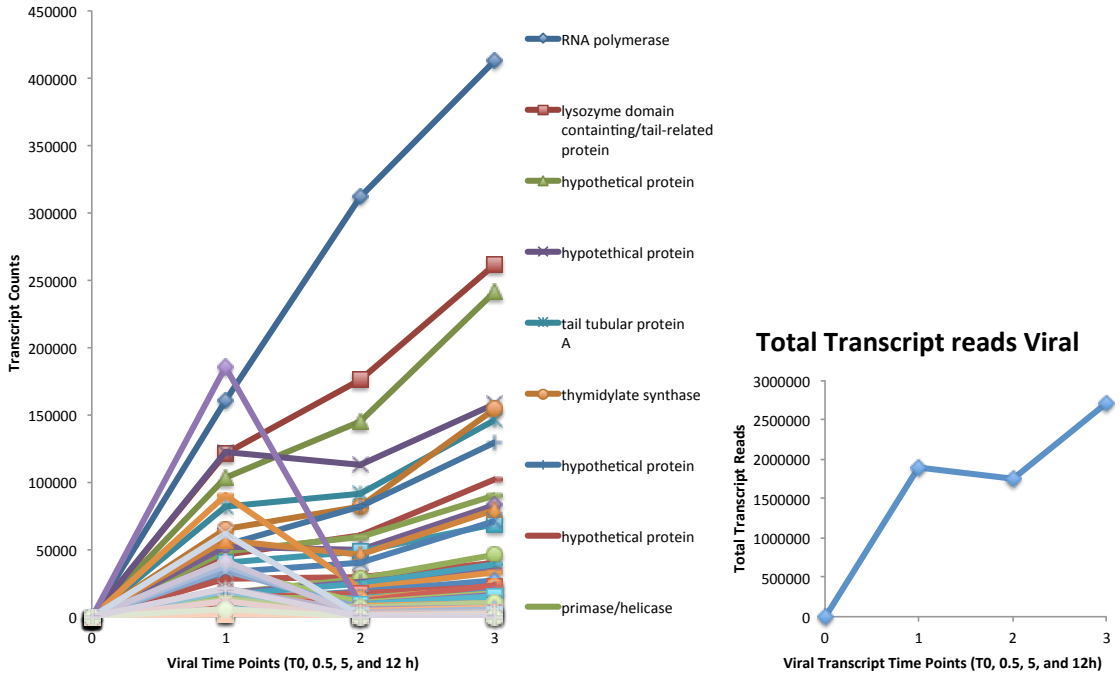


Figure 5.S4 Total viral transcripts broken down into clusters based on amount of reads mapping back to specific genes. Top nine most abundant viral genes are listed. Total reads mapping back to viral genes increased over the infection time series (0 min, 30 min, 5 h, and 12 h).

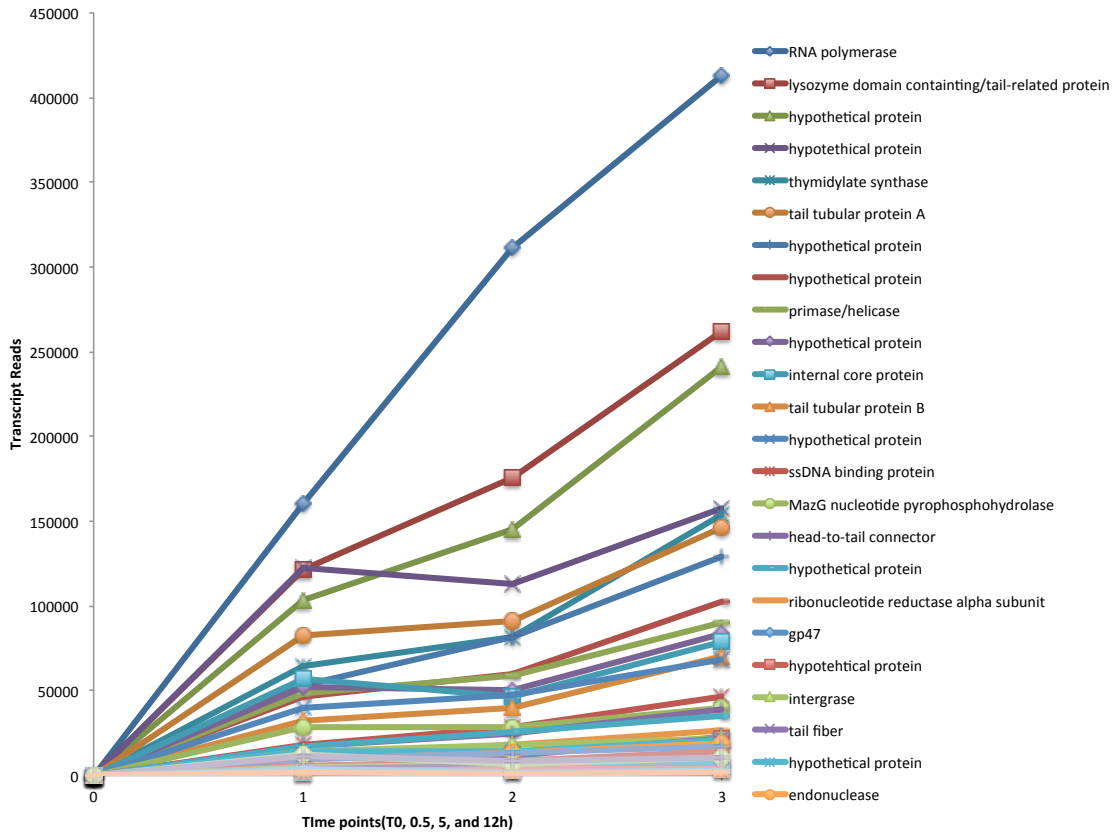


Figure 5.S5 Viral transcript cluster 1 reads mapping back to viral genes over the infection time series (0 min, 30 min, 5 h, and 12 h).

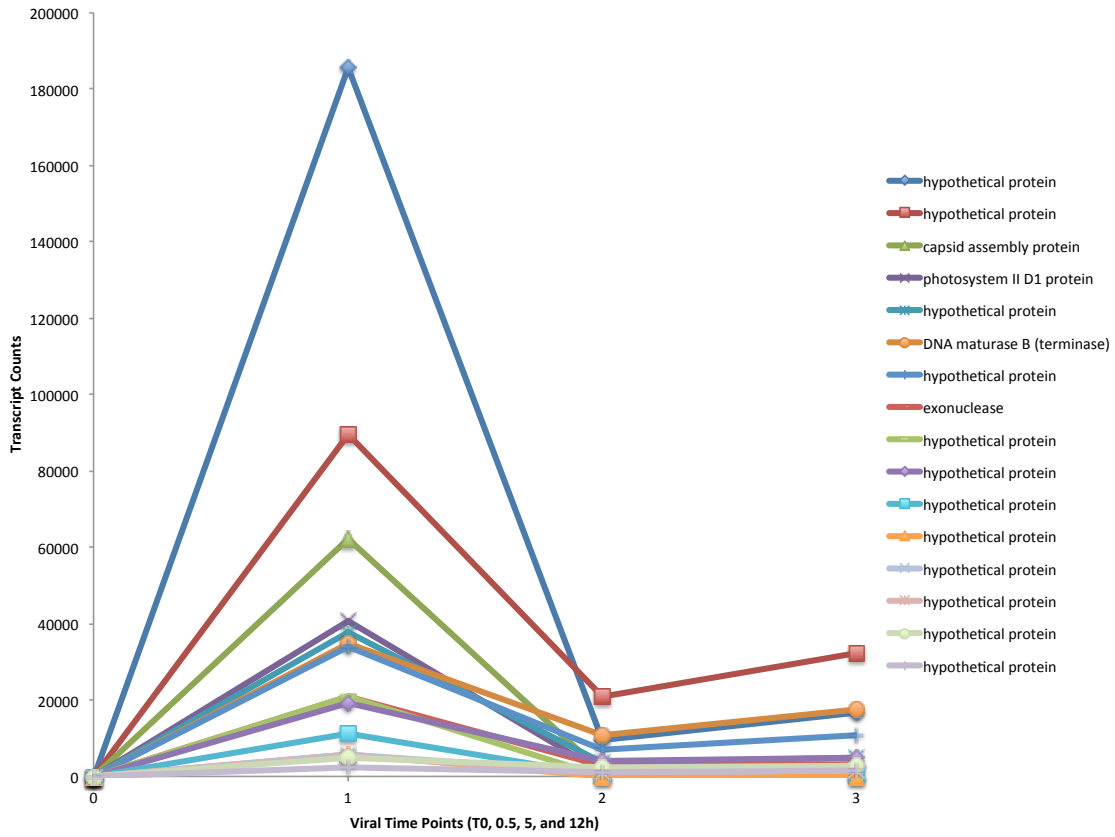


Figure 5.S6 Viral transcript cluster 2 reads mapping back to viral genes over the infection time series (0 min, 30 min, 5 h, and 12 h).

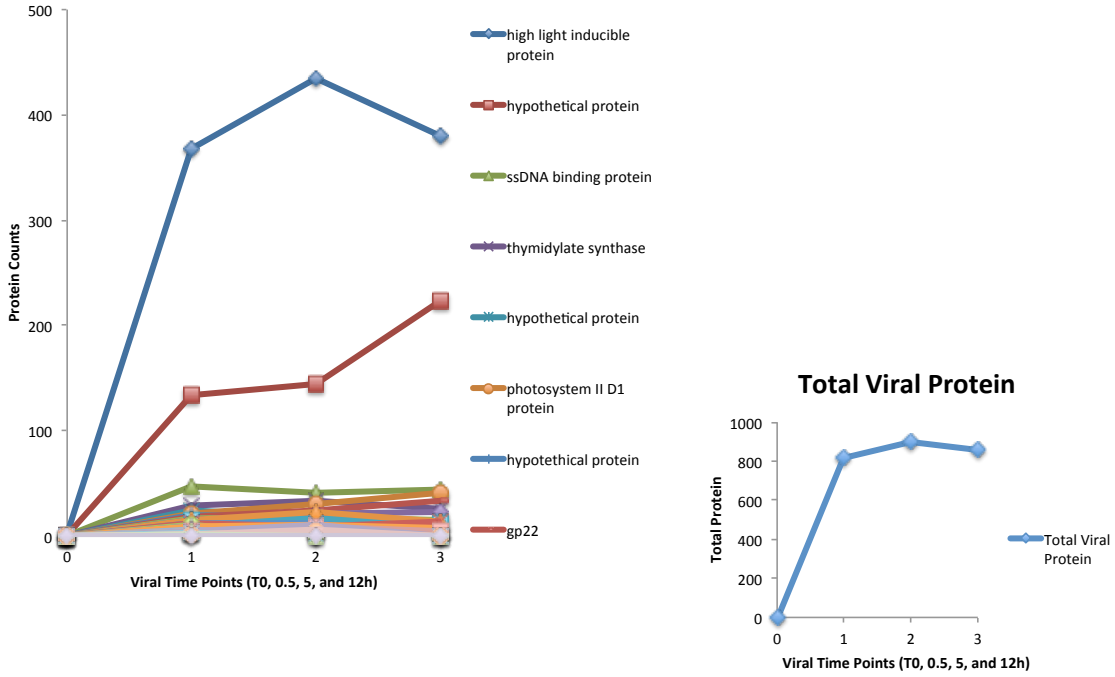


Figure 5.S7 Total viral protein broken down into clusters based on amount of counts mapping back to specific genes. Total counts mapping back to viral proteins was relatively constant over the infection time series (0 min, 30 min, 5 h, and 12 h).

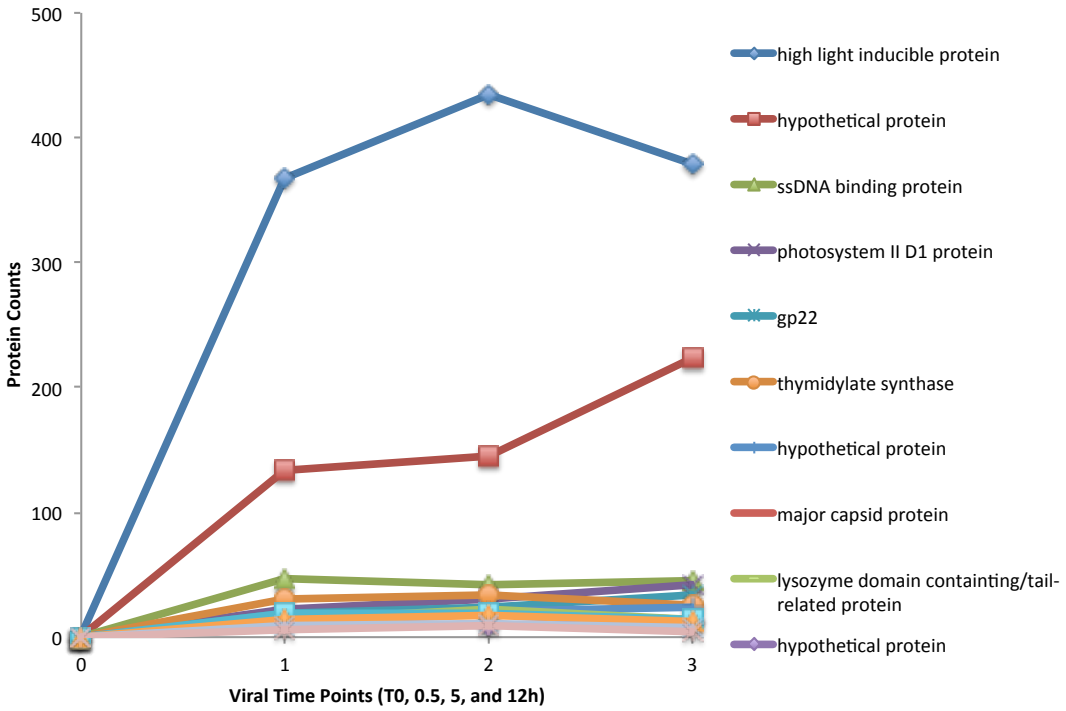


Figure 5.S8 Viral protein cluster 1 counts mapping back to viral proteins over the infection time series (0 min, 30 min, 5 h, and 12 h).

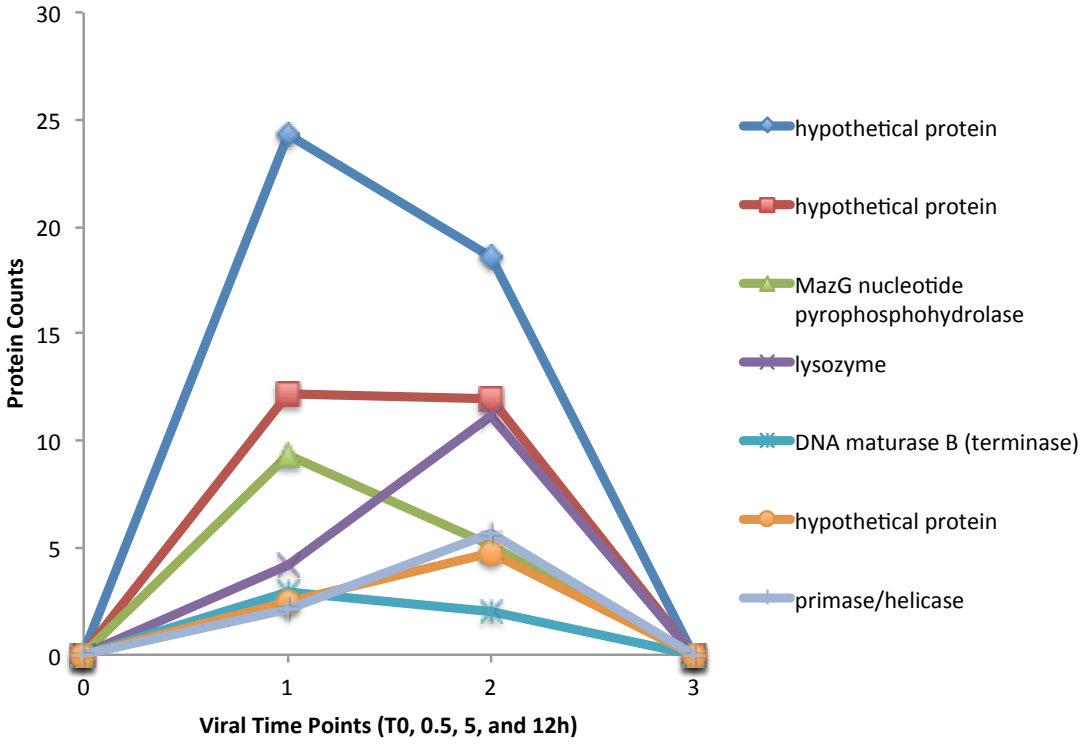


Figure 5.S9 Viral protein cluster 2 counts mapping back to viral proteins over the infection time series (0 min, 30 min, 5 h, and 12 h).

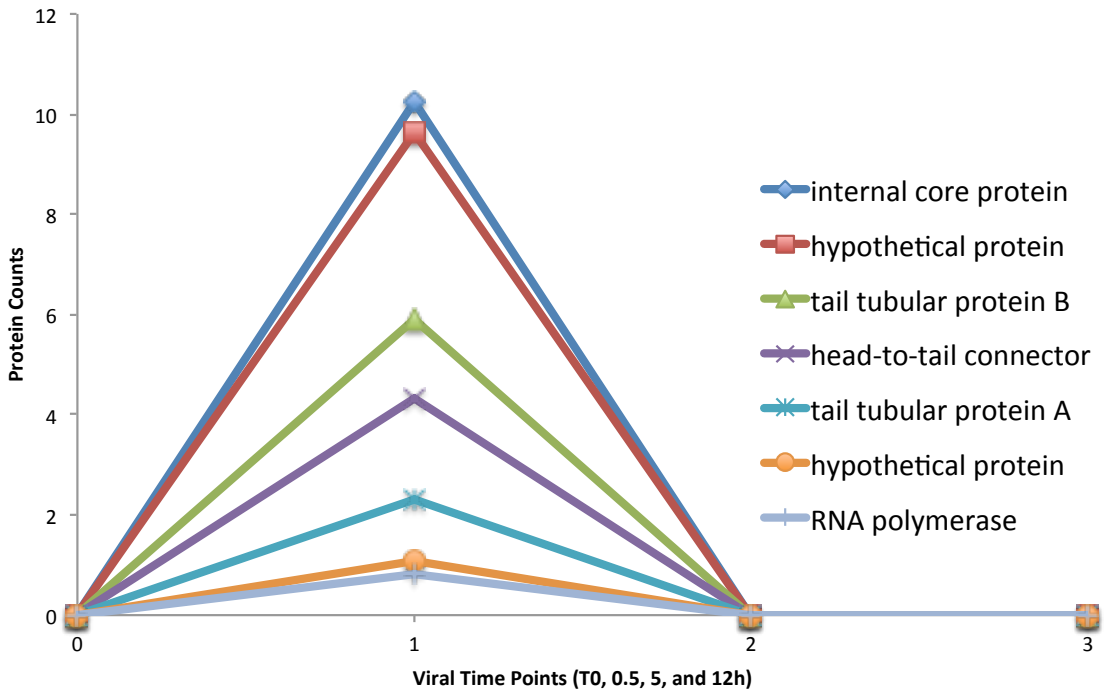


Figure 5.S10 Viral protein cluster 3 counts mapping back to viral proteins over the infection time series (0 min, 30 min, 5 h, and 12 h).

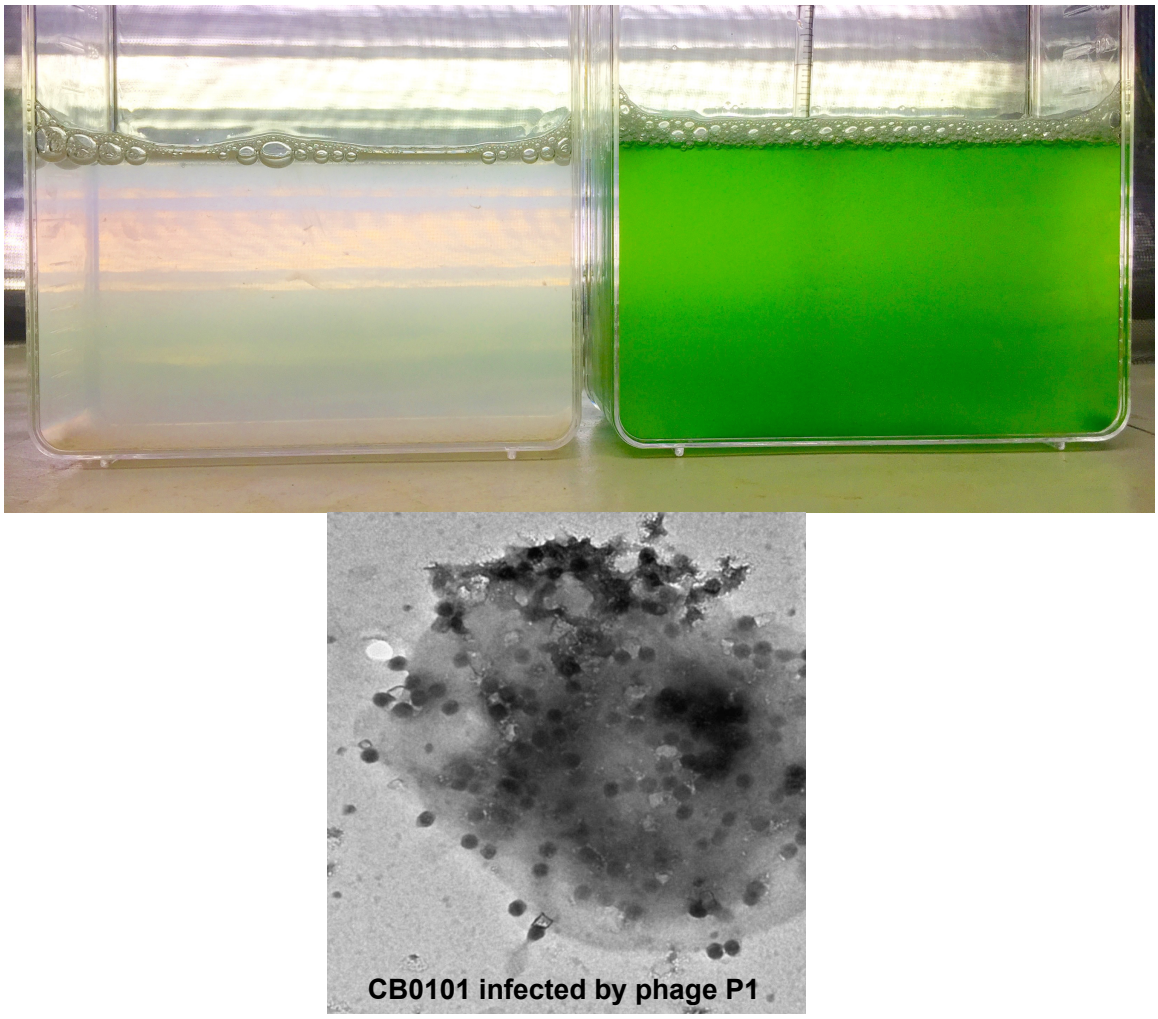


Figure 5.S11 Culture of CB0101 before and after infection by cyanopodovirus S-CBP1. Top left after 48 h of infection. Top right before infection. Bottom, TEM image of S-CBP1 bursting from CB0101 cell.

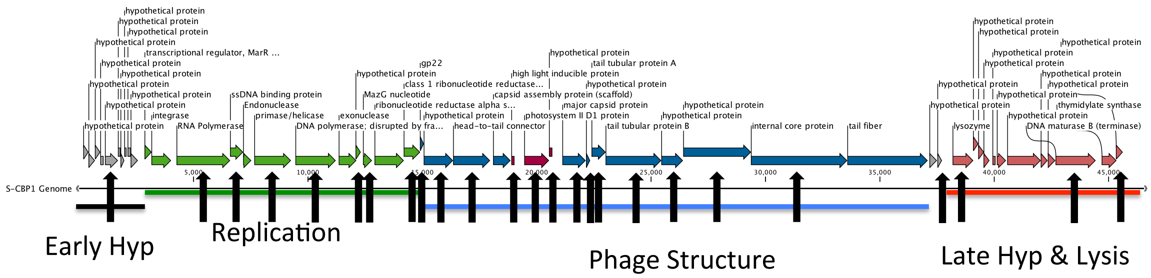


Figure 5.S12 Genome map of cyanopodovirus S-CBP1. Arrows note which proteins were identified through mass spec.

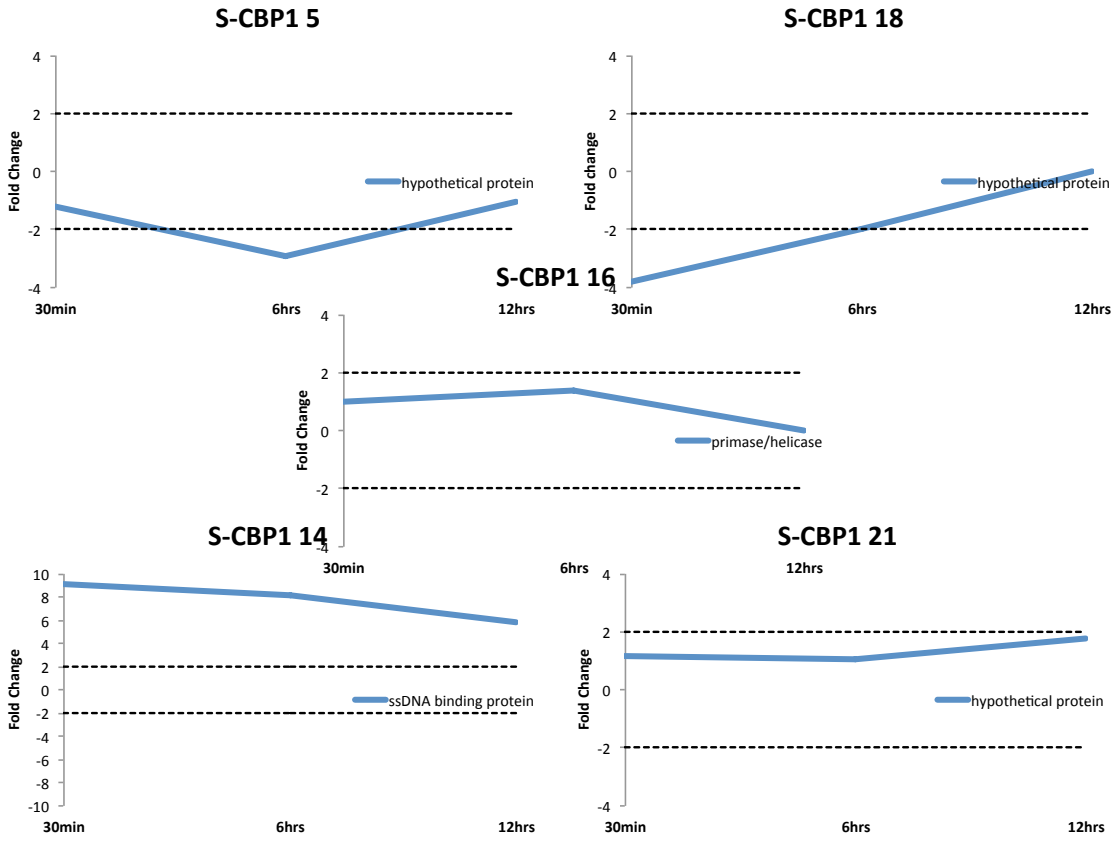


Figure 5.S13 S-CBP1 protein response at 30 min, 5 h, and 12 h post infection. Dashed lines delineate 2-fold increase in protein expression compared to control.

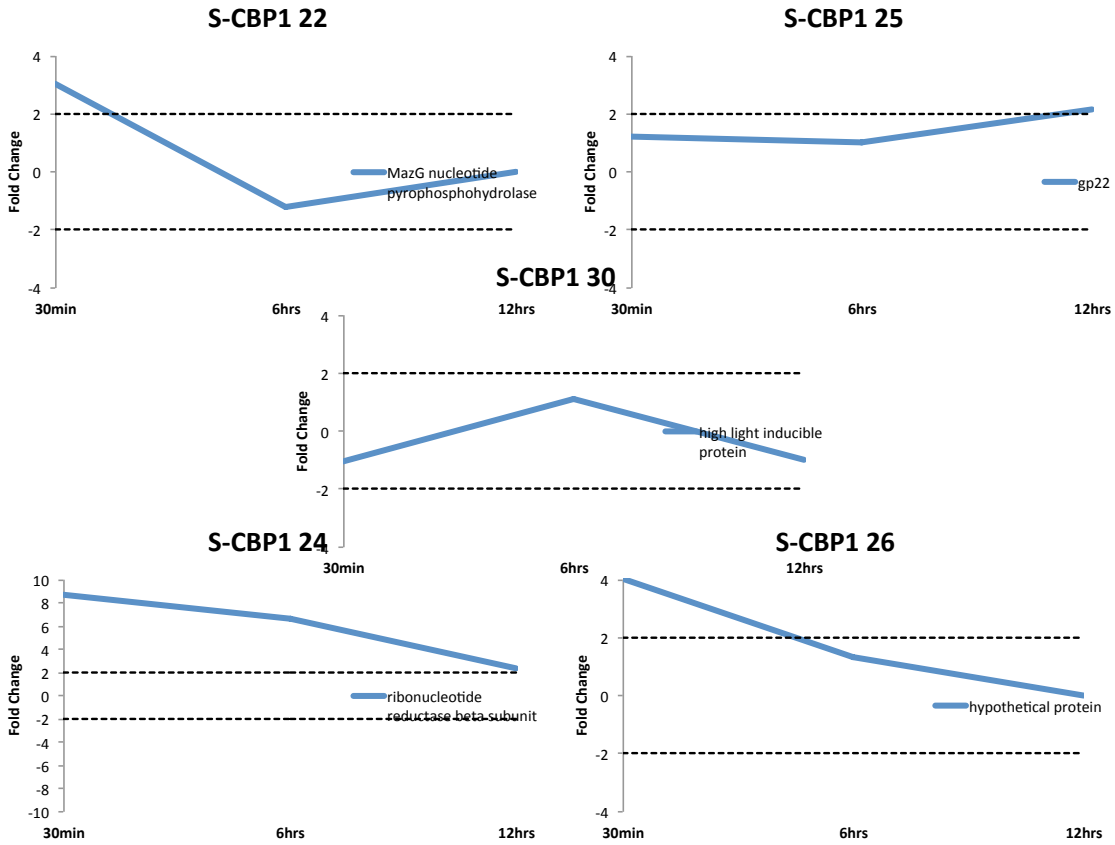


Figure 5.S14 S-CBP1 protein response at 30 min, 5 h, and 12 h post infection. Dashed lines delineate 2-fold increase in protein expression compared to control.

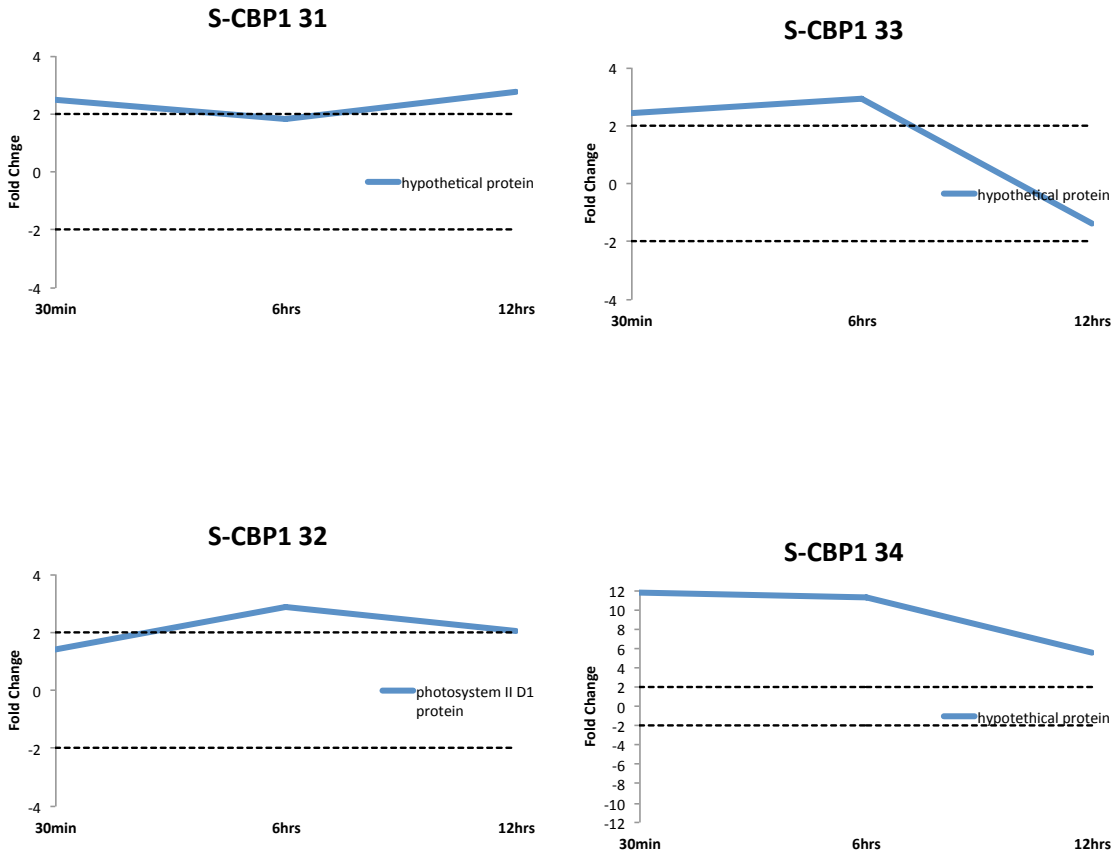
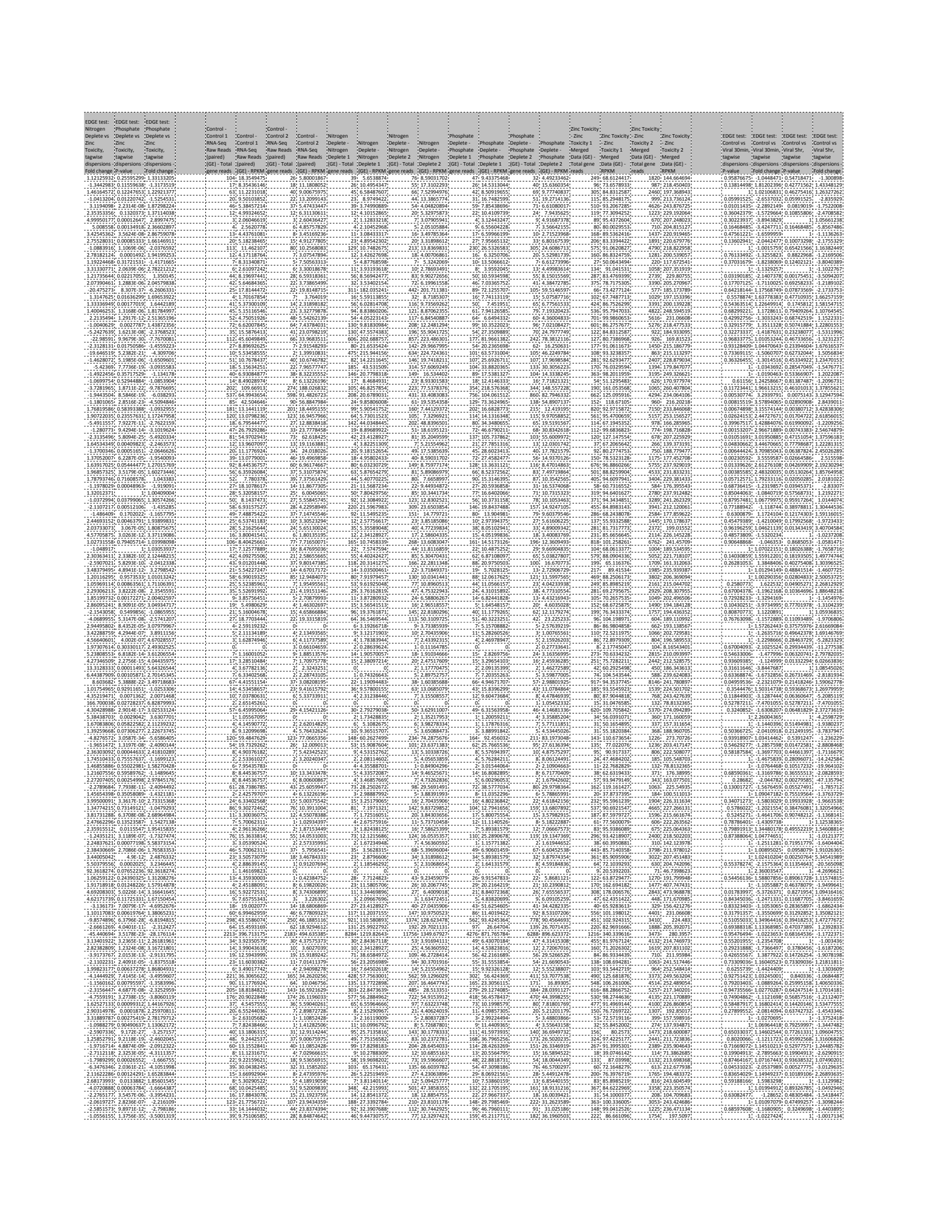


Figure 5.S15 S-CBP1 protein response at 30 min, 5 h, and 12 h post infection. Dashed lines delineate 2 fold increase in protein expression compared to control.

internal locu	external locu	molecule id	common_name	gene_symbo	ec_number	go_terms	product_nam	fmin	fmax	strand	TIGR_roles	feature_id	Category	Subcategory	Subsystem
gsyne_1		Synechococcus_assembled_mapped	RNA polymerase sigma factor rpoD2	rpoD2		GO:0003677,GO:0016987,GO	UniRef100_C	24	993	1	92,141,165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors cyanobac
gsyne_10		Synechococcus_assembled_mapped	cytochrome c6 domain protein	petJ		GO:0006810,GO:0009055,GO	UniRef100_P	7996	8344	1	92,141	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_100		Synechococcus_assembled_mapped	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain protein				PF00389.25	82991	83951	1	703	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine and Serine Utilization
gsyne_1000		Synechococcus_assembled_mapped	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L family protein				PF00420.19	870769	871129	1	703	fig|1129.58.peg.992			
gsyne_1001		Synechococcus_assembled_mapped	NADH-Ubiquinone/plastoquinone (complex I), various chains family protein				PF00361.15	871125	872586	1	112	fig|1129.58.peg.993			
gsyne_1002		Synechococcus_assembled_mapped	na+/H+ ion antiporter subunit				PF01899.11	872594	873005	1	141	fig|1129.58.peg.994			
gsyne_1003		Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	873001	873250	1	88	fig|1129.58.peg.995			
gsyne_1004		Synechococcus_assembled_mapped	na+/H+ antiporter subunit				PF03334.9	873246	873513	1	141	fig|1129.58.peg.996			
gsyne_1005		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF13244.1	873509	874010	1	156	fig|1129.58.peg.997			
gsyne_1006		Synechococcus_assembled_mapped	domain related to MnhB subunit of Na+/H+ antiporter family protein				PF04039.8	874006	874666	1	141	fig|1129.58.peg.998			
gsyne_1007		Synechococcus_assembled_mapped	sulfate transporter family protein				PF00916.15	874748	876434	1	143	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis
gsyne_1008		Synechococcus_assembled_mapped	phosphate-starvation-inducible E family protein				PF06146.7	876466	876958	1	149	fig|1129.58.peg.1000			
gsyne_1009		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	877000	877144	-1	856	fig|1129.58.peg.1001			
gsyne_101		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF04134.7	84381	84774	1	156	fig|1129.58.peg.100			
gsyne_1010		Synechococcus_assembled_mapped	RNA polymerase sigma factor rpoD2	rpoD2		GO:0003677,GO:0016987,GO	UniRef100_C	877252	878170	1	92,141,165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription initiation, bacterial s
gsyne_1011		Synechococcus_assembled_mapped	adenosylmethionine-8-amino-7-oxonor	bioA	2.6.1.62	GO:0004015,GO:0009102	TIGR00508	878180	879452	1	77	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Biotin	Biotin biosynthesis
gsyne_1012		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	879516	879756	1	856	fig|1129.58.peg.1004			
gsyne_1013		Synechococcus_assembled_mapped	beta-lg-H3/Fasciclin				UniRef100_C	879758	880160	-1	185	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1014		Synechococcus_assembled_mapped	CO2 hydration family protein				TIGR01964	880159	881464	-1	164	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1015		Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, chain M family protein				TIGR01972	881460	882954	-1	112	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1016		Synechococcus_assembled_mapped	NAD(P)H dehydrogenase, subunit NdhF3 family protein				TIGR01960	882964	884836	-1	703	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1017		Synechococcus_assembled_mapped	amino acid permease family protein				PF13520.1	884889	886749	-1	141	fig|1129.58.peg.1009			
gsyne_1018		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	886858	887242	1	856	fig|1129.58.peg.1010			
gsyne_1019		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	887248	887668	-1	156	fig|1129.58.peg.1011			
gsyne_102		Synechococcus_assembled_mapped	phycocyanin, beta subunit			GO:0009055,GO:0015979,GO	TIGR01339	84794	85313	-1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1020		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	887743	888052	-1	156	fig|1129.58.peg.1012			
gsyne_1021		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	888177	888987	1	156	fig|1129.58.peg.1013			
gsyne_1022		Synechococcus_assembled_mapped	non-canonical purine NTP pyrophospha	rdgB	3.6.1.-	GO:0006281,GO:0016462	TIGR00042	888991	889588	-1	132	fig|1129.58.p	Nucleosides and Nucleotides	Detoxification	Housecleaning nucleoside triphos
gsyne_1023		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF05982.7	889822	890809	1	156	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1024		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	890805	891087	1	156	fig|1129.58.peg.1016			
gsyne_1025		Synechococcus_assembled_mapped	major carboxysome shell protein 1A	csoS1A			UniRef100_P	891337	891652	1	185	fig|1129.58.peg.1017			
gsyne_1026		Synechococcus_assembled_mapped	ribulose bisphosphate carboxylase larg	cbbL2	4.1.1.39	GO:0000287,GO:0019253,GO	UniRef100_P	891723	893136	1	119,141,703	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1027		Synechococcus_assembled_mapped	ribulose bisphosphate carboxylase sma	cbbS2	4.1.1.39	GO:0019253,GO:0004497,GO	UniRef100_P	893217	893559	1	119,703	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1028		Synechococcus_assembled_mapped	carboxysome shell peptide mid-region family protein				PF12288.3	893731	896086	1	185	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1029		Synechococcus_assembled_mapped	carboxysome shell carbonic anhydrase		4.2.1.1	GO:0004089,GO:0015977,GO	TIGR02701	896234	897803	1	698	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_103		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	85378	85831	1	856	fig|1129.58.peg.102			
gsyne_1030		Synechococcus_assembled_mapped	carboxysome peptide A			GO:0015977,GO:0031470	TIGR02703	897819	898119	1	698	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1031		Synechococcus_assembled_mapped	carboxysome peptide B			GO:0015977,GO:0031470	TIGR02704	898118	898370	1	698	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1032		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	898625	898772	-1	856	fig|1129.58.peg.1024			
gsyne_1033		Synechococcus_assembled_mapped	major carboxysome shell protein 1C	csoS1C			UniRef100_P	898779	899085	1	185	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1034		Synechococcus_assembled_mapped	rubrerythrin family protein				PF02915.12	899090	899600	1	157	fig|1129.58.peg.1026			
gsyne_1035		Synechococcus_assembled_mapped	NAD(P)H dehydrogenase, subunit NdhF3 family protein				TIGR01960	899638	901501	1	703	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1036		Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, chain M family protein				TIGR01972	901509	903015	1	112	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1037		Synechococcus_assembled_mapped	CO2 hydration family protein				TIGR01964	903016	904159	1	164	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1038		Synechococcus_assembled_mapped	pterin 4 alpha carbinolamine dehydratase family protein				PF01329.14	904185	904440	1	76	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_1039		Synechococcus_assembled_mapped	cbbX protein	cbbX			TIGR02880	904477	905377	1	185	fig|1129.58.p	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome
gsyne_104		Synechococcus_assembled_mapped	arsenite methyltransferase	As3mt	2.1.1.137	GO:0009404,GO:0008276,GO	UniRef100_C	85958	87008	1	92,703	fig|1129.58.peg.103			
gsyne_1040		Synechococcus_assembled_mapped	chromosomal replication initiator prote	dnaA		GO:0003677,GO:0003688,GO	TIGR00362	905385	906816	-1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication
gsyne_1041		Synechococcus_assembled_mapped	putative serine protease HhoB			GO:0004252,GO:0006508	UniRef100_P	906876	907995	1	189,703	fig|1129.58.peg.1033			
gsyne_1042		Synechococcus_assembled_mapped	guanylyl transferase CofC like family protein				PF01983.11	907999	908653	1	703	fig|1129.58.peg.1034			
gsyne_1043		Synechococcus_assembled_mapped	bestrophin, RFP-TM, chloride channel family protein				PF01062.16	908681	909599	1	141	fig|1129.58.peg.1035			
gsyne_1044		Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	909595	910315	1	90	fig|1129.58.peg.1036			
gsyne_1045		Synechococcus_assembled_mapped	EAL domain protein				PF00563.15	910340	912497	1	264,710	fig|1129.58.peg.1037			
gsyne_1046		Synechococcus_assembled_mapped	acetyltransferase family protein				PF00583.19	912509	912917	-1	703	fig|1129.58.peg.1038			
gsyne_1047		Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	913804	915559	-1	141	fig|1129.58.peg.1040			
gsyne_1048		Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	913037	913853	1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_1049		Synechococcus_assembled_mapped	ATP phosphoribosyltransferase	hisG	2.4.2.17	GO:0000105,GO:0003879	TIGR00070	915603	916251	-1	161	fig|1129.58.p	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_105		Synechococcus_assembled_mapped	subtilase family protein				PF00082.17	87022	88441	-1	138	fig|1129.58.peg.104			
gsyne_1050		Synechococcus_assembled_mapped	hydroxyacylglutathione hydrolase	gloB	3.1.2.6	GO:0004416,GO:0019243	TIGR03413	916280	917054	1	96	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Non-redox reactions
gsyne_1051		Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	917055	918138	-1	141	fig|1129.58.p	Iron acquisition and metabolism	Iron acquisition and metabolism	Iron acquisition in Streptococcus
gsyne_1052		Synechococcus_assembled_mapped	reactive intermediate/imine deaminase family protein			GO:0008152,GO:0019239	TIGR00004	918226	918625	1	134	fig|1129.58.peg.1044			
gsyne_1053		Synechococcus_assembled_mapped	2OG-Fe(II) oxygenase superfamily protein				PF13532.1	918639	919230	-1	185	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_1054		Synechococcus_assembled_mapped	peptidase M23 family protein				PF01551.17	919226	919922	-1	138	fig|1129.58.peg.1046			
gsyne_1055		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	919988	920234	1	856	fig|1129.58.peg.1047			
gsyne_1057		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	920819	921083	1	856				
gsyne_1058		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	921075	921480	1	856				
gsyne_1059		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	921472	921787	1	856	fig|1129.58.peg.1051			
gsyne_106		Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	88494	89475	-1	154	fig|1129.58.peg.105			
gsyne_1060		Synechococcus_assembled_mapped	dnaJ domain protein				PF00226.26	921776	922808	1	95	fig|1129.58.peg.1052			
gsyne_1061		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF09664.5	922883	923768	1	156	fig|1129.58.peg.1053			
gsyne_1062		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	924389	924575	1	856	fig|1129.58.peg.1055			
gsyne_1063		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	924574	924763	1	856	fig|1129.58.peg.1056			
gsyne_1064		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF13148.1	924762	927357	1	156	fig|1129.58.peg.1057			
gsyne_1065		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	927664	928192	1	856	fig|1129.58.peg.1058			
gsyne_1066		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	928303	928546	1	856	fig|1129.58.peg.1059			
gsyne_1067		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	928562	928691	-1	856	fig|1129.58.peg.1060			
gsyne_1068		Synechococcus_assembled_mapped	terminase-like family protein				PF03237.10	929309	930818	1	185	fig|1129.58.peg.1062			
gsyne_1069		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	930994	931156	-1	856	fig|1129.58.peg.1063			
gsyne_107		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	90759	90924	-1	856	fig|1129.58.peg.107			
gsyne_1070		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	931527	931677	1	856	fig|1129.58.peg.1065			
gsyne_1071		Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	932010	932355	1	157	fig|1129.58.peg.1067			
gsyne_1072		Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	932659	933127	-1	157	fig|1129.58.peg.1068			
gsyne_1073		Synechococcus_assembled_mapped	transposase family protein				PF01527.15	933495	933774	-1	154	fig|1129.58.peg.1069			
gsyne_1074		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	933913	934048	1	856	fig|1129.58.peg.1070			
gsyne_1075		Synechococcus_assembled_mapped	FKBP-type peptidyl-prolyl cis-trans isomerase family protein				PF00254.23	934444	934573	1	95	fig|1129.58.peg.1071			
gsyne_1076		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	934937	935099	1	856	fig|1129.58.peg.1072			
gsyne_1077		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	935347	935509	1	856	fig|1129.58.peg.1073			
gsyne_1078		Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	936161	936524	1	157	fig|1129.58.peg.1075			
gsyne_1079		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF07864.6	937096	937237	1	156	fig|1129.58.peg.1077			
gsyne_108		Synechococcus_assembled_mapped	nitroreductase family protein				PF00881.19	90963	91611	-1	703	fig|1129.58.peg.108			
gsyne_1080		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	937391	938972	-1	856	fig|1129.58.peg.1078			
gsyne_1081		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF00565.12	939176	939746	-1	157	fig|1129.58.peg.1080			
gsyne_1082		Synechococcus_assembled_mapped	excalibur calcium-binding domain protein				PF05901.6	939835	940045	-1	157	fig|1129.58.peg.1081			
gsyne_1083		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	940096	940327	1	856	fig|1129.58.peg.1082			
gsyne_1084		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	940429	941275	1	856	fig|1129.58.peg.1083			
gsyne_1085		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	941601	941769	-1	856	fig|1129.58.peg.1085			
gsyne_1086		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF14311.1	941882	943262	-1	156	fig|1129.58.peg.1086			
gsyne_1087		Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	943277	944399	-1	132,152	fig|1129.58.peg.1087			
gsyne_1088		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	944979	945216	1	856	fig|1129.58.peg.1088			
gsyne_1089		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	945225	945342	-1	856	fig|1129.58.peg.1089			
gsyne_109		Synechococcus_assembled_mapped	L,D-transpeptidase catalytic domain protein				PF03734.9	91804	92314	-1	138	fig|1129.58.peg.109			
gsyne_1090		Synechococcus_assembled_mapped	transposase family protein				PF01527.15	946149	946428	1	154	fig|1129.58.peg.1090			
gsyne_1091		Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	946795	947257	1	157	fig|1129.58.peg.1091			
gsyne_1092		Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	947284	947485	1	165	fig|1129.58.peg.1092			
gsyne_1093		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	947606	947768	1	856	fig|1129.58.peg.1093			
gsyne_1094		Synechococcus_assembled_mapped	mannose-1-phosphate guanylyltransferase/mannose	5.3.1.8		GO:0004476,GO:0008905,GO	TIGR01479	948480	949947	-1	90	fig|1129.58.peg.1095			
gsyne_1095		Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	951035	952205	-1	90	fig|1129.58.peg.1097			
gsyne_1096		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	950343	951051	1	141	fig|1129.58.peg.1096			
gsyne_1097		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	952229	953183	-1	856	fig|1129.58.peg.1098			
gsyne_1098		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF04577.9	953408	954890	-1	156	fig|1129.58.peg.1099			
gsyne_1099		Synechococcus_assembled_mapped	glycosyltransferase like 2 family protein				PF10111.4	954886	955486	-1	703	fig|1129.58.peg.1100			
gsyne_11		Synechococcus_assembled_mapped	YCII-related domain protein				PF03795.9	8346	8604	-1	157	fig|1129.58.peg.12			
gsyne_110		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	92404	92743	-1	856	fig|1129.58.peg.110			
gsyne_1100		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	955516	955810	1	856				
gsyne_1101		Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	955897	956938	1	185	fig|1129.58.peg.1101			
gsyne_1102		Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	958863	960240	-1	90	fig|1129.58.peg.1103			
gsyne_1103		Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	957012	958875	1	90	fig|1129.58.peg.1102			
gsyne_1104		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	960236	961676	-1	856	fig|1129.58.peg.1104			
gsyne_1105		Synechococcus_assembled_mapped	undecaprenyl-phosphate glucose phosphotransferas	2.7.8.-			TIGR03023	961665	963057	-1	703	fig|1129.58.peg.1105			
gsyne_1106		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF02698.12	963121	963643	-1	156	fig|1129.58.peg.1106			
gsyne_1107		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	963609	963804	-1	856	fig|1129.58.peg.1107			
gsyne_1108		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	964309	964462	-1	856				
gsyne_1109		Synechococcus_assembled_mapped	NUDIX domain protein				PF00293.23	963837	964356	1	703	fig|1129.58.peg.1108			
gsyne_111		Synechococcus_assembled_mapped	polyphosphate kinase 2 family protein				PF03976.9	92830	93718	1	103	fig|1129.58.peg.111			
gsyne_1110		Synechococcus_assembled_mapped	coA-binding domain protein				PF13727.1	964581	965361	-1	157	fig|1129.58.peg.1110			
gsyne_1111		Synechococcus_assembled_mapped	prevent-host-death family protein			GO:0008219	TIGR01552	965422	965545	1	94,708	fig|1129.58.peg.1111			
gsyne_1112		Synechococcus_assembled_mapped	putative ribonuclease VapC30			GO:0045926,GO:0046872,GO	UniRef100_P	965582	965990	-1	141,703	fig|1129.58.peg.1112			
gsyne_1113		Synechococcus_assembled_mapped	antitoxin VapB30	vapB30		GO:0045927	UniRef100_P	965989	966211	-1	185	fig|1129.58.peg.1113			
gsyne_1114		Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF02698.12	966287	966986	-1	156	fig|1129.58.peg.1114			
gsyne_1115		Synechococcus_assembled_mapped	NUDIX domain protein				PF00293.23	966989	967247	1	703	fig|1129.58.peg.1115			
gsyne_1116		Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	967434	968592	-1	90	fig|1129.58.peg.1116			
gsyne_1117		Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	968595	968748	1	856				
gsyne_1118		Synechococcus_assembled_mapped	GDSL-like Lipase/Acylhydrolase family protein				PF13472.1	968784	969750	-1	703	fig|1129.58.peg.1117			
gsyne_1119		Synechococcus_assembled_mapped	putative ribonuclease VapC30			GO:0045926,GO:0046872,GO	UniRef100_P	969844	970243	-1	141,703	fig|1129.58.peg.1118			
gsyne_112		Synechococcus_assembled_mapped	marC integral membrane family protein				PF01914.12	93714	94398	1	88	fig|1129.58.peg.112			

function	evidence_cod	nucleotide_se	aa_sequence	Feature ID	EDGE test: Control vs Nitrogen Deplete, tagwise dispersions - P-value	EDGE test: Control vs Nitrogen Deplete, tagwise dispersions - Fold change	EDGE test: Control vs Phosphate Deplete, tagwise dispersions - P-value	EDGE test: Control vs Phosphate Deplete, tagwise dispersions - Fold change	EDGE test: Control vs Zinc Toxicity, tagwise dispersions - P-value	EDGE test: Control vs Zinc Toxicity, tagwise dispersions - Fold change	EDGE test: Nitrogen Deplete vs Phosphate Deplete, tagwise dispersions - P-value	EDGE test: Nitrogen Deplete vs Phosphate Deplete, tagwise dispersions - Fold change	EDGE test: Nitrogen Deplete vs Zinc Toxicity, tagwise dispersions - P-value
Cyanobacteria-specific Rpc	idu(1);Transcr	atggccagctctc	MASSLSAFLGEIGRHQLLTPEQELMLGRKVQAMVALHERCHSAGGVGEACSYNDIEKRTMRVGERAKDQMITANLRLVVNLAKRYQGKGLDLLD	rpoD2_1	0.00073059	-2.3461355	8.2615E-05	-2.785694	0.00219212	-2.0924111	0.53552882	-1.1873543	0.63731755
Cytochrome C553 (soluble	idu(1);Soluble_	ttgggtctgcagac	MGLQTDYTLAEAQVADLIPRWRRLGAALLAAAAALLLWPGMALADGAQLFEQHCAGCHVNGGNIIRRGKTLKLAALERENRASEAAIAIAAAGVC	petJ_1	0.913975804	1.06709764	0.91344741	1.04570773	0.26627922	-1.2597707	1	-1.020455	0.07119797
D-3-phosphoglycerate dehy	idu(1);Glycine_	atgagcatcgttgt	MSIVVLDGYTTNPGDLSWEPLSVLAPCTVWDRTAPAEVNARLADAEIVLTNKTPLAAETLAALPKLRLISVLATGVNVVDVAAAKAQGITVCNVPAYS	gsyne_100	5.02718E-05	-1.97779	0.00212015	-1.6632804	0.04248127	-1.3531254	0.31484605	1.18908993	0.00534372
Putative multicomponent Na	icw(2);CBSS-1	atggcaccgatcc	MAPIRLLELLILLAALAGFAGLLLRRNLFLKVLAMDVMGSAVVALFVLLAARSGLRSPILPRSGELLARDYADPIPQAVILTAIVIGLSIQALLLVVITQMA	gsyne_1000	0.165394891	-1.3552015	0.81094881	1.08096246	0.0943828	-1.411199	0.04868355	1.46492194	0.90165113
Na(+) H(+) antiporter subur	icw(1);Multi-su	atgacgctgagct	MTLSWSSPDALLTTWLLVPYLAAFLAVLLPSLSHGLVLLCCSATALVGAEALLTESARPLQLIGEFGVQLSLEPLAGWFVLLNGLVCLAVWNEARRQ	gsyne_1001	0.000181804	-1.9088877	0.41091209	-1.1461504	0.00027383	1.63415049	0.00105921	1.66547751	1.8979E-21
Putative Multisubunit sodiu	icw(1);CBSS-1	atggcgtttttgttga	MAFLLSCAFRLLLWALLTADLSAMNLAIGLAIALVLPHARGPQHPLKPTLKALLRSLIAVPLAYGEALALISCGDREEERWIERPAGDPRHRLLIFLEVP	gsyne_1002	0.121267984	-1.6069442	0.87787075	1.06816334	0.22075391	1.4646019	0.02270248	1.71647892	9.9363E-06
Na(+) H(+) antiporter subur	isu;Multi-subu	atgaccttgttgctc	MTLLLWGMVLALLIPIAVVCRPCSVWDRMAAFGSIASKVALITMVVAVLRGDWMLGLVGAISLSAGNAGMLLLANLLREVES	gsyne_1003	0.596270327	-1.4299416	0.88274425	1.20572492	0.00100357	3.49629782	0.24591029	1.72411625	4.6922E-08
Na(+) H(+) antiporter subur	icw(2);Multi-su	gtgagcctgctgtt	MSLLLLGAGLMLWFWGTWPLLEQRSYLSKLHKLSVSDTLGSGLMLLGLLLRIPAQWPLLALALLGLVVWNTIFGYVLARCSQPGELKR	gsyne_1004	0.08885276	-2.373764	0.89955034	-1.1213596	0.03805025	2.10996461	0.1173503	2.1168625	7.0062E-08
Putative multicomponent Na	icw(6);CBSS-1	atgaatcctccccct	MNPPLSLSGELDLLVPITALLPITALLLVSQSNPYQTLVLRGILGSVATLLYALLGAPDVALTEALVGTLLSTTLYAVALRSSMALRLEDRRSAPNPNQD	gsyne_1005	0.137591664	-1.6636348	0.3021853	-1.3926984	0.0020877	2.05901782	0.59604195	1.1945406	2.7762E-11
Multisubunit Na+/H+ antipo	icw(4);CBSS-1	atgacctggctcta	MTWLYLLSAIALFLAPLASALPNSSELSPLITALTEQTQVPNLVSGVILHTRLFDTVAEVVVFTLAAIGVRLVLAADPERKQIRALEDPPSQVLCELGST	gsyne_1006	0.037470766	-1.7349874	0.89856436	-1.0462195	0.02048656	1.58806939	0.02256844	1.65833978	8.471E-10
Sulfate permease	idu(1);Cystein	atgacctccgcctc	MTSASAPPGRSPLRLLNHISTNNIKGDLFGGVTAAVIALPMALAFGVASGAGAASGLWGAVLVGLFAALFGGTPTLISEPTGPMTVVMTAVIASLTAG	gsyne_1007	0.241374973	-1.2123726	0.00644989	1.54422389	0.08090824	-1.3195361	4.3356E-05	1.87217472	0.58383989
FIG01149328: hypothetical protein		atggatgcccttttt	MDALFSCVVCIPQPMKLFDDKQFLSAIHSYERQLAKLLALLLAAVVGFAALELLVETGVGLVQRETNWFDGSLIKLLDRLLLIFIALEVLQNVTAYLRD	gsyne_1008	0.361992275	-1.3556921	0.8559562	1.05662433	0.00239953	2.05195656	0.17085882	1.43245723	7.6063E-09
hypothetical protein		gtgggtttcggtgt	MGFGVDAATAIPSISSADQFLRPIASRAIWSCAKRCLVPALKRLTQP	gsyne_1009	0.096151504	-2.1360561	0.63526264	-1.2642309	0.16630424	-1.7916256	0.24714911	1.6896092	0.75570543
FIG01150548: hypothetical protein		atgaccctggtgc	MTLVLVYDGGCPFCRHFALRSELVGGVPGLQIRDGRADAALRTELKARGFNLARGAVLLEGDQVWFGAEAIAELCTRLQPSDPLLALLRQLFAAP	gsyne_101	0.720819052	-1.2212585	0.90945309	-1.0255009	0.0005496	2.71302741	0.72081905	1.19088968	2.4268E-08
RNA polymerase sigma fac	idu(5);CBSS-3	atgcctgcgccac	MPAPQKLRKGDCDAISRHLRAIGRVPLLTADEEISLGRAVQNGRLLLEAAEELKLRAGGEAPSLEAWASSVNLSPRQLQRQLRLAERASEQMVTA	rpoD2_2	0.569594995	-1.1066882	0.25450039	-1.2274051	0.59945426	1.09999952	0.49007479	-1.1090794	0.11333134
Adenosylmethionine-8-amir	isu;Biotin_bios	atgagctggcacc	MSWHPHLWHPTTQVATSPVPLQVRSARCCVLELQDGRQLIDAISSWWVTLHGHAEPSIAAAIGRQALQLEQVIFANFSHQPAEQLATRLAALTGL	bioA	0.138584935	-1.3268747	0.19402148	-1.3088924	0.00566122	1.56299962	0.893694	1.01373852	1.5969E-07
hypothetical protein		atgcctgacacctt	MPDTFALLLAAGIIGTSVALASAILFDEARGRRRTIEHYRKLERERILRVRRLHNQVRKPGSGRGSWDHYLDGKNQRAA	gsyne_1012	8.04188E-63	7.50751983	4.5521E-06	2.29554091	5.7938E-06	-2.7273019	1.6192E-22	-3.2704797	1.3668E-93
Sensory subunit of low CO2	icw(2);CO2_u	atggcttcgattctc	MASILETAASVGVFNTLLAAVEAAGLRSALEGPGPFTVFAPVDEAFAALPPGTVQTLVDNPPQLARILKYHVVPGAFTRTDLVAQECWDSLEGAPIP	gsyne_1013	0.063781308	2.02290857	0.28205078	1.56768809	0.00265849	2.65964434	0.36265194	-1.2903769	0.16167704
Low-affinity CO2 hydration	idu(1);CO2_u	atgaccgccacag	MTATVTPERTKAPLIPPSTHRYAEVIHRLEAGGSMLPDTPENLQQIIGIYKAYAVPMDFYWRDLLYIAERVFLNPLPAFKYFISQEYLDRPNSYAGEQS	gsyne_1014	0.052832002	1.45637384	0.37749783	1.18103766	0.00021841	1.94188445	0.25373454	-1.2331307	0.05422291
NADH dehydrogenase subu	icw(1);CO2_u	atgaccctgttgct	MTLLLLLLLPLLVAVLLPLLPAGSAWLRRAALAAPLLQLLVALLWWRDPSSDLSWSWLPRLGLRLELGLDGLTLPLVLLAALITAMAVLAAPADQTRP	gsyne_1015	0.011569157	1.49614196	0.40338747	1.15262029	4.6852E-07	2.09529075	0.06006671	-1.2980354	0.00419438
NADH dehydrogenase subu	icw(3);CO2_u	gtgtcctggctagg	MSWLGTAWLVPLYPLLGSIFSLLWSPGLIARTGPRPSGYVNLLMVSIAFGHSLMALLGLTGNSAAGGQAAIYAPPSFQWTWIHTAGLSIGFDGLVTEP	gsyne_1016	0.108352704	-1.2766489	0.02606777	-1.4497309	8.5271E-05	1.73387484	0.46385381	-1.1355753	6.7672E-11
Amino acid permease		gtgctgatcaattg	MLINWARRLLGNPLPRSQSDSEKLPSFEALPILSSDALSSVAYATEAALGVLILAGSQALELSLPITGAIVLLIGIVVLSYRQTIEAYPQGGGSYVVARE	gsyne_1017	0.332690073	1.15234756	0.126679	-1.2535879	0.31548178	1.14768461	0.005181	-1.444569	0.98527192
hypothetical protein		atgcgcgccacc	MRATLHELLQQLVQRGWPKIDQPEEHRRAGGRAPWWTIDVGCIALGNVTTVTLHPWQHGLLEFSITVLVDGDDTIQSFELDCNAMPIPVALVNWW	gsyne_1018	1.31999E-05	1.98904539	0.51762748	-1.1089537	9.8978E-08	-2.6358191	1.282E-08	-2.2057592	6.864E-45
FIG00940602: hypothetical protein		gtggccgccaag	MAAKRSASAPAASAPEAADLNAEQALALVGMGLMQKMAASGELPWMWNETEDGGSCDVAALRQRLELTQLALQTGAPLSTAEVTYLMGARPGS	gsyne_1019	4.79372E-15	3.91128979	0.11710721	1.32163659	1.3381E-20	-5.8768108	5.9054E-11	-2.9594291	3.0293E-79
Phycocyanin beta chain	idu(2);Phycob	atgttcgacgcctt	MFDAFTKVVAQADARGEFLNAGQIDALAAMVAESNKRMDAVNRITSNASKIVTGAARDLFDQQPALIAPGGNAYTHRRMAACLRDMEIILRYVTYA	gsyne_102	2.02831E-08	3.05413519	0.00178064	1.9225866	0.16337575	1.32052833	0.00449454	-1.5885553	5.3192E-09
FIG00941997: hypothetical protein		atgctcagtgcttc	MLSASTRLKLQAIVARIGSGDAVTLDERIYLQKFADRDRTVADWLRQARRRQLATTGDGLDRLMAELDLGDPEPGPPFRPDPDDPGDLGDWFGQ	gsyne_1020	2.06451E-81	43.8623307	2.1119E-22	9.62174271	0.00556402	2.23257519	7.1805E-27	-4.558668	2.737E-111
CsoS1D		gtgcagatcaccg	MQITGTDLGFSGSGTPLDELHPSAASCVITTDSEARLVSQASAVESIELRTYVFLDSLQPQLAAYMGTVSQGFLPIPGDACLWLEVSPGMAVHRVT	gsyne_1021	0.329978287	1.16259243	0.06067673	1.31213036	0.11266707	-1.2582287	0.30204407	1.12862455	0.0005183
Nucleoside 5-triphosphatas	idu(1);Heat_sh	atgcgcccacccct	MRPPSTRPLLVIASGNAYKVAEISAMLDAVDLEVRQQPEVLEIEETGSTYLENARLKATEVARLTGQWALADDSGLEVDALGGAPGLYSARYAPTD	rdgB_1	4.10107E-32	5.75173712	8.3721E-11	3.28066946	0.84034932	1.06048413	4.1707E-06	-1.7532206	4.5118E-56
putative sodium-dependent	isu;CO2_uptal	gtggacacgagc	MDTSLILQNLLTPPVLFFFLGVLAVLLGSDLEIPAPLPKLFSLYLLLAIGFKGGLELQHSGISGPVLLTIAAAVAMSLLVPLYSFALLRLKLDGFNAAAIAA	gsyne_1023	0.000347573	1.80510205	0.07408397	1.37196395	0.27166402	1.20965484	0.0523228	-1.3157066	0.00156129
FIG00940496: hypothetical protein		atgaaacggctgg	MKRLDLIVSERELEPVLQAIDQAGCSGYTVMRHVTGRGPRGAVSDNMEFSGLGANAHVIVFCPPELLGPLRSSLQPLLNYYGGVGFVSEAEPL	gsyne_1024	0.678753318	-1.1746867	0.67875332	-1.1580035	0.33304186	-1.2568859	1	1.01440683	0.52944884
carboxysome shell protein (	icw(4);CO2_u	atggctaacgaa	MANETMGIALGMIETRGLVPAIEAADAMTKAAEVRLVGREFVGGGYVTVLVRGETGAVNAAVRAGADACERVGDGLVAAHIIARPHREVEPALNSS	csoS1A	6.59073E-08	-3.3185666	0.27346404	-1.2640668	5.1567E-26	-12.372268	1.078E-05	2.62530944	7.4971E-09
Ribulose bisphosphate cart	icw(4);CO2_u	atggctaagaagt	MAKKYDAGVKEYRDTYWTPDYVPLDSDLLACFKCTGQEGVPREEVAAAVAAESSTGTWSTVWSELLTDLDFYKGRCYRIEDVPGDKESFYAFIA	cbbL2	4.48117E-12	-4.0148674	0.18208201	-1.2928006	2.5889E-23	-7.806309	1.0683E-08	3.10555806	0.00075458
Ribulose bisphosphate cart	icw(2);CO2_u	atgcctttcaagag	MPFKSTVGDYQTVATLETFGFLPPMTQDEIYDQIAYIIAQGWSPLVEHVHPSRSMATYWSYWKLPFFGEKDLSVIVNELEACHRAYPDHHVRLVGY	cbbS2	5.16993E-18	-4.5463451	0.25972013	-1.1897527	5.8589E-25	-5.3651715	1.4199E-15	3.82125216	0.47216508
carboxysome shell protein (	icw(4);CO2_u	atggccactaaat	MATKSSREAALERRKALTEGGKQAAKRHSSGGGRVRTAADARPRTRTNAAPVQASTPAASAPAAAPAPTRSLSASAPARTGTPKRVSNPSRDLVL	gsyne_1028	2.21085E-11	-3.2421685	0.00226407	-1.6771336	0.00021594	-1.8336026	0.00014893	1.93316051	0.00065974
carboxysome shell protein (	icw(2);CO2_u	atgcgtcggagaa	MRRRTATNERALSPTAPRRRFGSNGAAEPLSPNPAELNPTSSLSKVLRQRELANAARTGQSRSSRMKAAAPVVAPASTSSARRVRPVATQVVIKP	gsyne_1029	2.33144E-14	-3.1290281	5.2914E-06	-1.923596	0.00015083	-1.6406222	0.00116476	1.62665549	1.987E-06
hypothetical protein		gtgtctgccgatgg	VSADGYAWISIGRHSLQHLRSWLDHRFQRGAKGAATRCGLKAARPSWIGAQPGGHALAGLERRHRGGASPPLRTRGGKAIAQADLITRLQAGAS	gsyne_103	8.37885E-12	3.54861684	0.00544815	1.78506062	0.03657281	-1.5474073	4.783E-06	-1.9879531	3.7726E-33
putative carboxysome pepti	icw(5);CO2_u	atgttgatctgcaa	MLICKVVKPLVSTNRIADFQHKHLQVVLDGSTQKVAVDAVGAIPGDWVICVGSSAAREAAGSKSYPSDLTIVGIIDHWDPDAAKEMAAGKPANPAA	gsyne_1030	1.77001E-06	-2.4740551	0.94940015	-1.0215156	6.722E-10	-3.1687029	1.7475E-07	2.42194555	0.26695495
putative carboxysome pepti	isu;CO2_uptal	atggaaatcatgc	MEIMQVMGSLVCTNRVEGFAHQNLRILRTSKGKLNVACDPVGASPGNWVFTASGSAARHATGNANLFTDLTIGGIIDHWSPDG	gsyne_1031	1.41189E-08	-2.730424	0.40211338	-1.1502063	5.0753E-25	-6.3169714	2.7333E-07	2.37385593	4.5952E-06
hypothetical protein		atgctgctggaag	MLLEEEERLLPPPLALLPPPRRAVAAGLAADDRLVLAGLLATAVVATV	gsyne_1032	3.00084E-05	-4.875556	0.36118845	-1.3191335	0.00084061	-2.9632451	0.00026947	3.69602932	0.1694241
carboxysome shell protein (	icw(6);CO2_u	atggcctcttccgt	MASSVQGIALGMIETRGLVPAIEAADAMTKAAEVSLIAREFVGGGYVTVLVRGETGAVNAAVRAGADACERVGDGLVAAHIIARPHSEVEPVLSGTN	csoS1C	0.018329731	-1.7503167	0.51044033	-1.1614461	0.00017692	-2.3979943	0.06935326	1.50701501	0.16258672
bacterioferritin possible associated with ca		atgagcatggacc	MSMDAVHPRVLAYLGRALSLELTAVQQYMTQASLVGLWGDEASAERFREETVEEMQHAERIVQHMLQLGVAPAASQLQPVTHAPDLVGLLEQNA	gsyne_1034	2.76528E-08	-3.2129375	0.33373351	-1.1997486	4.856E-06	-2.3443199	6.7667E-07	2.67800903	0.08741315
NADH dehydrogenase subu	icw(8);CO2_u	ttgagcgacgctc	MSDALPLPLQLIWLVPLYGFSGMLLSLPWATGWIKRNGPRPAAYLNLLVTLLAVLHGSLAISEVVALGPQHLDFPWFQAADLNLRIGFDLSLTNLAAL	gsyne_1035	0.015992063	-1.4305594	0.51267492	-1.1085097	0.31778958	1.14582465	0.06262035	1.290525	6.1999E-05
NADH dehydrogenase subu	icw(3);CO2_u	atgttgttgtcgtcc	MLLSSLLLVPFLGTLALLVWPGSPTPGQLRQITIVILVAQLVLSLLTALQFDTATAGLQLTEHHSWVPSIGLDYAVGVDGLSLPLVLINGALTLVSAVITR	gsyne_1036	0.053973877	-1.3734031	0.48870218	-1.1181704	0.00702166	1.43335434	0.17594022	1.22825914	3.7958E-09
Low-affinity CO2 hydration	icw(1);CO2_u	atgcctgttgtttcc	MPVVSQDLVQANLSIDQAEVKRRLLAGQTLLTDTPDHLLEVVGVLESYGEVLDAYSINLIYQAEQQFLNPFPIFKYLDGDLNPAKIWRHLNHDRINF	gsyne_1037	0.003944281	-1.577772	0.59108123	1.08608625	0.37087481	1.13320393	6.7604E-05	1.7135965	5.3837E-07
Possible pterin-4 alpha-cart	icw(3);CO2_u	atggagcaccag	MEHQWNPRPKPDRVEWLERRIEFPDYASNRAFLDRLNDFCEGEGRYPDISFGRTYVNITLRAEGEEAAIGEADHAFAAAIDGLV	gsyne_1038	0.005625445	-2.0247973	0.35240648	-1.2637796	8.4766E-05	-2.4253081	0.04794977	1.60217593	0.29052656
probable RuBisCo-expressi	isu;CO2_uptal	atggcctcgtctga	MASSEQQPAGIAPDDTPVNLQAAYEGAQVQDVLAQLDQELIGLRPVKTRIREIAALLVVDRARKQVGLSTTAPSLHMSFTGRPGTGKTTVAARMS	cbbX	0.380712479	1.18433845	0.01229834	1.55710465	0.00699405	1.56347327	0.04684013	1.31474634	0.0202744
SAM-dependent methyltransferase SCO3		atgcaggagttgg	MQELVQAYYGQELQSSADLKTSACCDADAVPAWLKPLLAKVHPEVSSRYYGCGLVCPPLLEGCRILDLGSGSGRDVYLLAQLVGASGEVVGVDM	As3mt	0.073563677	1.3184738	0.91832275	-1.0272833	0.10452315	1.27106387	0.02842085	-1.3544461	0.73879811
Chromosomal replication in	isu;DNA-replic	gtggcggtgcagc	MAVQQGETLWRQVQEALQGNLSKPTFETWIRPACCAGFNGTELQLLAPNAFACGWLRKNYLVTIASVASEIAGRPISVQVEAGRDPDLAQGLNGN	dnaA	3.45518E-12	2.92008571	1.8609E-05	1.9856503	0.03578303	1.38345371	0.00362762	-1.4705941	1.3907E-09
Protease		atgatgcgcatctc	MMRISRRPSLLSALLLAGLLSACSGGLPGRRGGDPTRVSDAPPSAALQPGNNFIVSAVDKVGPSVVRIDTVRRVVNPLGGLFGGGPSIQQQQGQ	gsyne_1041	0.065286824	1.31579953	0.86485575	1.0319718	0.37987887	-1.1296622	0.0520854	-1.2750344	0.00011955
Glycosyltransferase (EC 2.4.1.-)		atgcccattgccc	MPIARRQLVVLARWPAPGRCKQRLTASCGSSALAAAMQRRLSWHTVQTAAAAARHCGSELRLSASGLGPRALRRWGGQLQLRPLQLDLQRGG	gsyne_1042	0.013369824	-2.1279448	0.0858758	-1.6862268	0.55652137	1.14990366	0.47087122	1.2619565	0.00013919
probable membrane protein STY1534		atgatctccccac	MISPPPKLAHRNVLRVVGQLALRMRWDLLLMALLCGVSVLSAQLGQARAVRLIDGSGLSMLGIAVSIFVAFRNTQAINRWWEARVLWGSITNCSR	gsyne_1043	0.063707304	-1.4790177	0.17461891	-1.3130824	0.05926345	1.37748912	0.59961844	1.12637077	3.5678E-07
Glycosyl transferase, group 2 family protei		atgagggcggcg	MRAAPLAVVIPSFNEAERLPALLADLAAGPVDLIAELVVVDGGSGDGTPLQARLGGAQLLHSAAGRGLQLQRGVAATTAPWLLLLHADCRLQPGW	gsyne_1044	0.15846028	-1.6196997	0.6680099	-1.192975	9.7993E-07	2.82586875	0.28539901	1.3576979	4.5646E-22
diguanylate cyclase/phosph	idu(5);Bacteria	atggacaagctcg	MDKLALLRSVRREWQCQRRDHPRRLNTALLIWAVLSAALAGVLVEQRWQLLQQRQSRQGQTDQGLLELRVNSHKITALDWGHWDPVYAYAGGA	gsyne_1045	0.551331788	1.10118784	0.61457525	1.08777704	0.42561582	1.13126743	0.95413094	-1.0123286	0.85664727
N-acetyltransferase (GNAT) family, Syn79		atggcaatgcttag	MAMLSSPPTELDGLYGQGYRVCPTPNPQLSLVLSTEREIDLYELEQLCDAVGWSRRPLRRVRKALENSLLVVGLWRHDPRLPRLVGFARCTGDG	gsyne_1046	0.738262454	-1.0745478	0.53767957	-1.1615328	0.49210347	-1.1271115	0.78087111	-1.0809503	0.72720641
ABC transporter, ATP-binding/permease p		atggcacctcgcg	MAPRDRQRLLRLLPYLGRDRKRLLLTLVLLIPVAGAAAVQPLLVGQAISALRQEPVLAWLEPMPLAQQLRTLVLLLLAAVMVRLGLQGLQSFNVQAV	gsyne_1047	0.778925392	1.04179827	0.48482564	1.12965037	9.3825E-10	2.39992204	0.59072865	1.08432736	5.4484E-13
Possible alpha/beta hydrola	isu;Synechocy	atgcaggctggac	MQAGDPSTTGSPLERSPLLVCVHGWLLSGRLWQPLTDALSPDWECWSPDLPGFGNEPRPRGLQPSLASYGRWLAEAARERTGERPLVLMGHS	gsyne_1048	0.0003882	1.66062115	0.08480061	1.308416	0.00409024	-1.5600801	0.03912678	-1.2691844	3.5874E-20
ATP phosphoribosyltransfer	isu;Riboflavin_	atgatcaccgtcg	MITVALAKGALLKDSVTRFAAAGLDFAAVLEPGNRQLMVPSACGRARALLVRNADVPVYVAYGQAQLGVVGYDVLREHQLPVAHLVDLGFGGCR	hisG	0.004782882	-2.0803162	0.00932517	-1.9585349	0.00862849	1.67464682	0.84959681	1.06217982	8.8101E-15
hypothetical protein		atggcctcagagg	MASEAICSQNHSFCSLPPLKHRLSRVSLGQFFSDNTPVDPKNADIYGEPSLDFSIARSIAPKSDIYMSSNSGDSKLYGSFAELIYNKSVDIISSSSEF	gsyne_105	0.021331445	-1.5040129	0.17498685	-1.2648177	0.1740065	-1.2521306	0.31492792	1.18911435	0.25117044
Hydroxyacylglutathione hyd	isu;CBSS-342	atgcagccggccc	MQPALTTASIAQRVSLIPVLNDNYVFVLHGDGPGPAVVVDPAVAEPVIAWLEQRGLELSAILHTHHHHDHIGGTPGLLQRWPQAAVIASGADQARIP	gloB_1	0.00616417	1.933839	0.43683405	1.19765956	0.00149546	2.04927205	0.02928674	-1.6146817	0.77856837
Ferric iron ABC transporter,	isu;Iron_acqui	atgcgaatcgagc	MRIELSNPELPLRPQVELDGLWHRYHGGASSGDWTLRDIQFQLRPGELVGLLGPSGCGKTTLLRLIAGFEKPDRGVVRIGGQEVAGPHRWLPPE	gsyne_1051	0.029608897	-1.5753623	0.02221289	-1.6176115	0.02859455	1.4555776	0.95442457	-1.0268187	1.7709E-08
Bona fide RidA/YjgF/TdcF/RutC subgroup		atgaccagccccc	MTSPTIEAVTTSAAPAPVGPYNQAVKAGGVLYCSGQIALDPATGAMVGNGDVEAETIQVLSNLKAVLAEAGCTPQQVVRTTVFLADLGDFAKVNAL	gsyne_1052	0.766495142	1.16473465	0.8402409	1.076376	0.01038633	2.15708545	0.84577482	-1.082089	0.00172271
Alkylated DNA repair protei	isu;DNA_repa	ttgatccggattga	MIRIERSGLQLRHGEAWLQQQGLDTQQLRRSLITGLAWEQPLVTVYGKQHRTPRLTCWVADRGCNYRYSGLQQAIHPWTPELLRLRGLLHEHLG	gsyne_1053	0.333167068	-1.5257718	0.23455711	-1.6262445	0.02866032	1.87508536	0.81848015	-1.0658504	0.0002044
hypothetical protein		ttgcgcatacggc	MRIRRWLLVVLGFIAAFSLAARAEPGLEGAMDAGLPPRPDLIPAETPVADVVLAAAVPSGLSREAAWPLRPGEPLRLVYPLAIQAEEVDPYGWRYS	gsyne_1054	1.90721E-10	3.12690268	0.03250063	1.57715692	0.06356943	1.45146646	7.1645E-07	-1.9826199	3.7047E-12
hypothetical protein		atgcgtccgatcg	MRPIVLSALAALALLPMAPAQAGSATAGSIMSKQAAIATATSSMPAGNSVTRSRCTTMVRALSARYSCTVWWSPTPLEGDG	gsyne_1055	0.005996081	1.67529365	0.82044455	1.05982129	0.0001173	-2.4288252	0.00351734	-1.5807322	5.8526E-22
				gsyne_1057	0.180642103	1.75100086	0.23415816	1.67433748	1.6609E-05	5.15662404	1	-1.0457873	4.9642E-05
				gsyne_1058	1	-1.0106682	0.79746948	-1.1489208	0.00029863	3.38675702	0.79746948	-1.1367933	7.4936E-07
hypothetical protein		atgcctaaccccca	MPNPKTLATGTWLPIEQLAEQLVCGERTVDTLRSEGIFKAGEHYYAVGSGKKRPKFVYCLESCRAALLKRTAELEAERKATVEDAVTYDEEHLEEL	gsyne_1059	0.285944852	-1.7536554	0.22845186	-1.7935487	0.00877901	2.60393569	1	-1.0227486	6.4107E-08
Mobile element protein		atgggcggcaag	MGGKQLGFTDYELTTAKKRTKREKFLSEMEAVVPWQALIDLIEPHYPKASKKGGRPPYPLATMLRIHLLQQWYSLSDPAMEEALIEVPTMRRFAGI	gsyne_106	0.609272871	-2.1292932	0.37248029	-2.690409	1	-1.0791744	1	-1.2635221	0.60927287
hypothetical protein		atggcgactgacc	MATDLGKRRSPALEQMQRLVASYDLFNKELFSNQLPPVWLDLRNKPGSYGYFQANKWKDANGNLLDVISLDSKTAAERPLIELLSTLVHEMAHAY	gsyne_1060	0.924652325	-1.0709842	0.40505461	1.35404753	6.5753E-12	4.89090843	0.19469839	1.45016348	1.7439E-24
hypothetical protein		atgcgaagaagc	MRRSKAEIEAIRAAIYDYCQRHYPLTVRQLFYALTVLHLINKTEGEYKQTVCRLAKDMRLQGELPWHWLVDNTRWMRKPISYGSLADCVEQSART	gsyne_1061	0.228385593	-1.4628358	0.31129681	-1.3844115	1.79E-07	2.92135658	0.92605	1.05664811	6.0406E-18
hypothetical protein		atgcacaaccata	MHNHTRTANPLPSTRAHIAARARAAARRIAYNQQVERWEQLLRMEQALEDSTALYFSGAPHPARFQSDFDWLEELIRGGETLSRWMADCVDRLS	gsyne_1062	0.014997159	-6.2969319	0.22552864	-2.6692483	0.13593705	2.11417775	0.51365359	2.35906559	8.884E-08
hypothetical protein		atggctctctccag	MALSSNDRIDLINALDVLIGAYGQNSEAENRLRKDYTADRPRGRRARALLERIARGALEVDC	gsyne_1063	0.050597273	-3.1949709	0.67585832	-1.3394207	0.03899184	2.01688191	0.09811871	2.38533782	3.9039E-08
hypothetical protein		atgcctcaggact	MPQDFTDWRHYLPQLDGFPLLPVGAGVKGKSPIDPATGKGLAGWQTKRFTPDQIAAMNGVVKSVGTLTGPQADHTAFIDIDGALCIERCKHHGC	gsyne_1064	5.95877E-12	-3.6945601	0.01777384	-1.5017485	4.2577E-10	2.32874328	7.3273E-07	2.46017225	8.6453E-68
hypothetical protein		ttggctcgcccaa	MARPSKPEQLKIQERCYQLWVEGKSHTDIARLAEVSTTTVTKYVRQFLAAQPIAKMTREEREAAVWQEWQEIAQKLRMDIEEQRHRGRVKVVRN	gsyne_1065	0.414559	1.2325474	0.29996572	1.28594728	0.32379918	1.25417817	0.82269845	1.04332481	0.92804184
hypothetical protein		gtgcaaaatccgt	MQNPCKWAAYPALGVTIQHMRNPAIGLLRSDMAELQDAWEVGQATRAEGWELDPTHDATLYASVVLLGMLGLIELGRLCLKQSAATREAVEG	gsyne_1066	0.006014938	-3.1048408	0.33663092	-1.4318917	0.31262448	1.40174488	0.05070658	2.16834898	1.9328E-07
hypothetical protein		atgtctgaagaca	MSEDICGLLFELQQLALQVAQSGDDLPLAIACEQLREALAEL	gsyne_1067	0.129299384	-84.785991	0.69276907	-3.473224	0.38436918	1.96612714	1	24.4113226	0.00148408
Terminase		atgtctgtacgcc	MSVRPLQLSPWQRKVAGLVQSVDSLNTLLLAGGRGGGKSVLLVWLICYFAITSGGSFRGVLIRADLSGLQKLEGMLMEQIPLLLPGSKYLRAKRQV	gsyne_1068	6.88411E-06	-2.2913976	0.00886279	-1.6105413	4.6495E-06	1.87845614	0.04351537	1.42274995	1.8177E-27
hypothetical protein		atgcctgaaccca	MPEPTSRELSLMYFDRFRPEILGMLEVIEDPAGFDEEKRLQLVDAYMDIVTDG	gsyne_1069	0.515667781	1.85178381	0.3992219	2.74617242	0.00107604	9.97072071	0.79627543	1.4829876	0.00021974
hypothetical protein		atgccgcgcaaa	MPRKSQPKPTPPSKAPASKPALSEGFKIKLQIAATVFVPMLALGLWLNSQGFFG	gsyne_107	1	-1.0637352	0.61127556	-1.3448497	0.52903965	1.57072743	0.73956386	-1.2642711	0.24436671
hypothetical protein		atgggcaatcatc	MGNHPSDSEYIERNTPPTSRQTLNKVNTMNTNITELKNEELETIQGGGSTILGNTAPADPQLQQLHDVLPKRGIRNI	gsyne_1070	0.305185388	-1.6720408	0.0511818	-2.6735636	0.67336251	-1.200664	0.29498892	-1.5989823	0.47972174
possible SAP domain		atgccagaagaa	MPEEQLKAFLEAVKADADLQEKLTAAADVDAVVEIANAAAFAISAEEQGQVEICDEELGGVTGGIRPSYAEIKEHTDSLVRQCNEAYEKKLRAETLE	gsyne_1071	0.022902962	-1.383862	0.23711478	-1.1806389	1.9054E-36	-6.6808112	0.2524121	1.17212971	4.7864E-29
Mobile element protein		gtggtgggtcaaa	MVGQNRSTQRHPAKVVSIEEGKLRHRLREIAAEHIRWGRRMAYRLLRREGWSVNHKRVQRLWREEGLQRPISRKRKRARPADGSVRRHRAEHP	gsyne_1072	0.592278596	-1.1135158	0.58841149	1.10090011	2.3277E-05	-2.1882225	0.21190361	1.22586968	1.0831E-05
Mobile element protein		atgaaacgcacc	MKRTRHTAEQIIRKLKTAEQLIAQGKTVADVCRVIEVTQPTYHRWRQQYGGMQAEEAKRLTQLEKENARLKKLLAEAELEKAMHKDLAEGNF	gsyne_1073	0.298204563	-1.4592504	0.29820456	-1.4932591	0.14273355	1.61934578	1	-1.0233057	0.00013808
hypothetical protein		atgaggactctca	MRTLIHPGPITRVHVKLTTVSSKPAELWPSTLGAKLAMGLGGIDKPEQKRQQGSGGIGWLRSPDGDKVIRIEGANESLHAK	gsyne_1074	0.837055997	-1.2250437	0.41430089	1.66656832	0.61316104	1.42452411	0.15259605	2.04161906	0.21998801
FKBP-type peptidyl-prolyl cis-trans isomer		atgaacaccccca	MNTPILALSDQELITAVGGSGSGAKPGQTVVVHYRGTFENGQEFDSSYGRDPFSFPLGLGRVIKGLDEGVVGMKVGEKRTLVVPPALAHGERGV	gsyne_1075	0.380190561	-2.4187512	0.38019056	-2.6067514	0.62061066	-1.6470236	1	-1.0777261	0.70091659
hypothetical protein		atgactaaccaac	MTNQPNRDLTQQAQELDDQQLEAVAGGFISYPVPTREDWEELKRRHERNPNGH	gsyne_1076	0.044322796	-2.0525356	0.3274077	-1.4690059	0.09620748	-1.6878356	0.37342246	1.39722759	0.56702427
hypothetical protein		atgaccaatcaat	MTNQFNRDLTLQAFDIVHQPLELSDKDLEGVAGGQLCPVGFPFFCPDDPVYSDW	gsyne_1077	0.028709623	-2.7203831	0.00737795	-3.5661381	0.83991006	-1.1973127	0.71383156	-1.3108956	0.01096903
possible SAP domain		atggagttcatcac	MEFITPRPLQAMSEEQLKAFLEAVKADAGLQEKLKAAGDADAVVAIAKGAGFLISAEELKKAQAEVSDQELAIVAGGGQLNRLNDFYSEAMKKRLQ	gsyne_1078	0.090745225	-1.2957149	0.19215208	-1.225547	1.7056E-11	-2.9528932	0.72958005	1.05725435	1.9986E-10
hypothetical protein		gtggaggtgactg	MEVTDADITSSGRPLVKHCRRMLRFNAEQLWQNLIRQGWKRVPPQW	gsyne_1079	0.477740107	-1.6069543	0.77511676	1.29807245	0.8708638	-1.1032652	0.14086738	2.08594307	0.47774011
Oxygen-insensitive NAD(P)H nitroreducta		atgcaaaccatct	MQTIWPDGMPADTTTLLDALRWRYATKAFDASRQIDASTWSALENALVLTASSYGLQPWKFLVISDAAIRAELRPHSWNQSQITDCSHLVVLLKKR	gsyne_108	0.000124539	-2.6880597	0.01179547	-1.8390184	0.02710935	1.48620247	0.15777168	1.46168177	2.1738E-20
hypothetical protein		atggcacctggat	MAPGLTKSASKKQGTKTTSSAKHETTFQRDTLANIAIGSGSATTTNILGDLIGAVANKWLPGSRPAFEYLVDTGAAIVLNEGLETARDGESLFNEDW	gsyne_1080	0.002663873	-1.5763662	0.44724794	-1.1161391	0.25942074	-1.1696349	0.01607209	1.4123385	0.02147649
Staphylococcal nuclease homologue		gtgctctcagttgg	MLSVGDGDTLTVNASGRRTTIRLACVDAPESAQRPYGGQSRAALQSLAPVGATVTVQGNKKDRYGRTVAEILRGSTNVNVELVRRGDAFVYRQY	gsyne_1081	0.044130746	-1.8299525	0.44070076	-1.2893707	0.00127401	2.08601742	0.18810662	1.41926017	1.4673E-13
hypothetical protein		atgaagccttcag	MKPSAIAALAGLGVLVLSSGTAWAQSCSSFQTCAQAVASYKAGNTKLDRDKDGIPCESLCGKNGENMPR	gsyne_1082	1	-1.1426755	0.41826716	1.40492004	0.03372396	2.16738953	0.1828191	1.60536773	0.00189453
hypothetical protein		atgtgggtggcaa	MWVAMISPSRFHADALGDLRDFLETTEENPALRAAATFRAMDRLRDALLLIEETASVETPVPLLLQDVALLGRQLLQRLR	gsyne_1083	0.582417388	1.45988238	0.25393831	1.7624411	0.00194402	3.44408899	0.63169009	1.2072487	0.00052747
hypothetical protein		gtgaaaccgctca	MKPLTFNALLESEGLDPARVRLIRHKHERRYQEQVFSDALNKREKFEKYQSSQGDTRVIKSIKTADYIASFVVSPSGETVFAGIWKVNGCKEIFTAD	gsyne_1084	0.009067627	-1.4279223	0.87773996	-1.0247533	1.0115E-05	-1.7756386	0.00520224	1.39343028	0.05725944
hypothetical protein		atgagcaccaca	MSTTFTADYLARAAEQLGWDATPAGQQKRQKDLALLQELMAATRGLHPGRHLRQN	gsyne_1085	0.71023223	-1.1922194	0.17686533	-2.9608182	0.22927878	1.8858745	0.24814834	-2.4834507	0.02228177
hypothetical protein		atgcttgctcgact	MLARLSPEEFVRRLAQRFPRIEALSDYVTAKEKISLRCKACSHEWQATPDNLLRGVKYGCPKCALAARNEEWKAEIRKWLRKHRPDVKLIGELTTH	gsyne_1086	0.001057509	-1.7360473	0.12426691	-1.2857283	0.02458059	1.37341114	0.05383313	1.35024432	1.1967E-12
hypothetical protein		atgcccgactacg	MPDYGRMRLQVRRPGIKTQSMNLPFAWEEAAWVDALQHIKVIAKAFNEGGVDLKGAAKVATVVRSAHDTDWTAAAAAYRQHKQRVSDRTWRQH	gsyne_1087	0.0540395	-1.5398741	0.6750716	-1.1135424	1.1617E-06	2.23398155	0.10588886	1.38286079	4.2803E-20
hypothetical protein		atgacccatacc	MTHTPHWSVQRQATDCLGVSERTLHRWRSAGLLKPGEHFRRKFPSPNSPLLYHLERCEEAMNHACARPWQQLERAPQCSREKLKRR	gsyne_1088	0.558488828	-1.5259787	1	1.11503183	0.00353804	3.60673158	0.34935523	1.70151482	5.7278E-07
hypothetical protein		atggattcccgca	MDSRRLVVWISTGILGFQGATLAFDLLNCTALSWLYVRIHGVPALERRVDVSVGSRAVVEPDATQQALGTPTPEHPVVLFCARPQGRIDDAVNQGL	gsyne_1089	0.502816048	-42.949429	0.50281605	-42.949429	0.56112025	2.15047856	1	1	0.00909655
FIG01152221: hypothetical protein		atgcccctgccga	MPLPMLLAATTLELGMASPPAALQPMPLLTLERTSRRLPRTGDPIWDLRLDIPGEPVRHFDAVSGRADRQGANRDQMGSEAPLPIGRYRLGAIEP	gsyne_109	0.002707212	2.39603749	0.02579355	1.94043279	0.00087196	2.54600841	0.40117333	-1.2347954	0.84850352
Mobile element protein		atgaaacgaacc	MKRTRHTPEQIIRKLKTADQLLAQGGQTVADACRFLEVSQPTYHRWRQLYGGMKAEEAKRLSQLEKENARLKRLLAEAELDKAMLKDLAEGNF	gsyne_1090	0.055539894	1.90925566	0.01103004	2.31796037	4.9195E-06	3.6604043	0.45276138	1.21406495	0.00037378
Mobile element protein		atggacttccaatt	MDFQFDATADGRRLKFLNVIDEHSRLCLAIRVGRRCKSRDVVAVLEELTSLYPAPAFIRSDNRPEFIAHALKRWSENSGTTTAYIEPGSPWQNGFAE	gsyne_1091	0.267941839	-1.3553387	0.76692897	1.09332638	3.389E-10	3.46192662	0.08677041	1.48182752	2.1546E-28
AbrB family transciptional regulator		atgaagggggtca	MKGVTSGRGKGGRKLSYTATVQGNGNLLIGKAYTAMLDLKPGDEFEIKLGRKQVRLIPVGGVDEDE	gsyne_1092	0.007834002	-4.235379	0.39609979	-1.5317802	0.91759334	1.09121695	0.06104465	2.76500439	0.00011153
hypothetical protein		atgcccaaacag	MPKQRPKRRNALAVFSLALSLAGYLLLQSGALPNKKKKVSTSTSVEIMSDTRS	gsyne_1093	0.943338951	-1.0228742	0.07057417	1.46365301	5.0907E-05	-3.2079103	0.0173198	1.49713282	3.1956E-09
Mannose-1-phosphate guanylyltransferas		atgctgatccaac	MLIQPPMTPLVPVILCGGTGTRLWPLSRASYPKQYWALAGDGDDTLLQQTQQRLNGIQGLQPPLLICHEDHRFIVAEQMRQIGVDPGVILLEPMGP	gsyne_1094	0.267357501	1.17437556	0.68206554	-1.0676345	0.05593125	1.29318811	0.07961022	-1.2538039	0.40789583
Glycosyltransferase		ttgatcaacctgcg	MINLRVWGHHRASFGLAGGAAATVRLLREVGCNVACHDLPLASHPAIQSAPCSQHQSLPVQIDLVHTNPNLLQADPCLLHAADLTAPLRIGYWAW	gsyne_1095	7.04105E-05	1.94788749	0.07654989	1.34756244	2.6072E-20	-5.0606052	0.02443714	-1.4454896	1.5441E-44
hypothetical protein		atggagcttataga	MELIDYYRWCLRQLELKQWEAAEGRLLWLRHQLGPTDQDIADALAYALLMQGAYEQCIAVLTPVLYSPKRSFWIHHKYADAKRGLHQLRDAVKHY	gsyne_1096	0.234474639	1.19240069	0.8818609	1.03421169	4.0127E-08	-2.235932	0.2690711	-1.1529561	7.5581E-16
hypothetical protein		atgtccttcgcgcc	MSFAPPDFVDTTVRQITVEDSLPQPPGGTTIVFTGLSSGTAAITDPNTGTAPVNVLLDPQFDGLPQNLFIAIATAKVELAFVATKASSTLATTGVQIRV	gsyne_1097	0.01014921	2.10606569	0.35267279	1.30589438	1.5381E-20	-21.576105	0.0965861	-1.6127382	2.1538E-29
Tetratricopeptide TPR_2		gtgagtgcaatat	MSAISEAWPLLDRGKPHHALGIWREQLLQSHRCLAYIEAAHQALPQDPLAEQRSLVLRLLAQLQAGVPGEAEISLLGQVLRGWAALCLDHAPGRS	gsyne_1098	0.005918207	-1.6574049	0.32702106	-1.196148	1.2685E-05	1.8909195	0.047821	1.38561855	3.5949E-20
Beta-1,3-glucosyltransferase		ttgttacctgaatcc	MLPESCDLAVVLPFRNAQRWLAESLLALVNASQDLRWQLIAVDDGSTDQGGHLLRRLTAHWPAQQCILLRTPGIGVAAARNLAIRTTKAPIIALLDA	gsyne_1099	0.143261037	-1.4737397	0.11185195	-1.6529529	0.00651213	1.9160969	0.84566258	-1.1216044	5.661E-09
FIG01150045: hypothetical protein		atgcgtttcgtgctc	MRFVLWGTYCDNALEKRTPYRDEHLAGLQQQKDSGVLITLGPTEGSTHVFGIYEAENQEQVETLLHNDVYWRNGIWTELKVYPWIQAF	gsyne_11	1.28885E-05	2.20823073	0.01197768	1.64216334	0.01026387	-1.7739889	0.02824275	-1.3447083	1.327E-27
hypothetical protein		atgctcaaccgcc	MLNRRPLHRTLTALIVLSAGAGSALAGQSLWSLETGVQSCIETSSAQACRQAEALVNSLKSNPAYGRSSHLCKEEISELEEVIKLLPMRDAVPTEVM	gsyne_110	0.000233782	2.05866021	0.00395904	1.79265161	1	-1.0250468	0.36493353	-1.1483883	9.1005E-09
				gsyne_1100	0.392629118	1.40799918	0.29193867	1.50612122	0.00145609	2.8135087	0.92211573	1.06968899	0.00160581
hypothetical protein		atgggcaagcgc	MGKRQAKQRSKKSKDATPAEPACSAAVSKPDAQCGSNAEARNTLIHRYLEMAEDLNQRGAMEMAVPFYRQVIALLMGPENVSLPAAVVQAEDQF	gsyne_1101	0.240992715	1.21617292	0.88524367	1.02586562	7.472E-13	-3.4078155	0.29596356	-1.185509	1.7208E-17
possible glycosyltransferase		ttgaagcccagga	MKPRIGLVSFAWTADHPGGLRSHVVDLAHALCDQGYAVFVHCVNTDPQAPLFETRSWIENGIHVQELNYAYQDLQALPGFQCVDQAEVILCEWVF	gsyne_1102	0.78693968	1.03852739	0.15109485	1.22034214	0.43894493	-1.1131302	0.20206843	1.17506978	0.21732178
Glycosyl transferase, group 2 family protei		gtgcaaaacgctt	MQNASWAQLYSTADALVQVGQWDQALPLLEQVCSIKHDHASAHHLLGKYFAACGQLDRAEQHQTLSCQFDPQLGWNWFALAELLLELKRYEKA	gsyne_1103	0.73035749	1.05737091	0.71232305	1.06177782	8.3835E-07	-2.1900023	0.9838313	1.00416779	4.6877E-08
hypothetical protein		atgcctactgagg	MPTEAGLDRAMHQLTSAVHRRNVANKMSHLSAWGVLSCRSSIRRLSPSAALAASLAVAAVAPAQASGLQWRLTNPGAAPPSSRPAAAASGGLPW	gsyne_1104	0.00115557	1.74095439	0.05401515	1.39323085	6.2882E-09	-2.7317884	0.17575193	-1.2495807	5.672E-20
Capsular polysaccharide synthesis enzym		atgacctcaccac	MTSPQSPSRRRWGGWLRLYGDDLNRLQRLVDPLYVTLLFDGLVLTQLRPRSTAEEWLIAAVVATLAALILPQGKLYQSYRQQSLLTLMRRLSLSWL	gsyne_1105	0.910442681	1.03408666	0.37217449	1.16577345	0.00027738	1.68067139	0.39094708	1.12734599	9.6193E-06
hypothetical protein		atggaggaacag	MEEQIPTSTSSPGPLHPPAVAVVLGRGPQIAAASTRLAAALLRDQDAAAVYVSGDATSTAEALERQGVASDQIAGDSCARTTWENATHTAAWLRIH	gsyne_1106	0.02494494	-1.9942648	0.16782783	-1.5522645	0.0977362	1.45574941	0.41952999	1.28474548	7.5422E-07
hypothetical protein		ttgcctgatccatc	MPDPSAIAWSHCPPEPLLWLQLREPLLQVLYRPWLALPLLGGLVWWLPCLRCQPCCTAPSALLL	gsyne_1107	1	-1.0698647	1	1.11516619	0.01489102	3.10216608	1	1.1930769	0.00033243
				gsyne_1108	0.73375503	1.14404957	1	-1.0859309	0.90490637	1.04115443	0.64585658	-1.2423587	0.82286699
NUDIX hydrolase		atgaagcgctgga	MKRWILRCRLYWLAACLFDLYRLIAKPRTRGALVALWCQGRVLLVVASYRRELSLPGGWINRGEAPEHAAQRELEEELGVVAPLELFQQPWVCTE	gsyne_1109	0.003437734	1.56545259	5.186E-06	1.96813944	0.00184519	-1.6549422	0.04963396	1.2572335	5.4731E-18
hypothetical protein		atggccgattccc	MADSRHRLSRQFRVSNGDGFELKHVDPGSTDHAEPGGKQVAAAALAQGVERMAELQDKLYAQDRWALLLIFQAMDAAGKDGTIKHVMSGVNPG	gsyne_111	0.045962495	-1.3830652	4.5916E-09	2.23867686	0.57312706	-1.0989547	4.8956E-20	3.09623603	0.05068822
sugar transferase		gtggttgtgttggct	MVVLAESFRRVLNPFAGRLRLHGSDISRLQRLLDPLGVTLLFLLLQRPEVWDGSQLTLQPWLWVLVSCLLLLPTSGIYASYRQRSLFTLVRRVTSGV	gsyne_1110	0.033970896	1.39349733	0.01219335	1.477998	0.02547835	-1.4149087	0.648302	1.06063927	5.5286E-08
hypothetical protein		gtgaccatttggg	MTIWEPQMRRLTVAQAKAQLSALLDAVEHGEDVEITRRGR	gsyne_1111	0.716566679	-1.2218695	0.46914652	1.30137784	0.03170602	-3.3127472	0.15003	1.59011394	0.00876867
hypothetical protein		atggtgatcgatc	MVIDPSAVLAILQNEPERPAFNAAIASADHCALSAASLVELSIVIEARYGSDGQGDLDLFLSTAQISIVSLDREQAEIARAAFARYGKGRHRASLNLGD	gsyne_1112	0.02300451	1.53394634	0.08209092	1.4212409	0.45518169	-1.1727463	0.58188024	-1.0793007	3.2448E-06
hypothetical protein		gtggctctcaaca	MALNIRNPEADRLAAQVACLSGETKTDAVILALKERLQRLQSQPEAGKVRQRSLIHRLDQIALRCAARPILDSSSADEICGYDASGLPS	vapB30	0.00390216	1.57420804	0.97081154	1.01808611	1.8062E-13	-4.0322717	0.00119434	-1.5462425	1.3557E-46
hypothetical protein		gtgcctgattcaac	MPDSTAIAWSHCPSAPWLWLQLREPLLAVGYQPWLLGPLLGLLVWWIARRPLPVVVAMVLIAVLYSPIGTTALSAWLQGQLPPSVPAASQPVAVLL	gsyne_1114	0.756326438	1.08045492	0.19908248	1.38336776	0.00014214	2.28648341	0.28630283	1.28035676	1.2069E-06
hydrolase, nudix family protein		atgaagcgctgga	MKRWILRLRLLTLAAWLYDVDRLVVKPRTRGALVALWCQGRVLLVQASYRRELSLPGGWIDRGEAPEQAARRELFE	gsyne_1115	0.32433444	-1.4642794	1	-1.0134186	0.08349634	1.83144004	0.33224757	1.44489095	5.3189E-05
Colanic acid biosynthesis glycosyl transfe		gtgagaattctgttt	MRILFYGLNYYPEPVGIGKYTGEWSCWLASRGHQVRVITAPPYFPQWRVQPGHRNAYATEQHDGLFVQRCPLWVPRQPSGLTRLLHLASFALSS	gsyne_1116	1.35368E-13	3.35014526	0.06850702	1.37099462	0.24470352	-1.2154962	2.5502E-09	-2.4435875	3.7564E-22
				gsyne_1117	0.008010327	-2.0726923	0.21140848	-1.3896709	9.8536E-07	-4.7185208	0.12892906	1.49149865	0.00359598
hypothetical protein		atgcgcatctccc	MRISRFLIALSALGGFALVGELAARYVFGLGTPPLYVADPLTEYRLKPSQQLRRFGNHIEVNRFSMRSKPLASNARGQRRVLVFGDSVVWGGSQL	gsyne_1118	0.243566802	-1.2136568	0.45579354	-1.1292437	1.4139E-08	-2.5025272	0.67576887	1.07475188	2.4625E-06
hypothetical protein		atggtgatcgatc	MVIDPSAVLAILQNEPERQAFNAAIASADHCALSAALLVELSIVIEARYGSDGQGDLDLFLNTAQISIVSLDRGQAEIARAAFARYGKGRHRASLNLG	gsyne_1119	0.252260876	1.23723142	0.12169789	1.33918492	5.6051E-05	-2.0894695	0.64647774	1.08240456	1.9483E-10
Putative membrane protein		atggcggattcttc	MADSSVVEHMMPQTFQHYLLGLFAVANNIPALGPFLNLQEGLPRTQARHVIRVATITSFLIMISSFLFGTAVLRFFGIGVSAFQIAGGLLLGASGLSML	gsyne_112	0.381885725	-1.1683135	9.8188E-14	2.83804469	0.22360272	-1.2332899	2.387E-23	3.31572598	0.78032519



EDGE test: Control vs Viral 12hr, tagwise dispersions - P-value	EDGE test: Control vs Viral 12hr, tagwise dispersions - Fold change	EDGE test: Viral 30min vs Viral 5hr, tagwise dispersions - P-value	EDGE test: Viral 30min vs Viral 5hr, tagwise dispersions - Fold change	EDGE test: Viral 30min vs Viral 12hr, tagwise dispersions - P-value	EDGE test: Viral 30min vs Viral 12hr, tagwise dispersions - Fold change	EDGE test: Viral 5hr vs Viral 12hr, tagwise dispersions - P-value	EDGE test: Viral 5hr vs Viral 12hr, tagwise dispersions - Fold change
0.59949562	1.25017209	0.60009161	-1.2450606	0.54712945	1.30623865	0.25056229	1.62634632
0.56510781	1.30066639	0.49558926	-1.2640723	0.37114324	-1.3931504	0.88549637	-1.102113
0.90094891	-1.0355556	0.51280595	1.23720677	0.86887875	-1.057373	0.36867844	-1.3081891
0.20407392	-2.2736109	1	-1.0686685	0.6927654	1.16717562	0.6927654	1.24732384
0.02726653	-1.9913965	0.47561518	1.30647972	0.7775231	1.14955251	0.73290059	-1.1365116
0.21536616	-1.7000578	0.58845438	-1.5708271	0.86598515	-1.0807973	0.84705062	1.45339657
0.54084613	-2.3055873	0.30223937	4.11485315	1	1.6891067	0.54084613	-2.436112
0.0684317	-7.3349647	1	-1.7101139	1	-2.1417387	1	-1.2523954
0.89837653	-1.1169847	0.55771628	1.49062202	0.65113456	1.48614027	1	-1.0030157
0.07192042	-2.6107566	1	-1.0642218	0.87123797	-1.2771234	1	-1.2000538
0.18945893	-1.5939699	0.65421566	1.16565852	0.19625492	-1.591462	0.07942898	-1.8551012
0.03425095	-5.1413723	1	1.08926547	0.17488327	-3.8785765	0.09157696	-4.2247995
0.03358858	-4.911048	0.72005433	-2.0857684	0.42071593	-2.6927456	1	-1.2910089
0.74823416	1.29523607	1	1.02780524	0.61743868	1.46740627	0.74823416	1.42770849
0.00787341	-2.9239943	0.35534943	-1.639351	0.5845226	-1.3658815	0.7968332	1.20021464
0.15235004	-1.7596175	0.3980117	1.40371494	1	-1.0284132	0.35377771	-1.4435989
0.23167551	-1.5817257	0.03150516	-2.5552102	0.13556435	-1.8596151	0.64242731	1.37405325
0.69109892	-1.3626118	1	1.01513494	0.34357637	-2.2316635	0.28412691	-2.2654396
0.32493975	-1.4564229	0.45746503	1.28948085	0.12573066	-1.7863014	0.01999824	-2.3034014
0.72764168	-1.1696444	0.92224996	-1.0588777	0.41761211	-1.3718304	0.5069829	-1.2955513
0.74213138	-1.1509574	0.21929985	1.50173341	0.67628826	1.13238279	0.46721938	-1.3261712
0.43153213	1.29149311	0.77273948	-1.1002571	0.86843417	-1.0461789	0.92123721	1.05169119
0.46451243	-1.3052359	0.88942591	-1.0792497	0.84503599	1.08697831	0.68771203	1.17312098
0.3032225	1.45811936	0.44330636	-1.3370594	0.33172673	1.44292188	0.07731129	1.92927225
0.44667811	1.37913871	0.30675376	1.60443673	0.55403618	1.32012082	0.71398438	-1.2153711
0.87170553	-1.4231772	0.33342642	2.26766569	1	1.05824541	0.42871684	-2.1428543
0.91696884	-1.0536342	0.09627988	1.60690431	0.45191771	1.23520252	0.36546052	-1.3009238
1	-1.0056316	0.36901324	-1.4962521	0.93280761	1.0285767	0.28547049	1.53901008
0.59969829	1.15777985	0.53366907	1.22510629	0.59969829	1.17983123	0.96126256	-1.0383742
0.90844326	-1.144531	0.45785774	-1.5031236	0.53362413	-1.422179	1	1.05691594
0.24884092	1.64324826	0.40687255	-1.4262256	0.67604761	-1.1964912	0.68224121	1.19200671
0.01309274	2.87328403	0.90233329	-1.0525657	0.74368856	-1.1464161	0.83870182	-1.0891635
0.18537701	1.87872764	0.62374818	-1.2584617	0.17217903	-1.9049811	0.38043423	-1.5137378
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0.78024661	1.12501196	0.86835164	1.06998941	0.0519737	-2.1753339	0.03501451	-2.3275843
0.63151099	1.20820094	0.18218763	-1.7445083	0.79861479	-1.1826185	0.33012928	1.4751235
0.51314862	1.28855994	0.66530886	-1.1649044	0.0136752	-2.3023523	0.04464926	-1.9764302
0.47445101	-1.3650907	0.06556954	-2.1944714	0.00119805	-4.1219036	0.1481746	-1.8783127
0.6835402	1.26088034	0.09913212	-2.8186699	0.13954425	-2.7335716	0.95065341	1.03113083
0.1313366	2.06421204	0.36568846	-1.5140622	0.2185323	-1.7972235	0.75587342	-1.1870209
0.11098559	1.95574233	0.38537759	-1.413564	0.13850177	-1.8182143	0.5323116	-1.2862625
0.0637598	2.05583421	0.64908132	-1.1917883	0.53432367	-1.2709007	0.87552541	-1.0663812
0.16699431	1.56192814	0.3488662	-1.3367432	0.13739957	-1.5898301	0.59744792	-1.189331
0.33791286	1.35635733	0.6744786	1.12596502	0.35856554	-1.3214299	0.1807015	-1.4878839
0.68736415	-1.3350356	0.13088784	-2.2995966	1	-1.0836454	0.15521307	2.12209327
0.64894043	1.19973585	0.45459366	1.32172979	0.51992613	1.30059987	1	-1.0162463
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0.5822026	1.21047395	0.25077613	1.45934049	0.37598183	1.35421053	0.82160081	-1.0776319
0.8208197	1.10258374	0.32304786	1.35716993	0.83249359	-1.06333	0.20069751	-1.4431196
0.45479389	-1.5229075	0.62455006	-1.3879919	1	-1.0717116	0.62455006	1.29511697
0.10143904	2.24127517	0.01847824	3.25655587	0.12199446	2.14227755	0.39730904	-1.5201372
0.79647589	-1.2611078	0.56754585	1.49652464	0.76317942	1.21482349	0.79647589	-1.2318865
0.84078431	1.06599024	0.98075069	-1.0112717	0.73284243	1.11540207	0.69697376	1.12797453
0.58463138	-1.3715876	0.15025741	-1.8898737	0.51811706	-1.4679026	0.58092686	1.28746536
0.05127178	1.77355558	0.88921953	-1.0409779	0.69782339	1.13753483	0.56675936	1.18414863
0.53437787	1.20946365	0.80856272	-1.0620226	0.64858048	-1.1450039	0.86365136	-1.0781351
0.55958811	-1.4046633	0.43569441	-1.4796771	0.50272668	-1.4228418	1	1.03994495
0.38105694	1.44303924	0.02947914	2.49329781	0.38105694	1.43886142	0.18519318	-1.7328269
0.28524786	1.58903116	0.42903499	1.39789495	1	-1.0210826	0.3941567	-1.4273661
0.63938358	1.21416836	0.04770706	2.25664164	0.37170906	1.45240857	0.28379546	-1.5537237
0.67906431	1.2908562	0.85751702	1.16055845	0.36134046	1.71608605	0.56938633	1.47867266
0.61514883	-1.6788249	0.21015746	3.03222447	0.37087975	2.36683374	0.90934903	-1.2811312
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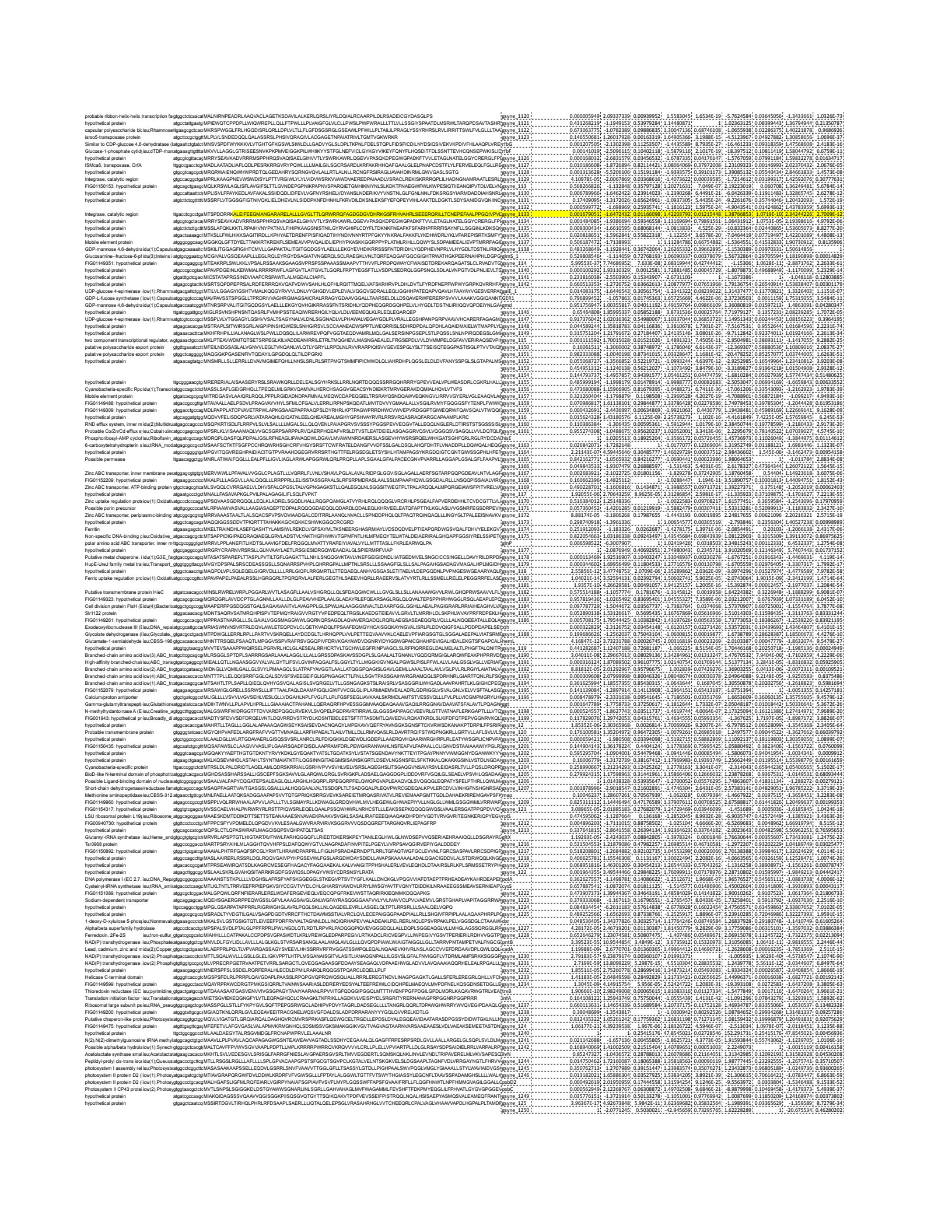
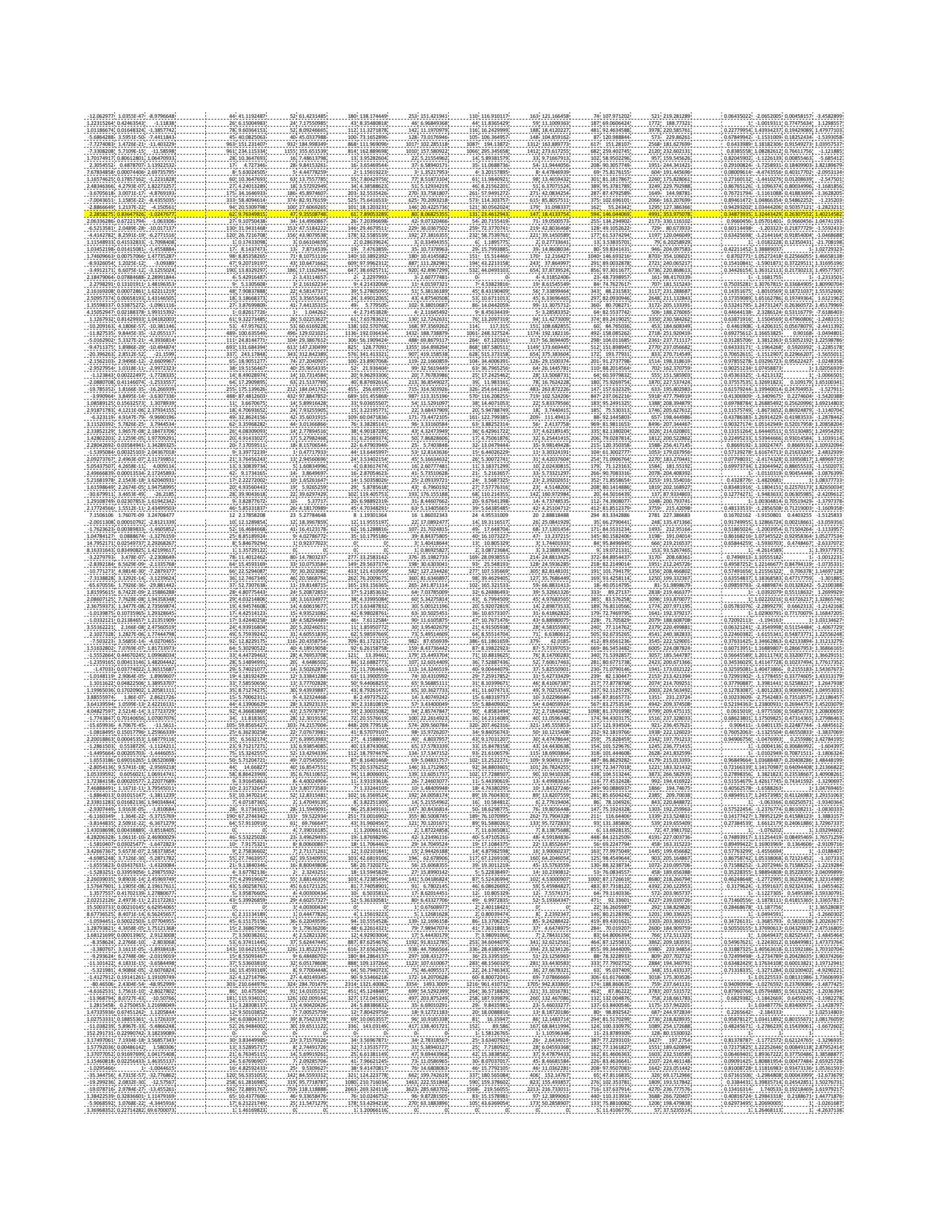
0.28463729	-2.7426353	0.20077387	-4.2950454	0.38967524	-2.2300266	1	1.92600632
0.29934439	-11.277538	1	-5.3637369	1	-5.3637369	1	1
0.56777445	1.40891957	0.02662818	4.13516724	0.31567513	2.08237746	0.22680437	-1.9857914
0.1410377	2.87990719	0.00908066	6.77996228	0.10538877	3.23989279	0.29819812	-2.0926502
0.55389112	-3.8446336	0.31611646	4.17330514	1	1.00003513	0.55389112	-4.1731585
0.12541383	-6.4434215	0.72698675	-1.6842274	0.43106194	-3.8507601	1	-2.286366
1	-1.0158081	0.00175139	3.55045292	0.05348858	2.19737163	0.21418246	-1.6157726
0.81221643	-1.1778151	0.73816572	-1.1837674	0.21674771	-1.7704297	0.39834895	-1.4955891
0.11844903	-2.9006196	1	-1.6647291	1	1.07864695	1	1.79565496
0.52787211	-7.4701055	1	1	1	1	1	1
0.92602545	1.05419309	0.00574605	3.86950723	0.26738291	1.71919989	0.09517443	-2.2507605
1	1.21983366	0.5276548	-9.6274986	1	-1.8527474	1	5.19633629
0.09051425	-20.634448	0.72282846	-1.694018	0.15737737	-18.03648	0.52117167	-10.64716
0.50366725	-1.7400381	0.49686347	-1.8538092	1	1.17301557	0.49686347	2.17454706
0.93918907	1.03578331	0.48039937	-1.2784396	1	1.00158459	0.48039937	1.28046536
0.01900139	-2.756401	0.07746323	-2.2405793	0.09492626	-2.1437916	1	1.04514792
0.13042491	-1.9701099	1	-1.2496021	0.63004612	-1.4382775	0.80079406	-1.1509884
0.28096071	-14.242584	0.52064048	-9.704783	0.52064048	-9.704783	1	1
0.30195879	-4.3124818	0.17356393	-18.546297	0.44713035	-4.0062192	1	4.62937639
0.18698169	-2.2299528	0.72697521	-1.5815437	0.44119064	-1.6932338	0.82354558	-1.0706209
0.00279585	-47.135794	0.07747076	-23.051745	0.07747076	-23.051745	1	1
0.30428122	-1.3511871	0.72860712	-1.1391041	0.66642025	1.16019904	0.40245039	1.32158753
0.08176454	-21.060996	0.75519564	-1.5008959	0.08176454	-22.966423	0.27218785	-15.30181
0.63279124	-1.3487628	0.81982515	-1.2442892	0.69777384	1.17166848	0.47032566	1.45789447
0.37468182	1.3294736	0.15377624	1.58750597	0.14338117	1.59823392	1	1.00675774
0.5245271	-1.5110112	0.68955672	1.28795959	1	-1.0319912	0.68955672	-1.3291629
0.78786401	-1.6618574	0.61108402	1.61039448	1	-1.1613472	0.61108402	-1.8702272
0.52011569	-4.0237658	0.83919821	1.14967735	0.37092996	-5.4111674	0.26451221	-6.2210966
0.17206164	1.50444548	0.87388064	-1.0604638	0.23907826	1.43588689	0.17206164	1.52270605
0.71951779	-3.4498914	1	-1.311169	1	-2.7574247	1	-2.1030276
0.25133238	1.55395507	0.10370024	1.89331798	0.26771423	1.54017017	0.63544892	-1.2292914
0.1427058	2.23830108	0.00340612	5.21961648	0.17319495	2.1856231	0.11021707	-2.3881595
0.66710502	1.29433323	0.53721976	-9.5317501	0.31000923	2.79257101	0.0730558	26.618089
1	1.09496977	0.52055798	-10.076554	1	-2.155343	1	4.67515091
0.6176282	1.38520503	0.73310042	-1.4233307	1	-1.1464574	0.81507285	1.24150332
0.04698675	-3.2358182	0.56749459	-1.7637336	0.09107773	-2.9267829	0.57653677	-1.6594245
0.8271954	1.15739874	0.01336045	5.878547	0.01003357	6.2182834	1	1.05779258
0.04617962	-4.8158227	0.2432077	-3.0840059	0.10898525	-3.8615145	1	-1.25211
0.49925734	-1.4139713	0.45154591	-1.5255889	0.72245443	-1.2792572	0.78640028	1.1925584
0.90654871	1.04664815	0.04146149	1.83045715	0.26408859	1.4182814	0.39316748	-1.2906163
0.83983649	-1.0992889	0.84802656	1.09123336	0.38773961	-1.4836489	0.29052672	-1.6190071
0.9185641	1.04897946	0.76599222	1.0931414	0.79646858	-1.080755	0.55761722	-1.1814181
0.84697064	-1.0779432	0.72427984	-1.1465932	0.89220618	-1.0543621	0.82861393	1.08747574
1	1.02585287	0.59403386	1.23124019	0.55201955	1.26741123	1	1.02937773
0.15423516	-2.0357502	1	1.0728533	0.84657138	-1.1722285	0.84657138	-1.2576292
0.52187058	-1.4172647	0.02598491	-2.6476574	0.18300372	-1.9668688	0.47700048	1.34612809
0.92916939	1.06878278	1	1.0497351	0.86830011	-1.085726	0.86830011	-1.1397247
0.05733663	-4.0495926	0.79838595	1.27608878	0.24679777	-2.8074583	0.09315522	-3.5825661
0.55601216	1.20615095	0.76214396	-1.1031199	0.62553626	1.1682415	0.42375684	1.28871042
0.86919242	1.05733981	0.1567084	1.5315787	0.64808911	1.15136529	0.34927851	-1.3302283
0.52159181	-1.2381856	0.69843892	1.13859935	0.47285619	-1.2724869	0.27107317	-1.4488528
0.6852979	-1.1514202	0.81149653	-1.0890789	0.94151819	-1.0352918	0.88841364	1.05195363
0.39950125	1.29113499	0.3644817	1.313993	0.80582069	1.10540094	0.53912151	-1.1887026
0.11887115	-2.3302878	0.61175879	1.43117642	0.8706624	-1.119572	0.32038452	-1.6023051
0.78735937	1.44628642	1	-1.3389958	0.78735937	1.48543669	0.55200564	1.98899349
0.1751711	-5.7038616	0.61976661	-1.4384021	0.1751711	-6.1011024	0.42049339	-4.2415834
0.68972356	1.13285572	0.91327359	-1.0455983	1	-1.0116252	0.95629535	1.03358264
0.3285864	1.44026865	0.34446731	1.4755393	0.23693077	1.61478932	0.83502963	1.09437229
0.33096967	1.35726048	0.81697019	1.08711511	0.59077683	1.18527461	0.78362164	1.09029357
0.03728848	-4.8189907	1	1.06103811	0.64155458	-1.7275054	0.64155458	-1.832949
0.87464167	1.14367863	1	1.00301172	1	1.0671885	1	1.06398408
0.00061672	-3.4581404	0.43376976	-1.4670197	0.18486162	-1.6837775	0.78483025	-1.1477538
0.41640664	1.49904427	0.18032417	1.97385942	0.60939002	1.3040924	0.44739056	-1.5135886
0.88300235	1.12466725	0.4881352	-1.7789382	0.80119889	-1.421158	0.76031403	1.25175266
1	-1.0138539	0.86744492	-1.0702271	1	-1.0340793	0.89326785	1.03495649
0.06494875	-3.0006395	0.90980224	-1.1984615	0.20342215	-2.3323691	0.2967763	-1.946136
0.98836485	1.01490318	0.46601456	-1.3241942	1	1.00388971	0.45717863	1.32934492
1	1.01852687	0.59389067	-1.2331146	0.71734166	1.18973152	0.34608081	1.46707537
0.24253189	1.56344717	1	1.02099312	0.24253189	1.59900378	0.2850177	1.56612591

Control - Control 1 RNA-Seq Raw Reads (paired) (GE) - Total gene reads	Control - Control 1 RNA-Seq Raw Reads (paired) (GE) - RPKM	Control - Control 2 RNA-Seq Raw Reads (paired) (GE) - Total gene reads	Control - Control 2 RNA-Seq Raw Reads (paired) (GE) - RPKM	Viral 30min - Viral 1a 30min (GE)-1 - Total gene reads	Viral 30min - Viral 1a 30min (GE)-1 - RPKM	Viral 30min - Viral 1b 30min (GE)-1 - Total gene reads	Viral 30min - Viral 1b 30min (GE)-1 - RPKM	Viral 5hr - Viral 5a 5hrs (GE)-1 - Total gene reads	Viral 5hr - Viral 5a 5hrs (GE)-1 - RPKM	Viral 5hr - Viral 5b 5hrs (GE)-1 - Total gene reads	Viral 5hr - Viral 5b 5hrs (GE)-1 - RPKM	Viral 12hr - Viral 11a 11hrs_ (GE)-1 - Total gene reads	Viral 12hr - Viral 11a 11hrs_ (GE)-1 - RPKM	Viral 12hr - Viral 11b 11hrs_ (GE)-1 - Total gene reads	Viral 12hr - Viral 11b 11hrs_ (GE)-1 - RPKM
107	11.4936369	23	2.93982441	49	10.6271617	28	3.71078609	24	6.96230516	42	5.87945252	32	6.63899108	104	7.98349593
17	5.08472126	18	6.406349	18	10.8702178	29	10.701642	7	5.65437212	30	11.6937387	7	4.04384667	36	7.69496772
63	6.8307248	45	5.80575378	27	5.91068094	55	7.3573789	28	8.19883957	69	9.74965464	17	3.5600293	80	6.198724
20	5.78262417	22	7.56898271	3	1.75131287	9	3.21049261	5	3.90420932	5	1.88399124	8	4.46748775	5	1.03312067
46	3.27721616	39	3.30621981	11	1.582295	16	1.40637596	15	2.88606849	18	1.67122015	8	1.10081834	30	1.52740632
12	3.03904336	13	3.91758893	3	1.53399668	9	2.81211031	2	1.36789816	5	1.6502113	1	0.48914099	13	2.35280035
3	1.25406307	3	1.49224194	0	0	1	0.51574179	4	4.51571198	0	0	1	0.8073773	1	0.29873369
4	1.55935933	6	2.78328271	1	0.78710691	1	0.48097268	1	1.05282049	0	0	0	0	1	0.27859434
13	2.70086638	8	1.97774181	4	1.67790455	5	1.28163378	9	5.04975577	3	0.81225969	3	1.20381406	14	2.07861404
20	3.15415864	15	2.81491093	2	0.63684104	11	2.14032841	4	1.70365498	7	1.43868422	4	1.21840575	7	0.78892851
113	6.97619073	84	6.17076559	38	4.73664691	115	8.75935113	50	8.33639	113	9.09143101	31	3.6964089	69	3.04421321
12	2.53871305	8	2.01392001	4	1.70859792	7	1.82710962	6	3.42808623	5	1.37853017	2	0.81722337	1	0.15118839
7	5.05979615	5	4.30055836	0	0	5	4.45901751	1	1.95210466	1	0.94199562	0	0	2	1.03312067
6	1.58911809	6	1.89093253	2	1.06950404	6	1.96060617	6	4.29164994	1	0.3451587	3	1.5346332	11	2.08201417
44	4.98893066	29	3.91266486	5	1.14464894	21	2.93770566	6	1.83727497	8	1.18211215	6	1.31396698	15	1.21543608
42	3.43684267	24	2.33690718	10	1.65218195	18	1.81725997	23	5.08283855	11	1.17305115	6	0.94828749	28	1.63739879
25	10.8424203	22	11.3534741	22	19.2644416	16	8.56131362	5	5.85631398	10	5.65197371	5	4.18826976	22	6.8185964
4	1.03569388	7	2.15669792	4	2.09111985	10	3.19452001	9	6.29335233	3	1.0122938	2	1.00018382	5	0.92518269
41	3.27017367	17	1.61345086	17	2.73768449	35	3.44420663	30	6.46213956	30	3.11833032	7	1.07835911	28	1.59599331
45	3.13515768	24	1.98965592	12	1.68801241	51	4.38380517	23	4.32755732	28	2.54225323	13	1.74931749	37	1.84219107
52	2.89131209	48	3.17579694	18	2.02074562	40	2.74401078	44	6.60712346	31	2.24629724	25	2.68478831	43	1.70862264
72	4.02918329	65	4.3283039	54	6.10134807	81	5.592471	52	7.85879553	62	4.52157896	28	3.02636267	143	5.71882279
35	9.48711778	42	13.5467588	19	10.3984202	20	6.68852627	18	13.1767065	16	5.65197371	14	7.32947208	37	7.16727463
112	27.756596	68	20.0528893	74	37.0277579	43	13.1477316	42	28.1103071	48	15.5025565	53	25.3689483	177	31.3478328
27	5.41494287	7	1.67050591	10	4.04927832	15	3.71155215	21	11.3741127	15	3.92044419	12	4.64825315	25	3.58307746
10	3.36851894	2	0.80165748	4	2.72048601	1	0.41559775	8	7.27774941	3	1.31696475	3	1.95181504	3	0.72218144
51	6.55364073	42	6.42216715	18	4.67016766	35	5.54899957	32	11.1053065	47	7.87089672	20	4.96387527	56	5.1426451
18	3.1383086	22	4.56421068	7	2.46415881	23	4.9474928	7	3.29601591	11	2.49936526	10	3.36745308	24	2.99033922
40	4.21832766	39	4.89400927	25	5.32313943	31	4.03344563	29	8.25936075	36	4.9476244	21	4.27738189	58	4.37113668
14	5.16745139	9	3.95285364	13	9.68811376	6	2.73233414	5	4.984097	8	3.84815231	6	4.27738189	10	2.63775489
202	66.7480047	281	110.487488	171	114.085524	612	249.50114	85	75.8532096	440	189.47569	150	95.7318803	611	144.282681
537	39.5575692	644	56.4496221	735	109.317619	2426	220.485635	503	100.067123	2379	228.382938	803	114.248174	2077	109.339701
85	25.8696345	100	36.2152283	85	52.2321383	479	179.862685	56	46.028573	361	143.183334	72	42.3235681	244	53.0697774
181	7.99991064	214	11.2548625	221	19.7217908	800	43.624528	190	22.6792287	861	49.5933693	196	16.7317376	653	20.6255632
120	7.9607828	129	10.1831959	122	16.341122	364	29.7927166	94	16.8411018	407	35.1870485	48	6.15026994	224	10.6196113
18	4.13591663	29	7.92897647	12	5.56708727	42	11.9064627	8	4.96429264	20	5.98884631	18	7.98822312	26	4.26931984
47	16.3070002	33	13.6241689	41	28.7215311	147	62.9256551	44	41.2284504	101	45.6679475	16	10.7219706	82	20.3318147
81	33.4566113	78	38.3364059	58	48.3695936	348	177.341497	40	44.6195351	122	65.6705516	16	12.7642507	102	30.108088
12	8.49691715	14	11.7958172	3	4.28892948	78	68.1410676	7	13.3858605	16	14.7643395	12	16.4111795	10	5.06018286
20	6.80308726	38	15.3808205	28	19.2301021	158	66.3082134	15	13.7795623	99	43.8859135	28	18.3955378	78	18.9608028
39	7.9596121	48	11.6570429	62	25.5485643	186	46.8354216	28	15.4331098	142	37.7684831	29	11.4315128	137	19.9817691
92	5.14011038	64	4.25485194	72	8.12203071	251	17.3018496	55	8.29880242	198	14.4166286	57	6.15088893	242	9.66242324
56	3.87044168	38	3.12518663	49	6.83779528	130	11.0853663	37	6.90625075	87	7.83620259	32	4.27170143	94	4.64286897
52	4.73537728	43	4.6595026	38	6.986865	92	10.3364941	58	14.2641978	72	8.54471615	23	4.04536292	96	6.24753285
27	11.0210014	14	6.79994169	9	7.4173251	15	7.55410026	2	2.20472997	8	4.25560373	11	8.6721821	11	3.20875125
28	3.23826954	29	3.99091816	17	3.96964251	21	2.99645977	29	9.05776562	16	2.41150878	15	3.35061581	45	3.7192344
51	5.05566571	28	3.30282882	23	4.60345098	38	4.64757025	29	7.7637991	23	2.97132332	18	3.44634769	43	3.04623008
58	4.21876984	29	2.51001142	21	3.08407298	35	3.14094315	43	8.4468428	29	2.74896834	23	3.23120183	66	3.43074033
49	4.55788608	41	4.53806909	26	4.88301712	53	6.08243461	44	11.0532039	53	6.42476368	13	2.33554989	84	5.58383717
25	3.97886984	12	2.27258864	3	0.96402543	17	3.33812687	3	1.28946363	10	2.07411879	6	1.84437568	14	1.59233277
28	3.17477406	25	3.37298695	17	3.89180638	23	3.21748715	87	26.6404871	20	2.95528037	38	8.3217909	44	3.56527916
16	2.31304967	6	1.03213401	5	1.45942739	5	0.8918035	8	3.12336746	6	1.13039474	5	1.39608992	9	0.9298086
106	5.11508898	80	4.59364231	56	5.45610686	70	4.16753793	47	6.12510169	74	4.65364177	43	4.00769068	128	4.41411222
17	4.33696813	16	4.85710121	10	5.15092021	16	5.03606684	4	2.75591246	9	2.99222137	7	3.44916333	13	2.37010035
42	2.49097657	23	1.6231851	29	3.47268877	44	3.21963931	21	3.36362649	47	3.63272156	24	2.74922323	76	3.22121726
43	5.4849891	40	6.07137651	36	9.27165638	47	7.39672317	21	7.23427021	57	9.47536768	20	4.92737619	70	6.38103941
21	3.37319743	14	2.67590298	15	4.86475798	9	1.78360701	8	3.47040828	8	1.67465888	6	1.86145323	15	1.72186778
57	4.18109401	89	7.76828131	33	4.88738476	83	7.51151195	159	31.4978071	72	6.88274176	52	7.36710453	127	6.65740337
25	3.3619908	7	1.12014543	14	3.80129926	23	3.81608941	29	10.5322856	16	2.80407998	9	2.33763894	36	3.45975293
35	3.3638534	22	2.51600533	12	2.32861545	23	2.72728827	47	12.1993023	19	2.3797784	16	2.97007496	42	2.88472474
9	2.34783237	5	1.55208121	1	0.52671064	7	2.25297727	5	3.52259487	3	1.01990503	6	3.02311201	8	1.49142232
19	3.34629013	4	0.83828143	1	0.35559652	3	0.65187667	9	4.28075743	1	0.22952178	4	1.36065617	6	0.7551745
21	3.14056313	15	2.66931208	18	5.43510891	9	1.66059963	11	4.44272095	15	2.92343468	10	2.88846191	29	3.099362
27	11.4242087	23	11.5800401	17	14.5230824	13	6.78640714	9	10.2842587	8	4.41129655	9	7.35501031	28	8.46654985
4	1.57707932	0	0	0	0	5	2.43219137	4	4.25913744	3	1.54144737	1	0.76150359	0	0
5	1.28502759	4	1.22326993	3	1.55672255	2	0.63417138	7	4.8585716	3	1.00479533	2	0.99277506	2	0.36733179
3	0.991307	6	2.35916344	4	2.66866723	1	0.4076816	1	0.8923907	0	0	0	0	3	0.7084256
0	0	3	0.37876477	0	0	1	0.13090694	0	0	0	0	0	0	0	0
7	0.70601807	9	1.08014024	3	0.6109231	5	0.62218849	22	5.99250733	6	0.78864749	5	0.97401622	15	1.08117279
17	1.99941582	7	0.97965262	2	0.4749323	15	2.17660516	72	22.8694024	9	1.37946477	26	5.90617024	12	1.00860594
4	2.23843516	2	1.33178581	0	0	1	0.69042852	4	6.04522733	0	0	1	1.08084381	0	0
7	3.85508278	2	1.31064636	0	0	4	2.71787734	1	1.48731784	1	0.71771095	0	0	1	0.39356978
67	2.68741609	37	1.76596339	9	0.7288701	26	1.28667141	71	7.69106668	29	1.51590509	22	1.70435949	65	1.86320028
14	2.75988881	24	5.62982185	23	9.15459001	17	4.13472533	20	10.6478436	12	3.08289475	7	2.66526258	22	3.099362
10	4.28342531	7	3.56787064	0	0	4	2.1139046	2	2.31360552	0	0	1	0.82731255	4	1.22443931
2	1.61375558	0	0	0	0	0	0	0	0	0	0	0	0	0	0
57	3.93172459	30	2.46234753	13	1.81050237	26	2.21266555	99	18.4421498	19	1.70795229	23	3.06418146	49	2.41540736
1	0.6425138	0	0	0	0	2	1.58542845	0	0	0	0	1	1.24096882	0	0
4	2.52332691	2	1.50128583	0	0	4	3.11320495	1	1.70365498	1	0.82210527	0	0	0	0
8	5.55131921	4	3.30282882	3	4.20315089	1	0.85613136	1	1.87402047	1	0.90431579	1	1.34024632	5	2.4794896
120	36.2042557	129	46.3114041	58	35.3308336	142	52.8568059	57	46.4431161	83	32.6340047	42	24.4740633	211	45.493244
54	12.0100656	27	7.14554312	9	4.04149124	40	10.9760431	3	1.80194276	17	4.92736169	5	2.14783065	21	3.33777446
8	2.98458022	7	3.10750023	3	2.25975854	5	2.30142839	2	2.01507578	4	1.94476515	0	0	7	1.8662825
2	1.54203311	2	1.8349049	0	0	2	1.90251414	0	0	0	0	0	0	0	0
6	4.84126675	0	0	1	1.62912825	3	2.98650475	0	0	0	0	0	0	1	0.57662549
8	5.14011038	10	7.64543708	1	1.29726879	10	7.92714224	2	3.47040828	4	3.34931775	0	0	8	3.67331793
8	5.14011038	6	4.58726225	1	1.29726879	4	3.1708569	0	0	0	0	0	0	0	0
61	17.4912434	44	15.0128583	18	10.4210353	31	10.966972	17	13.1646066	23	8.59473687	16	8.86113272	52	10.6556578
2	1.47641468	4	3.51364768	1	1.49047904	4	3.64311218	1	1.9936388	2	1.92407616	0	0	0	0
24	3.85508278	16	3.05817483	5	1.62158599	14	2.77449979	9	3.90420932	4	0.83732944	10	3.10242205	12	1.37749422
86	5.66192424	79	6.18888702	31	4.12073617	74	6.01078945	73	12.9794587	72	6.17748929	52	6.61222095	132	6.21048629
11	2.00870103	13	2.82478781	5	1.84348723	7	1.57708409	9	4.43846954	5	1.1898892	5	1.76348201	8	1.04399562
7	3.4695745	1	0.58979086	1	1.00075021	3	1.83456721	3	4.01575816	3	1.93781956	1	0.9573188	3	1.0626384
4	1.80237637	2	1.07234702	2	1.81954584	4	2.22371782	5	6.08448206	1	0.58721805	1	0.87028982	0	0
76	9.35062632	57	8.34491324	44	10.9301796	55	8.34879875	44	14.6200179	43	6.89460622	42	9.98055773	133	11.6940467
3	1.85870063	2	1.47447715	0	0	3	2.29320901	1	1.67323257	1	0.80742482	1	1.1966485	0	0
46	3.4695745	37	3.32077898	20	3.04576152	43	4.00148354	66	13.4440599	33	3.24374143	40	5.82715793	52	2.80290129
23	2.13369555	19	2.09738461	13	2.43498046	18	2.06020916	112	28.0601996	18	2.176161	31	5.5544968	32	2.12148843
4	1.75674658	2	1.04519899	0	0	2	1.08371059	0	0	0	0	4	3.39302867	1	0.31385944
1	0.88963449	0	0	1	1.79621833	1	1.09760431	0	0	0	0	0	0	1	0.63576656
13	2.65320403	1	0.24285506	5	2.06036808	11	2.76983676	5	2.75591246	5	1.32987617	7	2.75933067	6	0.87511398
4	1.49229011	10	4.43928605	2	1.5065057	8	3.68228543	2	2.01507578	3	1.45857386	0	0	4	1.06644714
15	3.37945569	9	2.41278079	2	0.90977292	1	0.27796473	11	6.69293026	6	1.76165414	6	2.61086946	18	2.89810473
9	4.66062247	3	1.84859822	2	2.09111985	5	3.19452001	0	0	2	1.34972506	0	0	2	0.74014615
18	11.5652483	14	10.7036119	5	6.48634397	17	13.4761418	5	8.67602071	8	6.6986355	6	7.44581291	13	5.96914163
60	4.25714663	50	4.22140698	14	2.00559347	49	4.28941071	42	8.04794068	60	5.54794965	22	3.01486903	82	4.15783532
298	26.5111077	264	27.9470131	110	19.7584016	517	56.7461429	87	20.902536	560	64.9252364	101	17.3544716	364	23.1419029
64	9.4090156	62	10.846154	31	9.20181339	79	14.3293173	44	17.4696824	64	12.2619091	25	7.09876231	96	10.0860594
2214	241.560942	2346	304.576903	988	217.647436	2508	337.606518	579	170.606581	2406	342.104371	931	196.190146	2772	216.136641
34	2.38796626	32	2.67435532	19	2.6943275	19	1.64640647	20	3.79356371	25	2.28824846	12	1.62782954	50	2.50960486
14	2.42870215	10	2.06426801	4	1.4010503	6	1.28419704	5	2.34252559	5	1.13039474	3	1.00518474	7	0.86782136
19	7.66533902	19	9.12118424	10	8.14564126	31	15.4302746	4	4.35818715	10	5.25764996	9	7.01291681	12	3.45975293
23	7.0619658	11	4.01892887	15	9.2990064	12	4.54583024	8	6.63370079	21	8.40293436	9	5.33726412	21	4.60790103
6	2.12422929	4	1.68511674	2	1.42964316	3	1.31040515	3	2.86839868	3	1.38415683	0	0	2	0.50601829
221	22.0972901	177	21.0591031	104	20.9955664	203	25.0424592	86	23.2227321	178	23.1942667	105	20.277502	308	22.0081498
90	6.80308726	65	5.84651071	31	4.7312156	77	7.18105827	58	11.8402165	92	9.0628598	33	4.81787894	112	6.0501707
205	11.4535068	150	9.97230924	83	9.36289651	194	13.3727443	86	12.9763092	212	15.4359862	59	6.36670959	193	7.70598217
176	12.7217732	178	15.3099878	68	9.92410627	181	16.1416434	63	12.2982594	149	14.0357347	70	9.77262945	194	10.0212705
37	2.76668657	37	3.29215157	29	4.37828218	33	3.04443265	34	6.86602328	44	4.28770419	18	2.59961571	69	3.68717204
20	3.98801667	8	1.89817748	2	0.80520132	8	1.96811807	8	4.30809304	4	1.03944344	0	0	12	1.70999283
3	1.60134208	1	0.63515939	0	0	3	1.97568776	0	0	2	1.39125507	3	3.09287613	1	0.38145994
7	4.76216108	1	0.80951687	3	4.12073617	3	2.51803342	1	1.83727497	3	2.65975233	0	0	1	0.48617443
40	8.02213758	33	7.87524213	27	10.9330515	33	8.16541473	19	10.2908639	37	9.670429	17	6.58502529	56	8.0260935
48	5.62633703	37	5.16067003	30	7.09991705	21	3.03695247	47	14.8782031	23	3.51338906	29	6.56539584	73	6.11495746
60	8.00671039	45	7.14554312	23	6.19695324	70	11.5248453	25	9.00971381	69	11.9995749	33	8.50540936	87	8.29675366
8	6.76990147	4	4.02784002	1	1.70859792	2	2.08812527	1	2.28539082	2	2.20564828	0	0	2	1.20950712
22	5.61254699	19	5.76780768	16	8.24147234	15	4.72131266	10	6.88978115	21	6.98184987	6	2.95642571	39	7.11030106
39	18.2855954	32	17.8531288	7	6.62658924	19	10.9908756	7	8.86361035	9	5.49921766	2	1.81114368	17	5.69612476
15	2.23363165	8	1.4175231	5	1.50327285	15	2.75578765	24	9.65160759	8	1.55247346	8	2.30085206	21	2.23473312
8	3.22751117	5	2.40031164	1	0.81456413	16	7.96401267	3	3.26864036	5	2.62882498	4	3.11685192	8	2.30650195
68	6.11220379	54	5.77567216	25	4.53707998	71	7.87374699	19	4.61222655	66	7.73119719	29	5.03460407	71	4.56071921
16	10.8849396	15	12.142753	3	4.12073617	16	13.4295116	9	16.5354748	4	3.54633644	2	2.62793397	7	3.40322102
123	13.2533436	115	14.7447715	39	8.48462137	156	20.7385858	37	10.7668878	95	13.3400622	39	8.11639855	197	15.1695482
33	8.60871869	47	14.5895634	16	8.42737021	37	11.9085941	7	4.93163282	35	11.898892	12	6.04622402	69	12.8635175
39	5.93479849	28	5.07013196	22	6.75945319	24	4.50595454	29	11.9181127	13	2.57809327	17	4.99653235	82	8.9174626

gsyne_1120	Synechococcus_assembled_mapped	rv0623-like transcription factor family protein					PF07704.6	970242	970425	-1	261	fig|1129.58.peg.1119			
gsyne_1121	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF02698.12	970562	971285	-1	156	fig|1129.58.peg.1120			
gsyne_1122	Synechococcus_assembled_mapped	undecaprenyl-phosphate glucose phosphotransferas		2.7.8.-			TIGR03023	972174	972663	-1	703	fig|1129.58.peg	Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_1123	Synechococcus_assembled_mapped	putative remnant of IsrsO5 transposase protein				GO:0003677,GO:0006355	UniRef100_C	972973	973165	-1	141	fig|1129.58.peg.1122			
gsyne_1124	Synechococcus_assembled_mapped	CDP-glucose 4,6-dehydratase	rfbG	4.2.1.45		GO:0009243,GO:0047733	TIGR02622	976252	977341	-1	90	fig|1129.58.peg.1125			
gsyne_1125	Synechococcus_assembled_mapped	glucose-1-phosphate cytidylyltransfera	rfbF	2.7.7.33		GO:0009103,GO:0047343	TIGR02623	977331	978033	-1	90	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	dTDP-rhamnose synthesis
gsyne_1126	Synechococcus_assembled_mapped	transposase family protein					PF01527.15	978303	978765	1	154	fig|1129.58.peg.1127			
gsyne_1127	Synechococcus_assembled_mapped	DDE_Tnp_1-associated family protein					PF13808.1	978914	979529	1	185	fig|1129.58.peg.1128			
gsyne_1128	Synechococcus_assembled_mapped	transposase DDE domain protein					PF01609.16	979813	980056	1	154	fig|1129.58.peg.1129			
gsyne_1129	Synechococcus_assembled_mapped	integrase core domain protein					PF00665.21	980109	981099	1	157	fig|1129.58.peg.1131			
gsyne_113	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	94399	95488	-1	156	fig|1129.58.peg.113			
gsyne_1130	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein					PF00535.21	981159	982035	-1	90	fig|1129.58.peg.1132			
gsyne_1131	Synechococcus_assembled_mapped	polysaccharide biosynthesis family protein					PF02719.10	982089	983064	-1	90	fig|1129.58.peg.1133			
gsyne_1132	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein					PF00534.15	984493	985276	-1	90				
gsyne_1133	Synechococcus_assembled_mapped	integrase core domain protein					PF00665.21	986227	987313	-1	157	fig|1129.58.peg.1137			
gsyne_1134	Synechococcus_assembled_mapped	transposase family protein					PF01527.15	987309	987816	-1	154	fig|1129.58.peg.1138			
gsyne_1135	Synechococcus_assembled_mapped	sulfotransferase family protein					PF03567.9	987990	988686	-1	703	fig|1129.58.peg.1139			
gsyne_1136	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_C	988703	989471	-1	703	fig|1129.58.peg.1140			
gsyne_1137	Synechococcus_assembled_mapped	transposase DDE domain protein					PF01609.16	989627	990608	1	154	fig|1129.58.peg.1141			
gsyne_1138	Synechococcus_assembled_mapped	short chain dehydrogenase family protein					PF00106.20	990749	991106	-1	703	fig|1129.58.peg.1142			
gsyne_1139	Synechococcus_assembled_mapped	glutamine-fructose-6-phosphate transa	glmS	2.6.1.16		GO:0004360,GO:0006040,G	TIGR01135	991102	992995	-1	89,100	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Sialic Acid Metabolism
gsyne_114	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	95729	96602	1	92	fig|1129.58.peg.114			
gsyne_1140	Synechococcus_assembled_mapped	cobQ/CobB/MinD/ParA nucleotide binding domain protein					PF01656.18	993208	995557	-1	157	fig|1129.58.peg.1144			
gsyne_1141	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	995535	995661	-1	856	fig|1129.58.peg.1145			
gsyne_1142	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	995697	995997	-1	856	fig|1129.58.peg.1146			
gsyne_1143	Synechococcus_assembled_mapped	UDP-glucose 4-epimerase GalE	galE	5.1.3.2		GO:0003978,GO:0006012	TIGR01179	995996	997034	-1	119	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_1144	Synechococcus_assembled_mapped	GDP-L-fucose synthase 1	GER1	1.1.1.271		GO:0016853,GO:0050577,G	UniRef100_C	997030	997996	-1	141,703	fig|1129.58.peg.1148			
gsyne_1145	Synechococcus_assembled_mapped	GDP-mannose 4,6-dehydratase	gmd	4.2.1.47		GO:0000271,GO:0008446	TIGR01472	998079	999270	-1	90	fig|1129.58.peg.1149			
gsyne_1146	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	999371	999578	-1	856	fig|1129.58.peg.1150			
gsyne_1147	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein					PF01370.16	999574	1000693	-1	119	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_1148	Synechococcus_assembled_mapped	dual specificity phosphatase, catalytic domain protein					PF00782.15	1001431	1001620	1	703	fig|1129.58.peg.1152			
gsyne_1149	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1001702	1002533	-1	856	fig|1129.58.peg.1153			
gsyne_115	Synechococcus_assembled_mapped	response regulator					PF00072.19	96616	97381	-1	699	fig|1129.58.peg.115			
gsyne_1150	Synechococcus_assembled_mapped	polysaccharide biosynthesis/export family protein					PF02563.11	1002536	1003436	-1	90,147	fig|1129.58.peg.1154			
gsyne_1151	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1003441	1003678	-1	856	fig|1129.58.peg.1155			
gsyne_1152	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1003798	1004386	-1	856	fig|1129.58.peg.1156			
gsyne_1153	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1004391	1004724	-1	856				
gsyne_1154	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	1005031	1005313	-1	156				
gsyne_1155	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_P	1005365	1005998	-1	92,141	fig|1129.58.peg.1157			
gsyne_1156	Synechococcus_assembled_mapped	sigma-70 factor, region 1.2 family protein					PF00140.15	1006982	1007231	-1	165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors cyanobacter
gsyne_1157	Synechococcus_assembled_mapped	putative mll6279 protein				GO:0015074,GO:0003677	UniRef100_C	1006036	1006990	1	92,141	fig|1129.58.peg.1158			
gsyne_1158	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF09980.4	1007495	1008008	1	156	fig|1129.58.peg.1160			
gsyne_1159	Synechococcus_assembled_mapped	matrixin family protein					PF00413.19	1008014	1008668	1	185	fig|1129.58.peg.1161			
gsyne_116	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	97553	97808	1	156	fig|1129.58.peg.116			
gsyne_1160	Synechococcus_assembled_mapped	acrB/AcrD/AcrF family protein					PF00873.14	1008664	1011820	1	185	fig|1129.58.peg.1162			
gsyne_1161	Synechococcus_assembled_mapped	efflux transporter, RND family, MFP subunit				GO:0005215,GO:0006810	TIGR01730	1011836	1012925	1	141	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Cobalt-zinc-cadmium resistance
gsyne_1162	Synechococcus_assembled_mapped	phosphoribosyl-ATP diphosphatase	hisE	3.6.1.31		GO:0000105,GO:0004636	TIGR03188	1012926	1013622	-1	161	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	Zinc regulated enzymes
gsyne_1163	Synechococcus_assembled_mapped	6-pyruvoyl tetrahydropterin synthase family protein					PF01242.14	1013671	1014148	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_1164	Synechococcus_assembled_mapped	peptidase M23 family protein					PF01551.17	1014249	1014702	1	138	fig|1129.58.peg.1166			
gsyne_1165	Synechococcus_assembled_mapped	putative permease family protein					PF03773.8	1014740	1015694	1	141	fig|1129.58.peg.1167			
gsyne_1166	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_D	1015669	1016341	1	156				
gsyne_1167	Synechococcus_assembled_mapped	fecCD transport family protein					PF01032.13	1017645	1018428	-1	145	fig|1129.58.peg.1170			
gsyne_1168	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_B	1016352	1017660	-1	156	fig|1129.58.peg.1169			
gsyne_1169	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	1018867	1019560	-1	141	fig|1129.58.peg.1172			
gsyne_117	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,G	TMHMM	97835	97955	1	88	fig|1129.58.peg.117			
gsyne_1170	Synechococcus_assembled_mapped	ferric uptake regulator family protein					PF01475.14	1018469	1018871	1	261	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	Zinc regulated enzymes
gsyne_1171	Synechococcus_assembled_mapped	carbohydrate-selective porin, OprB family protein					PF04966.7	1019633	1020977	1	144,182	fig|1129.58.peg.1173			
gsyne_1172	Synechococcus_assembled_mapped	periplasmic solute binding family protein					PF01297.12	1021013	1021955	1	185	fig|1129.58.peg.1174			
gsyne_1173	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1022079	1022220	1	856	fig|1129.58.peg.1175			
gsyne_1174	Synechococcus_assembled_mapped	ferritin-like domain protein					PF00210.19	1022227	1022767	-1	157	fig|1129.58.peg.1176			
gsyne_1175	Synechococcus_assembled_mapped	ferritin-like domain protein					PF00210.19	1022862	1023345	-1	157	fig|1129.58.p	Stress Response	Oxidative stress	Oxidative stress
gsyne_1176	Synechococcus_assembled_mapped	glutamine ABC superfamily ATP binding	glnP			GO:0006810,GO:0016021,G	UniRef100_D	1023407	1023641	-1	141	fig|1129.58.peg.1178			
gsyne_1177	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein					PF00528.17	1023644	1023770	-1	141	fig|1129.58.peg.1179			
gsyne_1178	Synechococcus_assembled_mapped	cobalamin synthesis cobW C-terminal domain protein					PF07683.9	1023883	1025053	1	157	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	Zinc regulated enzymes
gsyne_1179	Synechococcus_assembled_mapped	hupE / UreJ family protein					PF04955.7	1025113	1025821	1	185	fig|1129.58.p	Membrane Transport	Cation transporters	Transport of Nickel and Cobalt
gsyne_118	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	98045	98546	1	156	fig|1129.58.peg.118			
gsyne_1180	Synechococcus_assembled_mapped	ferric uptake regulator family protein					PF01475.14	1026012	1026495	-1	261	fig|1129.58.p	Stress Response	Oxidative stress	Oxidative stress
gsyne_1181	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1025913	1026033	1	856				
gsyne_1182	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF03706.8	1026517	1027513	-1	156	fig|1129.58.peg.1183			
gsyne_1183	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF01969.12	1027509	1028739	-1	156	fig|1129.58.peg.1184			
gsyne_1184	Synechococcus_assembled_mapped	peptidase M41 family protein					PF01434.13	1028738	1029395	-1	138	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_1185	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_B	1029397	1030054	-1	156	fig|1129.58.peg.1186			
gsyne_1186	Synechococcus_assembled_mapped	TPR repeat family protein					PF13414.1	1030157	1031006	1	185	fig|1129.58.peg.1187			
gsyne_1187	Synechococcus_assembled_mapped	exodeoxyribonuclease III	xth	3.1.11.2		GO:0006281,GO:0008853	TIGR00195	1031447	1032278	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_1188	Synechococcus_assembled_mapped	FAD linked oxidase, C-terminal domain protein					PF02913.14	1032289	1033744	-1	157	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Glycolate, glyoxylate interconver
gsyne_1189	Synechococcus_assembled_mapped	glutamate-1-semialdehyde-2,1-aminor	hemL	5.4.3.8		GO:0005737,GO:0006779,G	TIGR00713	1033960	1035187	1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi
gsyne_119	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	99200	101264	-1	856	fig|1129.58.peg.120			
gsyne_1190	Synechococcus_assembled_mapped	receptor ligand binding region family protein					PF01094.23	1035165	1036434	1	185	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter branched-chain
gsyne_1191	Synechococcus_assembled_mapped	branched-chain amino acid transport system / permease component family protein					PF02653.11	1036442	1037372	1	147	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter branched-chain
gsyne_1192	Synechococcus_assembled_mapped	branched-chain amino acid transport system / permease component family protein					PF02653.11	1037390	1038254	1	147	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter branched-chain
gsyne_1193	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	1038250	1039027	1	141	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter branched-chain
gsyne_1194	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	1039023	1039767	1	141	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter branched-chain
gsyne_1195	Synechococcus_assembled_mapped	sodium/calcium exchanger family protein					PF01699.19	1039776	1040463	1	145	fig|1129.58.peg.1196			
gsyne_1196	Synechococcus_assembled_mapped	sodium/calcium exchanger family protein					PF01699.19	1040456	1040906	1	145	fig|1129.58.peg.1197			
gsyne_1197	Synechococcus_assembled_mapped	gamma-glutamyltransferase	ggt	2.3.2.2		GO:0003840,GO:0006750	TIGR00066	1040929	1042747	-1	86	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Biosynthesis and ga
gsyne_1198	Synechococcus_assembled_mapped	hydantoinase B/oxoprolinase family protein					PF02538.9	1042813	1046416	-1	185	fig|1129.58.p	Nucleosides and Nucleotides	Nucleosides and Nucleotides -	Hydantoin metabolism
gsyne_1199	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF04461.8	1047350	1047842	-1	156	fig|1129.58.p	Miscellaneous	Miscellaneous - no subcategor	Broadly distributed proteins not ir
gsyne_12	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	8640	8940	-1	856	fig|1129.58.peg.13			
gsyne_120	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF07077.6	98551	99223	1	156	fig|1129.58.peg.119			
gsyne_1200	Synechococcus_assembled_mapped	lysR substrate binding domain protein					PF03466.15	1046488	1047400	1	157	fig|1129.58.peg.1200			
gsyne_1201	Synechococcus_assembled_mapped	MAPEG family protein					PF01124.13	1047929	1048334	1	185	fig|1129.58.peg.1202			
gsyne_1202	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1048432	1049269	1	856	fig|1129.58.peg.1203			
gsyne_1203	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1049392	1050889	1	856	fig|1129.58.peg.1204			
gsyne_1204	Synechococcus_assembled_mapped	DNA recombination-mediator A family protein					PF02481.10	1051027	1051540	-1	185	fig|1129.58.peg.1205			
gsyne_1205	Synechococcus_assembled_mapped	AAA domain protein					PF13500.1	1051577	1052696	-1	157	fig|1129.58.peg.1206			
gsyne_1206	Synechococcus_assembled_mapped	putative ligand-binding domain of nuclear horm					UniRef100_C	1052720	1053113	-1	157	fig|1129.58.peg.1207			
gsyne_1207	Synechococcus_assembled_mapped	short chain dehydrogenase family protein					PF00106.20	1053155	1053893	1	703	fig|1129.58.peg.1208			
gsyne_1208	Synechococcus_assembled_mapped	methionine aminopeptidase, type I	map	3.4.11.18		GO:0004239,GO:0006464	TIGR00500	1053911	1054787	-1	140	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba
gsyne_1209	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	1054863	1055157	1	156	fig|1129.58.peg.1210			
gsyne_121	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	101265	101787	-1	856	fig|1129.58.peg.121			
gsyne_1210	Synechococcus_assembled_mapped	ribosomal protein L19	rplS			GO:0000311,GO:0003735,G	TIGR01024	1055220	1055703	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_1212	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_B	1055911	1056100	1	156	fig|1129.58.peg.1212			
gsyne_1213	Synechococcus_assembled_mapped	putative lipoprotein				GO:0008150,GO:0003674,G	lipoP	1056101	1056218	1	88	fig|1129.58.peg.1213			
gsyne_1215	Synechococcus_assembled_mapped	glutamate--tRNA ligase	gltX	6.1.1.17		GO:0004818,GO:0006424,G	TIGR00464	1056434	1057856	1	137	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi
gsyne_1216	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	1059021	1059237	-1	156	fig|1129.58.peg.1215			
gsyne_1217	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF07799.7	1059272	1059830	-1	156	fig|1129.58.peg.1216			
gsyne_1218	Synechococcus_assembled_mapped	nucleotidyltransferase domain protein					PF01909.18	1059863	1060202	1	703	fig|1129.58.peg.1217			
gsyne_1219	Synechococcus_assembled_mapped	HEPN domain protein					PF05168.9	1060198	1060591	1	157	fig|1129.58.peg.1218			
gsyne_122	Synechococcus_assembled_mapped	heavy metal translocating P-type ATPase domain protein				GO:0016020,GO:0015662,G	UniRef100_C	101790	101976	-1	92,141,703	fig|1129.58.peg.122			
gsyne_1220	Synechococcus_assembled_mapped	DNA polymerase I	polA	2.7.7.7		GO:0003887,GO:0006260	TIGR00593	1060611	1063674	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_1221	Synechococcus_assembled_mapped	cysteine--tRNA ligase	cysS	6.1.1.16		GO:0004817,GO:0005737,G	TIGR00435	1063685	1065155	1	137	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	Zinc regulated enzymes
gsyne_1222	Synechococcus_assembled_mapped	putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase				GO:0016853,GO:0055114,G	UniRef100_A	1065156	1065372	-1	703	fig|1129.58.peg.1221			
gsyne_1223	Synechococcus_assembled_mapped	sodium:neurotransmitter symporter family protein					PF00209.13	1065415	1066777	-1	185	fig|1129.58.peg.1222			
gsyne_1224	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1066977	1067139	1	856	fig|1129.58.peg.1223			
gsyne_1225	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1067135	1067621	1	856	fig|1129.58.peg.1224			
gsyne_1226	Synechococcus_assembled_mapped	1-deoxy-D-xylulose 5-phosphate reduct	dxr	1.1.1.267		GO:0005737,GO:0019288,G	TIGR00243	1067617	1068868	1	76	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis
gsyne_1227	Synechococcus_assembled_mapped	alpha/beta hydrolase family protein					PF12697.2	1069187	1070270	-1	703	fig|1129.58.peg.1227			
gsyne_1228	Synechococcus_assembled_mapped	putative ferredoxin					UniRef100_B	1068864	1069206	1	112	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_1229	Synechococcus_assembled_mapped	NAD(P) transhydrogenase subunit beta	pntB	1.6.1.2		GO:0050661,GO:0016021,G	UniRef100_C	1070316	1071738	-1	141,703	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_123	Synechococcus_assembled_mapped	cadmium-translocating P-type ATPase	cadA	3.6.3.3		GO:0015434,GO:0015691	TIGR01512	101951	104249	-1	145	fig|1129.58.p	Membrane Transport	Cation transporters	Copper Transport System
gsyne_1230	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	PF12769.2	1071734	1072034	-1	156	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1231	Synechococcus_assembled_mapped	alanine dehydrogenase/PNT, C-terminal domain protein					PF01262.16	1072030	1073173	-1	703	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1232	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	1073283	1073460	-1	156	fig|1129.58.peg.1231			
gsyne_1233	Synechococcus_assembled_mapped	type III restriction enzyme, res subunit					PF04851.10	1073755	1075081	1	183	fig|1129.58.peg.1232			
gsyne_1234	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_B	1075175	1075421	1	156	fig|1129.58.peg.1233			
gsyne_1235	Synechococcus_assembled_mapped	thioredoxin-disulfide reductase	trxB	1.8.1.9		GO:0004791,GO:0055114	TIGR01292	1075532	1076936	1	112	fig|1129.58.p	Sulfur Metabolism	Sulfur Metabolism - no subcat	Thioredoxin-disulfide reductase
gsyne_1236	Synechococcus_assembled_mapped	translation initiation factor IF-1	infA			GO:0003743,GO:0006413	TIGR00008	1077050	1077317	-1	169	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation initiation factors bacte
gsyne_1237	Synechococcus_assembled_mapped	pseudouridine synthase family protein		5.4.99.-		GO:0001522,GO:0009982	TIGR00093	1077608	1078181	1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA pseudouridine syntheses
gsyne_1238	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_B	1078193	1078409	-1	156	fig|1129.58.peg.1237			
gsyne_1239	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein					PF01370.16	1078492	1079455	-1	119	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_124	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,G	UniRef100_A	104296	104626	-1	156	fig|1129.58.peg.124			
gsyne_1240	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1079646	1079769	-1	856	fig|1129.58.peg.1240			
gsyne_1241	Synechococcus_assembled_mapped	N2,N2-dimethylguanosine tRNA methyltransferase family protein					PF02005.11	1079746	1081084	-1	168	fig|1129.58.peg.1241			
gsyne_1242	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein					PF00561.15	1081155	1081785	1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_1243	Synechococcus_assembled_mapped	acetolactate synthase, small subunit	ilvN	2.2.1.6		GO:0003984,GO:0005948,G	TIGR00119	1081781	1082312	1	74	fig|1129.58.p	Carbohydrates	Fermentation	Acetolactate synthase subunits
gsyne_1244	Synechococcus_assembled_mapped	cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD family protein					PF00160.16	1082324	1083047	-1	95	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth
gsyne_1245	Synechococcus_assembled_mapped	ycf4 family protein					PF02392.11	1083049	1083616	-1	185	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_1246	Synechococcus_assembled_mapped	photosynthetic reaction centre family protein					PF00124.14	1083801	1084164	1	185	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_1247	Synechococcus_assembled_mapped	photosystem II D2 protein	psbD2			GO:0006810,GO:0009772,G	UniRef100_C	1084136	1084856	1	92,141	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_1248	Synechococcus_assembled_mapped	photosystem II 44 kDa subunit reaction	psbC			GO:0009538,GO:0009539,G	TIGR01153	1084839	1086228	1	112,164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_1249	Synechococcus_assembled_mapped	autotransporter beta-domain protein					PF03797.14	1088591	1089656	1	97,187	fig|1129.58.peg.1250			
gsyne_125	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	105752	106220	-1	856	fig|1129.58.peg.126			
gsyne_1250	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,G	default	1090301	1090418	-1	856				





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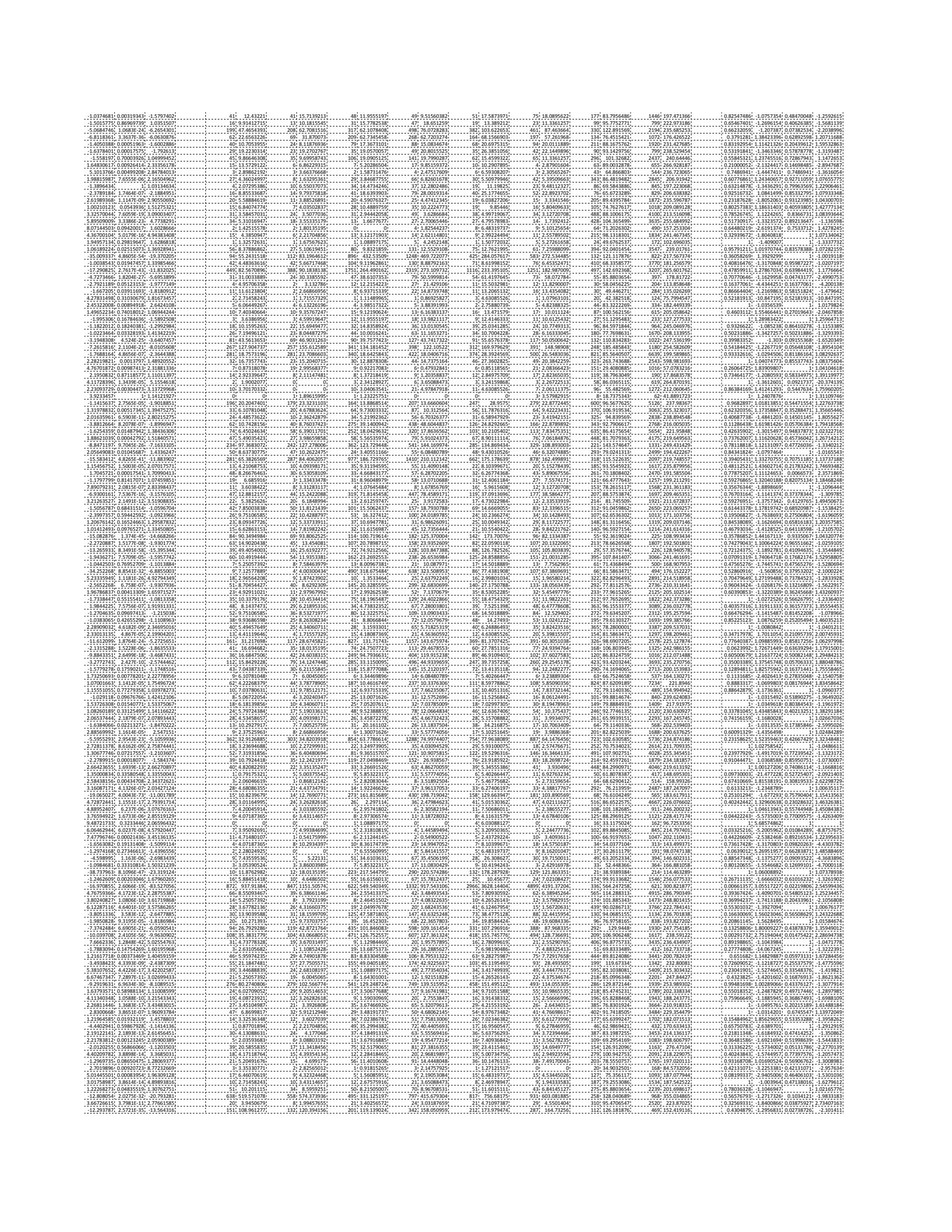
111	15.1028537	110	17.8093711	90	24.724417	133	22.326563	65	23.8845747	128	22.6965532	56	14.7164302	168	16.3354609
693	80.147171	636	87.5249637	271	63.2807718	574	81.9032337	159	49.6615425	664	100.077614	164	36.6333995	831	68.6818619
337	148.0059	349	182.387224	122	108.182365	350	189.649352	79	93.7010237	248	141.943238	64	54.2884587	346	108.595367
65	11.506242	76	16.0086091	22	7.86303738	97	21.1848832	39	18.6445914	57	13.1494899	23	7.86369017	65	8.22279714
38	11.8778226	41	15.2495475	14	8.83545233	54	20.8248169	10	8.44153366	51	20.7748223	15	9.05571841	43	9.60522998
14	5.16745139	14	6.14888344	3	2.23571856	12	5.46466827	9	8.9713746	10	4.81019039	5	3.5644849	17	4.48418332
72	11.8393064	41	8.02227379	51	16.9321245	52	10.549486	45	19.9836306	84	18.0005987	40	12.7037566	156	18.3317715
252	105.341298	228	113.410387	222	187.369377	161	83.0344273	69	77.8960317	157	85.5286623	68	54.9016566	259	77.3720249
490	53.4619971	433	56.2156006	156	34.3653847	374	50.3448317	104	30.6443599	341	48.4861141	78	16.4369832	338	26.3543234
11	2.23189003	14	3.38008797	8	3.27731064	16	4.00529292	14	7.67142884	15	3.96629734	12	4.70261868	11	1.59499331
18	2.86478629	24	4.54517727	5	1.60670906	12	2.35632485	12	5.15785451	14	2.90376631	1	0.30739595	7	0.79616639
49	20.0010766	42	20.3998251	34	28.021006	50	25.1803342	12	13.2283798	39	20.7460682	15	11.8257029	81	23.6280774
62	2.04480627	44	1.72676412	27	1.79792576	56	2.27867663	45	4.00812364	39	1.67625076	26	1.65619793	64	1.50843474
26	2.48509469	15	1.70600662	19	3.66666056	30	3.5377329	14	3.61381358	21	2.61578948	7	1.29224852	31	2.11747046
20	2.9910125	17	3.02522036	21	6.3409604	19	3.50571032	8	3.23106978	21	4.09280855	9	2.59961571	30	3.20623655
20	4.36424466	19	4.93347072	8	3.52465484	25	6.73059247	8	4.71451691	23	6.54064882	8	3.37168887	23	3.58668307
9	2.06795831	1	0.27341298	3	1.39177182	9	2.55138486	11	6.82590239	4	1.19776926	5	2.21895087	3	0.49261383
21	2.29122845	15	1.94742265	3	0.66087278	8	1.0768948	20	5.89314614	15	2.13282027	12	2.52876665	13	1.01362782
13	2.01359235	5	0.92154822	6	1.87640665	10	1.91100751	7	2.92815699	3	0.60556861	5	1.49581063	8	0.885532
42	5.58322334	15	2.37272185	20	5.3680088	18	2.95217711	20	7.18015507	13	2.25212745	14	3.59453037	34	3.22998645
17	1.35281575	10	0.94691193	6	0.96402543	7	0.68726142	8	1.71928484	12	1.24447128	6	0.92218784	10	0.56869028
20	3.00396061	19	3.39576556	10	3.0325764	14	2.59433746	35	14.1971248	8	1.56591479	19	5.51183553	28	3.00544194
28	24.2870215	22	22.7069481	3	5.25393862	17	18.1927915	6	14.0551536	8	9.04315793	3	5.02592372	1	0.6198724
9	2.33031123	10	3.08099703	3	1.56833989	12	3.83342401	6	4.19556822	3	1.0122938	8	4.0007353	5	0.92518269
46	3.56250954	27	2.48818019	16	2.50187553	25	2.38875938	20	4.18308141	22	2.22041824	12	1.79497276	47	2.60125025
12	1.32595204	23	3.0240869	4	0.89238872	10	1.3632665	8	2.38728723	8	1.15199464	6	1.28049012	13	1.02654028
10	7.38207341	12	10.540943	3	4.47143712	17	15.4832268	0	0	1	0.96203808	6	8.55476377	7	3.69285685
52	10.0232152	42	9.63325072	20	7.78361276	38	9.03694216	20	10.4112249	39	9.79675442	24	8.93497549	62	8.54046418
25	5.38753805	10	2.56430809	13	5.65641424	13	3.45643097	13	7.56592116	11	3.08927755	8	3.32980453	43	6.6222393
8	3.55853795	1	0.52929949	1	0.89810917	3	1.64640647	2	2.40259035	0	0	0	0	4	1.27153313
1	0.82608917	0	0	0	0	0	0	1	2.23097675	0	0	0	0	0	0
78	6.93914901	87	9.20981113	47	8.44222615	91	9.98819923	46	11.0519156	69	7.99971663	35	6.01392581	128	8.13781202
64	9.4090156	34	5.94789088	27	8.01448263	62	11.2457933	21	8.33780295	42	8.04687782	19	5.39505936	51	5.35821905
66	13.7120909	75	18.5413295	65	27.2659489	53	13.585318	52	29.1763666	58	15.7036874	50	20.0635677	150	22.2708647
36	7.75805479	48	12.3086788	33	14.35859	39	10.3692929	16	9.31190297	30	8.42530242	11	4.57848123	100	15.4005565
37	32.0935642	11	11.3534741	1	1.75131287	14	14.9822988	2	4.68505118	4	4.52157896	6	10.0518474	6	3.7192344
28	2.92614717	24	2.98448387	18	3.79802792	17	2.19190258	28	7.90249597	14	1.90668993	20	4.03688652	32	2.38986949
29	2.45408928	18	1.81252801	10	1.70859792	26	2.71456286	16	3.65662531	27	2.97762517	7	1.14411272	41	2.4794896
19	3.01013313	16	3.01628203	5	1.59937249	6	1.17278269	7	2.99500989	13	2.68404231	5	1.52996156	15	1.69828055
17	2.69327701	15	2.8277644	10	3.19874497	14	2.73649294	14	5.99001978	11	2.27111272	10	3.05992311	36	4.07587332
17	2.0841967	21	3.06357797	11	2.72288927	12	1.8151195	16	5.29758438	10	1.59773108	11	2.604719	45	3.94265131
24	3.00612953	21	3.12993706	5	1.26448583	9	1.39082712	13	4.39752097	8	1.30587118	5	1.2096086	28	2.50634328
49	3.50534331	34	2.89423144	15	2.16657263	22	1.94174123	42	8.11431545	22	2.05102551	20	2.76339448	44	2.24943386
92	7.80442187	122	12.3149485	74	12.6745381	147	15.3852458	64	14.6622629	141	15.5878395	59	9.66681334	200	12.1246435
64	3.22751117	40	2.40031164	36	3.66553857	51	3.1731613	44	5.99250733	51	3.35175185	14	1.36362271	75	2.70293198
33	2.70676025	28	2.73283708	20	3.31217564	34	3.44071706	18	3.9872776	41	4.38261791	19	3.01000947	52	3.04807232
28	3.13380923	21	2.79675021	16	3.61561367	36	4.97108533	18	5.4407046	44	6.41772498	17	3.67486895	23	1.83962132
29	3.49366877	14	2.00692723	13	3.16209269	32	4.75628535	15	4.88026165	31	4.86697736	10	2.32681653	28	2.41061489
19	2.54524771	12	1.91283522	8	2.16378424	11	1.81803957	10	3.61780014	21	3.66614511	5	1.29367406	14	1.34026465
33	4.61677252	13	2.16415195	13	3.67210763	35	6.04124953	13	4.91174721	27	4.92268678	8	2.16168762	19	1.89960897
35	5.30284313	30	5.40856248	15	4.58859268	10	1.86928245	19	7.77432074	28	5.52856817	10	2.92630202	24	2.59859172
16	3.70087947	9	2.47712161	0	0	7	1.99763985	13	8.12075538	6	1.80863159	2	0.89349755	10	1.65299307
44	2.51916301	30	2.04382972	31	3.58354449	33	2.33105074	41	6.3395082	28	2.0891784	11	1.21639518	59	2.41402453
93	2.68668134	43	1.47816028	21	1.22489826	27	0.96234583	63	4.91520774	39	1.46828959	26	1.45072458	59	1.21806733
34	7.19302031	28	7.04872004	19	8.11584014	35	9.13554807	27	15.426388	26	7.1683569	15	6.12917526	97	14.6652739
105	36.4305323	105	43.3496283	52	36.4273077	100	42.8065681	35	32.7953583	65	29.3902633	33	22.1140643	171	42.3992722
25	3.87229297	22	4.05481217	13	4.06554774	17	3.24871276	11	4.60138955	12	2.42227445	15	4.48743189	20	2.21383
35	3.99457591	27	3.66679186	20	4.60871808	22	3.09784375	30	9.24681154	29	4.31334835	13	2.86565826	27	2.20217826
23	5.91112693	13	3.97562728	13	6.74579773	12	3.80502828	7	4.8585716	8	2.6794542	2	0.99277506	19	3.48965203
75	9.32681318	54	7.99071489	53	13.307467	30	4.60285679	41	13.7696845	29	4.6998491	31	7.44581291	146	12.9751069
50	3.47652756	51	4.21954584	22	3.08848763	59	5.06129763	52	9.76443533	48	4.34941464	37	4.9688491	111	5.51549791
44	8.92756013	40	9.65739421	30	12.2899149	39	9.7629015	17	9.31530644	58	15.3363497	33	12.9322014	39	5.65497628
58	5.39504883	39	4.31669986	32	6.00986723	68	7.80387837	44	11.0532039	47	5.69743194	22	3.95246905	59	3.92198087
9	2.38367714	8	2.52124337	10	5.34752022	7	2.28737387	2	1.43054998	7	2.4161109	3	1.5346332	10	1.89274015
10	1.41039614	13	2.18174668	5	1.4238316	5	0.8700522	6	2.28539082	11	2.02184425	0	0	8	0.80633808
53	6.29751537	52	7.35218744	44	10.5558584	49	7.18329397	43	13.7984384	49	7.58758114	29	6.65533277	98	8.32157469
7	2.4782675	2	0.84255837	3	2.14446474	3	1.31040515	2	1.91226579	1	0.46138561	2	1.36759829	5	1.26504571
28	5.58322334	28	6.64362119	4	1.61040264	33	8.11848706	11	5.92362793	26	6.75638236	8	3.08102603	22	3.13498685
190	40.9452892	139	35.6438824	146	63.5258831	294	78.1685157	56	32.5916604	292	82.0062769	76	31.6331431	355	54.6719757
64	35.2464711	62	40.6300371	41	45.5897319	125	84.9336669	15	22.3097675	159	114.116041	35	37.2290646	79	31.0920124
0	0	4	4.23439592	0	0	3	3.29281293	1	2.40259035	2	2.31875844	0	0	1	0.63576656
46	3.36709762	23	2.00329807	24	3.54696278	30	2.70927646	42	8.30262235	37	3.52950257	32	4.52403822	59	3.08628452
10	4.81885348	8	4.58726225	4	3.89180638	12	7.13442802	3	3.90420932	1	0.62799708	2	1.86145323	1	0.34437356
9	1.67882637	7	1.55375012	3	1.12987927	5	1.1507142	3	1.51130683	8	1.94476515	1	0.36028127	11	1.46636482
55	16.8873095	71	25.9403591	40	24.7973504	58	21.9715128	26	21.5595276	56	22.407825	18	10.6745282	73	16.0179417
21	5.56191333	18	5.67279759	8	4.27801618	16	5.22828313	13	9.29857487	8	2.7612696	9	4.60389959	20	3.78548031
4	2.23843516	2	1.33178581	3	3.38963782	6	4.14257111	1	1.51130683	8	5.83429544	1	1.08084381	4	1.59967071
77	2.61662328	57	2.3048634	28	1.92112675	49	2.05437986	64	5.87352156	51	2.25857519	33	2.16592207	90	2.18564216
43	3.04472865	46	3.87576851	14	2.00150043	36	3.14497235	25	4.78066447	40	3.69108487	13	1.77787778	51	2.58069326
5	2.40942674	4	2.29363112	1	0.9729516	5	2.97267834	4	5.20561243	6	3.76798247	0	0	1	0.34437356
43	3.28616087	30	2.72810751	21	3.24031456	22	2.07432709	39	8.04920688	23	2.29066776	20	2.95208441	40	2.18457234
0	0	3	2.29363112	0	0	0	0	1	1.73520414	2	1.67465888	0	0	1	0.45916474
6	1.28502759	2	0.50969581	4	1.72969173	1	0.26423808	3	1.73520414	1	0.27910981	0	0	3	0.45916474
46	3.82734837	44	4.35624904	17	2.85585792	32	3.2849165	30	6.74108084	45	4.87940176	28	4.49962795	40	2.37840729
15	1.44165146	10	1.14363879	10	1.94051288	15	1.77866627	27	7.0081098	12	1.50301794	11	2.04192653	26	1.78578198
7	2.13044048	4	1.44860913	1	0.61449574	8	3.00396969	2	1.64387761	3	1.1898892	1	0.58782734	2	0.43499818
53	3.87948204	38	3.30979681	24	3.54696278	29	2.61896725	31	6.12812602	63	6.00969356	19	2.6861477	59	3.08628452
143	6.477143	128	6.89885915	88	8.0478085	204	11.4001826	90	11.0092587	248	14.6390546	74	6.47377467	212	6.86229498
15	5.20436176	9	3.71568242	4	2.8021006	10	4.28065681	19	17.8031945	10	4.52157896	6	4.02073897	6	1.48769376
37	3.36940306	34	3.68425787	27	4.96435145	33	3.70765551	29	7.13209891	28	3.32294517	24	4.22124826	47	3.05868796
16	9.4090156	8	5.59801495	5	5.9366538	8	5.80428042	3	4.76445883	0	0	0	0	3	1.26075742
32	2.51190914	31	2.89557956	18	2.85281735	29	2.80857574	41	8.69172391	31	3.17124317	19	2.88061993	52	2.91704659
303	128.205009	327	164.637961	158	134.979236	307	160.263615	91	103.985282	218	120.207831	98	80.0878901	238	71.9656738
86	6.37571383	96	8.46879184	58	8.68172193	83	7.59176315	34	6.80733933	75	7.24612014	51	7.3026242	133	7.04641275
181	70.5610096	126	58.448937	64	50.3748422	129	62.0454751	29	30.5317942	166	84.3350683	37	27.8590528	184	51.261358
11	1.99818427	15	3.24230578	5	1.83383547	16	3.58589052	6	2.94348765	10	2.36731883	1	0.35084982	20	2.59632419
12	5.78262417	7	4.01385447	4	3.89180638	2	1.18907134	7	9.10982174	6	3.76798247	2	1.86145323	7	2.41061489
34	3.67493873	40	5.14459318	19	4.14641054	39	5.200798	31	9.04900851	22	3.09890147	16	3.34017775	54	4.171104
52	16.4016249	32	12.0102866	10	6.36841044	41	15.9551754	11	9.37010237	24	9.8652632	8	4.873623	46	10.3687747
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	2.33379451	23	2.12906566	19	2.98429996	11	1.05576738	18	3.78165566	7	0.70966486	17	2.55428111	35	1.9457878
13	2.14783184	9	1.76937258	10	3.33583404	9	1.83456721	23	10.2624931	19	4.0909524	12	3.82927521	27	3.1879152
21	4.11644433	15	3.49875934	19	7.51976148	31	7.49719555	15	7.94076472	19	4.85367234	9	3.40740591	49	6.86412375
24	3.45517793	8	1.37046839	15	4.36011503	27	4.79575659	25	9.7200232	32	6.0037563	9	2.50253463	34	3.49803512
16	2.93720593	26	5.67946755	11	4.0771305	25	5.66224446	13	6.44504396	18	4.30626568	14	4.96387527	38	4.98521719
116	33.2620366	137	46.7445814	3	1.73683921	177	62.6178724	5	3.87194313	9	3.36315791	3	1.66146239	1	0.2049165
265	38.3098851	324	55.7352363	224	65.3823472	398	70.9875588	179	69.8853468	479	90.2431802	248	69.2460601	689	71.1820139
592	44.3625941	814	72.5837651	648	98.0432606	1227	113.442028	420	84.9987688	1309	127.834706	672	97.2619363	1795	96.1270806
65	6.35274205	48	5.58224589	37	7.30124803	72	8.68189551	55	14.51706	53	6.75052634	40	7.55068352	96	6.70509864
17	3.78094657	25	6.61624363	14	6.28676416	24	6.58562587	10	6.00647588	19	5.5070513	13	5.58435968	45	7.15237385
1	0.88963449	0	0	0	0	1	1.09760431	0	0	0	0	0	0	0	0

gsyne_1251	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1089776	1090340	1	156	fig|1129.58.peg.1251			
gsyne_1252	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1090510	1090786	-1	156	fig|1129.58.peg.1252			
gsyne_1253	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1090979	1091696	1	156	fig|1129.58.peg.1253			
gsyne_1254	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1091724	1092192	1	141	fig|1129.58.peg.1254			
gsyne_1255	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1092188	1092827	1	156	fig|1129.58.peg.1255			
gsyne_1256	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1093601	1093859	-1	856				
gsyne_1257	Synechococcus_assembled_mapped	mce related family protein				PF02470.15	1092838	1093618	1	185	fig|1129.58.peg.1256			
gsyne_1258	Synechococcus_assembled_mapped	maf-like family protein				PF02545.9	1093936	1094125	-1	185	fig|1129.58.peg.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1259	Synechococcus_assembled_mapped	helix-turn-helix family protein				PF01381.17	1094383	1094560	1	261	fig|1129.58.peg.1258			
gsyne_126	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	104741	105800	1	856	fig|1129.58.peg.125			
gsyne_1260	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01934.12	1094684	1095014	-1	156	fig|1129.58.peg.1259			
gsyne_1261	Synechococcus_assembled_mapped	nucleotidyltransferase domain protein				PF01909.18	1095010	1095319	-1	703	fig|1129.58.peg.1260			
gsyne_1262	Synechococcus_assembled_mapped	septum formation protein Maf	maf		GO:0000917,GO:0030428	TIGR00172	1095507	1096119	-1	93	fig|1129.58.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1263	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1096169	1096544	1	156	fig|1129.58.peg.1262			
gsyne_1264	Synechococcus_assembled_mapped	cobyric acid synthase CobQ	cobQ	6.3.5.10	GO:0005737,GO:0009236,G	TIGR00313	1096567	1098046	1	79	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis
gsyne_1265	Synechococcus_assembled_mapped	fusaric acid resistance -like family protein				PF13515.1	1098247	1099342	-1	94	fig|1129.58.peg.1265			
gsyne_1266	Synechococcus_assembled_mapped	2Fe-2S iron-sulfur cluster binding domain protein				PF00111.22	1098042	1098282	1	112	fig|1129.58.1	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_1267	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1099338	1099923	-1	156	fig|1129.58.peg.1266			
gsyne_1268	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1100024	1100153	-1	856	fig|1129.58.peg.1267			
gsyne_1269	Synechococcus_assembled_mapped	tRNA (5-methylaminomethyl-2-thiouridtrmU		2.1.1.61	GO:0004808,GO:0005737,G	TIGR00420	1100293	1101436	-1	168	fig|1129.58.1	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_127	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	106240	106531	-1	156	fig|1129.58.peg.127			
gsyne_1270	Synechococcus_assembled_mapped	yjeF-related family protein				PF03853.10	1101554	1103156	1	185	fig|1129.58.1	Cell Wall and Capsule	Cell Wall and Capsule - no sut	YjeE
gsyne_1271	Synechococcus_assembled_mapped	RNA polymerase sigma factor, cyanobacterial RpoD-like family protein				TIGR02997	1103287	1104217	1	135	fig|1129.58.1	RNA Metabolism	Transcription	Transcription factors cyanobacter
gsyne_1272	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1104673	1104844	-1	856	fig|1129.58.peg.1271			
gsyne_1273	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1105057	1105195	-1	856				
gsyne_1274	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1105506	1105668	1	856	fig|1129.58.peg.1274			
gsyne_1275	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1105718	1105844	-1	856	fig|1129.58.peg.1275			
gsyne_1276	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1106004	1106145	1	856	fig|1129.58.peg.1276			
gsyne_1277	Synechococcus_assembled_mapped	FKBP-type peptidyl-prolyl cis-trans isomerase family protein				PF00254.23	1106450	1106681	1	95	fig|1129.58.peg.1277			
gsyne_1278	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07864.6	1107373	1107514	1	156	fig|1129.58.peg.1278			
gsyne_1279	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1107687	1107990	1	856				
gsyne_128	Synechococcus_assembled_mapped	carbonic anhydrase family protein				PF00484.14	107526	108144	-1	102	fig|1129.58.1	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Cyanate hydrolysis
gsyne_1280	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	1108118	1108436	1	157	fig|1129.58.peg.1281			
gsyne_1281	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	1108603	1108960	1	157	fig|1129.58.peg.1282			
gsyne_1282	Synechococcus_assembled_mapped	hemolysin-type calcium-binding repeat family protein				PF00353.14	1109339	1111901	-1	97	fig|1129.58.1	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1283	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	1112319	1112646	1	154	fig|1129.58.peg.1284			
gsyne_1284	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	1112626	1113997	1	157	fig|1129.58.peg.1285			
gsyne_1285	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	1114038	1114857	1	154	fig|1129.58.peg.1286			
gsyne_1286	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1114843	1115023	1	856				
gsyne_1287	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	1115423	1115885	1	157	fig|1129.58.peg.1288			
gsyne_1288	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1116167	1116281	-1	88	fig|1129.58.peg.1289			
gsyne_1289	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1117815	1119474	-1	132,152	fig|1129.58.peg.1290			
gsyne_129	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	106634	107558	1	156	fig|1129.58.peg.128			
gsyne_1290	Synechococcus_assembled_mapped	histone deacetylase domain protein				PF00850.14	1119524	1120439	1	157	fig|1129.58.peg.1291			
gsyne_1291	Synechococcus_assembled_mapped	pyruvate dehydrogenase (acetyl-transfpdhA		1.2.4.1	GO:0004739,GO:0006086,G	TIGR03182	1120460	1121447	-1	118	fig|1129.58.1	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-Co
gsyne_1292	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF13355.1	1121700	1123662	1	156	fig|1129.58.peg.1293			
gsyne_1293	Synechococcus_assembled_mapped	signal recognition particle protein	ffh		GO:0003924,GO:0005048,G	TIGR00959	1123731	1125195	1	97	fig|1129.58.1	Membrane Transport	Protein translocation across cy	Bacterial signal recognition partic
gsyne_1294	Synechococcus_assembled_mapped	ribosomal protein S16	rpsP		GO:0000314,GO:0003735,G	TIGR00002	1125292	1125703	1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_1295	Synechococcus_assembled_mapped	AAA domain protein				PF13604.1	1125715	1126705	1	157	fig|1129.58.1	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1296	Synechococcus_assembled_mapped	inhibitor of apoptosis-promoting Bax1 family protein				PF01027.15	1126813	1127548	1	185	fig|1129.58.peg.1297			
gsyne_1297	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1127606	1128134	-1	156	fig|1129.58.peg.1298			
gsyne_1298	Synechococcus_assembled_mapped	GTP-binding protein Era	era		GO:0003924,GO:0005525,G	TIGR00436	1128166	1129159	1	93,262	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Universal GTPases
gsyne_1299	Synechococcus_assembled_mapped	cpeS-like family protein				PF09367.5	1129171	1129657	1	185	fig|1129.58.1	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_13	Synechococcus_assembled_mapped	putative oRF2			GO:0008152,GO:0008168,G	UniRef100_C	9007	9529	-1	92,703	fig|1129.58.peg.14			
gsyne_130	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07077.6	108254	108878	1	156	fig|1129.58.peg.130			
gsyne_1300	Synechococcus_assembled_mapped	tRNA (guanine(37)-N(1))-methyltransfe trmD			GO:0006400,GO:0009019	TIGR00088	1129677	1130376	1	168	fig|1129.58.1	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_1301	Synechococcus_assembled_mapped	SPFH domain / Band 7 family protein				PF01145.20	1130379	1131294	-1	157	fig|1129.58.peg.1302			
gsyne_1302	Synechococcus_assembled_mapped	nfeD-like C-terminal, partner-binding family protein				PF01957.13	1131363	1131819	1	157	fig|1129.58.peg.1303			
gsyne_1303	Synechococcus_assembled_mapped	2-C-methyl-D-erythritol 2,4-cyclodiphosispF		4.6.1.12	GO:0008685,GO:0019288	TIGR00151	1131848	1132334	1	76	fig|1129.58.1	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis
gsyne_1304	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1132384	1132771	1	92,703	fig|1129.58.peg.1305			
gsyne_1305	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1133449	1133608	-1	156				
gsyne_1306	Synechococcus_assembled_mapped	AIR carboxylase family protein				PF00731.15	1132767	1133490	1	125	fig|1129.58.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_1307	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1133718	1133853	-1	856	fig|1129.58.peg.1307			
gsyne_1308	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07466.6	1134013	1134991	-1	156	fig|1129.58.peg.1308			
gsyne_1309	Synechococcus_assembled_mapped	thiamine biosynthesis protein ThiS	thiS		GO:0003824,GO:0009228	TIGR01683	1134997	1135225	-1	162	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Cofactors, Vitamins, Prosthetic	Thiamin biosynthesis
gsyne_131	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	108881	109097	-1	856	fig|1129.58.peg.131			
gsyne_1310	Synechococcus_assembled_mapped	thiamine-phosphate pyrophosphorylasthiE		2.5.1.3	GO:0004789,GO:0009228	TIGR00693	1135229	1136267	-1	162	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Cofactors, Vitamins, Prosthetic	Thiamin biosynthesis
gsyne_1311	Synechococcus_assembled_mapped	riboflavin biosynthesis protein RibF	ribF	2.7.1.26	GO:0003919,GO:0005737,G	TIGR00083	1136397	1137399	-1	85	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metabo
gsyne_1312	Synechococcus_assembled_mapped	5'/3'-nucleotidase SurE	surE	3.1.3.5	GO:0006950,GO:0008253,G	TIGR00087	1138047	1138845	-1	149	fig|1129.58.1	Nucleosides and Nucleotides	Detoxification	Housecleaning nucleoside tripho
gsyne_1313	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12263.3	1137490	1138069	1	156	fig|1129.58.peg.1312			
gsyne_1314	Synechococcus_assembled_mapped	phenylalanine--tRNA ligase, alpha subu pheS		6.1.1.20	GO:0004826,GO:0006432,G	TIGR00468	1138913	1139921	1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Phe
gsyne_1315	Synechococcus_assembled_mapped	ATP-NAD kinase family protein				PF01513.16	1139980	1140892	1	163	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynth
gsyne_1316	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein				PF00486.23	1140888	1141542	1	261	fig|1129.58.peg.1316			
gsyne_1317	Synechococcus_assembled_mapped	precorrin-6Y C5,15-methyltransferase (cbiT		2.1.1.132	GO:0046025,GO:0046140	TIGR02469	1142026	1143271	-1	79	fig|1129.58.peg.1318			
gsyne_1318	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02643.10	1141569	1142073	1	156	fig|1129.58.peg.1317			
gsyne_1319	Synechococcus_assembled_mapped	extracellular substrate-binding orphan	grrP			TIGR04262	1143359	1144241	1	185	fig|1129.58.peg.1319			
gsyne_132	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10184.4	109412	109832	-1	156	fig|1129.58.peg.132			
gsyne_1320	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	TIGR04260	1144282	1144651	1	156	fig|1129.58.1	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1321	Synechococcus_assembled_mapped	radical SAM/SPASM domain , GRRM sy grrM			GO:0051539	TIGR04261	1144647	1145856	1	157	fig|1129.58.peg.1321			
gsyne_1322	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01594.11	1145857	1146901	1	156	fig|1129.58.peg.1322			
gsyne_1323	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1146906	1147158	1	156	fig|1129.58.peg.1323			
gsyne_1324	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04685.8	1147185	1149696	1	156	fig|1129.58.peg.1324			
gsyne_1325	Synechococcus_assembled_mapped	antitoxin RelJ	relJ		GO:0003677,GO:0006355,G	UniRef100_P	1149748	1149991	1	92,141	fig|1129.58.1	Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1326	Synechococcus_assembled_mapped	addiction module toxin, Txe/YoeB family			GO:0008219	TIGR02116	1149987	1150257	1	94,708	fig|1129.58.1	Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1327	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11320.3	1150325	1150823	1	156	fig|1129.58.peg.1327			
gsyne_1328	Synechococcus_assembled_mapped	ion channel family protein				PF07885.11	1151895	1152603	-1	141	fig|1129.58.peg.1329			
gsyne_1329	Synechococcus_assembled_mapped	riboflavin biosynthesis protein RibD	ribD	3.5.4.26	GO:0008703,GO:0008835,G	TIGR00326	1150843	1151899	1	85	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metabo
gsyne_133	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	109905	110121	1	185	fig|1129.58.peg.134			
gsyne_1330	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02586.9	1152678	1153326	-1	156	fig|1129.58.peg.1330			
gsyne_1331	Synechococcus_assembled_mapped	ATP-dependent metallopeptidase HflB	hflB	3.4.24.-	GO:0004222,GO:0006508,G	TIGR01241	1153411	1155292	1	93,138	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_1332	Synechococcus_assembled_mapped	ornithine carbamoyltransferase	argF	2.1.3.3	GO:0004585,GO:0042450	TIGR00658	1155456	1156407	1	73	fig|1129.58.1	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine and Ornithine Degradati
gsyne_1333	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02638.10	1156475	1157690	1	156	fig|1129.58.peg.1333			
gsyne_1334	Synechococcus_assembled_mapped	repressor LexA	lexA	3.4.21.88	GO:0006282,GO:0006355,G	TIGR00498	1157755	1158373	1	132,261	fig|1129.58.1	DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_1336	Synechococcus_assembled_mapped	phage integrase family			GO:0015074,GO:0003677,G	UniRef100_C	1158617	1160036	1	92,141	fig|1129.58.peg.1335			
gsyne_1337	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1160196	1160412	1	856	fig|1129.58.peg.1336			
gsyne_1338	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1160411	1160660	1	156	fig|1129.58.peg.1337			
gsyne_1339	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1160662	1161685	1	156	fig|1129.58.peg.1338			
gsyne_134	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	110184	110421	-1	185	fig|1129.58.peg.135			
gsyne_1340	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1161698	1163288	1	856	fig|1129.58.peg.1339			
gsyne_1341	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1163605	1163890	-1	856	fig|1129.58.peg.1340			
gsyne_1342	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1163880	1164258	-1	156	fig|1129.58.peg.1341			
gsyne_1343	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1164257	1164386	-1	856	fig|1129.58.peg.1342			
gsyne_1344	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1164403	1164706	-1	856	fig|1129.58.peg.1343			
gsyne_1345	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1164738	1165137	-1	156	fig|1129.58.peg.1344			
gsyne_1346	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1165507	1165675	1	856	fig|1129.58.peg.1345			
gsyne_1347	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1165688	1165838	-1	856	fig|1129.58.peg.1346			
gsyne_1348	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1165883	1166090	-1	856				
gsyne_1349	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1166730	1166898	1	856	fig|1129.58.peg.1348			
gsyne_135	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	110425	110569	-1	185	fig|1129.58.peg.136			
gsyne_1350	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1167090	1167555	-1	156	fig|1129.58.peg.1349			
gsyne_1351	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1167644	1167803	1	856	fig|1129.58.peg.1350			
gsyne_1352	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	1167863	1169183	-1	141	fig|1129.58.peg.1351			
gsyne_1353	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1169236	1169692	-1	156	fig|1129.58.peg.1352			
gsyne_1354	Synechococcus_assembled_mapped	carbon-nitrogen hydrolase family protein				PF00795.17	1169807	1171109	-1	703	fig|1129.58.1	Protein Metabolism	Protein processing and modific	Lipoprotein Biosynthesis
gsyne_1355	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1171329	1171698	1	156	fig|1129.58.peg.1354			
gsyne_1356	Synechococcus_assembled_mapped	FKBP-type peptidyl-prolyl cis-trans isomerase family protein				PF00254.23	1172030	1172363	1	95	fig|1129.58.peg.1355			
gsyne_1357	Synechococcus_assembled_mapped	superoxide dismutase [Fe]	sodB	1.15.1.1	GO:0006801,GO:0004784,G	UniRef100_P	1172587	1173187	1	92,141,703	fig|1129.58.1	Stress Response	Oxidative stress	Protection from Reactive Oxygen
gsyne_1358	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1173445	1173967	1	156	fig|1129.58.peg.1357			
gsyne_1359	Synechococcus_assembled_mapped	tRNA ribosyltransferase-isomerase	queA	5.-.-.-	GO:0005737,GO:0006400,G	TIGR00113	1174073	1175192	-1	168	fig|1129.58.1	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_136	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	110915	111110	-1	856	fig|1129.58.peg.137			
gsyne_1360	Synechococcus_assembled_mapped	e3 binding domain protein				PF02817.12	1175225	1176545	-1	157	fig|1129.58.1	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-Co
gsyne_1361	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11068.3	1176595	1177039	-1	156	fig|1129.58.peg.1360			
gsyne_1362	Synechococcus_assembled_mapped	AMP-binding enzyme family protein				PF00501.23	1177146	1179081	-1	185	fig|1129.58.peg.1361			
gsyne_1363	Synechococcus_assembled_mapped	lipoyl(octanoyl) transferase	lipB	2.3.1.181	GO:0009107,GO:0016979	TIGR00214	1179106	1179790	-1	140	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Biotin	Biotin biosynthesis
gsyne_1364	Synechococcus_assembled_mapped	ribosomal subunit interface protein	raiA		GO:0005840,GO:0009386,G	TIGR00741	1179837	1180425	1	169	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Lipoic acid	Lipoic acid metabolism
gsyne_1365	Synechococcus_assembled_mapped	deoxyribose-phosphate aldolase	deoC	4.1.2.4	GO:0004139,GO:0009264	TIGR00126	1180474	1181155	1	122,184	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome activity modulation
gsyne_1366	Synechococcus_assembled_mapped	DNA repair protein RecO	recO		GO:0003677,GO:0006281,G	TIGR00613	1181144	1181939	1	132	fig|1129.58.1	Carbohydrates	Monosaccharides	Deoxyribose and Deoxynucleosic
gsyne_1367	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	1181973	1183311	1	141	fig|1129.58.1	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa
gsyne_1368	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1183339	1184509	1	90	fig|1129.58.peg.1367			
gsyne_1369	Synechococcus_assembled_mapped	orotidine 5'-phosphate decarboxylase	pyrF	4.1.1.23	GO:0004590,GO:0009220	TIGR01740	1184519	1185239	-1	126	fig|1129.58.peg.1368			
gsyne_137	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	110749	110944	1	856				
gsyne_1370	Synechococcus_assembled_mapped	tyrosine--tRNA ligase	tyrS	6.1.1.1	GO:0004831,GO:0005737,G	TIGR00234	1185755	1186997	-1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Tyr
gsyne_1371	Synechococcus_assembled_mapped	cupin domain protein				PF07883.6	1185339	1185759	1	157	fig|1129.58.peg.1370			
gsyne_1372	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08855.5	1187060	1187384	-1	156	fig|1129.58.peg.1372			
gsyne_1373	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	1187507	1188245	1	261	fig|1129.58.peg.1373			
gsyne_1374	Synechococcus_assembled_mapped	helix-hairpin-helix motif family protein				PF12836.2	1188277	1188967	1	185	fig|1129.58.peg.1374			
gsyne_1375	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1188986	1189139	-1	856				
gsyne_1376	Synechococcus_assembled_mapped	putative cyanobacteria-specific protein containing UvrC-like endo			GO:0004519	UniRef100_C	1189142	1189592	1	703	fig|1129.58.peg.1375			
gsyne_1377	Synechococcus_assembled_mapped	cytosol aminopeptidase family, N-terminal domain protein				PF02789.12	1189626	1190256	1	138	fig|1129.58.1	Protein Metabolism	Protein degradation	Aminopeptidases (EC 3.4.11.-)
gsyne_1378	Synechococcus_assembled_mapped	cytosol aminopeptidase family, catalytic domain protein				PF00883.16	1190263	1191118	1	138	fig|1129.58.1	Protein Metabolism	Protein degradation	Aminopeptidases (EC 3.4.11.-)
gsyne_1379	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1191384	1191594	-1	156	fig|1129.58.peg.1379			
gsyne_138	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	111185	112052	-1	156	fig|1129.58.peg.138			
gsyne_1380	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1191151	1191388	1	88	fig|1129.58.peg.1378			



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0.6201915	1.26515752	0.03251186	-2.5910674	0.39954811	-1.4672454	0.22083251	1.76594006
0.28471371	-14.24616	0.65750783	2.04366664	1	-5.3983786	0.52314247	-11.032486
0.21811348	-1.7968426	0.66160134	1.19811881	1	-1.1101947	0.59427299	-1.3301452
0.36481586	-2.3374932	1	1.0956926	1	-1.3813589	1	-1.5135447
0.798108	-1.2042584	0.41950093	-1.447193	0.53677183	1.30653048	0.13220598	1.89080179
0.69698171	-1.3074671	0.64044567	1.30582558	0.7209097	1.20423354	1	-1.0843624
0.20442523	1.62711048	0.51251086	-1.3228903	0.27074028	1.60006106	0.08369368	2.11670524
1	-1.1573822	1	1.09051291	0.65278643	2.78675278	0.65278643	2.55545142
0.23453522	-2.1584105	0.38051973	1.92176573	0.83971291	1.3623454	0.62427347	-1.4106303
0.89732479	-1.0789693	0.47138016	-1.6215334	0.89732479	-1.0747091	0.64812688	1.50881146
0.27198497	-1.523871	0.74662182	1.12861991	0.43984678	-1.3794499	0.25326565	-1.5568746
0.01422833	-2.8560728	0.28969734	-1.5595404	0.05761101	-2.2458124	0.38988126	-1.4400476
0.93272386	1.0796696	0.0028466	5.03092863	0.24912034	1.98668559	0.08049565	-2.5323225
0.0037619	-2.7140868	0.15704135	-1.6218557	0.03508096	-2.094715	0.4939487	-1.2915545

41	7.56662525	42	9.22332516	19	7.07977544	39	8.88008594	21	10.4666037	24	5.77222847	20	7.12896981	65	8.5727034
16	6.03404261	14	6.28255482	4	3.04576152	14	6.51404298	6	6.11093633	7	3.44033182	5	3.64197371	7	1.88656817
199	28.8889258	208	35.9303554	34	9.96562973	256	45.8513868	30	11.7616348	109	20.6214271	24	6.72927025	71	7.36584777
62	13.7893346	69	18.2608324	32	14.3697466	114	31.2817229	27	16.2174849	91	26.3758773	27	11.5982855	88	13.9868644
40	6.51563287	24	4.65187158	10	3.28885046	46	9.24461096	19	8.35830727	54	11.4631579	11	3.46072994	39	4.53991054
29	11.699728	23	11.0414336	2	1.62912825	30	14.9325238	8	8.71637429	20	10.5152999	6	4.67527787	30	8.64938233
45	6.00503279	37	5.87522434	21	5.65808774	57	9.38451686	20	7.20777105	47	8.17362351	6	1.54643807	57	5.43580412
15	8.26089167	7	4.58726225	0	0	8	5.43575468	2	2.97463567	3	2.15313284	2	2.12737512	3	1.18070933
3	1.76419043	3	2.09925561	1	1.18733076	2	1.45107011	1	1.58815294	2	1.53273863	1	1.13580197	1	0.42025248
27	2.6537822	8	0.93564556	12	2.38138861	19	2.30403624	11	2.91986193	14	1.79326078	12	2.27803908	28	1.96673396
4	1.26166346	11	4.12853602	1	0.63684104	8	3.11320495	6	5.11096493	7	2.87736843	1	0.60920287	10	2.25408146
16	5.3896303	14	5.61160236	6	4.08072902	19	7.89635723	14	12.7360615	7	3.07291774	6	3.90363007	16	3.85163433
20	3.40154363	12	2.4285506	4	1.37357872	9	1.88852506	15	6.88978115	6	1.32987617	4	1.31396698	20	2.43087216
15	4.1634894	7	2.31198017	7	3.92294083	12	4.10943054	6	4.49764914	16	5.78762107	7	3.75268971	21	4.16554253
31	2.18167971	24	2.00983498	15	2.13141526	31	2.6916909	20	3.80125857	20	1.83431195	7	0.95149333	40	2.01175627
34	3.23193241	18	2.03599037	11	2.11117168	17	1.99373057	19	4.87758753	10	1.23878876	7	1.28516771	19	1.29069322
2	0.86739363	2	1.03213401	0	0	1	0.5350821	2	2.34252559	2	1.13039474	0	0	1	0.3099362
15	2.66890346	7	1.48203857	2	0.71848733	7	1.53664604	10	4.8051807	5	1.15937922	1	0.3436529	9	1.14437982
1	0.80687779	1	0.96012466	0	0	1	0.99550158	0	0	1	1.05152999	1	1.55842596	0	0
56	5.09963707	30	3.25081577	25	4.59662171	38	4.26942149	27	6.64023002	35	4.15368146	21	3.69359223	62	4.03486497
94	33.6226808	115	48.9465611	107	77.2744236	95	41.9239585	55	53.1294464	93	43.351221	57	39.3783714	304	77.7077153
42	2.72887882	46	3.5564168	23	3.01724315	25	2.00405282	24	4.21128196	36	3.04825548	16	2.00785966	58	2.69307859
449	50.2528694	408	54.3368612	285	64.4031185	536	74.0139371	188	56.8251369	558	81.3884214	219	47.3409589	666	53.2690346
31	18.8696157	24	17.3833096	5	6.14495745	33	24.78275	6	9.86326565	9	7.13933521	3	3.52696401	10	4.34998175
4	3.01702131	3	2.69252349	0	0	1	0.93057757	0	0	1	0.98295195	0	0	1	0.53901948
11	7.06765177	2	1.52908742	1	1.29726879	7	5.54899957	1	1.73520414	5	4.18664719	3	3.72290646	6	2.75498844
2	1.65217834	1	0.98298477	0	0	0	0	0	0	0	0	0	0	0	0
5	3.69103671	4	3.51364768	0	0	7	6.37544632	4	7.9745552	2	1.92407616	0	0	1	0.52755098
10	4.50594091	11	5.89790861	3	2.72931876	24	13.342307	3	3.65068923	4	2.34887219	4	3.48115928	5	1.61005818
3	2.21462202	3	2.63523576	1	1.49047904	5	4.55389023	4	7.9745552	1	0.96203808	0	0	1	0.52755098
18	6.18340011	23	9.40161669	11	7.62948182	17	7.20506592	13	12.0605278	12	5.37217303	11	7.29837107	21	5.15537442
26	4.37907462	23	4.60953051	13	4.42078977	13	2.70138537	12	5.45831206	13	2.85342362	7	2.27711754	28	3.37018004
81	26.5127863	71	27.6534017	34	22.4696746	51	20.595613	15	13.2595788	52	22.1813308	17	10.7472583	63	14.7365891
267	77.8467557	267	92.6318587	102	60.0450127	233	83.8145409	59	46.45681	146	55.4748344	96	54.0603559	280	58.3409318
281	11.4162814	297	14.3580234	142	11.6480762	285	14.2855643	169	18.5427084	270	14.2953902	147	11.5349069	490	14.2265797
27	8.59435886	23	8.71158978	8	5.14146898	33	12.9597867	22	18.9121332	13	5.39270886	6	3.68875135	30	6.8242833
7	0.53144467	17	1.53577927	6	0.91972667	31	2.90372782	10	2.05035063	7	0.69258321	3	0.4399058	9	0.48830211
16	2.03345026	6	0.90737056	2	0.51320524	12	1.88160739	10	3.43227193	10	1.65625603	8	1.96373088	5	0.45411897
5	2.89131209	1	0.68808934	2	2.33508383	1	0.7134428	0	0	0	0	0	0	1	0.41324827
7	1.57707932	2	0.53617351	1	0.45488646	9	2.50168255	7	4.25913744	3	0.88082707	0	0	3	0.48301746
0	0	1	1.08645685	0	0	1	1.12648864	0	0	1	1.1898892	0	0	0	0
197	12.359967	185	13.8115581	96	12.1610152	199	15.4041719	100	16.9441272	240	19.6234892	52	6.30133896	261	11.7024735
33	3.71740125	21	2.81491093	18	4.09397814	28	3.89150619	24	7.30137847	25	3.6701128	14	3.04601437	40	3.22011636
24	2.73015699	10	1.35361837	4	0.91872151	13	1.82454225	21	6.45154589	19	2.81672132	7	1.53798759	11	0.89424215
62	6.53840788	43	5.39595894	58	12.3496835	60	7.80666896	49	13.9554716	81	11.1321549	31	6.3142304	118	8.89300221
74	3.92581825	60	3.78764773	36	3.85610174	36	2.35632485	36	5.15785451	59	4.07910029	30	3.07395946	60	2.2747611
47	3.34159839	28	2.36883215	25	3.58875589	35	3.07014321	22	4.22422648	44	4.07683349	16	2.19712512	65	3.30259885
234	59.2613455	250	75.3382486	87	44.4859036	360	112.484413	56	38.3011484	220	72.6092972	55	26.9027547	266	48.1419149
50	5.25693107	48	6.00514331	13	2.75964453	60	7.78301239	21	5.96279241	48	6.57684213	10	2.03067625	59	4.43302686
281	39.7938953	307	51.7330841	211	60.3309414	378	66.0444194	142	54.3083484	348	64.2248767	207	56.6185692	684	69.2233015
13	2.56275389	10	2.34575911	10	3.98025653	14	3.40506792	17	9.05066706	9	2.31217106	9	3.42676617	16	2.25408146
48	5.03140714	32	3.99133392	26	5.50261446	38	4.91434921	70	19.8159265	51	6.9667833	30	6.07362382	76	5.6930879
19	4.06925405	4	1.01939161	10	4.32422931	11	2.90661882	8	4.62721104	10	2.79109813	5	2.06828136	17	2.60193353
11	2.19340917	8	1.89817748	4	1.61040264	3	0.73804428	8	4.30809304	3	0.77958258	2	0.77025651	5	0.71249701
47	7.83990393	47	9.32890352	27	9.0933553	34	6.99722748	19	8.55922812	31	6.73889173	13	4.18826976	62	7.39078631
22	3.27599309	22	3.89818852	8	2.40523656	16	2.93950682	32	12.8688101	8	1.55247346	10	2.87606507	14	1.48982208
42	4.77777473	53	7.17417735	41	9.41689544	38	5.33327734	25	7.68041177	32	4.7439517	23	5.05338778	110	8.94242151
26	5.93479849	23	6.24712688	9	4.14784628	11	3.09784375	12	7.39744924	8	2.3797784	5	2.20435251	24	3.91498358
23	4.92593911	12	3.05817483	11	4.75665224	10	2.64238075	14	8.09761933	14	3.90753738	9	3.72290646	25	3.82637284
15	4.03438896	14	4.48058173	6	3.25825651	9	2.98650475	4	2.9054581	13	4.55662996	3	1.55842596	11	2.11429346
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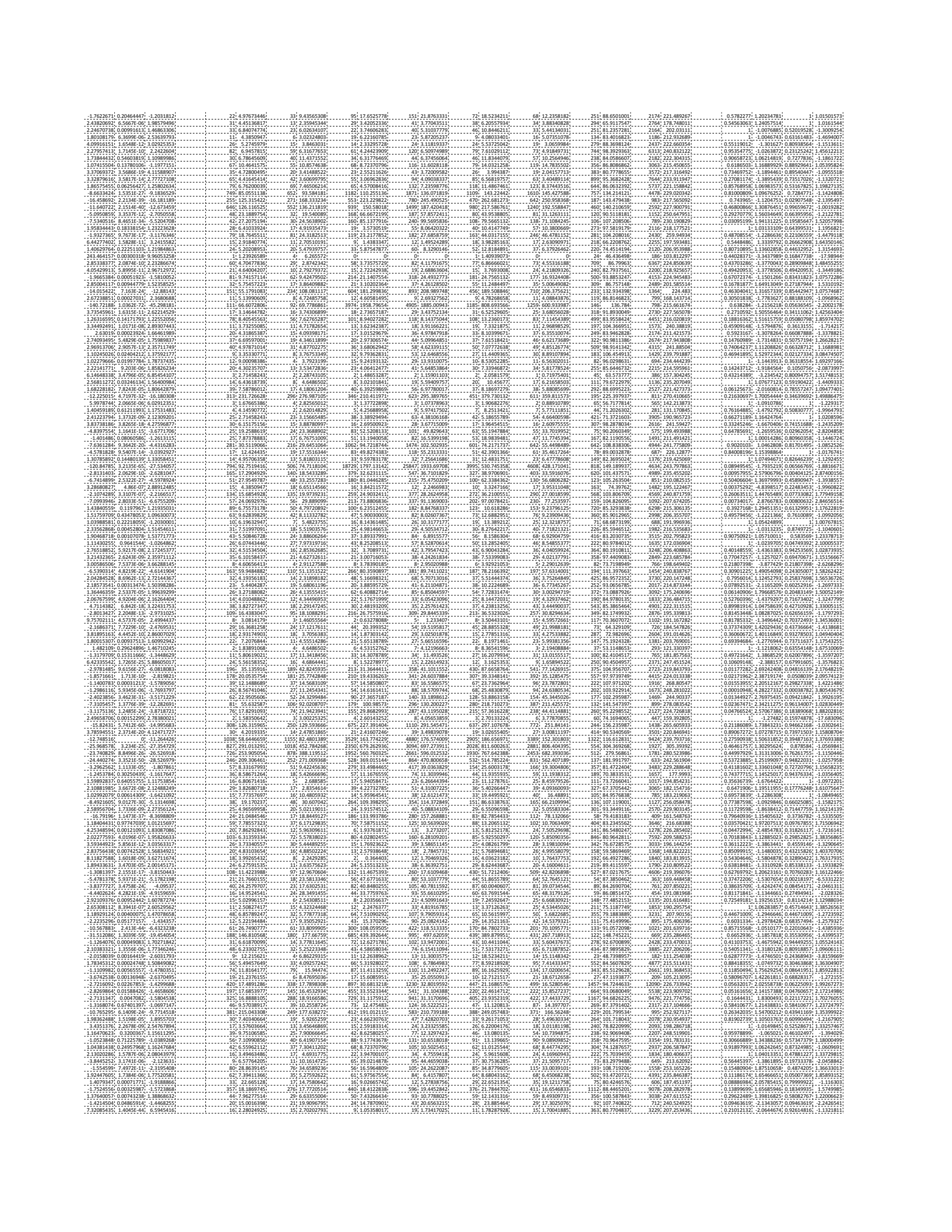
63	9.06984206	49	8.39411889	37	10.7549504	52	9.23627196	30	11.6640278	45	8.4427823	22	6.11730687	76	7.81913733
39	30.0696457	16	14.6792392	10	15.5672255	24	22.8301697	8	16.6579598	20	20.0959065	7	10.4241381	22	12.1219492
60	6.38571995	55	6.96532151	64	13.752641	79	10.3733708	41	11.7844846	84	11.6506943	40	8.22237009	130	9.88753522
7	3.19566073	8	4.34582739	4	3.68697447	2	1.12648864	1	1.23290821	6	3.5696676	1	0.881741	8	2.60998905
9	4.33696813	4	2.29363112	2	1.94590319	4	2.37814267	3	3.90420932	1	0.62799708	2	1.86145323	9	3.099362
18	1.80498096	10	1.1932185	4	0.80985566	24	2.96924172	5	1.35406104	10	1.30681473	7	1.3557405	19	1.36156943
51	5.29785328	41	5.06796338	19	3.9850233	49	6.2800055	14	3.92758782	27	3.65516862	16	3.21017084	46	3.41486592
23	3.00000803	11	1.70728933	9	2.37019787	9	1.44834253	17	5.98841129	15	2.54976257	9	2.26733401	24	2.23713347
35	6.29197449	30	6.41741351	24	8.71119356	20	4.4359138	12	5.82597038	25	5.85696757	8	2.77771259	39	5.01036759
48	4.95653501	30	3.68619288	36	7.50562659	35	4.45901751	37	10.3182675	32	4.30626568	12	2.39329701	68	5.01801467
52	5.93479849	40	5.43228424	15	3.45653856	47	6.61812073	16	4.93163282	45	6.69312676	19	4.18826976	76	6.198724
38	6.04788216	25	4.73455966	16	5.14146898	35	6.87261415	19	8.16660298	46	9.54094644	11	3.3813554	25	2.84345138
40	3.3441682	25	2.48706989	22	3.71362729	23	2.37241221	25	5.64463998	15	1.63430565	13	2.09918099	44	2.62885644
13	2.68478979	4	0.98298477	12	5.00375106	7	1.78360701	15	8.36616283	6	1.61484963	4	1.59553134	16	2.36141867
161	19.0000509	127	17.8341522	90	21.4446474	140	20.3840801	70	22.3097675	147	22.6078948	93	21.1977735	307	25.891269
41	10.1608968	35	10.3213401	27	13.5101279	74	22.6263289	21	14.0551536	42	13.5647369	20	9.57318803	78	13.8142992
36	10.1548522	43	14.4330934	18	10.2515875	58	20.185211	17	12.950548	59	21.6888747	19	10.351496	57	11.4903177
112	9.64248993	84	8.60538526	66	11.4726203	136	14.445889	74	17.205647	192	21.5420139	47	7.81533216	118	7.26004399
43	4.28711792	31	3.67771887	35	7.04551155	65	7.99547968	11	2.96181397	89	11.5638083	25	4.81410318	63	4.48873117
9	3.71740125	7	3.44044669	0	0	5	2.54801001	2	2.23097675	3	1.61484963	0	0	2	0.59035467
62	2.57005519	46	2.26896842	37	3.09670615	32	1.6365713	76	8.50809773	50	2.7010627	34	2.72212515	87	2.57724726
10	4.28342531	11	5.60665386	6	5.18907518	7	3.69933305	7	8.09761933	6	3.34931775	5	4.13656273	10	3.06109827
8	3.08406623	4	1.8349049	1	0.77836128	8	3.80502828	2	2.08224497	2	1.00479533	0	0	7	1.92849191
18	3.76218922	10	2.48706989	6	2.53201861	14	3.61019249	6	3.38678399	10	2.72384275	7	2.82582056	24	3.58480424
24	3.52838085	18	3.14888341	22	6.53031918	20	3.62767526	19	7.54372648	20	3.83184658	21	5.96296034	32	3.3620198
28	2.75988881	21	2.46304706	14	2.78617957	16	1.9457531	12	3.19435308	23	2.9544408	11	2.09413488	25	1.76100114
13	6.26450952	7	4.01385447	2	1.94590319	13	7.72896369	3	3.90420932	2	1.25599416	3	2.79217984	8	2.75498844
9	1.44565604	8	1.52908742	1	0.3243172	8	1.58542845	5	2.16900518	7	1.46532652	3	0.93072661	8	0.91832948
362	20.0316742	319	21.0048324	252	28.1550778	536	36.5938126	162	24.2098339	506	36.4899355	181	19.3448632	550	21.7499088
18	1.9701054	11	1.43261502	11	2.43084436	10	1.35036493	7	2.06910778	12	1.71163873	7	1.47976724	22	1.72078143
52	4.45476233	37	3.77174896	15	2.59453759	29	3.06516167	30	6.94081657	21	2.34452243	12	1.98555011	52	3.1835422
39	6.56861192	37	7.41533169	25	8.5015188	32	6.64956398	16	7.27774941	34	7.46280023	22	7.15665513	63	7.58290509
40	2.93410106	24	2.09481743	19	2.8139488	27	2.44350389	20	3.96198832	16	1.52949817	13	1.84177613	39	2.04439946
1	0.48188535	5	2.86703891	0	0	0	0	0	0	2	1.25599416	1	0.93072661	3	1.03312067
3	1.25406307	2	0.99482796	2	1.68801241	5	2.57870892	8	9.03142397	0	0	1	0.8073773	3	0.89620106
28	2.84891748	21	2.54250019	11	2.25975854	18	2.25958424	13	3.57217979	21	2.7845501	13	2.55472173	24	1.74509532
15	6.58779969	14	7.31639295	3	2.66022208	10	5.41855293	10	11.8608891	13	7.44057298	3	2.5447715	20	6.27718886
28	1.83298276	24	1.86952575	16	2.1147929	36	2.90761595	23	4.06627084	29	2.47407151	11	1.39082166	30	1.40348468
7	2.55652858	4	1.73833096	1	0.73739489	8	3.60476363	8	7.89061252	2	0.95191136	2	1.4107856	6	1.56599343
9	2.4782675	7	2.29363112	0	0	2	0.67946934	6	4.46195351	1	0.35885547	4	2.12737512	5	0.98392444
0	0	0	0	1	1.62912825	0	0	0	0	0	0	1	1.55842596	0	0
7	2.4046556	8	3.27012754	0	0	2	0.84765481	0	0	1	0.44768109	1	0.66348828	2	0.49098804
11	2.8695729	1	0.31041624	2	1.05342128	1	0.3218539	6	4.22711385	3	1.01990503	0	0	0	0
4	2.4782675	10	7.37238576	3	3.7528133	5	3.82201501	2	3.34646513	0	0	1	1.1966485	2	0.885532
2	1.3878298	0	0	5	7.00525149	3	2.56839409	2	3.74804095	0	0	0	0	2	0.99179584
9	4.52553196	5	2.99169277	0	0	10	6.20385045	1	1.35798585	1	0.6553013	2	1.94238598	3	1.07803896
3	1.85870063	5	3.68619288	0	0	4	3.05761201	1	1.67323257	0	0	0	0	1	0.442766
10	7.22828022	12	10.3213401	4	5.83770957	14	12.485249	4	7.80841864	13	12.245943	4	5.58435968	17	8.78152567
16	3.58149626	11	2.92992879	3	1.35585513	9	2.48554267	5	3.02261367	9	2.62543295	4	1.7293501	8	1.27973657
872	570.843201	848	660.565764	1591	2102.89719	2209	1784.14545	545	963.529394	2857	2437.387	607	767.480678	1755	821.038537
66	5.20436176	39	3.6593842	22	3.50262574	31	3.0159173	57	12.1385417	23	2.36355264	22	3.35061581	53	2.98665793
14	3.19566073	8	2.1729137	4	1.84348723	5	1.40811079	3	1.84936231	4	1.1898892	8	3.52696401	11	1.79436747
29	2.31837928	26	2.47331651	18	2.90540384	8	0.78906116	24	5.18162343	11	1.14602232	11	1.69846884	54	3.08507923
30	8.46237684	32	10.7409067	31	17.6555119	39	13.5728143	14	10.6651572	42	15.4395379	14	7.6274181	56	11.2887331
20	6.25148559	17	6.3229831	15	9.46655606	28	10.7980532	10	8.44153366	16	6.5175913	10	6.0371456	15	3.35066162
94	16.3070002	126	26.009777	72	25.2189054	252	53.9362758	50	23.4252559	178	40.2420528	78	26.1348033	218	27.0264366
108	21.53529	117	27.7608457	185	74.4811221	268	65.9319555	126	67.8524654	242	62.8863281	170	65.4718032	717	102.172071
31	2.88356058	19	2.10300763	12	2.25370021	21	2.41002126	21	5.27539275	9	1.09099761	13	2.33554989	28	1.86127906
3	1.60134208	1	0.63515939	0	0	0	0	1	1.44155421	1	0.69562753	0	0	0	0
46	3.62728244	31	2.90874129	23	3.661836	42	4.0860815	33	7.02757677	56	5.75473686	20	3.04601437	71	4.00099458
55	12.893689	60	16.7373082	19	8.99322826	62	17.9324812	11	6.96426527	47	14.3590683	27	12.2252199	86	14.407845
39	2.09788226	24	1.53619945	11	1.19469405	19	1.26096867	13	1.88854776	17	1.19173399	18	1.87011115	37	1.42234287
21	3.19566073	20	3.62152283	9	2.76523085	12	2.25297727	7	2.87678581	8	1.58651894	5	1.46956834	22	2.39248997
276	48.8572736	306	64.4557155	198	70.7673365	214	46.7377836	126	60.2363723	184	42.447476	163	55.7296303	650	82.2279714
24	3.6682726	33	6.00183651	13	4.01181803	21	3.96007899	12	4.95335808	19	3.78458151	13	3.83770974	35	3.82300159
19	2.48761946	12	1.86952575	7	1.85044379	12	1.93841063	7	2.47512138	5	0.85312811	2	0.50575333	21	1.96487855
27	2.10041506	21	1.94392952	14	2.19895787	19	1.82359819	31	6.51285142	19	1.92623319	9	1.35226647	41	2.27935143
47	4.18128209	33	3.49337664	23	4.13130216	33	3.62209423	20	4.8051807	44	5.10126858	15	2.57739678	39	2.4794896
14	2.02391846	12	2.06426801	20	5.83770957	13	2.31868911	4	1.56168373	9	1.69559211	8	2.23374387	20	2.06624133
2	1.06756139	2	1.27031878	0	0	1	0.65856259	2	2.88310842	0	0	0	0	0	0
30	2.51418442	25	2.49307731	9	1.52288076	16	1.65436012	15	3.39496463	12	1.3106026	10	1.61865498	14	0.83847474
5	1.23913375	6	1.76937258	0	0	5	1.528806	1	0.66929303	4	1.2918797	1	0.4786594	3	0.5313192
39	12.529019	17	6.49862152	8	5.18907518	18	7.13442802	4	3.47040828	13	5.44264135	14	8.68678173	21	4.82122978
18	2.53871305	15	2.51740002	7	1.99336424	8	1.39208352	11	4.18988317	7	1.28662816	8	2.17926232	12	1.20950712
21	3.16787237	16	2.87202506	15	4.56864227	11	2.04727065	10	4.07395755	9	1.76931351	16	4.66172634	33	3.55752856
3	2.04092618	2	1.61903374	0	0	1	0.83934447	1	1.83727497	0	0	0	0	4	1.94469773
17	3.93218444	9	2.47712161	4	1.86806706	2	0.57075424	7	4.37271444	4	1.20575439	3	1.34024632	7	1.15709515
10	1.65217834	10	1.96596954	8	2.66866723	6	1.2230448	6	2.6771721	2	0.43062657	3	0.9573188	14	1.65299307
51	6.20871227	34	4.92527105	10	2.45798298	51	7.66012272	19	6.24673491	42	6.66337953	12	2.82157121	36	3.13198686
639	316.722587	560	330.282882	176	176.132037	576	352.236903	70	93.7010237	398	257.084061	81	77.542823	304	107.680691
20	2.40108962	9	1.28570326	5	1.21198123	6	0.88871768	35	11.3478748	13	2.03392825	9	2.08688874	15	1.28693232
151	66.3171835	137	71.5961311	53	46.9972568	116	62.855214	23	27.2800449	78	44.6434379	22	18.6616577	72	22.5978799

gsyne_1381	Synechococcus_assembled_mapped	peptide-methionine (S)-S-oxide reducta	msrA	1.8.4.11	GO:0000317,GO:0006979,G(	TIGR00401	1191744	1192377	-1	140,149	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Peptide methionine sulfoxide red
gsyne_1382	Synechococcus_assembled_mapped	lipid-A-disaccharide synthase	lpxB	2.4.1.182	GO:0008915,GO:0009245	TIGR00215	1192373	1193564	-1	90	fig|1129.58.peg.1381			
gsyne_1383	Synechococcus_assembled_mapped	acyl-[acyl-carrier-protein]-UDP-N-acety	lpxA	2.3.1.129	GO:0008780,GO:0009245	TIGR01852	1193560	1194385	-1	90	fig|1129.58.peg.1382			
gsyne_1384	Synechococcus_assembled_mapped	beta-hydroxyacyl-(acyl-carrier-protein)	fabZ	4.2.1.-	GO:0006633,GO:0016836	TIGR01750	1194411	1194840	-1	176	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_1385	Synechococcus_assembled_mapped	UDP-3-O-[3-hydroxymyristoyl] N-acetyl	lpxC	3.5.1.-	GO:0008759,GO:0009245	TIGR00325	1194875	1195718	-1	90	fig|1129.58.peg.1384			
gsyne_1386	Synechococcus_assembled_mapped	tlr1789 protein			GO:0019867	UniRef100_C	1195726	1197745	-1	185	fig|1129.58.peg.1385			
gsyne_1387	Synechococcus_assembled_mapped	phosphoribosylaminoimidazolesuccino(	purC	6.3.2.6	GO:0004639,GO:0009152	TIGR00081	1197970	1198726	-1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_1388	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1198722	1199817	-1	156	fig|1129.58.peg.1387			
gsyne_1389	Synechococcus_assembled_mapped	phosphoribosylamine--glycine ligase	purD	6.3.4.13	GO:0004637,GO:0006189,G(	TIGR00877	1199920	1201186	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_139	Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	112060	114577	-1	185	fig|1129.58.peg.139			
gsyne_1390	Synechococcus_assembled_mapped	HAMP domain protein				PF00672.20	1201182	1203180	1	129	fig|1129.58.peg.1389			
gsyne_1391	Synechococcus_assembled_mapped	circadian clock protein KaiC	kaiC	2.7.11.1	GO:0004674,GO:0007623,G(	TIGR02655	1203190	1204696	-1	92	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_1392	Synechococcus_assembled_mapped	circadian clock protein KaiB	kaiB		GO:0007623	TIGR02654	1204812	1205160	-1	92	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_1393	Synechococcus_assembled_mapped	circadian clock protein kaiA	kaiA		GO:0007623,GO:0042802,G(	UniRef100_C	1205160	1206036	-1	92,141	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_1394	Synechococcus_assembled_mapped	ribosomal protein L21	rplU		GO:0000311,GO:0003735,G(	TIGR00061	1206191	1206545	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_1395	Synechococcus_assembled_mapped	ribosomal protein L27	rpmA		GO:0000315,GO:0003735,G(	TIGR00062	1206584	1206848	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_1396	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	1206932	1207679	-1	703	fig|1129.58.peg.1395			
gsyne_1397	Synechococcus_assembled_mapped	conserved hypothetical integral membrane family protein				TIGR00697	1207685	1208405	-1	156	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth
gsyne_1398	Synechococcus_assembled_mapped	tRNA pseudouridine(55) synthase	truB	5.4.99.25	GO:0004730,GO:0006400,G(	TIGR00431	1208550	1209429	1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA pseudouridine syntheses
gsyne_1399	Synechococcus_assembled_mapped	glucosamine-6-phosphate isomerases/6-phosphogluconolactonase family protein				PF01182.15	1210254	1211043	-1	703	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular pol	Sialic Acid Metabolism
gsyne_14	Synechococcus_assembled_mapped	methyltransferase type 11 domain protein			GO:0008152,GO:0008168,G(	UniRef100_A	9535	9673	1	92,703				
gsyne_140	Synechococcus_assembled_mapped	type II secretion system (T2SS), E, N-terminal domain protein				PF05157.10	114573	116754	-1	157	fig|1129.58.peg.140			
gsyne_1400	Synechococcus_assembled_mapped	DNA-binding regulatory , YebC/PmpR family protein			GO:0003677,GO:0005737,G(	TIGR01033	1209488	1210262	1	156	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metab(
gsyne_1401	Synechococcus_assembled_mapped	spoIID/LytB domain protein			GO:0003674,GO:0005575,G(	TIGR02669	1211039	1212461	-1	157	fig|1129.58.peg.1400			
gsyne_1402	Synechococcus_assembled_mapped	ribonuclease Z	rnz	3.1.26.11	GO:0016891,GO:0042779	TIGR02651	1212578	1213529	1	166	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA processing
gsyne_1403	Synechococcus_assembled_mapped	cytochrome c-550	psbV		GO:0009523,GO:0009538,G(	TIGR03045	1213678	1214146	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_1404	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1214206	1214572	-1	156	fig|1129.58.peg.1403			
gsyne_1405	Synechococcus_assembled_mapped	ferredoxin	petF		GO:0006810,GO:0009055,G(	UniRef100_P	1214706	1215006	-1	92,141	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_1406	Synechococcus_assembled_mapped	ribosomal protein L11 methyltransferas	prmA	2.1.1.-	GO:0006464,GO:0008757	TIGR00406	1215187	1216111	-1	158	fig|1129.58.peg.1405			
gsyne_1407	Synechococcus_assembled_mapped	phosphoglycerate dehydrogenase	serA	1.1.1.95	GO:0004617,GO:0006564	TIGR01327	1216129	1217716	-1	75	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine and Serine Utilization
gsyne_1408	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1217813	1218317	1	156	fig|1129.58.peg.1407			
gsyne_1409	Synechococcus_assembled_mapped	photosystem II S4 domain protein			GO:0003674,GO:0015979,G(	TIGR03069	1218326	1219118	1	164	fig|1129.58.peg.1408			
gsyne_141	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	116752	117697	1	856	fig|1129.58.peg.141			
gsyne_1411	Synechococcus_assembled_mapped	UDP-N-acetylmuramoylalanine--D-gluta	murD	6.3.2.9	GO:0008764,GO:0009252	TIGR01087	1219254	1220628	1	89	fig|1129.58.peg.1409			
gsyne_1412	Synechococcus_assembled_mapped	EVE domain protein				PF01878.13	1220686	1221145	1	157	fig|1129.58.peg.1410			
gsyne_1413	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF10929.3	1221916	1222144	-1	156	fig|1129.58.peg.1412			
gsyne_1414	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1221141	1221936	1	88	fig|1129.58.peg.1411			
gsyne_1415	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1222272	1222461	1	856	fig|1129.58.peg.1413			
gsyne_1416	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF08848.6	1223359	1223731	-1	156				
gsyne_1417	Synechococcus_assembled_mapped	NAD binding domain of 6-phosphogluconate dehydrogenase family protein				PF03446.10	1222518	1223397	1	157	fig|1129.58.peg.1414			
gsyne_1418	Synechococcus_assembled_mapped	RNA polymerase Rpb6 family protein				PF01192.17	1223742	1223973	-1	135	fig|1129.58.peg.1415			
gsyne_1419	Synechococcus_assembled_mapped	putative ribosomal protein L36			GO:0005840	UniRef100_C	1223976	1224282	-1	158	fig|1129.58.peg.1416			
gsyne_142	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	118284	118449	-1	88				
gsyne_1420	Synechococcus_assembled_mapped	hsp70 family protein				PF00012.15	1224376	1225951	1	95	fig|1129.58.p	Protein Metabolism	Protein folding	Protein chaperones
gsyne_1421	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_D	1226033	1226867	1	141	fig|1129.58.peg.1418			
gsyne_1422	Synechococcus_assembled_mapped	ferredoxin-thioredoxin reductase, varia	ftrV		GO:0005515,GO:0009536,G(	UniRef100_C	1226907	1227129	1	92,141,703	fig|1129.58.peg.1419			
gsyne_1423	Synechococcus_assembled_mapped	phosphoribosyl transferase domain protein				PF00156.22	1227137	1227680	-1	703	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	pyrimidine conversions
gsyne_1424	Synechococcus_assembled_mapped	2,3-bisphosphoglycerate-independent (	gpmI		GO:0006096,GO:0046537	TIGR01307	1227925	1229500	1	116	fig|1129.58.peg.1421			
gsyne_1425	Synechococcus_assembled_mapped	preprotein translocase, SecG subunit	secG		GO:0005887,GO:0015450,G(	TIGR00810	1229522	1229756	1	97	fig|1129.58.peg.1422			
gsyne_1426	Synechococcus_assembled_mapped	methionine-R-sulfoxide reductase	msrB	1.8.4.-	GO:0000318,GO:0006979,G(	TIGR00357	1229790	1230273	1	140,149	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Peptide methionine sulfoxide red
gsyne_1427	Synechococcus_assembled_mapped	ammonium transporter family protein	amt		GO:0008519,GO:0015696	TIGR00836	1230295	1231621	-1	145	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation
gsyne_1428	Synechococcus_assembled_mapped	chaperonin GroL	groL		GO:0005515,GO:0006457,G(	TIGR02348	1231892	1233524	-1	95	fig|1129.58.p	Protein Metabolism	Protein folding	GroEL GroES
gsyne_1429	Synechococcus_assembled_mapped	10 kDa chaperonin	groS		GO:0006457,GO:0005524,G(	UniRef100_C	1233583	1233895	-1	92,141,149	fig|1129.58.p	Protein Metabolism	Protein folding	GroEL GroES
gsyne_143	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	117703	118288	1	264,710	fig|1129.58.peg.142			
gsyne_1430	Synechococcus_assembled_mapped	ATP synthase F1, beta subunit	atpD	3.6.3.14	GO:0000275,GO:0015986,G(	TIGR01039	1234177	1235638	1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1431	Synechococcus_assembled_mapped	ATP synthase F1, epsilon subunit	atpC	3.6.3.14	GO:0000275,GO:0015986,G(	TIGR01216	1235654	1236059	1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1432	Synechococcus_assembled_mapped	FHA domain protein				PF00498.21	1237227	1239480	-1	157	fig|1129.58.p	Membrane Transport	Protein and nucleoprotein sec(	Type IV pilus
gsyne_1433	Synechococcus_assembled_mapped	rhomboid family protein				PF01694.17	1236134	1237253	1	140	fig|1129.58.peg.1429			
gsyne_1434	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1239557	1239833	1	156	fig|1129.58.peg.1431			
gsyne_1435	Synechococcus_assembled_mapped	FHA domain protein				PF00498.21	1239829	1240534	1	157	fig|1129.58.peg.1432			
gsyne_1436	Synechococcus_assembled_mapped	tyrosine kinase family protein				PF07714.12	1240530	1241865	1	703	fig|1129.58.peg.1433			
gsyne_1437	Synechococcus_assembled_mapped	von Willebrand factor type A domain protein				PF00092.23	1241868	1242600	1	157	fig|1129.58.peg.1434			
gsyne_1438	Synechococcus_assembled_mapped	phosphatase 2C family protein				PF13672.1	1242593	1243805	1	703	fig|1129.58.peg.1435			
gsyne_1439	Synechococcus_assembled_mapped	putative serine/threonine kinase			GO:0016310,GO:0016301	UniRef100_A	1243801	1244782	1	92,703	fig|1129.58.peg.1436			
gsyne_144	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	118677	118974	-1	156	fig|1129.58.peg.143			
gsyne_1440	Synechococcus_assembled_mapped	putative 30S ribosomal PSRP-3 domain protein			GO:0005840,GO:0006412,G(	UniRef100_C	1244863	1245328	-1	92	fig|1129.58.peg.1437			
gsyne_1441	Synechococcus_assembled_mapped	aminopeptidase P, N-terminal domain protein				PF05195.11	1246159	1247464	-1	138	fig|1129.58.p	Protein Metabolism	Protein degradation	Aminopeptidases (EC 3.4.11.-)
gsyne_1442	Synechococcus_assembled_mapped	putative imidazoleglycerol-phosphate dehydratase			GO:0016829,GO:0004424	UniRef100_C	1245440	1246163	1	703	fig|1129.58.peg.1438			
gsyne_1443	Synechococcus_assembled_mapped	small GTP-binding domain protein			GO:0005525	TIGR00231	1247508	1248867	1	157	fig|1129.58.peg.1440			
gsyne_1444	Synechococcus_assembled_mapped	cytidylyltransferase family protein				PF01467.21	1248863	1249460	1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	NAD and NADP	NAD and NADP cofactor biosynth
gsyne_1445	Synechococcus_assembled_mapped	NAD+ synthetase	nadE	6.3.1.5	GO:0005737,GO:0008795,G(	TIGR00552	1249463	1251161	1	163	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	NAD and NADP	NAD and NADP cofactor biosynth
gsyne_1446	Synechococcus_assembled_mapped	alanine dehydrogenase	ald	1.4.1.1	GO:0000286,GO:0005737,G(	TIGR00518	1251222	1252356	1	109	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pyruvate Alanine Serine Intercon
gsyne_1447	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1252732	1253176	-1	156	fig|1129.58.p	Miscellaneous	Miscellaneous - no subcategor	Broadly distributed proteins not ir
gsyne_1448	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1252440	1252743	1	856	fig|1129.58.peg.1444			
gsyne_1449	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11805.3	1253175	1254225	-1	156	fig|1129.58.peg.1446			
gsyne_145	Synechococcus_assembled_mapped	prokaryotic cytochrome b561 family protein				PF01292.15	119214	119736	-1	112	fig|1129.58.peg.145			
gsyne_1450	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1254224	1254410	-1	156	fig|1129.58.peg.1447			
gsyne_1451	Synechococcus_assembled_mapped	2Fe-2S iron-sulfur cluster binding domain protein				PF00111.22	1254430	1254754	-1	112	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_1452	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR02466	1254786	1255524	-1	156	fig|1129.58.peg.1449			
gsyne_1453	Synechococcus_assembled_mapped	ATP synthase F1, gamma subunit	atpG	3.6.3.14	GO:0000275,GO:0015986,G(	TIGR01146	1255700	1256654	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1454	Synechococcus_assembled_mapped	ATP synthase F1, alpha subunit	atpA	3.6.3.14	GO:0000275,GO:0015986,G(	TIGR00962	1256684	1258202	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1455	Synechococcus_assembled_mapped	ATP synthase F1, delta subunit	atpH	3.6.3.14	GO:0000275,GO:0015986,G(	TIGR01145	1258254	1258803	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1456	Synechococcus_assembled_mapped	ATP synthase B/B' CF family protein				PF00430.13	1258802	1259321	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1457	Synechococcus_assembled_mapped	ATP synthase B/B' CF family protein				PF00430.13	1259317	1259779	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1458	Synechococcus_assembled_mapped	ATP synthase F0, C subunit	atpE	3.6.3.14	GO:0000276,GO:0015986,G(	TIGR01260	1259884	1260133	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1459	Synechococcus_assembled_mapped	ATP synthase F0, A subunit	atpB	3.6.3.14	GO:0000276,GO:0015986,G(	TIGR01131	1260303	1261032	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_146	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	118998	119214	1	856	fig|1129.58.peg.144			
gsyne_1460	Synechococcus_assembled_mapped	ATP synthase I chain family protein				PF03899.10	1261082	1261499	-1	111	fig|1129.58.p	Respiration	ATP synthases	F0F1-type ATP synthase
gsyne_1461	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	1261582	1262803	-1	703	fig|1129.58.peg.1458			
gsyne_1462	Synechococcus_assembled_mapped	phycobiliprotein ApcE	apcE	4.-.-.-	GO:0006810,GO:0022900,G(	UniRef100_P	1262956	1265983	1	92,703	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1463	Synechococcus_assembled_mapped	allophycocyanin subunit alpha 1	apcA1		GO:0006810,GO:0022900,G(	UniRef100_P	1266405	1266891	1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1464	Synechococcus_assembled_mapped	allophycocyanin, beta subunit	apcB		GO:0009055,GO:0015979,G(	TIGR01337	1266932	1267421	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1465	Synechococcus_assembled_mapped	phycobilisome 7.8 kDa linker polypepti(	apcC		GO:0030089,GO:0015979	UniRef100_P	1267454	1267655	1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1466	Synechococcus_assembled_mapped	cell cycle family protein				PF01098.14	1267812	1268982	1	93,705	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1467	Synechococcus_assembled_mapped	cytochrome C biogenesis transmembrane region family protein				PF02683.10	1269007	1269724	1	88	fig|1129.58.p	Respiration	Respiration - no subcategory	Biogenesis of c-type cytochrome:
gsyne_1468	Synechococcus_assembled_mapped	7-cyano-7-deazaguanine reductase	queF	1.7.1.13	GO:0033739	TIGR03139	1271025	1271427	-1	703	fig|1129.58.peg.1466			
gsyne_1469	Synechococcus_assembled_mapped	resB-like family protein				PF05140.9	1269742	1271038	1	185	fig|1129.58.p	Respiration	Respiration - no subcategory	Biogenesis of c-type cytochrome:
gsyne_147	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	119779	120109	-1	856	fig|1129.58.peg.146			
gsyne_1470	Synechococcus_assembled_mapped	nitrogen regulatory protein P-II	glnB		GO:0006355,GO:0000166,G(	UniRef100_C	1271615	1271954	1	92,141	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation
gsyne_1471	Synechococcus_assembled_mapped	hemolysin TlyA family protein				TIGR00478	1271981	1272842	-1	157	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_1472	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1272961	1273156	1	156	fig|1129.58.peg.1469			
gsyne_1473	Synechococcus_assembled_mapped	adenylosuccinate lyase	purB	4.3.2.2	GO:0004018,GO:0009152	TIGR00928	1273230	1274526	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_1474	Synechococcus_assembled_mapped	putative SPOUT methyltransferase family protein				PF02590.12	1274536	1274971	-1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_1475	Synechococcus_assembled_mapped	helicase conserved C-terminal domain protein				PF00271.26	1275125	1277915	-1	703	fig|1129.58.peg.1473			
gsyne_1476	Synechococcus_assembled_mapped	aminotransferase class-III family protein				PF00202.16	1277980	1279171	1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	Biotin	Biotin biosynthesis
gsyne_1477	Synechococcus_assembled_mapped	alpha/beta hydrolase family protein				PF12697.2	1279167	1279875	1	703	fig|1129.58.peg.1475			
gsyne_1478	Synechococcus_assembled_mapped	putative sAM dependent methyltransferase			GO:0008168,GO:0016740,G(	UniRef100_B	1279861	1280632	1	92,703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	Biotin	Biotin biosynthesis Experimental
gsyne_1479	Synechococcus_assembled_mapped	dethiobiotin synthase	bioD	6.3.3.3	GO:0004141,GO:0009102	TIGR00347	1280628	1281282	1	77	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr(	Biotin	Biotin biosynthesis
gsyne_148	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	120170	121787	-1	88	fig|1129.58.peg.147			
gsyne_1480	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1281295	1281460	1	856	fig|1129.58.peg.1478			
gsyne_1481	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1281468	1281750	-1	156	fig|1129.58.peg.1479			
gsyne_1482	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11341.3	1281797	1281980	-1	156	fig|1129.58.peg.1480			
gsyne_1483	Synechococcus_assembled_mapped	dnaJ domain protein				PF00226.26	1282005	1282515	-1	95				
gsyne_1484	Synechococcus_assembled_mapped	16S rRNA (guanine(527)-N(7))-methyltr	gidB	2.1.1.170	GO:0005575,GO:0008168,G(	TIGR00138	1282572	1283322	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_1485	Synechococcus_assembled_mapped	aldo/keto reductase family protein				PF00248.16	1283329	1284526	-1	703	fig|1129.58.peg.1482			
gsyne_1486	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF06902.6	1284525	1284918	-1	156	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_1487	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF06868.6	1284914	1285304	-1	156	fig|1129.58.peg.1484			
gsyne_1488	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11211.3	1285303	1285522	-1	156	fig|1129.58.peg.1485			
gsyne_1489	Synechococcus_assembled_mapped	HEAT repeats family protein				PF13646.1	1285582	1286383	-1	185	fig|1129.58.peg.1486			
gsyne_149	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	121869	123186	-1	699	fig|1129.58.peg.148			
gsyne_1490	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1286420	1286546	-1	88	fig|1129.58.peg.1487			
gsyne_1491	Synechococcus_assembled_mapped	sodium:solute symporter family protein				PF00474.12	1286569	1288312	-1	145	fig|1129.58.peg.1488			
gsyne_1492	Synechococcus_assembled_mapped	23S rRNA m2A2503 methyltransferase	rlmN	2.1.1.-	GO:0008757,GO:0016433,G(	TIGR00048	1288359	1289430	-1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_1493	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	1289426	1289579	-1	185	fig|1129.58.peg.1490			
gsyne_1494	Synechococcus_assembled_mapped	DNA-directed RNA polymerase, beta'' subunit		2.7.7.6		TIGR02388	1289616	1293723	-1	135	fig|1129.58.peg.1491			
gsyne_1495	Synechococcus_assembled_mapped	DNA-directed RNA polymerase, gamma	rpoC1	2.7.7.6		TIGR02387	1293769	1295674	-1	135	fig|1129.58.peg.1492			
gsyne_1496	Synechococcus_assembled_mapped	DNA-directed RNA polymerase, beta su	rpoB	2.7.7.6	GO:0000345,GO:0003899,G(	TIGR02013	1295754	1299045	-1	135	fig|1129.58.peg.1493			
gsyne_1497	Synechococcus_assembled_mapped	hydrolase, TatD family protein			GO:0008152,GO:0016787	TIGR00010	1299377	1300199	-1	703	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate(	YcfH
gsyne_1498	Synechococcus_assembled_mapped	ribosomal protein S20	rpsT		GO:0000312,GO:0003735,G(	TIGR00029	1300252	1300555	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_1499	Synechococcus_assembled_mapped	ribose 5-phosphate isomerase A	rpiA	5.3.1.6	GO:0004751,GO:0006098	TIGR00021	1301998	1302691	-1	117	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway
gsyne_15	Synechococcus_assembled_mapped	tryptophan synthase, alpha subunit	trpA	4.2.1.20	GO:0000162,GO:0004834	TIGR00262	9773	10586	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn
gsyne_150	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein				PF00486.23	123200	123884	-1	261	fig|1129.58.peg.149			
gsyne_1500	Synechococcus_assembled_mapped	histidinol dehydrogenase	hisD	1.1.1.23	GO:0000105,GO:0004399	TIGR00069	1300655	1302002	1	161	fig|1129.58.p	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_1501	Synechococcus_assembled_mapped	putative serine protease HhoA			GO:0004252,GO:0006508,G(	UniRef100_P	1302743	1303838	-1	189,703	fig|1129.58.peg.1498			
gsyne_1502	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	1303864	1304647	-1	703	fig|1129.58.peg.1499			
gsyne_1503	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1304744	1304978	1	156	fig|1129.58.peg.1500			
gsyne_1504	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF02576.12	1305150	1305624	1	156	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors bacterial
gsyne_1505	Synechococcus_assembled_mapped	transcription termination factor NusA	nusA		GO:0003715,GO:0006353	TIGR01953	1305676	1307110	1	165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors bacterial
gsyne_1506	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04296.8	1307136	1307385	1	156	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors bacterial
gsyne_1507	Synechococcus_assembled_mapped	translation initiation factor IF-2	infB		GO:0003743,GO:0005737,G(	TIGR00487	1307449	1310806	1	169	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation initiation factors bacte
gsyne_1508	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1310822	1311767	1	156	fig|1129.58.peg.1507			
gsyne_151	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF07862.6	123993	124221	-1	156	fig|1129.58.peg.150			
gsyne_1510	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1312339	1313539	1	856	fig|1129.58.peg.1508			



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0.38360433	-1.4141403	0.6700464	1.16714313	0.29548339	-1.4948879	0.14013767	-1.7447481
1	-1.0263429	0.04749392	2.15039467	0.95088824	-1.0023169	0.06216711	-2.1553768
0.81738106	-1.0891309	0.32511817	1.47761778	0.59729303	1.31879312	0.70650384	-1.1204318
0.88623073	-1.1037356	0.45128927	1.29632169	0.94014278	1.01990244	0.54526521	-1.2710252
0.04412794	-8.5575821	1	1.476087	1	-2.2070248	0.64758405	-3.2577607
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0.04124596	-2.2776849	0.29309256	1.66690191	0.88148637	-1.0761457	0.18035969	-1.7938293
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1	1.0345687	0.41174059	1.81575728	0.65847498	1.3962996	0.85421763	-1.3004066
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1	-1.026151	0.94934185	1.0795124	0.83471813	-1.1008416	0.68667143	-1.1883721
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26	3.21028246	16	2.35076784	4	0.99718882	21	3.19906737	13	4.3349228	11	1.77001312	8	1.90782395	21	1.85299935
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48	14.1135234	39	13.6451614	13	7.71764994	101	36.6395202	13	10.3229941	39	14.9442017	25	14.1975246	127	26.6860321
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25	1.65217834	23	1.80869197	19	2.53523387	21	1.71226273	17	3.03412839	16	1.37800502	12	1.53171008	30	1.4168512
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25	11.7215355	25	13.9477568	9	8.51990046	21	12.1478099	1	1.26623005	12	7.33229021	10	9.05571841	12	4.02079395
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14	3.01702131	14	3.59003133	6	2.61065273	17	4.51994819	3	1.74598181	15	4.21265121	10	4.16225566	23	3.542128
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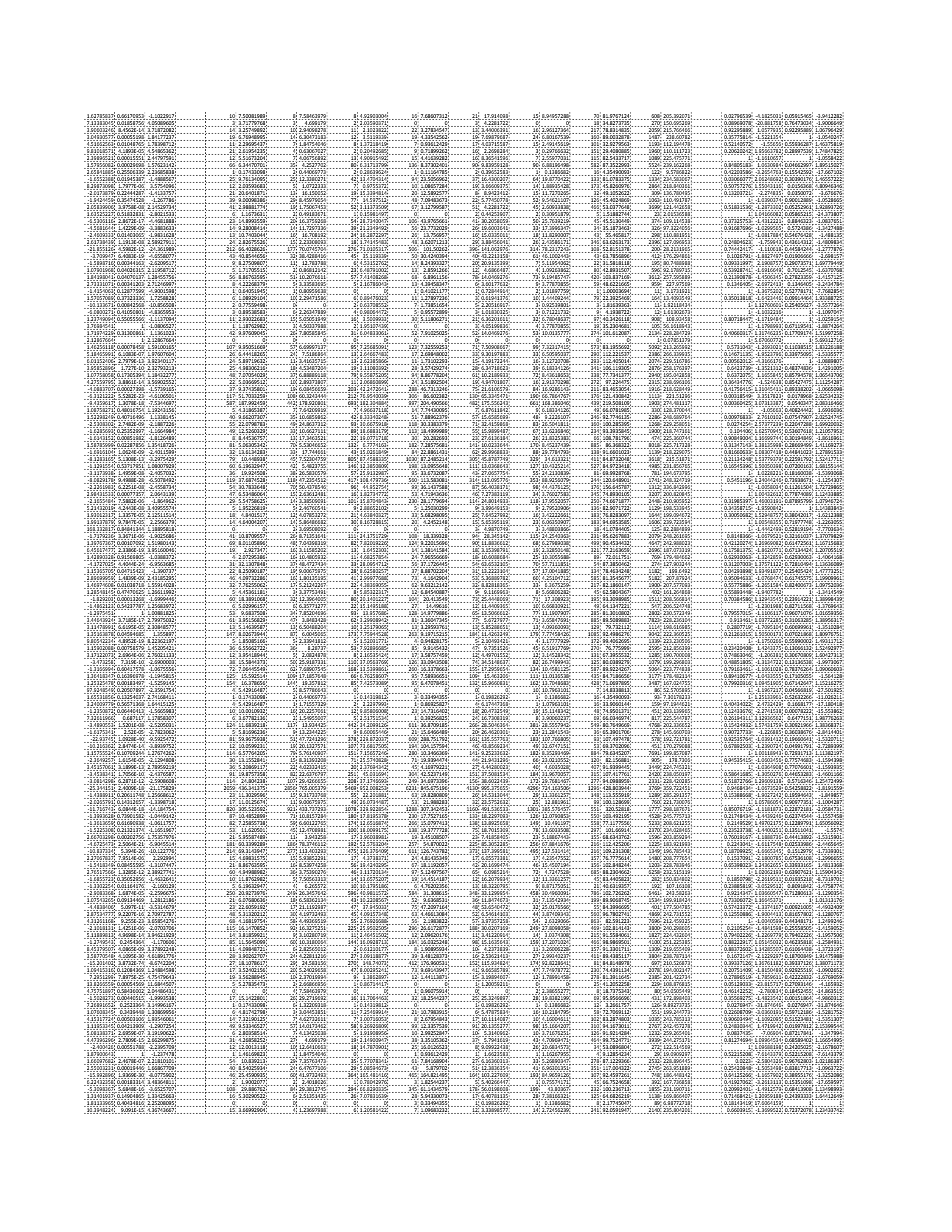
57	14.6493146	58	17.737414	87	45.144954	162	51.3678817	41	28.4573479	212	71.0055363	48	23.8266013	153	28.1008821
89	4.11174608	54	2.96858782	58	5.41018091	72	4.1039586	44	5.48980698	71	4.27472845	43	3.83692356	111	3.66475826
64	5.95315732	46	5.09149215	19	3.56835867	49	5.62338294	29	7.28506618	39	4.72765629	18	3.23383832	37	2.45954732
10	3.77127663	8	3.59003133	5	3.8072019	9	4.18759906	2	2.03697878	11	5.40623572	3	2.18518422	12	3.23411687
31	4.57688552	19	3.3379653	11	3.27905389	25	4.55389023	16	6.37964416	14	2.69370662	11	3.13674672	29	3.05979568
43	3.35262255	25	2.31940226	20	3.14842764	32	3.07822512	17	3.57958967	42	4.26755767	13	1.95766317	26	1.44869055
26	3.69708759	28	4.73766429	15	4.30650706	24	4.21048211	44	16.8969059	30	5.5593184	17	4.66889088	23	2.3372238
32	2.74817782	17	1.73725526	8	1.38717851	17	1.80126648	18	4.17479808	15	1.67880407	7	1.16110449	34	2.08669917
35	3.71361185	21	2.65135341	14	2.99919024	22	2.8799526	21	6.01749693	22	3.04204089	14	2.86902883	27	2.04728499
8	2.80369657	4	1.66809536	2	1.41520232	0	0	1	0.94647499	2	0.9134503	0	0	1	0.2504535
163	36.4864932	113	30.0983594	101	45.6471226	206	56.8913099	57	34.4577958	273	79.6381327	87	37.6133646	437	69.90561
32	2.55233067	14	1.32872424	19	3.05976502	16	1.57449446	29	6.24673491	16	1.6631095	12	1.84861562	37	2.10899115
23	3.31121218	19	3.25486243	3	0.87202301	12	2.13144738	8	3.11040742	15	2.81426077	2	0.55611881	15	1.54325079
26	1.99136727	27	2.46071684	28	4.32995677	42	3.96882089	23	4.75744712	32	3.19405137	19	2.8106711	38	2.07992505
14	2.44090669	12	2.48956946	6	2.11213613	7	1.50575868	8	3.76687532	5	1.13607512	2	0.67349062	13	1.61976708
38	2.32939631	18	1.31296199	19	2.35158619	22	1.66385954	27	4.46983682	21	1.67761764	11	1.3023595	22	0.96375921
109	10.0048577	99	10.8128324	76	14.0846326	82	9.28608092	44	10.9069975	80	9.56947929	41	7.26853165	179	11.7414984
8	1.87544568	3	0.83686541	1	0.4733278	5	1.44616784	5	3.16557512	5	1.52756046	2	0.90557184	8	1.34026465
29	9.96214461	24	9.81038263	32	22.1948562	18	7.62889333	13	12.0605278	12	5.37217303	8	5.30790623	35	8.59229069
18	1.7843526	20	2.35916344	19	3.80285081	19	2.32378513	14	3.74804095	13	1.67944362	5	0.9573188	20	1.4168512
22	4.38681834	11	2.60999404	9	3.62340594	9	2.21413283	15	8.07767445	10	2.5986086	4	1.54051302	26	3.70498446
2	1.11921758	4	2.66357163	1	1.12987927	3	2.07128555	4	6.04522733	3	2.18786079	2	2.16168762	4	1.59967071
11	3.53382588	18	6.88089337	19	12.3240535	8	3.1708569	6	5.20561243	9	3.76798247	6	3.72290646	30	6.88747111
24	3.38495074	18	3.02088002	4	1.13906528	9	1.56609396	15	5.71347705	4	0.73521609	1	0.27240779	15	1.5118839
196	21.3847988	197	25.5761508	293	64.5452417	493	66.3636418	118	34.7695622	540	76.7815296	173	36.4563859	740	57.6988146
178	12.2052226	191	15.5839996	182	25.1967544	517	43.7371457	129	23.8882056	456	40.7478262	166	21.9842776	554	27.146981
39	7.39417517	39	8.7985194	38	14.5464239	95	22.2219889	18	9.21649413	64	15.8131723	25	9.15468801	58	7.85849163
26	5.21438943	27	6.44337992	40	16.1971133	143	35.3834638	36	19.4984789	114	29.7953758	34	13.1700506	123	17.6287411
62	13.9684168	56	15.0128583	48	21.8345501	221	61.4302049	38	23.1210318	138	40.5180453	63	27.4141294	131	21.0917622
81	33.859703	123	61.1819194	94	79.3365831	295	152.143827	40	45.1571198	118	64.2826889	65	52.4795247	190	56.7594005
76	10.8513441	83	14.101584	57	16.4320714	286	50.3813929	27	10.4112249	211	39.261447	46	12.685459	125	12.7545761
2	0.9637707	3	1.72022334	0	0	3	1.78360701	0	0	0	0	0	0	0	0
308	76.8797804	270	80.1945846	151	76.100214	676	208.181583	62	41.7947012	374	121.659751	73	35.1935186	261	46.5573227
30	2.55742592	15	1.52157347	20	3.44238402	12	1.26211012	18	4.14402562	16	1.7775249	7	1.15254598	33	2.01039697
1038	35.6929468	1216	49.7552012	786	54.5701454	1868	79.2494244	521	48.3827882	1842	82.5445833	687	45.6268199	2398	58.9278103
828	177.333808	1131	288.232978	524	226.589616	1536	405.869683	430	248.712594	929	259.293016	553	228.751919	1789	273.81524
726	154.534423	946	239.60706	459	197.264444	1302	341.927311	339	194.875135	762	211.376882	542	222.826229	1434	218.134238
246	127.390347	252	155.282251	142	148.469509	342	218.505169	80	111.881819	286	193.010684	111	111.020404	325	120.273749
57	5.07091658	51	5.3988548	55	9.87920082	43	4.71969854	21	5.04543974	71	8.23159247	26	4.46748775	106	6.73912558
36	5.22613733	18	3.10935768	16	4.68970811	29	5.19410241	8	3.13643594	29	5.48643473	13	3.64502138	41	4.25351772
16	4.14277553	6	1.84859822	1	0.52277996	9	2.87506801	7	4.89482959	6	2.0245876	2	1.00018382	24	4.4408769
29	2.32911251	17	1.62465538	18	2.91885479	21	2.08087484	19	4.12110984	32	3.34931775	8	1.24096882	44	2.52540607
15	4.73123796	16	6.00514331	3	1.91052313	17	6.61556053	11	9.37010237	8	3.28842107	2	1.21840575	14	3.15571404
38	11.6675957	50	18.2678585	16	9.91894016	47	17.8045018	19	15.7550394	35	14.0048906	22	13.0466456	51	11.1906168
25	3.02227744	20	2.87702859	5	1.22042709	13	1.93897347	18	5.87671925	17	2.67828719	11	2.5684163	21	1.81426068
24	12.8107366	20	12.7031878	8	8.62184798	32	21.0740028	3	4.32466263	18	12.5212956	4	4.12383484	17	6.48481895
59	4.73853925	37	3.53601465	67	10.8646262	62	6.14353524	43	9.32672226	70	7.32663258	39	6.04972299	160	9.18329482
21	5.02490101	12	3.41671947	1	0.48312079	9	2.6569594	5	3.23106978	8	2.49466426	4	1.84861562	23	3.9329835
103	3.84264703	72	3.19628595	54	4.06756538	90	4.14257111	65	6.54899628	101	4.91053199	25	1.80140635	121	3.2260026
26	2.27226542	32	3.32778722	12	2.11745637	19	2.04867706	14	3.30431821	16	1.82229883	10	1.68796766	27	1.68630275
20	2.94031738	16	2.79900747	12	3.56199228	10	1.81383763	10	3.97038236	26	4.98140055	10	2.83950492	21	2.20632549
19	2.56505508	8	1.2851474	5	1.36288939	7	1.16593765	23	8.38569472	5	0.87968462	10	2.60748312	14	1.35069472
24	3.81971505	11	2.08320625	10	3.21341811	8	1.57088323	11	4.7280333	8	1.65929503	6	1.84437568	14	1.59233277
108	6.95202312	103	7.88941021	44	5.71857264	161	12.7863775	43	7.47522081	139	11.6604727	59	7.33529992	117	5.38219449
21	13.2474663	18	13.5115724	3	3.82104627	17	13.2311211	1	1.70365498	3	2.4663158	0	0	2	0.90163258
40	14.7641468	23	10.1017371	12	8.94287424	20	9.10778045	12	11.9618328	8	3.84815231	11	7.84186679	19	5.0117343
16	9.10052329	24	16.2434204	1	1.14840188	30	21.0524106	5	7.68041177	9	6.67118208	2	2.19712512	4	1.62589482
16	3.26548189	7	1.69998542	7	2.88451532	13	3.27344344	10	5.51182492	7	1.86182663	6	2.36514057	13	1.89608028
11	1.52661278	15	2.47712161	6	1.68126036	15	2.56839409	11	4.12284504	14	2.53208422	10	2.68049265	28	2.77702835
48	4.17392421	33	3.41457867	16	2.8091234	30	3.21853896	12	2.8180759	33	3.73965178	9	1.511556	30	1.8642779
12	3.17823619	17	5.35764217	2	1.06950404	16	5.22828313	7	5.00692493	9	3.1064283	4	2.04617759	22	4.16402834
61	16.2803111	65	20.6426801	27	14.5493685	65	21.4032841	21	15.1363192	41	14.2603644	26	13.4024632	53	10.1086884
188	89.3534256	181	102.365071	62	59.4966565	184	107.896007	32	41.0744213	165	102.200073	69	63.3404085	173	58.760507
31	4.02834493	15	2.31940226	7	1.83658279	16	2.5651876	19	6.66786311	12	2.03217032	9	2.25884212	19	1.7644308
48	3.79361221	33	3.10345533	25	3.98932317	16	1.56014827	31	6.61670099	27	2.78092556	11	1.6791241	88	4.97027528
9	7.43480251	4	3.93193907	0	0	7	7.13442802	2	4.46195351	0	0	1	1.59553134	0	0
57	3.40388549	34	2.41601075	24	2.89373555	37	2.72606372	43	6.9348434	38	2.95731499	22	2.53747153	95	4.05424289
74	7.19183511	81	9.36726661	74	14.5206894	130	15.5878259	46	12.0735213	172	21.7846382	34	6.38212535	117	8.12605835
19	12.9258658	6	4.85710121	4	5.49431489	24	20.1442674	2	3.67454995	12	10.6390093	2	2.62793397	1	0.48617443
421	10.6697653	357	10.7661604	347	17.7561889	872	27.2661267	267	18.2747796	887	29.2961325	229	11.2095109	934	16.9163133
197	10.7638768	153	9.94749625	145	15.9962436	445	29.9983036	115	16.9694767	456	32.4699214	87	9.18121498	399	15.5797851
325	10.2790494	311	11.7044185	191	12.1969283	761	29.6953494	143	12.2144452	692	28.5226312	123	7.51368723	691	15.6182982
46	5.82483311	41	6.17773639	29	7.41431727	49	7.65518919	13	4.44566901	68	11.2214369	20	4.89140994	58	5.24855463
381	130.881969	256	104.644081	295	204.608831	403	170.802445	120	111.327949	528	236.375613	151	100.18673	730	179.210635
30	4.50594091	21	3.75321457	13	3.94234932	29	5.37398474	10	4.05632137	19	3.71904763	10	2.90096607	30	3.22011636
17	2.17648585	13	1.98047854	7	1.80947455	15	2.36936724	13	4.49488305	14	2.33587105	10	2.4727792	12	1.09792897
39	5.93479849	26	4.70797968	24	7.37394893	17	3.1917178	12	4.93163282	20	3.96629734	8	2.35130934	86	9.35246077
56	4.32730896	42	3.86188225	35	5.46066374	62	5.91092923	27	5.63458271	54	5.43797916	31	4.62668553	95	5.24613613
42	3.9923871	41	4.63753362	20	3.83849397	47	5.51207864	19	4.87758753	36	4.45963953	13	2.38674003	62	4.21173576
16	2.12694222	17	2.68908477	11	2.95240484	14	2.29613775	15	5.3851163	15	2.5986086	12	3.08102603	26	2.46998964
10	4.44817244	11	5.82229439	5	4.49054583	6	3.29281293	3	3.60388553	4	2.31875844	1	0.85913226	12	3.81459939
80	17.5674658	85	22.2104786	50	22.1685174	204	55.2692399	29	17.1982892	145	41.4955032	26	11.0273432	187	29.3458579
62	4.50028492	38	3.28209977	38	5.56902838	86	7.70160012	38	7.44903535	94	8.89180801	33	4.62637329	124	6.43214875
33	13.7946938	17	8.45603764	16	13.5040993	65	33.523216	4	4.51571198	29	15.798288	5	4.03688652	18	5.37720636
357	11.0691519	284	10.4781433	294	18.4052184	483	18.4768297	208	17.4171697	522	21.0926204	159	9.52185726	706	15.6436073
44	4.84638978	29	3.80087444	31	6.89405702	42	5.70754242	21	6.24673491	41	5.88522976	9	1.91463761	67	5.27383502
20	9.13045922	21	11.4077969	2	1.84348723	13	7.32217613	3	3.69872462	10	5.94944601	2	1.76348201	10	3.26248632
16	1.3878298	15	1.54820101	4	0.70052515	7	0.74911494	11	2.57677815	7	0.79127632	8	1.34024632	8	0.49589792

gsyne_1511	Synechococcus_assembled_mapped	putative predicted protein				UniRef100_C	1313554	1313782	-1	185	fig|1129.58.peg.1509				
gsyne_1512	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1314076	1314214	-1	88					
gsyne_1513	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1314221	1314956	-1	856	fig|1129.58.peg.1510				
gsyne_1514	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04250.8	1314977	1315457	-1	156	fig|1129.58.peg.1511				
gsyne_1515	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	1315570	1316389	-1	154	fig|1129.58.peg.1512				
gsyne_1516	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	1316430	1317801	-1	157	fig|1129.58.peg.1513				
gsyne_1517	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04250.8	1317888	1318260	1	156	fig|1129.58.peg.1514				
gsyne_1518	Synechococcus_assembled_mapped	eco57I restriction-modification methylase family protein				PF07669.6	1318341	1320120	1	183	fig|1129.58.1	DNA Metabolism	DNA Metabolism - no subcate	Type I Restriction-Modification	
gsyne_1519	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1320332	1321313	-1	154	fig|1129.58.peg.1516				
gsyne_152	Synechococcus_assembled_mapped	eamA-like transporter family protein				PF00892.15	124231	124669	-1	141	fig|1129.58.peg.151				
gsyne_1520	Synechococcus_assembled_mapped	type I restriction modification DNA specificity domain protein				PF01420.14	1321543	1322551	-1	183	fig|1129.58.1	DNA Metabolism	DNA Metabolism - no subcate	Restriction-Modification System	
gsyne_1521	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1323063	1323237	1	856	fig|1129.58.peg.1519				
gsyne_1522	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1323291	1324032	-1	856					
gsyne_1523	Synechococcus_assembled_mapped	DEAD/DEAH box helicase family protein				PF00270.24	1324049	1326395	1	703	fig|1129.58.1	DNA Metabolism	DNA Metabolism - no subcate	Type I Restriction-Modification	
gsyne_1524	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08401.6	1326429	1327308	-1	156					
gsyne_1525	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04365.8	1327502	1327766	1	156	fig|1129.58.peg.1525				
gsyne_1526	Synechococcus_assembled_mapped	helix-turn-helix , CopG family protein			GO:0006355		UniRef100_A	1327752	1328010	1	185	fig|1129.58.peg.1526			
gsyne_1527	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1328041	1328248	-1	156	fig|1129.58.peg.1527				
gsyne_1528	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1328329	1329781	1	156	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Biotin	Biotin biosynthesis	
gsyne_1529	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11103.3	1329808	1330354	-1	156	fig|1129.58.peg.1529				
gsyne_153	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	124732	124912	-1	856	fig|1129.58.peg.152				
gsyne_1530	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11103.3	1330481	1330667	-1	156	fig|1129.58.peg.1530				
gsyne_1531	Synechococcus_assembled_mapped	cytidine and deoxycytidylate deaminase zinc-binding region family protein				PF00383.17	1331069	1331567	1	703	fig|1129.58.1	Amino Acids and Derivatives	Amino Acids and Derivatives - Creatine and Creatinine Degrada		
gsyne_1532	Synechococcus_assembled_mapped	photosystem II o(b) protein	psbA	1.10.3.9	GO:0009055,GO:0009538,G	TIGR01151	1331666	1332746	-1	112,164	fig|1129.58.1	Photosynthesis	Electron transport and photop	Photosystem II	
gsyne_1533	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1332966	1333290	-1	156	fig|1129.58.peg.1533				
gsyne_1534	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1333395	1333662	1	156	fig|1129.58.peg.1534				
gsyne_1535	Synechococcus_assembled_mapped	succinylglutamate desuccinylase / Aspartoacylase family protein				PF04952.9	1333696	1334638	-1	185	fig|1129.58.peg.1535				
gsyne_1536	Synechococcus_assembled_mapped	glutathione S-transferase C terminus d	ecm4	2.5.1.18	GO:0004364,GO:0016740	UniRef100_A	1334694	1335135	1	703	fig|1129.58.peg.1536				
gsyne_1537	Synechococcus_assembled_mapped	glutathione S-transferase, C-terminal domain protein				PF00043.20	1335086	1335659	1	703	fig|1129.58.peg.1537				
gsyne_1538	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10063.4	1335655	1336297	1	156	fig|1129.58.peg.1538				
gsyne_1539	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1337065	1337209	-1	856					
gsyne_154	Synechococcus_assembled_mapped	RNA methyltransferase, RsmE family protein		2.1.1.-	GO:0016436,GO:0031167	TIGR00046	125079	125799	1	156	fig|1129.58.peg.153				
gsyne_1540	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1337262	1338243	-1	154	fig|1129.58.peg.1541				
gsyne_1541	Synechococcus_assembled_mapped	secretin and TonB N terminus short domain protein				PF07660.9	1338208	1340047	-1	157	fig|1129.58.1	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus	
gsyne_1542	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1340124	1340814	-1	156	fig|1129.58.peg.1543				
gsyne_1543	Synechococcus_assembled_mapped	fimbrial assembly family protein				PF05137.8	1340810	1341506	-1	185	fig|1129.58.1	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus	
gsyne_1544	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1341505	1342363	-1	156	fig|1129.58.peg.1545				
gsyne_1545	Synechococcus_assembled_mapped	dihydroorotate dehydrogenase	pyrD	1.3.98.1	GO:0004152,GO:0009220	TIGR01036	1342391	1343552	-1	126	fig|1129.58.1	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis	
gsyne_1546	Synechococcus_assembled_mapped	RNase H family protein				PF00075.19	1343544	1344291	-1	134	fig|1129.58.1	RNA Metabolism	RNA processing and modificat	Ribonuclease H	
gsyne_1547	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12565.3	1344372	1345047	1	156	fig|1129.58.peg.1548				
gsyne_1548	Synechococcus_assembled_mapped	sigma-54 interaction domain protein			GO:0000315,GO:0003735,G	TIGR00855	1345308	1345695	-1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_1549	Synechococcus_assembled_mapped	ribosomal L10 family protein				PF00466.15	1345757	1346291	-1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_155	Synechococcus_assembled_mapped	oxidoreductase, short-chain dehydrogenase/reductase family dom			GO:0008152,GO:0055114,G	UniRef100_B	125806	126004	1	141,703	fig|1129.58.peg.154				
gsyne_1550	Synechococcus_assembled_mapped	ribosomal protein L1	rplA		GO:0000311,GO:0003735,G	TIGR01169	1346593	1347301	-1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_1551	Synechococcus_assembled_mapped	ribosomal protein L11	rplK		GO:0000315,GO:0003735,G	TIGR01632	1347394	1347820	-1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_1552	Synechococcus_assembled_mapped	transcription termination/antiterminati	nusG		GO:0003715,GO:0006353	TIGR00922	1347938	1348607	-1	165	fig|1129.58.1	RNA Metabolism	Transcription	Transcription factors bacterial	
gsyne_1553	Synechococcus_assembled_mapped	preprotein translocase, SecE subunit	secE		GO:0005887,GO:0015450,G	TIGR00964	1348633	1348795	-1	97	fig|1129.58.peg.1554				
gsyne_1554	Synechococcus_assembled_mapped	sigma-54 interaction domain protein				PF00158.21	1348948	1351684	-1	263	fig|1129.58.1	Protein Metabolism	Protein folding	Protein chaperones	
gsyne_1555	Synechococcus_assembled_mapped	lactoylglutathione lyase	gloA	4.4.1.5	GO:0004462,GO:0005975,G	TIGR00068	1351673	1352075	-1	100,184	fig|1129.58.1	Stress Response	Oxidative stress	Glutathione: Non-redox reactions	
gsyne_1556	Synechococcus_assembled_mapped	phosphopyruvate hydratase	eno	4.2.1.11	GO:0004634,GO:0006096	TIGR01060	1352201	1353494	1	116	fig|1129.58.peg.1557				
gsyne_1557	Synechococcus_assembled_mapped	ABC1 family protein				PF03109.11	1353517	1355173	-1	185	fig|1129.58.peg.1558				
gsyne_1558	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1355184	1355493	-1	156	fig|1129.58.peg.1559				
gsyne_1559	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1355543	1356083	-1	156	fig|1129.58.peg.1560				
gsyne_156	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	126007	126307	-1	856	fig|1129.58.peg.155				
gsyne_1560	Synechococcus_assembled_mapped	glutamate N-acetyltransferase/amino-a	argJ	2.3.1.35	GO:0004042,GO:0004358,G	TIGR00120	1357151	1358381	-1	73	fig|1129.58.1	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis extended	
gsyne_1561	Synechococcus_assembled_mapped	lysR substrate binding domain protein				PF03466.15	1356270	1357164	1	157	fig|1129.58.peg.1561				
gsyne_1562	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1359067	1359505	-1	856	fig|1129.58.peg.1564				
gsyne_1563	Synechococcus_assembled_mapped	dephospho-CoA kinase	coaE	2.7.1.24	GO:0004140,GO:0005737,G	TIGR00152	1358446	1359082	1	83	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Coenzyme A	Coenzyme A Biosynthesis	
gsyne_1564	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1359591	1360107	-1	856	fig|1129.58.peg.1565				
gsyne_1565	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1360128	1360245	-1	856	fig|1129.58.peg.1566				
gsyne_1566	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1360299	1360944	-1	856	fig|1129.58.peg.1567				
gsyne_1567	Synechococcus_assembled_mapped	aspartyl/glutamyl-tRNA(Asn/Gln) amid	gatB	6.3.5.-	GO:0006424,GO:0030956,G	TIGR00133	1360945	1362418	-1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Asp and As	
gsyne_1568	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	1362520	1363630	1	157	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Cofactors, Vitamins, Prosthetic	Thiamin biosynthesis	
gsyne_1569	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11750.3	1363737	1364067	1	156	fig|1129.58.peg.1570				
gsyne_157	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	126472	126637	-1	157	fig|1129.58.peg.156				
gsyne_1570	Synechococcus_assembled_mapped	nucleoside diphosphate kinase family protein				PF00334.14	1364101	1364557	-1	124	fig|1129.58.1	Nucleosides and Nucleotides	Purines	Purine conversions	
gsyne_1571	Synechococcus_assembled_mapped	arginine decarboxylase	speA	4.1.1.19	GO:0008295,GO:0008792	TIGR01273	1364644	1366564	-1	104	fig|1129.58.1	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Polyamine Metabolism	
gsyne_1572	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	1366813	1367518	-1	157	fig|1129.58.1	Stress Response	Oxidative stress	Oxidative stress	
gsyne_1573	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1366662	1366854	1	156					
gsyne_1574	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	1367627	1368185	1	157	fig|1129.58.peg.1574				
gsyne_1575	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1369113	1369317	-1	856	fig|1129.58.peg.1576				
gsyne_1576	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	1368181	1369117	1	264,710	fig|1129.58.peg.1575				
gsyne_1577	Synechococcus_assembled_mapped	alanine--tRNA ligase	alaS	6.1.1.7	GO:0004813,GO:0005737,G	TIGR00344	1369411	1372051	-1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Ala	
gsyne_1578	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1372092	1372524	1	156	fig|1129.58.peg.1578				
gsyne_1579	Synechococcus_assembled_mapped	helicase conserved C-terminal domain protein				PF00271.26	1372543	1375675	1	703	fig|1129.58.peg.1579				
gsyne_158	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	126818	127280	-1	157	fig|1129.58.peg.157				
gsyne_1580	Synechococcus_assembled_mapped	SWIM zinc finger family protein				PF04434.12	1375679	1376618	1	185	fig|1129.58.peg.1580				
gsyne_1581	Synechococcus_assembled_mapped	MEKHLA domain protein				PF08670.6	1376623	1377142	1	157	fig|1129.58.peg.1581				
gsyne_1582	Synechococcus_assembled_mapped	hsp20/alpha crystallin family protein				PF00011.16	1377304	1377721	1	185	fig|1129.58.peg.1582				
gsyne_1583	Synechococcus_assembled_mapped	diflavin flavoprotein A 1	dfa1	1.-.-.-	GO:0006810,GO:0022900,G	UniRef100_C	1377886	1379629	1	92,141,703	fig|1129.58.peg.1583				
gsyne_1584	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1379883	1381254	1	132,152	fig|1129.58.peg.1584				
gsyne_1585	Synechococcus_assembled_mapped	DNA methylase family protein				PF01555.13	1381250	1382858	1	183	fig|1129.58.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton	
gsyne_1586	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1383620	1383746	-1	856	fig|1129.58.peg.1586				
gsyne_1587	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1383799	1384780	-1	154	fig|1129.58.peg.1587				
gsyne_1588	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1385216	1385342	1	856	fig|1129.58.peg.1589				
gsyne_1589	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1385637	1385808	-1	156					
gsyne_159	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	127647	127926	-1	154	fig|1129.58.peg.158				
gsyne_1590	Synechococcus_assembled_mapped	putative diflavin flavoprotein A 5			GO:0006810,GO:0009055,G	UniRef100_C	1386066	1387881	1	92,141,703	fig|1129.58.peg.1592				
gsyne_1591	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1387891	1388038	-1	856					
gsyne_1592	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1388306	1388537	-1	856	fig|1129.58.peg.1593				
gsyne_1593	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1388115	1388319	1	156					
gsyne_1594	Synechococcus_assembled_mapped	glycine dehydrogenase	gcvP	1.4.4.2	GO:0004375,GO:0019464	TIGR00461	1388678	1391642	-1	109	fig|1129.58.1	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine cleavage system	
gsyne_1595	Synechococcus_assembled_mapped	glycine cleavage system H protein	gcvH		GO:0003824,GO:0019464	TIGR00527	1391631	1392021	-1	109	fig|1129.58.1	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine cleavage system	
gsyne_1596	Synechococcus_assembled_mapped	aluminium resistance family protein				PF06838.6	1392165	1393347	-1	96,145	fig|1129.58.peg.1596				
gsyne_1597	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1394573	1395356	-1	156	fig|1129.58.peg.1598				
gsyne_1598	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	1393800	1394586	1	121	fig|1129.58.peg.1597				
gsyne_1599	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	1395530	1396337	1	121	fig|1129.58.peg.1599				
gsyne_16	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11460.3	10633	10981	-1	156	fig|1129.58.peg.16				
gsyne_160	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	128119	128383	1	856	fig|1129.58.peg.159				
gsyne_1600	Synechococcus_assembled_mapped	ribosomal protein L9	rplI		GO:0000311,GO:0003735,G	TIGR00158	1396380	1396839	1	158	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_1601	Synechococcus_assembled_mapped	recG DNA helicase	dnaB	3.6.4.12	GO:0004003,GO:0006260	TIGR00665	1396957	1398376	1	132	fig|1129.58.1	DNA Metabolism	DNA replication	DNA-replication	
gsyne_1602	Synechococcus_assembled_mapped	tRNA uridine 5-carboxymethylaminom	gidA		GO:0006400,GO:0016740	TIGR00136	1398385	1400317	1	168	fig|1129.58.1	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_1603	Synechococcus_assembled_mapped	type IV pilus biogenesis family protein				PF11356.3	1400396	1401176	1	91	fig|1129.58.peg.1603				
gsyne_1604	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01947.11	1401205	1401808	1	156	fig|1129.58.peg.1604				
gsyne_1605	Synechococcus_assembled_mapped	viral (Superfamily 1) RNA helicase			GO:0004386		UniRef100_C	1402383	1402896	-1	703	fig|1129.58.peg.1605			
gsyne_1606	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1401904	1402432	1	156					
gsyne_1607	Synechococcus_assembled_mapped	sprT-like family protein				PF10263.4	1403042	1403588	-1	185	fig|1129.58.peg.1607				
gsyne_1608	Synechococcus_assembled_mapped	lumazine binding domain protein				PF12870.2	1403723	1404128	1	157	fig|1129.58.peg.1608				
gsyne_1609	Synechococcus_assembled_mapped	DNA ligase, NAD-dependent	ligA	6.5.1.2	GO:0003911,GO:0006260,G	TIGR00575	1404153	1406226	1	132	fig|1129.58.1	DNA Metabolism	DNA repair	DNA Repair Base Excision	
gsyne_161	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	128633	128777	-1	856	fig|1129.58.peg.160				
gsyne_1610	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1406387	1406525	-1	856					
gsyne_1611	Synechococcus_assembled_mapped	subtilase family protein				PF00082.17	1406504	1408547	1	138	fig|1129.58.peg.1610				
gsyne_1612	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09335.6	1408756	1409347	-1	156	fig|1129.58.peg.1612				
gsyne_1613	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1408607	1408781	1	156	fig|1129.58.peg.1611				
gsyne_1614	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_D	1409460	1411005	1	156	fig|1129.58.peg.1613				
gsyne_1615	Synechococcus_assembled_mapped	valine--tRNA ligase	valS	6.1.1.9	GO:0004832,GO:0005737,G	TIGR00422	1411012	1413802	-1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Val	
gsyne_1616	Synechococcus_assembled_mapped	bacterial extracellular solute-binding family protein				PF13416.1	1413924	1415142	1	185	fig|1129.58.peg.1615				
gsyne_1617	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1416391	1417018	-1	703	fig|1129.58.peg.1617				
gsyne_1618	Synechococcus_assembled_mapped	mechanosensitive ion channel family protein				PF00924.13	1415138	1416395	1	141	fig|1129.58.1	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis	
gsyne_1619	Synechococcus_assembled_mapped	putative protein phosphatase 2A regulatory B s				UniRef100_C	1417017	1417476	-1	129	fig|1129.58.peg.1618				
gsyne_162	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	129558	130785	1	132,152	fig|1129.58.peg.161				
gsyne_1620	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1417531	1417786	1	156	fig|1129.58.peg.1619				
gsyne_1621	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	1417797	1418622	1	703	fig|1129.58.peg.1620				
gsyne_1622	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	1418659	1419571	1	703	fig|1129.58.peg.1621				
gsyne_1623	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1419581	1419743	1	856	fig|1129.58.peg.1622				
gsyne_1624	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1420476	1420590	-1	856					
gsyne_1625	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1420811	1421003	-1	856	fig|1129.58.peg.1624				
gsyne_1626	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1421343	1422324	1	154	fig|1129.58.peg.1625				
gsyne_1627	Synechococcus_assembled_mapped	DDE_Tnp_1-associated family protein				PF13808.1	1422541	1422754	1	185	fig|1129.58.peg.1627				
gsyne_1628	Synechococcus_assembled_mapped	putative ISMca6, transposase, OrfA				UniRef100_A	1422822	1423149	1	154	fig|1129.58.peg.1628				
gsyne_1629	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1423117	1423996	1	154	fig|1129.58.peg.1629				
gsyne_163	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	130822	131188	-1	856	fig|1129.58.repeat.4				
gsyne_1630	Synechococcus_assembled_mapped	transposase, Mutator family protein				PF00872.13	1424346	1425588	-1	154	fig|1129.58.peg.1630				
gsyne_1631	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1425711	1425882	-1	856	fig|1129.58.peg.1631				
gsyne_1632	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1428343	1428460	-1	856	fig|1129.58.peg.1634				
gsyne_1633	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein				PF01370.16	1428456	1429308	-1	119	fig|1129.58.peg.1635				
gsyne_1634	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1429358	1430159	1	156	fig|1129.58.peg.1636				
gsyne_1635	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1430183	1430492	1	156	fig|1129.58.peg.1637				
gsyne_1636	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1430906	1431086	-1	856	fig|1129.58.peg.1639				
gsyne_1637	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1431321	1431939	-1	856	fig|1129.58.peg.1641				
gsyne_1639	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09988.4	1431937	1432453	1	156	fig|1129.58.peg.1643				
gsyne_164	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	132443	133424	1	154	fig|1129.58.peg.163				
gsyne_1640	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	1432469	1433168	1	703	fig|1129.58.peg.1644				



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0.13253503	1.69473884	0.01245808	2.48317921	0.02814383	2.18168851	0.73143185	-1.1381914
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0.04655297	-3.6727759	0.72473087	-1.3036947	0.07436956	-3.5659524	0.18855622	-2.7352665
0.62219409	-1.3486005	0.67725412	-1.3756248	0.75946937	-1.2466398	1	1.10346617
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0.07238099	-1.9681271	0.45328905	-1.4330938	0.93235185	-1.0453472	0.56300272	1.37092617
0.17628216	1.96408697	0.57964622	-1.2904246	0.79272979	-1.1154678	0.8246265	1.15684612
0.40096002	1.81031162	1	1.03334484	0.1336931	3.06244063	0.27959898	2.96361923
0.32614347	-1.3397295	0.95702694	1.02466746	0.83270986	1.08278166	0.95872426	1.05671517
0.58679606	-1.2657404	1	-1.2025169	0.45052733	2.13095925	0.33626152	2.5625146
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0.25405627	-4.4299511	0.25405627	-4.0117137	0.25405627	-4.9952395	1	-1.2451635
0.62254787	-1.4188141	1	-1.0058766	0.79030437	-1.2860645	0.79030437	-1.278551
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1	1.00465091	0.38824511	2.24087575	0.34358715	1.96819568	1	-1.1385432
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43	24.8652839	32	22.0188588	14	16.3455868	14	9.98819923	12	18.7402047	6	4.52157896	7	7.81810356	27	11.1577032
9	5.03647912	12	7.99071489	21	23.7274647	10	6.90428518	7	10.5791478	19	13.8564517	8	8.64675048	30	11.9975303
8	1.6720841	3	0.74612097	0	0	5	1.28935446	4	2.25785599	0	0	6	2.42213191	9	1.34430159
56	5.39711589	55	6.30748559	15	2.91885479	44	5.23191388	26	6.76729615	27	3.39118422	15	2.79217984	61	4.20135738
8	2.57005519	7	2.67590298	1	0.6486344	3	1.18907134	2	1.73520414	1	0.41866472	1	0.62048441	10	2.2958237
0	0	2	0.9277609	1	0.78710691	0	0	0	0	0	0	0	0	1	0.27859434
13	1.43644804	14	1.84074855	5	1.11548591	7	0.95428655	16	4.77457445	20	2.8799866	4	0.85366008	26	2.05308056
3	0.70807643	3	0.84255837	2	0.95309544	3	0.87360343	1	0.63742193	0	0	0	0	1	0.16867276
2	0.36330623	5	1.08076859	1	0.36676709	4	0.89647263	4	1.9623251	0	0	0	0	5	0.64908105
9	1.45916685	15	2.89383366	7	2.2914374	8	1.60024554	4	1.751421	13	2.74675358	7	2.19199165	35	4.05524
0	0	3	2.58033502	0	0	2	1.78360701	1	1.95210466	0	0	0	0	0	0
42	6.07175538	28	4.81662536	19	5.54582409	51	9.09639573	37	14.4455745	33	6.21717108	24	6.70123162	58	5.99209987
0	0	0	0	1	0.21422787	0	0	0	0	1	0.13827459	0	0	0	0
107	6.05619041	57	3.83893236	47	5.37107373	39	2.72341951	113	17.2727825	74	5.45834981	53	5.79388704	140	5.66278212
26	3.9221277	24	4.30803759	10	3.04576152	8	1.48892411	11	4.48135331	11	2.16249429	5	1.45678948	30	3.23411687
24	3.589215	11	1.95749553	0	0	6	1.10706642	11	4.44272095	10	1.94895645	8	2.31076952	14	1.49624372
25	3.03284485	19	2.74273372	13	3.18420522	9	1.34705984	30	9.8287787	8	1.26477733	6	1.40585279	28	2.42747234
48	4.30334822	37	3.94717914	39	7.05955576	28	3.09711604	31	7.50576675	29	3.38826331	19	3.29001036	73	4.67707341
22	3.06548751	10	1.6580466	2	0.5626708	14	2.406795	10	3.76309332	14	2.54225323	6	1.61475461	22	2.1907137
37	5.70552252	23	4.22028127	27	8.40630178	28	5.32703959	13	5.41383692	26	5.22493569	13	3.87182271	62	6.83237134
117	31.4682339	112	35.8446539	178	96.6616097	414	137.379219	77	55.9300684	387	135.647369	99	51.4280566	470	90.3379932
587	114.417991	494	114.578472	891	350.656128	1568	377.082578	351	184.769996	1345	341.658635	425	160.001317	2058	286.673573
5	2.62846553	7	4.37875033	1	1.06140174	8	5.18867492	7	9.93798736	7	4.79561405	5	5.07669062	4	1.50272097
40	5.88063475	38	6.64764275	46	13.6543038	122	22.1288191	19	7.54372648	102	19.5424176	23	6.53086132	127	13.3430161
55	13.4384928	57	16.5722925	70	34.5329299	151	45.5196605	17	11.2177282	133	42.3500002	45	21.2362974	158	27.5886871
49	7.62372873	35	6.47976506	31	9.73824198	72	13.8209547	21	8.82386321	51	10.3408308	30	9.0151098	85	9.45096933
8	5.14011038	13	9.93906821	5	6.48634397	14	11.0979991	2	3.47040828	6	5.02397663	3	3.72290646	3	1.37749422
81	3.08152999	73	3.30463958	57	4.37828218	101	4.74063967	52	5.34260223	102	5.05702911	47	3.45348559	166	4.51310607
32	8.28555105	36	11.0915893	25	13.069499	28	8.94465603	23	16.0830115	38	12.8223881	12	6.00110294	53	9.80693648
79	6.35954491	51	4.88527465	72	11.7025083	63	6.25710857	43	9.34836199	97	10.1761754	59	9.17337971	160	9.20460176
60	3.77127663	45	3.36565437	44	5.58389611	71	5.50591728	49	8.31766333	72	5.89771169	27	3.27777634	114	5.12068504
36	12.1266682	40	16.0331496	26	17.6831591	30	12.4679325	11	10.0069054	24	10.535718	13	8.45786515	55	13.239993
119	22.9377426	125	28.6703891	89	34.6370768	133	31.6292976	37	19.260766	125	31.3998539	44	16.3807884	198	27.2743856
54	18.7357023	71	29.3126058	28	19.6147042	69	29.536532	82	76.8348394	60	27.1294738	54	36.1866507	161	39.9197826
47	3.97731711	15	1.51044001	22	3.75891543	20	2.08812527	17	3.8851644	30	3.30847241	15	2.45167011	46	2.78186638
29	3.37643156	14	1.93958068	25	5.87688883	17	2.44198543	14	4.40206151	17	2.57942424	9	2.0238619	33	2.74574352
5	1.18821045	6	1.69665864	2	0.95962349	2	0.58639134	2	1.28357567	7	2.16788033	4	1.83595387	5	0.84914027
18	2.94586514	14	2.72639171	16	5.28698225	19	3.83643771	8	3.53588769	5	1.06641013	4	1.26438332	31	3.62566876
14	2.82407227	14	3.3604363	7	2.85097444	14	3.48425555	5	2.72386697	11	2.89170748	3	1.16881947	19	2.73897107
0	0	2	2.11719796	0	0	1	1.09760431	0	0	0	0	0	0	0	0
41	6.61639789	30	5.76074794	12	3.90990781	39	7.76491236	29	12.6387427	37	7.78132194	11	3.42853711	56	6.45820547
69	4.8757768	50	4.20421184	48	6.84831103	59	5.14376277	46	8.77850731	46	4.23610249	39	5.32277053	109	5.50436592
19	1.78167339	17	1.89689493	6	1.13598673	8	0.92554742	16	4.05193616	13	1.58866288	8	1.44891495	36	2.41247637
4	1.26166346	16	6.00514331	3	1.91052313	9	3.50235557	5	4.25913744	5	2.05526317	3	1.82760862	7	1.57785702
31	19.5557836	37	27.7737878	23	29.294688	48	37.3584595	18	30.6657896	37	30.4178949	12	14.620869	31	13.975305
22	5.02175257	21	5.70389845	22	10.1391798	40	11.2648864	14	8.63035744	31	9.22164131	13	5.73131652	50	8.15621579
46	2.49375667	16	1.03213401	18	1.97022698	22	1.47147578	22	3.22097269	27	1.90754113	19	1.98942814	38	1.47219695
32	4.72452698	19	3.3379653	12	3.5771497	17	3.09664535	16	6.37964416	22	4.23296754	14	3.99222309	30	3.16530587
5	2.71060508	3	1.93525126	0	0	3	2.00655788	2	2.92815699	2	1.41299343	0	0	2	0.7748405
60	11.1921758	32	7.10285768	31	11.6754191	43	9.89614209	34	17.1281441	53	12.8840691	22	7.92618794	63	8.39827123
6	3.06138927	6	3.6428259	4	4.12073617	3	1.88852506	2	2.75591246	4	2.65975233	4	3.94190095	10	3.64630824
53	5.89382848	35	4.63137054	26	5.83770957	30	4.11601617	31	9.31003761	28	4.05782728	22	4.72522742	75	5.96031154
61	2.40504596	48	2.25192874	39	3.10460009	40	1.9457531	54	5.74983554	45	2.31217106	24	1.82760862	92	2.59219367
13	3.13225476	13	3.72715058	5	2.43237899	6	1.78360701	7	4.55491087	6	1.88399124	4	1.86145323	21	3.61592233
147	4.88532042	91	3.59862814	95	6.37451045	166	6.80640834	94	8.43668221	210	9.0951301	55	3.53034233	209	4.96372918
6	1.35178227	6	1.60852053	5	2.2744323	2	0.55592946	7	4.25913744	5	1.46804512	5	2.17572455	5	0.80502909
36	3.99056492	37	4.88037805	29	6.4904886	48	6.56458553	35	10.4777503	41	5.92283507	22	4.71013085	58	4.59458137
12	2.40664127	6	1.43186221	3	1.2147835	8	1.97949448	7	3.7913709	13	3.3977183	2	0.77470886	15	2.14984647
38	9.48516771	51	15.147866	7	3.52782449	50	15.3980461	19	12.8080536	10	3.25293451	16	7.71364791	41	7.31360242
72	4.29964482	65	4.61884409	41	4.94346491	47	3.4628377	47	7.57994511	54	4.20250024	38	4.38290536	97	4.13959537
125	9.49008343	123	11.1118147	56	8.58411561	126	11.8022485	44	9.02154276	66	6.53007028	54	7.91830432	205	11.1224369
154	9.96855361	153	11.7848137	95	12.4160241	153	12.219039	120	20.9778411	115	9.7011489	130	16.2529871	343	15.8668831
4	3.30435667	4	3.93193907	1	1.66791702	4	4.07681601	0	0	0	0	0	0	0	0
1	0.1061032	2	0.25250985	0	0	3	0.39272081	0	0	0	0	0	0	0	0
4	3.30435667	1	0.98298477	1	1.66791702	9	9.17283603	0	0	0	0	0	0	1	0.59035467
10	6.08697281	16	11.5888731	1	1.22899149	8	6.00793939	0	0	1	0.79325947	1	1.17565467	3	1.30499453
2	0.74614505	0	0	2	1.5065057	3	1.38085704	0	0	3	1.45857386	1	0.72056254	6	1.59967071
124	7.11119402	124	8.46179284	103	11.9262959	190	13.443385	86	13.3194844	157	11.7336843	79	8.75036856	283	11.5982737
5	3.54038215	9	7.58302535	0	0	10	8.73603431	3	5.73679737	0	0	1	1.36759829	0	0
81	36.4981214	51	27.344849	33	30.0225064	60	33.3557674	11	13.3858605	52	30.5353385	24	20.8869557	79	25.4389193
12	6.12277854	19	11.5356154	6	6.18110425	13	8.18360861	2	2.75591246	6	3.9896285	3	2.95642571	9	3.28167741
114	4.0033552	83	3.46830456	54	3.82878118	90	3.89938374	56	5.3109892	96	4.39343705	45	3.05218039	128	3.21229422
30	8.00671039	16	5.08127511	15	8.08298249	15	4.9392194	7	5.04543974	21	7.3040891	3	1.54643807	37	7.05700886
36	3.1701696	23	2.4100591	17	3.02257044	24	2.60750669	17	4.04293757	17	1.95093509	11	1.87090223	43	2.70604195
91	12.0969839	88	13.9199682	10	2.6840044	109	17.8770725	11	3.94908529	85	14.7254487	8	2.05401736	23	2.18499084
114	15.0966219	114	17.963859	45	12.0319205	198	32.3500019	51	18.2395122	162	27.9578547	53	13.5559266	250	23.6592519
2060	265.699758	3218	493.889551	26	6.77087504	4691	746.48926	20	6.96661886	2480	416.859325	25	6.22791043	89	8.20351578
23	6.87932876	16	5.69453245	5	3.01950495	10	3.69022139	8	6.46213956	6	2.33874774	5	2.88846191	17	3.63373476
17	6.70258711	13	6.09897367	6	4.77630783	18	8.75588893	6	6.38870616	13	6.67960529	7	5.33052515	21	5.91696382
820	185.951052	988	266.600888	104	47.6173957	1350	377.705013	59	36.1330745	658	194.457448	66	28.9072737	260	42.1351174
88	6.45502233	78	6.80815666	31	4.59117962	54	4.88700778	35	6.93347955	66	6.30917995	15	2.12512631	81	4.24606041
82	4.4177812	62	3.97467754	69	7.50562659	83	5.51699558	74	10.7668878	85	5.96792255	50	5.20281958	108	4.15815026
53	7.07259418	49	7.78070251	23	6.19695324	28	4.60993811	19	6.8473825	26	4.52157896	13	3.35061581	48	4.57751926
21	3.62492859	12	2.46479763	8	2.7881598	12	2.55561601	9	4.19556822	5	1.12477089	3	1.00018382	8	0.98686153
181	36.724736	201	48.5284059	45	18.4348723	145	36.2979671	20	10.9591841	100	26.4419823	37	14.4997409	160	23.1999027
214	42.1868718	305	71.5456527	85	33.8321805	152	36.9693088	42	22.3604716	191	49.0694081	90	34.2676617	256	36.0653033
15	2.85953943	16	3.62948222	6	2.30942357	4	0.9408037	9	4.6335671	7	1.73906883	3	1.10459862	7	0.95364985
21	5.39711589	17	5.19889722	5	2.59453759	33	10.4638278	18	12.4934698	20	6.6986355	8	3.97110022	25	4.59164741
60	3.01265514	38	2.27039608	22	2.23032609	53	3.28328236	38	5.15287829	37	2.42110596	24	2.32749	63	2.26060557
10	7.22828022	5	4.30055836	0	0	5	4.45901751	0	0	1	0.94199562	0	0	0	0
5	3.77127663	4	3.59003133	1	1.52288076	1	0.93057757	3	6.11093633	1	0.98295195	1	1.45678948	0	0
250	12.7370577	262	15.8836481	144	14.8128666	253	15.9031744	132	18.162313	181	12.0177062	155	15.2524361	607	22.1005901
21	3.6985312	18	3.77226642	11	3.91156174	23	4.99772115	12	5.70767657	15	3.44282662	11	3.74180446	19	2.39138591
23	13.7586575	17	12.1008815	5	6.0390099	18	13.284797	2	3.23106978	4	3.11833032	0	0	12	5.12997848
48	3.23377818	30	2.40497244	13	1.76831591	16	1.3299128	30	5.45831206	13	1.14136945	16	2.08193604	41	1.97396259
68	2.53689319	60	2.66357163	35	2.63638497	59	2.7156855	48	4.83618187	61	2.96576685	22	1.58523759	92	2.45282842
115	9.82761251	93	9.45699139	40	6.9017256	62	6.53696361	33	7.61609306	71	7.90719474	26	4.29142912	136	8.30567945
14	2.32411689	9	1.77783848	8	2.68143598	5	1.02408058	6	2.68998154	7	1.51440444	5	1.60316546	13	1.54226626
85	7.0385163	63	6.207584	50	8.35948865	60	6.12981882	31	6.93253397	50	5.39567896	34	5.43775358	125	7.39704535
11	2.49446533	7	1.88887269	6	2.74715745	9	2.51803342	3	1.83727497	6	1.77316822	5	2.18994497	8	1.29646515
28	2.37525883	24	2.42261283	9	1.54149788	8	0.83729229	49	11.225795	10	1.10552053	7	1.14691006	27	1.63682688
27	11.0210014	29	14.0855935	28	23.0761225	26	13.0937738	21	23.1496647	33	17.5543654	25	19.7095048	43	12.5433003
17	2.14482788	21	3.15270024	8	2.03789134	7	1.08962173	11	3.74804095	13	2.13747369	13	3.16785495	29	2.61473449
19	2.16848406	10	1.35807106	3	0.69130771	9	1.26729971	8	2.46581641	3	0.44620845	5	1.10217625	14	1.14187021
5	3.21256898	2	1.52908742	0	0	0	0	0	0	1	0.83732944	0	0	0	0
0	0	4	4.34582739	0	0	1	1.12648864	0	0	0	0	0	0	0	0
17	9.21605727	27	17.4172614	6	6.56742327	17	11.3704947	3	4.39223548	3	2.11949014	3	3.14120232	11	4.26162275
2	0.21220639	7	0.88378447	0	0	0	0	0	0	0	0	0	0	0	0
6	2.93203479	3	1.74445184	1	0.98665514	1	0.60290941	1	1.31973273	3	1.91052632	0	0	1	0.34922389
14	4.45633422	9	3.40888296	6	3.85610174	9	3.53448728	5	4.29821209	5	2.07411879	0	0	12	2.72971332
49	5.80236009	58	8.17252865	56	13.3888766	55	8.03536262	74	23.665105	83	12.8085684	36	8.23359516	134	11.3396453
5	1.42195676	6	2.03042755	0	0	1	0.35087351	5	3.84020589	0	0	0	0	3	0.60971056
31	2.59799057	28	2.79224659	20	3.38417946	27	2.7917327	27	6.11093633	18	1.9659039	12	1.94238598	56	3.35389898
12	7.30436738	10	7.24304566	3	3.68697447	16	12.0158788	2	3.28775522	5	3.96629734	3	3.52696401	2	0.86999635
1	0.88963449	1	1.05859898	0	0	0	0	0	0	0	0	0	0	0	0
54	6.59707828	29	4.21575862	6	1.47998271	18	2.71309235	34	11.2177282	19	3.02500001	15	3.5393829	23	2.00803735
40	5.19786442	24	3.71104362	11	2.88605867	20	3.2064845	19	6.66786311	20	3.38695054	15	3.76473687	47	4.36464461
46	15.4951871	62	24.8513819	27	18.3632806	42	17.4551055	15	13.6457801	45	19.7544712	16	10.4096802	92	22.1468974
2	1.15652483	3	2.06426801	0	0	1	0.7134428	0	0	0	0	0	0	1	0.41324827
108	18.1900023	88	17.6364646	35	11.9021263	62	12.8835302	68	30.930435	82	17.9985182	47	15.2892178	153	18.4156266
16	3.22751117	6	1.44018699	8	3.25825651	11	2.73762936	12	6.53728072	12	3.15458998	12	4.67527787	21	3.02728381
0	0	0	0	0	0	4	0.52362775	0	0	0	0	0	0	0	0
15	2.23363165	4	0.70876155	3	0.90196371	7	1.28603424	9	3.61935285	6	1.1643551	4	1.15042603	6	0.63849518

gsyne_1641	Synechococcus_assembled_mapped	RF-1 domain protein				PF00472.15	1433984	1434389	-1	169	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba
gsyne_1642	Synechococcus_assembled_mapped	mazG family protein				TIGR00444	1433178	1434003	1	157	fig|1129.58.p	Nucleosides and Nucleotides	Detoxification	Nucleoside triphosphate pyropho
gsyne_1643	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_F	1434394	1436185	1	156	fig|1129.58.peg.1647			
gsyne_1644	Synechococcus_assembled_mapped	methyltransferase domain protein				PF13659.1	1436211	1437084	1	703	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Polyamine Metabolism
gsyne_1645	Synechococcus_assembled_mapped	agmatinase	speB	3.5.3.11	GO:0008295,GO:0008783	TIGR01230	1437088	1437949	1	185	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Polyamine Metabolism
gsyne_1646	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	1437950	1438346	-1	157	fig|1129.58.peg.1650			
gsyne_1647	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1438456	1438693	-1	156	fig|1129.58.peg.1651			
gsyne_1648	Synechococcus_assembled_mapped	glycine cleavage system T protein	gcvT	2.1.2.10	GO:0004047,GO:0005737,G(	TIGR00528	1438848	1439988	1	109	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine cleavage system
gsyne_1649	Synechococcus_assembled_mapped	aspartate--tRNA ligase	aspS	6.1.1.-	GO:0004815,GO:0005737,G(	TIGR00459	1440055	1441885	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Asp and As
gsyne_165	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	133703	134006	-1	856	fig|1129.58.peg.164			
gsyne_1650	Synechococcus_assembled_mapped	RNA polymerase sigma factor, cyanobacterial RpoD-like family protein				TIGR02997	1441978	1443124	1	135	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors cyanobacte
gsyne_1651	Synechococcus_assembled_mapped	CTP synthase	pyrG	6.3.4.2	GO:0003883,GO:0009220	TIGR00337	1443178	1444834	1	126	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	pyrimidine conversions
gsyne_1652	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	1444830	1445481	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_1653	Synechococcus_assembled_mapped	queuosine biosynthesis protein QueC	queC		GO:0008616	TIGR00364	1445528	1446206	1	157	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_1654	Synechococcus_assembled_mapped	chorismate binding enzyme family protein				PF00425.13	1446205	1447528	1	185	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn
gsyne_1655	Synechococcus_assembled_mapped	aminotransferase class IV family protein				PF01063.14	1447524	1448340	1	703	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn
gsyne_1656	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1448356	1448839	-1	156	fig|1129.58.peg.1660			
gsyne_1657	Synechococcus_assembled_mapped	urea ABC transporter, ATP-binding prot	urtE		GO:0005524,GO:0009898,G(	TIGR03410	1450496	1451198	-1	142	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_1658	Synechococcus_assembled_mapped	amino acid permease family protein				PF00324.16	1448968	1450507	1	142	fig|1129.58.peg.1661			
gsyne_1659	Synechococcus_assembled_mapped	urea ABC transporter, ATP-binding prot	urtD		GO:0005524,GO:0009898,G(	TIGR03411	1451200	1451953	-1	142	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_166	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	134405	134684	1	154	fig|1129.58.peg.165			
gsyne_1660	Synechococcus_assembled_mapped	urea ABC transporter, permease protei	urtC		GO:0005887,GO:0015840,G(	TIGR03408	1451985	1453092	-1	142	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_1661	Synechococcus_assembled_mapped	urea ABC transporter, permease protei	urtB		GO:0005887,GO:0015840,G(	TIGR03409	1453143	1454301	-1	142	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_1662	Synechococcus_assembled_mapped	periplasmic binding domain protein				PF13433.1	1454426	1455593	-1	157	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_1663	Synechococcus_assembled_mapped	urease accessory protein UreG	ureG		GO:0016530,GO:0019627,G(	TIGR00101	1455900	1456491	-1	160	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1664	Synechococcus_assembled_mapped	ABC transporter substrate binding family protein				PF04392.7	1456505	1457516	-1	141	fig|1129.58.peg.1668			
gsyne_1665	Synechococcus_assembled_mapped	ureF family protein				PF01730.11	1457588	1458269	-1	160	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1666	Synechococcus_assembled_mapped	ureE urease accessory , N-terminal domain protein				PF02814.10	1458265	1458769	-1	160	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1667	Synechococcus_assembled_mapped	ureD urease accessory family protein				PF01774.12	1458861	1459773	1	160	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1668	Synechococcus_assembled_mapped	urease subunit gamma	ureA	3.5.1.5	GO:0019627,GO:0009039,G(	UniRef100_C	1459845	1460148	1	92,141,703	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1669	Synechococcus_assembled_mapped	urease subunit beta	ureB	3.5.1.5	GO:0006807,GO:0009039,G(	UniRef100_C	1460170	1460488	1	141,160,703	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_167	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	135052	135514	1	157	fig|1129.58.peg.166			
gsyne_1670	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1462191	1462569	-1	856	fig|1129.58.peg.1675			
gsyne_1671	Synechococcus_assembled_mapped	urease, alpha subunit	ureC	3.5.1.5	GO:0009039,GO:0016151,G(	TIGR01792	1460494	1462207	1	160	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urease subunits
gsyne_1672	Synechococcus_assembled_mapped	A circularly permuted ATPgrasp family protein				PF04174.8	1462702	1464142	1	185	fig|1129.58.peg.1676			
gsyne_1673	Synechococcus_assembled_mapped	A predicted alpha-helical domain with a conserved ER motif family protein				PF04168.7	1464135	1465176	1	157	fig|1129.58.peg.1677			
gsyne_1674	Synechococcus_assembled_mapped	transglutaminase-like superfamily protein				PF01841.14	1465160	1466030	1	138	fig|1129.58.peg.1678			
gsyne_1675	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1468122	1468284	-1	856				
gsyne_1676	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09899.4	1466088	1468134	1	156	fig|1129.58.peg.1679			
gsyne_1677	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1468271	1468475	1	856	fig|1129.58.peg.1680			
gsyne_1678	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1468484	1468961	-1	156	fig|1129.58.peg.1681			
gsyne_1679	Synechococcus_assembled_mapped	uroporphyrinogen-III C-methyltransfera	cobA	2.1.1.107	GO:0004851,GO:0019354	TIGR01469	1469562	1470357	-1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi
gsyne_168	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	135541	135718	1	856	fig|1129.58.peg.167			
gsyne_1680	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1469198	1469576	1	156	fig|1129.58.peg.1682			
gsyne_1681	Synechococcus_assembled_mapped	putative dNA mismatch repair proteins, mutS fa			GO:0046872,GO:0016829,G(	UniRef100_C	1470353	1471013	-1	92,141,703	fig|1129.58.peg.1684			
gsyne_1682	Synechococcus_assembled_mapped	putative ferredoxin-nitrite reductase			GO:0048307,GO:0055114,G(	UniRef100_C	1471022	1471241	1	703	fig|1129.58.peg.1685			
gsyne_1683	Synechococcus_assembled_mapped	ferredoxin--nitrite reductase, chloropla	NIR1	1.7.7.1	GO:0006810,GO:0016020,G(	UniRef100_C	1471523	1473098	1	##########	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Nitrate and nitrite ammonification
gsyne_1684	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1473184	1473319	1	156	fig|1129.58.peg.1687			
gsyne_1685	Synechococcus_assembled_mapped	formate/nitrite transporter family protein				PF01226.12	1473422	1474277	1	143	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Nitrate and nitrite ammonification
gsyne_1686	Synechococcus_assembled_mapped	HEAT repeats family protein				PF13646.1	1474280	1475078	1	185	fig|1129.58.peg.1689			
gsyne_1687	Synechococcus_assembled_mapped	cyanate hydratase	cynS	4.2.1.104	GO:0008824,GO:0009636	TIGR00673	1475134	1475548	-1	96	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Cyanate hydrolysis
gsyne_1688	Synechococcus_assembled_mapped	glycosyl transferase family, helical bundle domain protein				PF02885.12	1475819	1476905	1	703	fig|1129.58.peg.1691			
gsyne_1689	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1476907	1477117	-1	856	fig|1129.58.peg.1692			
gsyne_169	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	135982	136183	1	856	fig|1129.58.peg.168			
gsyne_1690	Synechococcus_assembled_mapped	putative lipoprotein			GO:0008150,GO:0003674,G(	lipoP	1477141	1477300	-1	88	fig|1129.58.peg.1693			
gsyne_1691	Synechococcus_assembled_mapped	nitrate reductase	narB	1.7.99.4	GO:0042128,GO:0009055,G(	UniRef100_P	1477783	1480039	-1	141,160,703	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Nitrate and nitrite ammonification
gsyne_1692	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR02664	1477358	1477823	1	185	fig|1129.58.peg.1694			
gsyne_1693	Synechococcus_assembled_mapped	nitrite transporter family protein	narK		GO:0005887,GO:0015514,G(	TIGR00886	1480129	1481686	-1	143	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Nitrate and nitrite ammonification
gsyne_1694	Synechococcus_assembled_mapped	mobA-like NTP transferase domain protein				PF12804.2	1482064	1482607	1	703	fig|1129.58.peg.1698			
gsyne_1695	Synechococcus_assembled_mapped	molybdenum Cofactor Synthesis C family protein				PF06463.8	1482606	1483635	1	82	fig|1129.58.peg.1699			
gsyne_1696	Synechococcus_assembled_mapped	sulfite exporter TauE/SafE family protein				PF01925.14	1483645	1484221	-1	141	fig|1129.58.peg.1700			
gsyne_1697	Synechococcus_assembled_mapped	HPP family protein				PF04982.8	1484382	1484823	-1	185	fig|1129.58.peg.1701			
gsyne_1698	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1484188	1484404	1	856				
gsyne_1699	Synechococcus_assembled_mapped	molybdenum cofactor synthesis domain protein			GO:0003824,GO:0006777	TIGR00177	1484912	1485314	-1	76	fig|1129.58.peg.1702			
gsyne_17	Synechococcus_assembled_mapped	NADH dehydrogenase transmembrane subunit				PF10716.4	10980	11256	-1	703	fig|1129.58.peg.17			
gsyne_170	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04250.8	136201	136900	1	156	fig|1129.58.peg.169			
gsyne_1700	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1485415	1485568	-1	856				
gsyne_1701	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1485317	1485431	1	856				
gsyne_1702	Synechococcus_assembled_mapped	thiS family protein				PF02597.15	1485568	1485748	1	162	fig|1129.58.peg.1703			
gsyne_1703	Synechococcus_assembled_mapped	moaE family protein				PF02391.12	1485758	1486211	1	82	fig|1129.58.peg.1704			
gsyne_1704	Synechococcus_assembled_mapped	moeA C-terminal region family protein				PF03454.10	1486213	1487449	-1	82	fig|1129.58.peg.1705			
gsyne_1705	Synechococcus_assembled_mapped	molybdenum cofactor biosynthesis pro	moaC		GO:0003824,GO:0006777	TIGR00581	1487441	1487999	-1	82	fig|1129.58.peg.1706			
gsyne_1706	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1488075	1488216	1	856	fig|1129.58.peg.1707			
gsyne_1707	Synechococcus_assembled_mapped	sugar (and other) transporter family protein				PF00083.19	1488264	1489521	1	141	fig|1129.58.peg.1708			
gsyne_1708	Synechococcus_assembled_mapped	polyphosphate kinase 1	ppk1	2.7.4.1	GO:0006799,GO:0008976,G(	TIGR03705	1489557	1491696	1	703	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Polyphosphate
gsyne_1709	Synechococcus_assembled_mapped	RNA polymerase sigma factor, cyanobacterial RpoD-like family protein				TIGR02997	1491907	1492873	1	135	fig|1129.58.p	RNA Metabolism	Transcription	Transcription initiation, bacterial s
gsyne_171	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	136908	137115	-1	856	fig|1129.58.peg.170			
gsyne_1710	Synechococcus_assembled_mapped	cytidylyltransferase family protein				PF01148.15	1492883	1493561	1	176	fig|1129.58.peg.1711			
gsyne_1711	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1493565	1493898	-1	156	fig|1129.58.peg.1712			
gsyne_1712	Synechococcus_assembled_mapped	3-deoxy-7-phosphoheptulonate synthase		2.5.1.54	GO:0003849,GO:0009423	TIGR00034	1494032	1495106	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_1713	Synechococcus_assembled_mapped	aconitate hydratase 2	acnB	4.2.1.3	GO:0003994,GO:0006099	TIGR00117	1495246	1497862	1	120	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	TCA Cycle
gsyne_1714	Synechococcus_assembled_mapped	voltage gated chloride channel family protein				PF00654.15	1497869	1499243	1	143	fig|1129.58.peg.1715			
gsyne_1715	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1499258	1500335	-1	856	fig|1129.58.peg.1716			
gsyne_1716	Synechococcus_assembled_mapped	O-Antigen ligase family protein				PF04932.10	1502113	1503430	-1	90	fig|1129.58.peg.1718			
gsyne_1717	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	1500588	1502142	1	703	fig|1129.58.peg.1717			
gsyne_1718	Synechococcus_assembled_mapped	formyltetrahydrofolate deformylase	purU	3.5.1.10	GO:0008864,GO:0009152	TIGR00655	1503441	1504314	-1	125	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	5-FCL-like protein
gsyne_1719	Synechococcus_assembled_mapped	photosystem II protein PsbQ	psbQ		GO:0003674,GO:0009654,G(	TIGR03042	1504460	1504952	1	164	fig|1129.58.peg.1720			
gsyne_172	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	137302	137437	1	856	fig|1129.58.peg.171			
gsyne_1720	Synechococcus_assembled_mapped	FAD dependent oxidoreductase family protein				PF01266.19	1505026	1506076	1	703	fig|1129.58.peg.1721			
gsyne_1721	Synechococcus_assembled_mapped	phosphate ABC transporter, phosphate	pstS		GO:0006817,GO:0015415,G(	TIGR00975	1506163	1507162	1	143	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1722	Synechococcus_assembled_mapped	chaperone protein DnaK	dnaK		GO:0005524,GO:0006457,G(	TIGR02350	1507371	1509273	-1	95	fig|1129.58.p	Protein Metabolism	Protein folding	Protein chaperones
gsyne_1723	Synechococcus_assembled_mapped	shikimate 5-dehydrogenase	aroE	1.1.1.25	GO:0004764,GO:0009423	TIGR00507	1509326	1510256	1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_1724	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1510280	1510742	1	88	fig|1129.58.peg.1725			
gsyne_1725	Synechococcus_assembled_mapped	ribosomal protein S6	rpsF		GO:0000314,GO:0003735,G(	TIGR00166	1510831	1511200	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_1726	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1511452	1511659	1	856	fig|1129.58.peg.1727			
gsyne_1727	Synechococcus_assembled_mapped	argininosuccinate synthase	argG	6.3.4.5	GO:0004055,GO:0042450	TIGR00032	1511661	1512819	-1	73	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis extended
gsyne_1728	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1512860	1513085	-1	856	fig|1129.58.peg.1729			
gsyne_1729	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11332.3	1513240	1513516	1	156	fig|1129.58.peg.1730			
gsyne_173	Synechococcus_assembled_mapped	thiamine pyrophosphate enzyme, C-terminal TPP binding domain protein				PF02775.16	137441	139052	-1	157	fig|1129.58.peg.172			
gsyne_1730	Synechococcus_assembled_mapped	phospho-N-acetylmuramoyl-pentapept	mraY	2.7.8.13	GO:0008963,GO:0009252	TIGR00445	1513529	1514624	1	89	fig|1129.58.peg.1731			
gsyne_1731	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1514623	1514866	1	156	fig|1129.58.peg.1732			
gsyne_1732	Synechococcus_assembled_mapped	putative 5'-phosphoribosylglycinamide transformylase			GO:0016740,GO:0004644	UniRef100_A	1514889	1515060	-1	703	fig|1129.58.peg.1733			
gsyne_1733	Synechococcus_assembled_mapped	phosphoribosylglycinamide formyltrans	purT	2.1.2.-	GO:0004644,GO:0009152	TIGR01142	1515110	1516301	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_1734	Synechococcus_assembled_mapped	cell envelope-related function transcriptional attenuator common domain protein				TIGR00350	1516441	1517419	1	129	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	Cell envelope-associated LytR-C
gsyne_1735	Synechococcus_assembled_mapped	sucrose-phosphate synthase, putative, glycosyltransf		2.4.1.14		TIGR02472	1517423	1519544	-1	703	fig|1129.58.peg.1736			
gsyne_1736	Synechococcus_assembled_mapped	excinuclease ABC subunit B	uvrB	3.1.25.-	GO:0006289,GO:0009380,G(	TIGR00631	1519658	1521668	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, UvrABC system
gsyne_1737	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04020.8	1521686	1522124	-1	156	fig|1129.58.peg.1738			
gsyne_1738	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04481.7	1522186	1522942	-1	156	fig|1129.58.peg.1739			
gsyne_1739	Synechococcus_assembled_mapped	tRNA(Ile)-lysidine synthetase	tilS	6.3.4.-	GO:0006400,GO:0016879	TIGR02432	1522940	1523978	1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_174	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	139070	139187	1	856				
gsyne_1740	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1524003	1525434	1	856	fig|1129.58.peg.1741			
gsyne_1741	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR00649	1525455	1527432	-1	156	fig|1129.58.peg.1742			
gsyne_1742	Synechococcus_assembled_mapped	dihydrodipicolinate synthase	dapA		GO:0008840,GO:0009089	TIGR00674	1527518	1528439	-1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa
gsyne_1743	Synechococcus_assembled_mapped	aspartate-semialdehyde dehydrogenas	asd	1.2.1.11	GO:0004073,GO:0009086,G(	TIGR01296	1528441	1529476	-1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Threonine and Homoserine Biosy
gsyne_1744	Synechococcus_assembled_mapped	trigger factor	tig	5.2.1.8	GO:0003755,GO:0005854,G(	TIGR00115	1529769	1531188	1	95	fig|1129.58.peg.1745			
gsyne_1745	Synechococcus_assembled_mapped	ATP-dependent Clp endopeptidase, pro	clpP	3.4.21.92	GO:0004176,GO:0004252,G(	TIGR00493	1531322	1531907	1	138	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria
gsyne_1746	Synechococcus_assembled_mapped	ATP-dependent Clp protease, ATP-bind	clpX		GO:0004252,GO:0005524,G(	TIGR00382	1532010	1533363	1	95,138	fig|1129.58.p	Protein Metabolism	Protein degradation	Proteolysis in bacteria, ATP-depe
gsyne_1747	Synechococcus_assembled_mapped	lecithin retinol acyltransferase family protein				PF04970.8	1533375	1534044	1	703	fig|1129.58.peg.1748			
gsyne_1748	Synechococcus_assembled_mapped	DNA polymerase III, subunit gamma an	dnaX	2.7.7.7	GO:0003887,GO:0006260,G(	TIGR02397	1534053	1535922	1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication
gsyne_1749	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	1535937	1537293	-1	90	fig|1129.58.peg.1750			
gsyne_175	Synechococcus_assembled_mapped	phenolic acid decarboxylase subunit C	bsdC	4.1.1.61	GO:0019439,GO:0018799,G(	UniRef100_P	139333	140782	1	92,703	fig|1129.58.peg.173			
gsyne_1750	Synechococcus_assembled_mapped	spoIID/LytB domain protein			GO:0003674,GO:0005575,G(	TIGR02669	1537317	1538829	-1	157	fig|1129.58.peg.1751			
gsyne_1751	Synechococcus_assembled_mapped	ribosomal protein L35	rpmI		GO:0000315,GO:0003735,G(	TIGR00001	1538922	1539120	1	158	fig|1129.58.p	Virulence, Disease and Defense	Invasion and intracellular resis	Mycobacterium virulence operon
gsyne_1752	Synechococcus_assembled_mapped	ribosomal protein L20	rplT		GO:0000315,GO:0003735,G(	TIGR01032	1539222	1539513	1	158	fig|1129.58.p	Virulence, Disease and Defense	Invasion and intracellular resis	Mycobacterium virulence operon
gsyne_1753	Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	1539548	1540070	1	185	fig|1129.58.p	Photosynthesis	Electron transport and photopt	Photosystem I
gsyne_1754	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1540095	1540626	-1	156	fig|1129.58.peg.1755			
gsyne_1755	Synechococcus_assembled_mapped	thiazole biosynthesis ThiG family protein				PF05690.9	1540709	1541525	1	162	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Cofactors, Vitamins, Prosthetic	Thiamin biosynthesis
gsyne_1756	Synechococcus_assembled_mapped	putative high light inducible protein				UniRef100_B	1541594	1541762	1	185	fig|1129.58.peg.1757			
gsyne_1757	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein				PF01370.16	1541830	1543024	1	119	fig|1129.58.peg.1758			
gsyne_1758	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1543044	1544196	1	90	fig|1129.58.peg.1759			
gsyne_1759	Synechococcus_assembled_mapped	penicillin-binding protein 2	mrdA		GO:0003824,GO:0009252	TIGR03423	1544196	1545981	-1	89	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	16S rRNA modification within P s
gsyne_176	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF08327.6	141054	141453	1	156	fig|1129.58.peg.175			
gsyne_1760	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1545992	1546376	-1	156	fig|1129.58.peg.1761			
gsyne_1761	Synechococcus_assembled_mapped	putative membrane protein				UniRef100_B	1546421	1547033	-1	88	fig|1129.58.peg.1762			
gsyne_1762	Synechococcus_assembled_mapped	GMP synthase (glutamine-hydrolyzing),	guaA	6.3.5.2	GO:0003922,GO:0006177	TIGR00888	1547103	1548699	-1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_1763	Synechococcus_assembled_mapped	cobalamin biosynthesis protein CbiD	cbiD		GO:0005737,GO:0009236	TIGR00312	1548733	1549885	-1	79	fig|1129.58.peg.1764			
gsyne_1764	Synechococcus_assembled_mapped	soluble hydrogenase 42 kDa subunit		1.12.-.-	GO:0030170,GO:0005737,G(	UniRef100_P	1549977	1551129	1	141,703	fig|1129.58.p	Carbohydrates	CO2 fixation	Photorespiration (oxidative C2 cy
gsyne_1765	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1551199	1551661	1	156	fig|1129.58.peg.1766			
gsyne_1767	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1551843	1552053	-1	856	fig|1129.58.peg.1767			
gsyne_1768	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1552166	1552409	-1	156	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthe
gsyne_1769	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1552434	1552677	-1	856	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_177	Synechococcus_assembled_mapped	ubiE/COQ5 methyltransferase family protein				PF01209.13	141479	142238	-1	703	fig|1129.58.peg.176			
gsyne_1770	Synechococcus_assembled_mapped	membrane AbrB duplication domain protein				TIGR03082	1552760	1553285	1	88	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation elongation factors ba

2.93339059	4.5094E-05	2.46052931		8	3.37814703	6	3.20240347	11	3.81543436	12	3.24523087	9	4.32213158	14	4.70239286	113	74.4990483	1079	205.201893		0.420215	1.74857931	0.54467347	1.51061354
4.62086296	1.0985E-14	3.43969666		21	4.3532031	12	3.14417795	13	2.21358258	19	2.52242945	20	4.71505263	16	2.63822561	265	85.7668046	2311	215.755034		1	-1.0791621	0.60076706	1.25608297
2.36376445	9.3428E-16	2.58117091		37	3.5330495	29	3.50011434	50	3.92175757	90	5.50384633	45	4.88683219	62	4.70914432	610	90.9413828	5038	216.659391		0.96089442	1.03284308	0.28787688	1.52583844
1.43162722	0.41215727	-1.1253253		35	6.85641955	27	6.68542992	39	6.27562072	82	10.2877164	63	14.0357881	99	15.4264803	327	100.014004	2551	225.066655		0.41478648	1.26418117	0.44841725	1.25916844
-1.1774228	2.6295E-07	-1.8943527		40	7.94511932	34	8.53602318	63	10.2788309	124	15.7738574	101	22.8154333	149	23.5412226	270	83.731316	2534	226.682712		0.86147802	-1.0622041	0.39198635	1.32304504
-21.882928	1.982E-75	-27.057142		168	72.5533851	168	91.7051902	731	259.315524	1087	300.644826	850	417.478618	1042	357.946755	172	115.973981	1146	222.897077		0.49442119	1.28754279	0.86569656	1.06789127
-42.640618	2.7618E-63	-19.624217		73	52.676644	62	56.5487701	589	349.11883	903	417.309989	259	212.550395	317	181.951991	83	93.5097834	433	140.719568		0.52781746	-1.2246468	0.2384981	-1.4483851
2.21903057	0.00027645	1.63363498		19	2.85031156	18	3.41308791	28	3.45032103	57	5.4763271	50	8.53052285	46	5.48907137	326	76.3554522	3001	202.757107		0.93879366	1.07360634	0.60886325	1.2470371
2.61810726	3.061E-19	3.10291737		44	4.11192487	32	3.77988606	48	3.68465196	71	4.24939043	46	4.88896851	38	2.82473951	547	79.811145	4971	209.222128		0.50937685	1.28148002	0.032971	2.0927739
4.11298865	0.00016335	2.55220679		7	3.95092691	6	4.28044028	9	4.17259474	5	1.80736868	9	5.77710657	10	4.48955471	97	85.4784051	933	237.166834		0.67245624	-1.3673171	0.35895004	-2.1689771
-3.0000947	3.9942E-13	-2.9403292		157	23.4292625	111	20.9371797	266	32.6064369	436	41.6697839	265	44.9750603	308	36.560489	432	100.652933	3536	237.652605		0.48248792	1.28005191	0.98946579	1.00842803
-1.5682857	0.22609267	-1.2173177		93	9.60431068	107	13.9670043	202	17.1355229	296	19.577208	163	19.1442241	161	13.2254799	589	94.9690879	4869	226.461502		0.440706	1.31219482	0.35777673	1.38805651
1.66396595	9.9037E-05	1.94773307		8	2.10161221	11	3.65251087	30	6.47361088	34	5.72028023	20	5.97529711	26	5.43298188	183	75.0580722	1715	202.907489		0.28006785	1.70666636	0.09995949	2.23680144
2.30019162	0.00973397	1.51592654		23	5.8015191	9	2.86941019	18	3.72948733	30	4.84630717	25	7.1716785	36	7.22301811	197	77.5825119	1730	196.53113		0.65877916	-1.2677969	0.46893097	1.33959919
5.11375544	7.4173E-14	3.07997824		37	4.78283572	18	2.94098278	16	1.69889471	28	2.31802205	32	4.7043609	29	2.98183804	389	78.508569	3619	210.689882		0.56931206	1.21687683	1	1.00940041
2.15746795	0.0010871	1.82013509		27	5.65870677	22	5.82790337	41	7.05829853	26	3.48981629	29	6.91223249	40	6.66830921	267	87.3671979	2360	222.759783		0.93590467	-1.0266368	0.36700673	1.37015139
-3.8234037	8.0496E-11	-2.6742513		49	17.3497225	47	21.0344203	168	48.8616891	164	37.1891364	95	38.2548913	106	29.8541446	170	93.9786269	1349	215.11949		0.21895906	1.46801041	0.6120864	1.17753063
-5.8256494	0.10860959	-1.2486562		18	4.3850947	15	4.61885116	257	51.4283198	389	60.6920582	54	14.9612247	62	12.0143554	203	77.2122539	1713	187.946911		1	-1.01054	0.45311778	-1.4412751
1.19113501	2.5611E-08	2.03966161		35	3.88931401	25	3.51140731	99	9.03655507	120	8.54008124	57	7.20355263	51	4.50793301	471	81.7164689	4144	207.393943		0.63121702	1.19271537	0.51895742	1.25140354
-4.5446562	0.5943926	-1.0695238		19	4.31521271	11	3.15774844	235	43.8408748	343	49.8905762	61	15.7559777	53	9.57473561	223	79.0746342	2027	207.335522		0.58321061	-1.3759335	0.09271002	2.2940178
4.92368681	0.07951343	1.9625503		13	7.96861295	10	7.74775033	2	1.00700614	9	3.53311426	1	0.697118	22	10.7266565	98	93.7884108	797	220.023495		0.02618933	-4.9732744	0.27736023	-2.0848573
-6.2364142	0.03337653	-1.4257351		36	5.56158352	34	6.63912914	552	70.0483293	759	75.0954339	138	24.246104	114	14.0088707	394	95.0333208	3234	225.012858		0.10468112	-1.7223511	0.19630568	-1.5376876
-6.1478001	1.6259E-05	-2.0282124		61	9.00875673	48	8.9600926	657	79.7008834	757	71.598957	197	33.0878208	204	23.9644522	433	99.8404757	3646	242.506312		0.01360568	-2.3385292	0.1345313	-1.6685669
-65.000672	1.9673E-55	-12.156327		59	8.6461893	39	7.2239307	6191	745.240199	7916	742.940965	1016	169.329782	1240	144.542887	395	90.3760891	3485	230.010079		0.0156088	-2.2966096	0.37541817	-1.3519085
2.09125849	6.8465E-05	1.78504175		22	6.3661781	18	6.58362134	24	5.70466421	31	5.74504704	25	8.22740783	29	6.67507906	223	100.749915	1744	227.286657		0.56199538	-1.3222418	0.80068865	1.11264361
1.20485109	0.00434261	-1.3645618		70	11.8410569	57	12.1871883	61	8.475884	80	8.66678868	89	17.1217972	106	14.2626625	305	80.551937	2673	203.639839		0.63664344	-1.1852604	0.69223056	-1.1387133
1.91605285	2.9497E-11	4.13717136		11	2.76241649	8	2.53935077	35	7.21983475	28	4.50329394	8	2.28482727	17	3.39584381	225	88.2191179	1909	215.910497		1	-1.0721864	0.78372316	-1.2631806
-1.3678348	0.00265822	1.64320766		15	5.08984207	11	4.71782654	50	13.9362457	79	17.1678508	25	9.64761513	23	6.20787833	172	91.1224137	1459	222.966541		0.57860144	-1.4277067	0.74979165	-1.2752895
-1.8541779	0.76748807	-1.0375118		37	6.93825839	29	6.87357981	123	18.9459592	147	17.6539492	62	13.2223104	66	9.84453017	260	76.121233	2333	197.031127		0.03789897	1.84181564	0.03789897	1.86583678
-3.4021302	0.00028453	-1.7569688		15	8.46627195	9	6.42066042	76	35.2352444	128	46.2686382	40	25.6760292	48	21.5498626	113	99.5779358	914	232.33707		0.13545503	1.83490548	0.56480073	1.32729707
1.04297612	0.08702458	1.42115649		12	6.4535356	11	7.47730998	32	14.1360862	32	11.0215388	13	7.95109111	27	11.5500148	132	110.834283	998	241.723215		0.31037868	-1.883248	0.74263985	-1.3096276
9.78451702	0.00303398	2.32610323		21	7.77357697	4	1.87153449	9	2.73657187	1	0.23707044	17	7.15677632	20	5.88889644	214	123.679893	1383	230.565937		0.18582674	-2.5441641	0.72150452	-1.232912
-1.5173277	0.6695569	1.10173333		14	6.33402568	8	4.5748621	25	9.29083043	69	19.9929402	22	11.3198684	24	8.63704811	112	79.1140336	928	189.091113		0.43487569	1.40291747	0.71968165	1.16334331
-1.0898232	0.00141604	1.49391028		67	6.68899735	65	8.2023031	140	11.4809281	192	12.2761798	79	8.96974767	93	7.38535681	567	88.3797972	4690	210.877586		0.35022539	-1.368861	0.40853218	1.30720248
-6.6084005	0.0649755	-1.3849316		49	5.81938609	24	3.6027039	693	67.6047276	1004	76.364339	167	22.5561242	130	12.2808028	454	84.1822764	4127	220.742989		0.10916098	-1.8274584	0.73046765	-1.1844635
-6.3252318	0.07288347	-1.3395048		23	3.778511	13	2.69943232	519	70.0362611	698	73.4385459	109	20.3650868	109	14.2436622	367	94.1331603	2924	216.342369		0.61442962	1.24383749	0.13428571	1.75586401
-3.0256329	0.8161157	-1.0212015		26	5.11090348	20	4.96924676	178	28.7413441	272	34.2427809	65	14.5313044	62	9.69434193	252	77.340788	2406	213.005742		0.59373482	-1.2361729	0.47651368	-1.3315935
-2.9228217	0.59955799	1.25881054		2	2.11134189	0	0	32	27.7486136	28	18.9305134	10	12.0059211	4	3.35885204	46	75.8176155	286	135.977158		0.43162865	2.48733774	0.65897719	1.47667828
-15.876219	1.5823E-12	-3.3793443		57	4.7644504	34	3.59213879	2215	152.080813	3122	167.127011	492	46.7702801	463	30.7837312	604	78.8240261	5358	201.702844		0.1424315	-1.7493019	0.52387539	-1.3100757
-11.457375	2.2375E-16	-17.97433		432	362.157233	490	519.213209	299	205.895733	603	323.747573	505	481.472746	652	434.77376	215	281.407454	584	220.494429		0.89012249	-1.0494445	0.11759031	-1.7010106
-9.901271	8.7402E-22	-7.9291324		349	125.126885	350	158.609606	561	165.215507	698	160.271544	388	158.206326	476	135.748322	300	167.930732	1518	245.114122		0.95240633	-1.0219939	0.19997655	-1.5512
1.05792034	4.2382E-05	-1.866104		59	12.6919533	56	15.2265222	49	8.65835277	81	11.1593081	74	18.1040228	142	24.2978089	252	84.6370888	2104	203.841942		0.37211682	-1.3484879	0.70803909	1.12970676
2.28533475	0.16197955	1.74180633		7	6.76345115	3	3.66376668	5	3.9682869	4	2.47517609	2	2.19769402	8	6.14840713	30	45.255909	358	155.784664		0.82835864	-1.2399922	0.16709207	-5.7072554
-1.4309326	2.9112E-16	-4.9773628		92	41.6235973	138	78.9163712	41	15.2369619	79	22.8904678	136	69.9773684	211	75.934048	171	120.790176	1133	230.862318		0.74992202	1.1239911	0.16923776	-1.6337669
3.02596834	3.1434E-07	2.46802453		18	4.66414618	11	3.6027039	18	3.83120062	16	2.6551889	18	5.30443421	17	3.50389338	185	74.8436738	1611	188.003765		0.26924613	-1.9067536	1	-1.0487686
-8.1576368	0.00252538	-1.9937137		4	3.1236291	4	3.94816866	132	84.6712831	117	58.51418	29	25.7551676	24	14.9077817	52	63.3996023	525	184.641844		0.84256806	1.19270412	0.05843882	-27.544442
-9.6607996	8.5741E-06	-2.0622878		42	4.56049849	26	3.56839244	1187	105.870871	1645	114.394388	254	31.3663263	256	22.1108432	536	90.8681186	4611	225.491152		0.03396255	-2.2967934	0.57061736	1.24540568
-21.560212	5.0161E-11	-4.8902593		3	3.80041541	2	3.20240347	149	155.045378	154	124.941389	36	51.8655789	23	23.1760791	26	51.4241218	225	128.370044		0.72044645	-1.7962194	0.72044645	-1.6892396
-9.8212322	1.3949E-06	-2.323078		25	5.00054659	9	2.27539194	670	110.081671	959	122.849069	172	39.1266648	151	24.0246312	297	92.7507946	2639	237.732314		0.9378266	1.03423478	0.82056453	1.11231951
-5.2084926	0.11797178	-1.2456195		19	4.07187365	10	2.70879993	319	56.1557351	420	57.6455484	66	16.0861288	84	14.3193166	265	88.668689	2202	212.534464		0.53970205	-1.3733157	1	-1.086948
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-3.4434687	2.0239E-27	-9.0646527		337	39.7745339	379	56.5393283	373	36.1615278	586	44.2943779	855	114.764674	1269	119.134935	555	102.270859	3904	207.518283		0.86046889	-1.0723341	0.40756729	-1.3828286
1.57611489	0.01353059	1.36165507		59	6.67334849	31	4.43189766	56	5.20286504	93	6.73675159	68	8.74717105	76	6.83766309	410	72.4034682	3737	190.364625		0.68064554	1.14014531	0.31030515	1.34971483
-8.6355242	4.3626E-28	-5.8396257		95	82.0544236	67	73.1458065	186	131.963577	219	121.142993	125	122.787829	108	74.2000952	112	151.035882	612	238.068082		0.39049596	1.33988623	0.76572175	1.1176978
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2.94201297	6.0156E-06	1.94078265		34	7.12577889	17	4.50337988	21	3.61522608	31	4.1609348	34	8.10399671	32	5.33464736	289	94.5659933	2315	218.512244		0.32715183	1.41747646	0.7354644	1.11885263
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38	3.14663081	28	2.75892622	16	2.67503637	34	3.473564	26	5.81438333	31	3.34532095	18	2.87881072	60	3.55058177
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3	1.50851065	4	2.39335422	0	0	2	1.24077009	2	2.7159717	2	1.3106026	1	0.97119299	1	0.35934632
25	3.83802489	9	1.64410727	15	4.6495032	17	3.21996309	8	3.3168504	28	5.60195624	1	0.29651467	32	3.51078174
13	4.06346563	5	1.85970091	0	0	6	2.31386855	5	4.22076683	4	1.62939783	1	0.60371456	5	1.11688721
35	3.39204211	37	4.26692271	33	6.45735472	25	2.98928548	20	5.23469406	30	3.78903265	13	2.43340813	82	5.67927786
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40	3.03019607	27	2.43385312	21	3.21201487	23	2.14967482	26	5.31927209	38	3.7515284	17	2.48735672	46	2.49031707
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38	3.00327634	24	2.25705842	19	3.03188561	34	3.31531507	15	3.20162951	19	1.95694762	17	2.59500997	54	3.04994165
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24	2.86150475	21	2.97935589	11	2.64803321	18	2.64782896	27	8.69390941	22	3.41837585	11	2.53311161	29	2.47096902
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19	1.8834833	16	1.88733075	5	1.00075021	12	1.46765376	3	0.80315163	3	0.38756391	3	0.57439128	9	0.63758304
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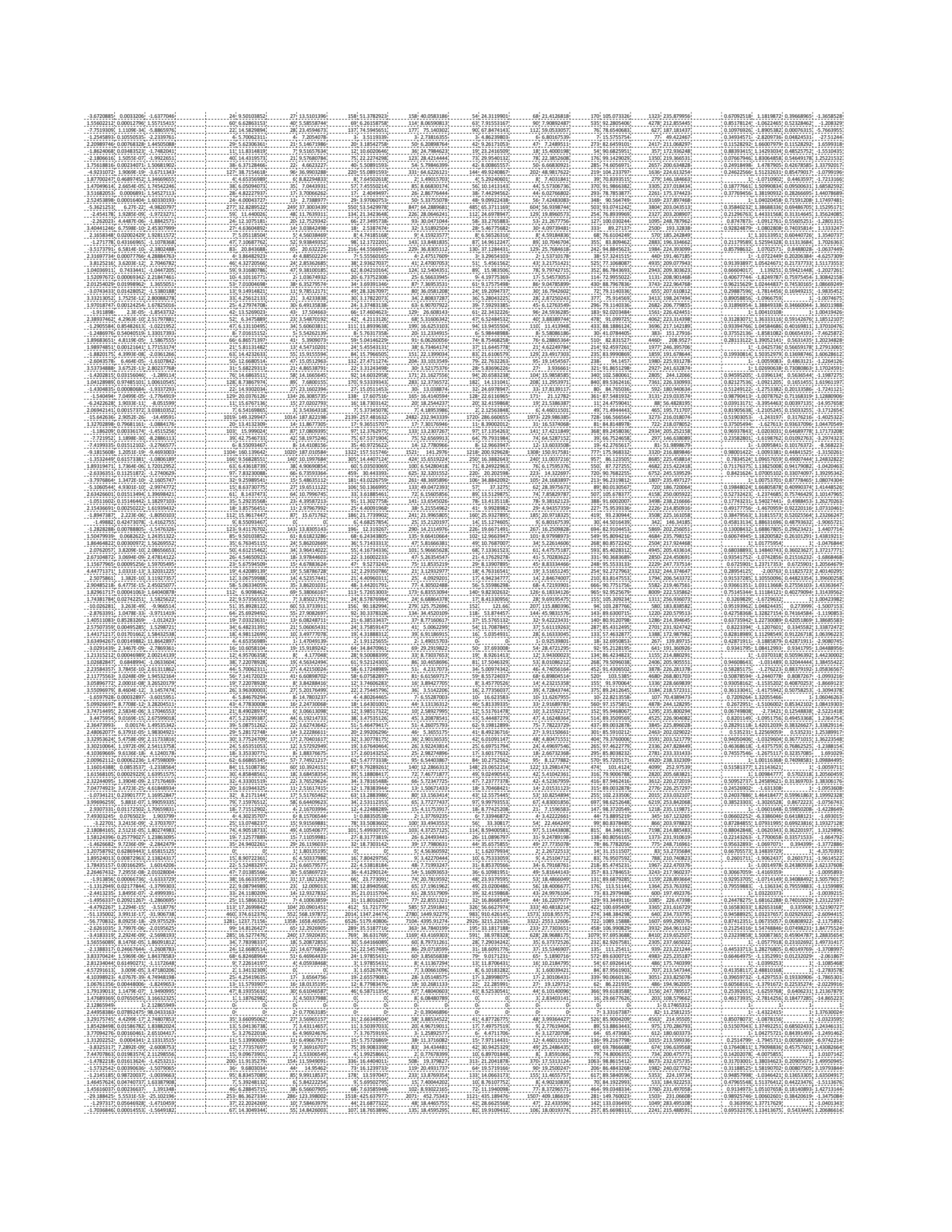
142	6.35715586	122	6.49911477	81	7.32161768	138	7.62233084	83	10.0350774	174	10.1516741	72	6.22566034	224	7.16652478
13	1.45498286	8	1.06542865	11	2.4857344	20	2.76171407	16	4.83618187	13	1.89614602	14	3.02636267	23	1.83962132
23	5.18183205	23	6.16599536	6	2.72931876	14	3.89150619	9	5.47603385	11	3.22969926	12	5.22173892	25	4.02514546
191	53.8771325	198	66.4593604	137	78.0259718	370	128.767725	58	44.1842225	282	103.665469	72	39.2267217	553	111.47624
22	11.0624115	13	7.77840121	4	4.06101536	19	11.7873159	0	0	4	2.6212052	1	0.97119299	6	2.15607791
44	3.95495539	39	4.17131878	28	5.08152958	35	3.88142457	24	5.82597038	29	3.39704119	21	3.64574777	72	4.62495469
5	2.31304967	6	3.30282882	2	1.86806706	3	1.71226273	2	2.49869396	1	0.6028772	1	0.89349755	1	0.33059861
45	16.9707449	63	28.2714967	17	12.9444864	70	32.5702149	12	12.2218727	31	15.2357552	16	11.6543159	71	19.1351915
316	20.416863	354	27.2160475	198	25.8294189	333	26.5448551	174	30.3612255	353	29.7228561	163	20.3407962	701	32.3672665
22	2.09125039	31	3.50642786	22	4.22234336	40	4.69113075	15	3.850727	38	4.70739728	18	3.30471696	47	3.19276743
17	7.28182303	15	7.64543708	5	4.32422931	10	5.2847615	11	12.7248304	9	5.02397663	5	4.13656273	8	2.44887862
3	1.82609184	1	0.72430457	0	0	0	0	2	3.28775522	1	0.79325947	0	0	2	0.86999635
50	4.36974119	27	2.80782047	11	1.94100167	31	3.34257837	41	9.67693191	19	2.16397986	22	3.71352886	59	3.68488379
88	9.36572259	56	7.09196372	32	6.87632048	55	7.22196701	19	5.46110261	46	6.3801421	10	2.05559252	57	4.3353039
907	44.5106658	864	50.4533964	627	62.1257805	873	52.8573324	318	42.1455807	939	60.0532199	323	30.6152449	1590	55.7622131
90	4.66062247	65	4.00529614	30	3.13667977	68	4.34454721	66	9.23025009	66	4.45409271	31	3.10056985	84	3.10861383
12	2.85170507	10	2.8277644	7	3.35868222	6	1.75917403	2	1.28357567	2	0.61939438	4	1.83595387	8	1.35862444
38	5.23189806	24	3.93193907	32	8.89555744	41	6.96456069	24	8.92390701	47	8.43310362	37	9.83910992	85	8.36335778
18	1.80498096	17	2.02847146	8	1.61971133	18	2.22693129	11	2.97893428	7	0.91477031	9	1.74309493	34	2.43649267
1	0.88963449	0	0	0	0	0	0	1	2.40259035	0	0	0	0	0	0
43	3.12770867	32	2.76966777	30	4.40581855	59	5.29473274	30	5.89314614	52	4.92918462	26	3.65266294	62	3.22281667
158	8.31855496	109	6.82868629	104	11.0553286	370	24.0340367	91	12.9389881	372	25.5239359	68	6.91477618	263	9.89538338
69	7.79806647	67	9.01016005	37	8.44281124	104	14.5012478	30	9.15645182	131	19.294034	21	4.58390437	99	7.99574822
99	9.95617031	70	8.37673976	40	8.12203071	114	14.144779	79	21.4561764	138	18.0863159	52	10.1004071	107	7.69001122
67	4.91461928	48	4.18963487	46	6.81271815	55	4.97750792	30	5.94298247	64	6.11799268	48	6.80040418	113	5.92351638
62	10.9194731	59	12.364651	33	11.7346852	55	11.9510723	26	12.3666326	61	14.0008283	28	9.52459317	100	12.5862416
491	37.772973	469	42.933113	298	46.287471	392	37.2065958	154	31.9954715	340	34.0872915	127	18.8704305	735	40.4085334
40	6.22345202	33	6.10949277	15	4.71205257	31	5.95068884	13	5.46239151	22	4.46075055	11	3.30554026	51	5.6705816
73	4.06547253	59	3.90984953	56	6.29685527	56	3.8477814	41	6.16652002	86	6.24166599	30	3.22691731	97	3.86052153
40	3.07041991	39	3.56223241	52	8.05913888	47	4.45112545	45	9.32864174	49	4.90171171	35	5.18900679	76	4.16905331
338	24.2798381	398	34.0198207	258	37.4193558	211	18.7001778	205	39.7695856	139	13.0124115	185	25.6672433	595	30.5444371
59	4.06160507	32	2.62129271	26	3.61382021	50	4.24668335	37	6.87884499	45	4.03712408	30	3.98882835	63	3.099362
95	49.9408451	68	42.5364318	52	55.1928905	112	72.6414489	31	44.0110869	102	69.8789476	29	29.4448056	116	43.5789081
48	17.1690285	47	20.0042467	42	30.3320168	70	30.8913378	16	15.455839	58	27.0362454	15	10.3627293	68	17.381989
98	19.5412817	84	19.9308636	89	35.8314588	147	36.1641696	51	27.4640931	127	33.0023292	59	22.722567	233	33.2023607
92	18.0339466	95	22.1588092	37	14.6437461	88	21.2823616	26	13.7639922	102	26.0565567	40	15.1440263	116	16.2497624
34	4.33696813	17	2.58033502	25	6.43865026	25	3.93442722	21	7.23427021	16	2.65975233	19	4.68100738	57	5.19598924
165	102.228535	186	137.126375	28	35.0262574	88	67.2674642	20	33.4646513	44	35.5266919	11	13.1631335	40	17.71064
225	19.6144287	189	19.6053595	161	28.3378264	259	27.8565355	121	28.4869946	226	25.6752976	102	17.1740107	381	23.7358175
63	5.69227067	39	4.1930444	44	8.02685066	94	10.4786912	32	7.80841864	95	11.186198	35	6.1078934	105	6.77985438
87	5.07315936	60	4.1632296	40	4.70941276	67	4.8202354	26	4.09449851	77	5.85145513	30	3.37877225	72	3.00039078
95	24.782675	100	31.0416242	29	15.2746085	75	24.1390422	33	23.2491262	57	19.3781956	24	12.092448	87	16.2192177
23	6.23439169	16	5.16067003	18	9.8511349	27	9.02951046	8	5.85631398	19	6.71171878	12	6.28240464	31	6.00501388
96	16.3274094	83	16.797475	69	23.694233	77	16.1573811	26	11.9422873	76	16.8450981	33	10.8402276	147	17.8669104
82	5.3478404	55	4.26822333	43	5.66213936	73	5.8738336	130	22.8968667	70	5.94944601	54	6.80200202	145	6.75800737
31	2.80095858	15	1.61270938	15	2.73642636	13	1.44918069	33	8.05243172	9	1.05974507	8	1.39608992	21	1.35597088
57	5.15014965	53	5.69823983	44	8.02685066	73	8.13770696	31	7.56440556	61	7.18271658	29	5.06082596	173	11.1706172
106	23.8814868	75	20.1065066	120	54.5863752	72	20.0134604	73	44.416719	54	15.8548873	91	39.5981868	314	50.5558269
16	7.93045601	14	8.25707205	6	6.00450127	13	7.94979122	5	6.69293026	14	9.04315793	7	6.70123162	10	3.542128
151	64.6797222	175	89.196766	81	70.0525149	144	76.1005656	40	46.2721104	137	76.4760887	49	40.5383147	150	45.9164741
24	10.2802208	17	8.66482869	19	16.4320714	18	9.51257069	7	8.09761933	11	6.14041588	8	6.61850037	29	8.87718499
49	6.71972928	52	8.48552859	27	7.47596009	26	4.39909396	23	8.51827488	40	7.14874145	21	5.56228712	86	8.42830457
24	4.7582736	23	5.42607592	17	6.80510144	22	5.38139714	8	4.28347537	17	4.39239099	15	5.74391282	34	4.81729408

gsyne_1771	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1553353	1553785	1	156	fig|1129.58.peg.1771		
gsyne_1772	Synechococcus_assembled_mapped	helicase conserved C-terminal domain protein				PF00271.26	1554150	1555698	-1	703	fig|1129.58.peg.1772		
gsyne_1773	Synechococcus_assembled_mapped	HNH endonuclease family protein				PF01844.18	1556069	1556327	1	157	fig|1129.58.peg.1774		
gsyne_1774	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1556340	1556460	-1	156	fig|1129.58.peg.1775		
gsyne_1775	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1556603	1557485	1	92,141,703	fig|1129.58.peg.1776		
gsyne_1776	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1557490	1557649	-1	156	fig|1129.58.peg.1777		
gsyne_1777	Synechococcus_assembled_mapped	acetyl-CoA carboxylase, biotin carboxyl	accB		GO:0003989,GO:0006633,G	TIGR00531	1558663	1559137	-1	176	fig|1129.58.peg.1779		
gsyne_1778	Synechococcus_assembled_mapped	4-hydroxythreonine-4-phosphate dehy	pdxA	1.1.1.262	GO:0008615,GO:0050570	TIGR00557	1557647	1558667	1	84	fig|1129.58.peg.1778		
gsyne_1779	Synechococcus_assembled_mapped	translation elongation factor P	efp		GO:0003746,GO:0005737,G	TIGR00038	1559142	1559703	-1	169	fig|1129.58.peg.1780		
gsyne_178	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	142331	142478	-1	856	fig|1129.58.peg.177		
gsyne_1780	Synechococcus_assembled_mapped	peptidyl-prolyl cis-trans isomerase, chl	CTLP40	5.2.1.8	GO:0006457,GO:0003755,G	UniRef100_C	1559769	1560843	1	92,703	fig|1129.58.peg.1781		
gsyne_1781	Synechococcus_assembled_mapped	thiamine-monophosphate kinase	thiL	2.7.4.16	GO:0009030,GO:0009228	TIGR01379	1560847	1561840	1	162	fig|1129.58.s Cofactors, Vitamins, Prosthetic Gro	Folate and pterines	5-FCL-like protein
gsyne_1782	Synechococcus_assembled_mapped	glyceraldehyde-3-phosphate dehydrog	gap	1.2.1.-	GO:0006094,GO:0006096,G	TIGR01534	1561910	1562933	-1	116	fig|1129.58.s Carbohydrates	CO2 fixation	Calvin-Benson cycle
gsyne_1783	Synechococcus_assembled_mapped	UDP-N-acetylmuramate--alanine ligase	murC	6.3.2.8	GO:0008763,GO:0009252	TIGR01082	1563124	1564567	1	89	fig|1129.58.peg.1784		
gsyne_1784	Synechococcus_assembled_mapped	UDP-N-acetylenolpyruvoylglucosamine	murB		GO:0008762,GO:0009252	TIGR00179	1564599	1565481	1	89	fig|1129.58.peg.1785		
gsyne_1785	Synechococcus_assembled_mapped	DNA-binding protein, YbaB/EbfC family			GO:0003677,GO:0005737,G	TIGR00103	1565530	1565869	1	156	fig|1129.58.s DNA Metabolism	DNA uptake, competence	DNA processing cluster
gsyne_1786	Synechococcus_assembled_mapped	ribosome small subunit-dependent GTF	rsgA	3.6.-.-	GO:0005525,GO:0006412,G	TIGR00157	1565872	1566868	-1	169	fig|1129.58.s Protein Metabolism	Protein biosynthesis	Universal GTPases
gsyne_1787	Synechococcus_assembled_mapped	sirA-like family protein				PF01206.12	1566878	1567115	-1	185	fig|1129.58.peg.1788		
gsyne_1788	Synechococcus_assembled_mapped	chaperone protein DnaJ	dnaJ		GO:0005515,GO:0006457,G	TIGR02349	1567122	1568253	-1	95	fig|1129.58.s Protein Metabolism	Protein folding	GroEL GroES
gsyne_1789	Synechococcus_assembled_mapped	grpE family protein				PF01025.14	1568256	1568937	-1	95	fig|1129.58.s Stress Response	Heat shock	Heat shock dnaK gene cluster ex
gsyne_179	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	142532	142709	-1	856	fig|1129.58.peg.178		
gsyne_1790	Synechococcus_assembled_mapped	type II/IV secretion system family protein				PF00437.15	1569056	1570874	1	185	fig|1129.58.s Membrane Transport	Protein and nucleoprotein secr	Type IV pilus
gsyne_1791	Synechococcus_assembled_mapped	twitching mobility protein	pilT		GO:0006810,GO:0005524,G	UniRef100_P	1570957	1572040	1	141,703	fig|1129.58.s Membrane Transport	Protein and nucleoprotein secr	Type IV pilus
gsyne_1792	Synechococcus_assembled_mapped	PIN domain protein				PF01850.16	1573339	1573756	-1	157	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Phd-Doc, YdcE-YdcD toxin-antito
gsyne_1793	Synechococcus_assembled_mapped	type II secretion system (T2SS), F family protein				PF00482.18	1572054	1573347	-1	97	fig|1129.58.s Membrane Transport	Protein and nucleoprotein secr	Type IV pilus
gsyne_1794	Synechococcus_assembled_mapped	prevent-host-death family protein			GO:0008219	TIGR01552	1573752	1573995	-1	94,708	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Phd-Doc, YdcE-YdcD toxin-antito
gsyne_1795	Synechococcus_assembled_mapped	flavo, HI0933 family protein			GO:0050662	TIGR00275	1574019	1575345	-1	156	fig|1129.58.peg.1796		
gsyne_1796	Synechococcus_assembled_mapped	tRNA dihydrouridine synthase A family	dusA	1.-.-.-		TIGR00742	1575370	1576369	1	168	fig|1129.58.peg.1797		
gsyne_1797	Synechococcus_assembled_mapped	RNA recognition motif family protein				PF14259.1	1576397	1576928	-1	185	fig|1129.58.peg.1798		
gsyne_1798	Synechococcus_assembled_mapped	argininosuccinate lyase	argH	4.3.2.1	GO:0004056,GO:0042450	TIGR00838	1576990	1578391	-1	73	fig|1129.58.s Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis extended
gsyne_1799	Synechococcus_assembled_mapped	stage II sporulation E family protein				PF07228.7	1578417	1579728	-1	185	fig|1129.58.s Stress Response	Stress Response - no subcate	SigmaB stress responce regulati
gsyne_180	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	142780	142975	1	88	fig|1129.58.peg.179		
gsyne_1800	Synechococcus_assembled_mapped	signal recognition particle-docking prot	ftsY		GO:0003924,GO:0005047,G	TIGR00064	1579886	1581530	-1	97	fig|1129.58.s Membrane Transport	Protein translocation across cy	Bacterial signal recognition partic
gsyne_1801	Synechococcus_assembled_mapped	transcription antitermination factor Nu	nusB		GO:0006355,GO:0030401	TIGR01951	1581542	1582160	-1	165	fig|1129.58.s RNA Metabolism	Transcription	Transcription factors bacterial
gsyne_1802	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04367.8	1582159	1582906	-1	156	fig|1129.58.peg.1803		
gsyne_1803	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1582965	1583640	-1	156	fig|1129.58.peg.1804		
gsyne_1804	Synechococcus_assembled_mapped	epoxyqueuosine reductase	queG	1.-.-.-	GO:0008616,GO:0051539	TIGR00276	1583651	1584584	1	112	fig|1129.58.s RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth
gsyne_1805	Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	1584610	1585495	1	185	fig|1129.58.peg.1806		
gsyne_1806	Synechococcus_assembled_mapped	DNA gyrase/topoisomerase IV, subunit A family protein				PF00521.15	1585557	1588062	1	132	fig|1129.58.peg.1807		
gsyne_1807	Synechococcus_assembled_mapped	putative excision endonuclease subunit	UvrA		GO:0003677,GO:0005524,G	UniRef100_D	1588090	1588342	-1	92,141,703	fig|1129.58.peg.1808		
gsyne_1808	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1588539	1589640	1	132,152	fig|1129.58.peg.1809		
gsyne_1809	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1590852	1590972	-1	856	fig|1129.58.peg.1812		
gsyne_181	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	142991	143174	1	856	fig|1129.58.peg.180		
gsyne_1810	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1591919	1593086	1	856	fig|1129.58.peg.1813		
gsyne_1811	Synechococcus_assembled_mapped	excinuclease ABC subunit A domain protein			GO:0003677,GO:0005524,G	UniRef100_C	1594866	1595121	-1	92,141,703	fig|1129.58.s DNA Metabolism	DNA repair	DNA repair, UvrABC system
gsyne_1812	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1595317	1596418	1	132,152	fig|1129.58.peg.1818		
gsyne_1813	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1597338	1597494	-1	856	fig|1129.58.peg.1819		
gsyne_1814	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1597630	1597750	-1	856	fig|1129.58.peg.1821		
gsyne_1815	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1598697	1599876	1	856	fig|1129.58.peg.1822		
gsyne_1816	Synechococcus_assembled_mapped	excinuclease ABC subunit A	uvrA	3.1.25.-	GO:0006289,GO:0009380,G	TIGR00630	1600144	1603111	-1	132	fig|1129.58.s DNA Metabolism	DNA repair	DNA repair, UvrABC system
gsyne_1817	Synechococcus_assembled_mapped	DNA repair protein RecN	recN		GO:0005524,GO:0005737,G	TIGR00634	1603157	1604831	-1	132	fig|1129.58.s DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_1818	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1604925	1607043	1	141,703	fig|1129.58.peg.1825		
gsyne_1819	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07176.6	1607070	1607661	1	156	fig|1129.58.peg.1826		
gsyne_182	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	143357	143654	1	88	fig|1129.58.peg.181		
gsyne_1820	Synechococcus_assembled_mapped	threonine synthase	thrC	4.2.3.1	GO:0004795,GO:0009088	TIGR00260	1607740	1608799	1	71	fig|1129.58.s Amino Acids and Derivatives	Lysine, threonine, methionine,	Threonine and Homoserine Biosy
gsyne_1821	Synechococcus_assembled_mapped	DNA polymerase III, beta subunit	dnaN	2.7.7.7	GO:0003887,GO:0006260,G	TIGR00663	1609271	1610402	1	132	fig|1129.58.s DNA Metabolism	DNA replication	DNA-replication
gsyne_1822	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1610398	1611196	1	156	fig|1129.58.peg.1829		
gsyne_1823	Synechococcus_assembled_mapped	putative peptidase, metallopeptidases			GO:0006508,GO:0008237,G	UniRef100_C	1611295	1612495	1	141,189,703	fig|1129.58.peg.1830		
gsyne_1824	Synechococcus_assembled_mapped	phosphoribosylformylglycinamidine syr	purL	6.3.5.3	GO:0004642,GO:0005524,G	UniRef100_D	1612500	1612680	-1	92,141,703			
gsyne_1825	Synechococcus_assembled_mapped	phosphoribosylformylglycinamidine syr	purL	6.3.5.3	GO:0004642,GO:0009152	TIGR01736	1612653	1614888	1	125	fig|1129.58.s Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_1826	Synechococcus_assembled_mapped	amidophosphoribosyltransferase	purF	2.4.2.14	GO:0004044,GO:0009152	TIGR01134	1614967	1616497	1	125	fig|1129.58.s Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_1827	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1616506	1617391	-1	156	fig|1129.58.peg.1833		
gsyne_1828	Synechococcus_assembled_mapped	aspartate kinase, monofunctional class		2.7.2.4	GO:0004072,GO:0009089	TIGR00656	1617390	1619244	-1	71	fig|1129.58.s Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa
gsyne_1829	Synechococcus_assembled_mapped	DNA polymerase III, delta subunit	holA	2.7.7.7	GO:0003887,GO:0006260,G	TIGR01128	1619304	1620282	-1	132	fig|1129.58.peg.1835		
gsyne_183	Synechococcus_assembled_mapped	cupin domain protein				PF07883.6	143668	144361	1	157	fig|1129.58.peg.182		
gsyne_1830	Synechococcus_assembled_mapped	antitoxin Phd_YefM, type II toxin-antitoxin system family protein				PF02604.14	1620281	1621016	-1	94,708	fig|1129.58.peg.1836		
gsyne_1831	Synechococcus_assembled_mapped	precorrin-8X methylmutase family protein				PF02570.10	1621145	1621814	1	79	fig|1129.58.s Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Cobalamin synthesis
gsyne_1832	Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	1621842	1623801	1	185	fig|1129.58.peg.1839		
gsyne_1833	Synechococcus_assembled_mapped	DNA mismatch repair protein MutS	mutS		GO:0005524,GO:0006298	TIGR01070	1624193	1626965	-1	132	fig|1129.58.s DNA Metabolism	DNA repair	DNA repair system including Rec
gsyne_1834	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14063.1	1623800	1624193	1	156	fig|1129.58.peg.1840		
gsyne_1835	Synechococcus_assembled_mapped	photosystem II core protein PsbZ	psbZ		GO:0003674,GO:0009523,G	TIGR03043	1627057	1627300	1	164	fig|1129.58.s Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_1836	Synechococcus_assembled_mapped	6,7-dimethyl-8-ribityllumazine synthas	ribH	6.3.3.-	GO:0000906,GO:0009231,G	TIGR00114	1627376	1627802	1	85	fig|1129.58.s Cofactors, Vitamins, Prosthetic Gro	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metabo
gsyne_1837	Synechococcus_assembled_mapped	clan AA aspartic protease, AF_0612 family protein		3.4.23.-	GO:0004190,GO:0008150	TIGR03698	1627803	1628265	-1	138	fig|1129.58.peg.1844		
gsyne_1838	Synechococcus_assembled_mapped	glucose-1-phosphate thymidylyltransfe	rfbA	2.7.7.24	GO:0008879,GO:0009243,G	TIGR01207	1628294	1629191	-1	90	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_1839	Synechococcus_assembled_mapped	dTDP-4-dehydrorhamnose 3,5-epimera	rfbC	5.1.3.13	GO:0008830,GO:0009243,G	TIGR01221	1629190	1629808	1	90	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	dTDP-rhamnose synthesis
gsyne_184	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	144552	144699	1	856			
gsyne_1840	Synechococcus_assembled_mapped	antidote-toxin recognition MazE family protein				PF04014.13	1629847	1630105	1	185	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1841	Synechococcus_assembled_mapped	PIN domain protein				PF01850.16	1630101	1630515	1	157	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1842	Synechococcus_assembled_mapped	dTDP-4-dehydrorhamnose reductase	rfbD	1.1.1.133	GO:0008831,GO:0009243,G	TIGR01214	1630511	1631411	1	90	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	dTDP-rhamnose synthesis
gsyne_1843	Synechococcus_assembled_mapped	bacterial sugar transferase family protein				PF02397.11	1631397	1632717	1	90	fig|1129.58.peg.1850		
gsyne_1844	Synechococcus_assembled_mapped	dolichyl-phosphate-mannose-mannosyltransferase family protein				PF02366.13	1632725	1634066	1	90	fig|1129.58.peg.1851		
gsyne_1845	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	1634204	1634654	1	154	fig|1129.58.peg.1852		
gsyne_1846	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	1634617	1635739	1	157	fig|1129.58.peg.1853		
gsyne_1847	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1635753	1635870	1	856	fig|1129.58.peg.1854		
gsyne_1848	Synechococcus_assembled_mapped	HAD phosphoserine phosphatase-like hydrolase, IB family protein			GO:0008152,GO:0016787	TIGR01488	1635943	1637482	-1	703	fig|1129.58.peg.1855		
gsyne_1849	Synechococcus_assembled_mapped	gtrA-like family protein				PF04138.9	1637499	1637922	-1	185	fig|1129.58.peg.1856		
gsyne_185	Synechococcus_assembled_mapped	sulfate transporter family protein				PF00916.15	144726	146262	1	143	fig|1129.58.s Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis
gsyne_1850	Synechococcus_assembled_mapped	flavin containing amine oxidoreductase family protein				PF01593.19	1637918	1639229	-1	109	fig|1129.58.peg.1857		
gsyne_1851	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein				PF01370.16	1639228	1640167	-1	119	fig|1129.58.peg.1858		
gsyne_1852	Synechococcus_assembled_mapped	putative decaprenylphosphoryl-beta-D-ribose oxidase			GO:0003885,GO:0050660,G	UniRef100_P	1640166	1641525	-1	92,141,703	fig|1129.58.peg.1859		
gsyne_1853	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	1641530	1642256	-1	703	fig|1129.58.s Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_1854	Synechococcus_assembled_mapped	ubiA prenyltransferase family protein				PF01040.13	1642252	1643170	-1	76	fig|1129.58.peg.1861		
gsyne_1855	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1643180	1644770	-1	88	fig|1129.58.peg.1862		
gsyne_1856	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1644822	1646070	-1	90	fig|1129.58.peg.1863		
gsyne_1857	Synechococcus_assembled_mapped	dTDP-glucose 4,6-dehydratase	rfbB	4.2.1.46	GO:0008460,GO:0009243,G	TIGR01181	1646288	1647344	1	90	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	dTDP-rhamnose synthesis
gsyne_1858	Synechococcus_assembled_mapped	glycosyltransferase like 2 family protein				PF13641.1	1647340	1648603	1	703	fig|1129.58.peg.1865		
gsyne_1859	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	1648599	1649544	1	90	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_186	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	146265	146931	-1	156	fig|1129.58.peg.185		
gsyne_1860	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	1649540	1651427	1	90	fig|1129.58.peg.1867		
gsyne_1861	Synechococcus_assembled_mapped	fic family protein				UniRef100_F	1651449	1651848	-1	185	fig|1129.58.peg.1868		
gsyne_1862	Synechococcus_assembled_mapped	filamentation induced by cAMP Fic domain protein			GO:0006355,GO:0005622,G	UniRef100_C	1651922	1652081	-1	92,165	fig|1129.58.peg.1869		
gsyne_1863	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1652276	1652603	1	156	fig|1129.58.peg.1870		
gsyne_1864	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	1653030	1655610	-1	90	fig|1129.58.peg.1872		
gsyne_1865	Synechococcus_assembled_mapped	toxin with endonuclease activity YhaV family protein				PF11663.3	1652599	1653055	1	185	fig|1129.58.peg.1871		
gsyne_1866	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1655639	1655879	-1	856	fig|1129.58.peg.1873		
gsyne_1867	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1656163	1656283	-1	856			
gsyne_1868	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1656302	1656590	-1	856	fig|1129.58.peg.1874		
gsyne_1869	Synechococcus_assembled_mapped	RES domain protein				PF08808.6	1656657	1657338	-1	157	fig|1129.58.peg.1875		
gsyne_187	Synechococcus_assembled_mapped	cbiX family protein				PF01903.12	147034	148180	1	79	fig|1129.58.peg.186		
gsyne_1870	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09722.5	1657385	1657775	-1	156	fig|1129.58.peg.1876		
gsyne_1871	Synechococcus_assembled_mapped	PIN domain protein				PF01850.16	1658083	1658497	-1	157	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1872	Synechococcus_assembled_mapped	prevent-host-death family protein			GO:0008219	TIGR01552	1658504	1658738	-1	94,708	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1873	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1658853	1659222	-1	856	fig|1129.58.peg.1879		
gsyne_1874	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1659445	1660564	-1	856	fig|1129.58.peg.1880		
gsyne_1875	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1661166	1661376	-1	856			
gsyne_1876	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1661594	1661771	-1	856			
gsyne_1877	Synechococcus_assembled_mapped	hlyD secretion family protein				PF00529.15	1662174	1663317	-1	97	fig|1129.58.peg.1882		
gsyne_1878	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	1663316	1666265	-1	141	fig|1129.58.peg.1883		
gsyne_1879	Synechococcus_assembled_mapped	PPIC-type PPIASE domain protein				PF00639.16	1666261	1667008	-1	157	fig|1129.58.peg.1884		
gsyne_188	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10929.3	148519	148843	1	156	fig|1129.58.peg.187		
gsyne_1881	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1667196	1668900	1	90	fig|1129.58.peg.1885		
gsyne_1882	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	1668990	1669203	1	261	fig|1129.58.peg.1886		
gsyne_1883	Synechococcus_assembled_mapped	addiction module toxin, RelE/StbE family protein				TIGR02385	1669180	1669435	-1	94,708	fig|1129.58.s Regulation and Cell signaling	Programmed Cell Death and T	Toxin-antitoxin replicon stabilizati
gsyne_1884	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF13635.1	1669442	1670447	-1	156	fig|1129.58.peg.1888		
gsyne_1885	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03683.8	1670693	1670885	1	156	fig|1129.58.peg.1889		
gsyne_1886	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1670966	1671947	1	154	fig|1129.58.peg.1890		
gsyne_1887	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1672089	1672233	-1	856			
gsyne_1888	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	1672286	1672727	-1	154	fig|1129.58.peg.1892		
gsyne_1889	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF05598.6	1672704	1673265	-1	156	fig|1129.58.peg.1893		
gsyne_189	Synechococcus_assembled_mapped	GMC oxidoreductase family protein				PF05199.8	149011	150646	-1	703	fig|1129.58.s Respiration	Electron donating reactions	Respiratory dehydrogenases 1
gsyne_1890	Synechococcus_assembled_mapped	acetyltransferase family protein				PF00583.19	1673566	1674007	-1	703	fig|1129.58.peg.1895		
gsyne_1891	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1673352	1673613	1	856			
gsyne_1892	Synechococcus_assembled_mapped	putative ribonuclease VapC30			GO:0045926,GO:0046872,G	UniRef100_P	1674003	1674369	-1	141,703	fig|1129.58.peg.1896		
gsyne_1893	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	1674401	1674665	-1	261	fig|1129.58.peg.1897		
gsyne_1894	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1674638	1674920	1	856	fig|1129.58.peg.1898		
gsyne_1895	Synechococcus_assembled_mapped	preprotein translocase, SecA subunit	secA		GO:0009898,GO:0015450,G	TIGR00963	1674950	1677821	1	97	fig|1129.58.peg.1899		
gsyne_1896	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1677836	1678472	1	856	fig|1129.58.peg.1900		
gsyne_1897	Synechococcus_assembled_mapped	carbamoyltransferase family protein				PF02543.10	1678468	1680307	1	703	fig|1129.58.peg.1901		
gsyne_1898	Synechococcus_assembled_mapped	putative sxtJ				UniRef100_C	1680495	1680717	1	185	fig|1129.58.peg.1902		
gsyne_1899	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	1680729	1681980	-1	141	fig|1129.58.s Cell Wall and Capsule	Capsular and extracellular poly	Rhamnose containing glycans
gsyne_19	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09990.4	11530	12031	1	156	fig|1129.58.peg.18		
gsyne_190	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	150645	150930	-1	856	fig|1129.58.peg.189		
gsyne_1900	Synechococcus_assembled_mapped	ABC-2 type transporter family protein				PF01061.19	1681989	1682790	-1	141	fig|1129.58.peg.1904		



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0.3379318	1.39424842	0.64207916	-1.1720652	0.58147029	-1.2111744	0.93854749	-1.0333678
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1	1.03548284	0.28158651	-1.5702032	0.93541752	1.11240433	0.21516232	1.74670089
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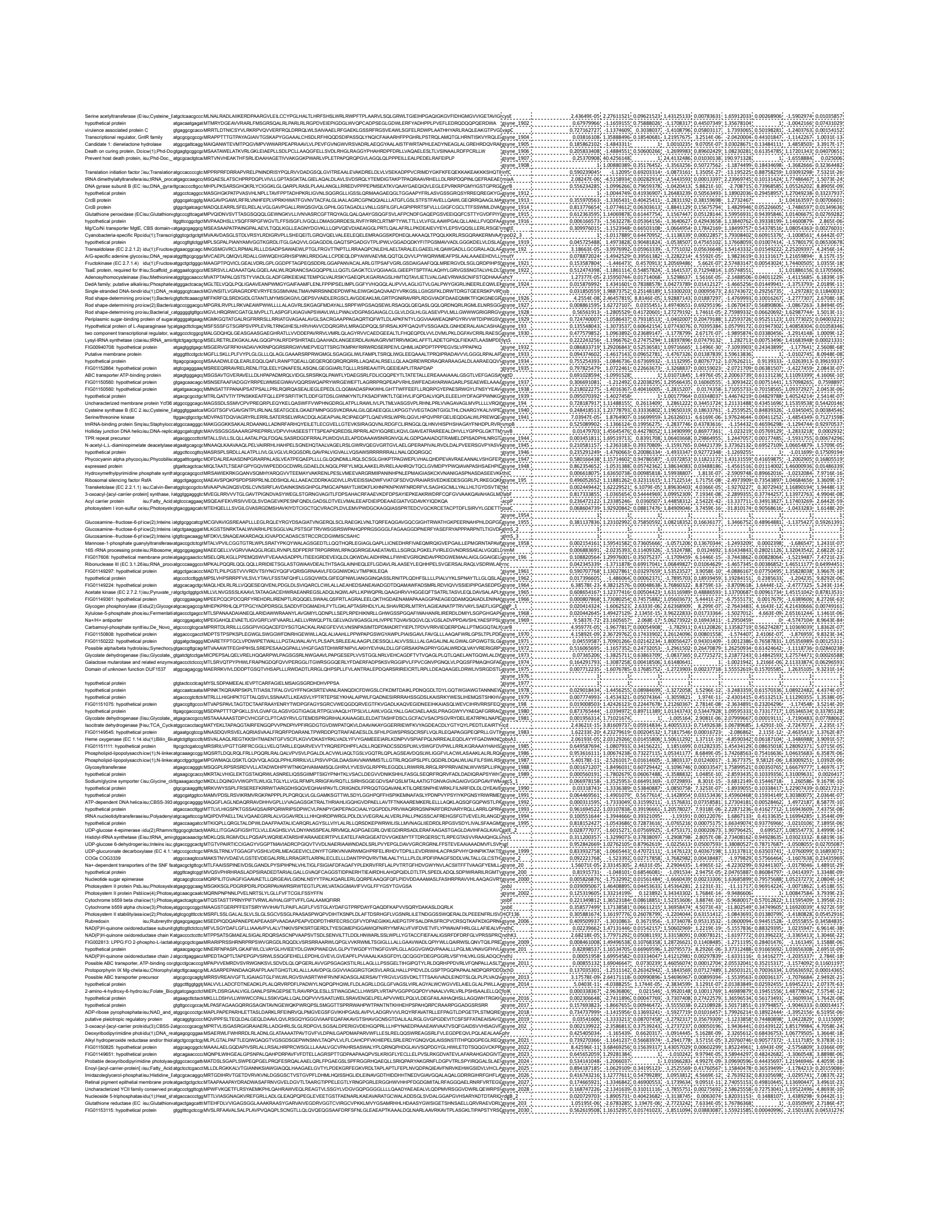
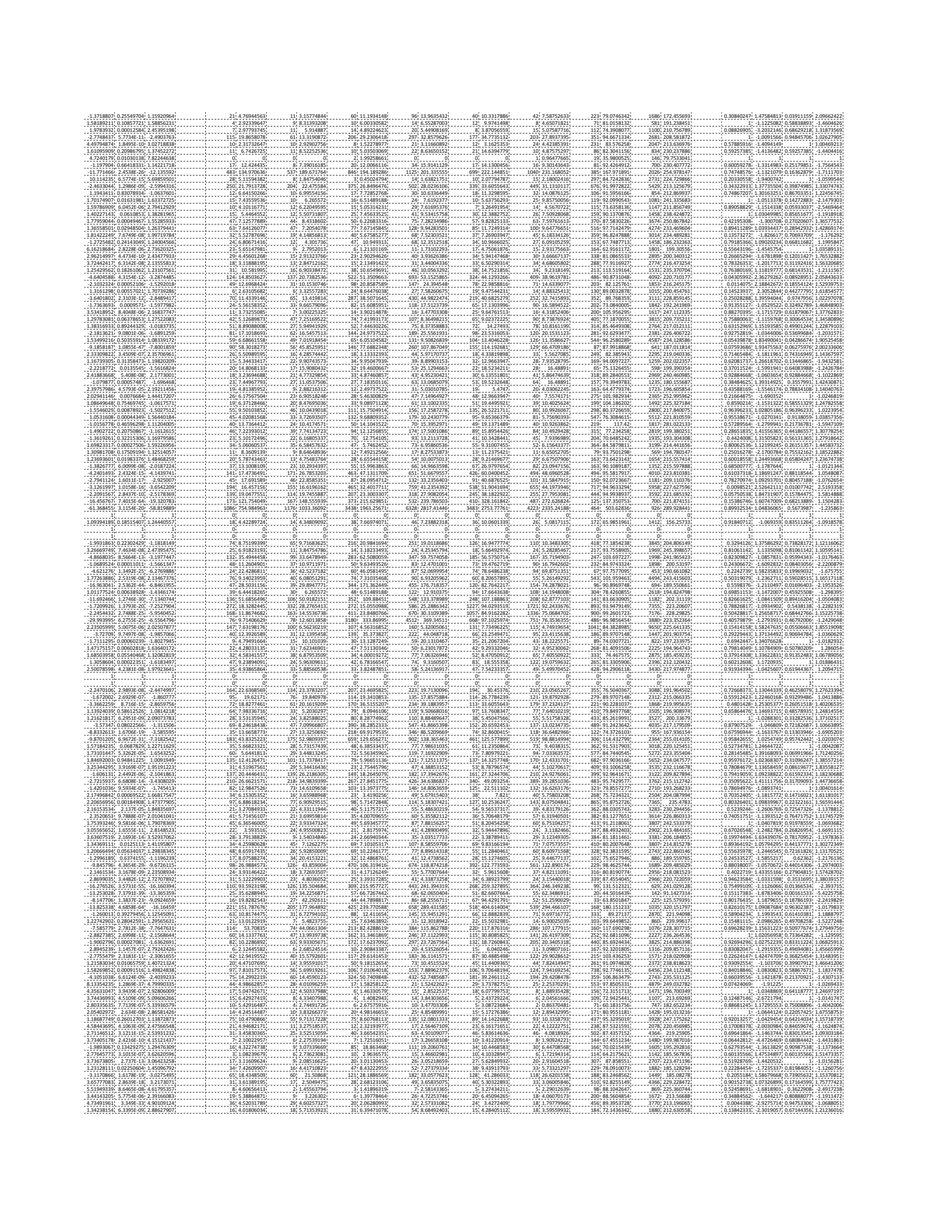
105	9.92657555	97	10.9119345	50	9.54393936	99	11.5472759	63	16.0849169	102	12.5667862	78	14.2423996	132	8.91805524
39	26.0218088	49	38.9035125	4	5.38865499	42	34.5745358	6	10.8116566	13	11.3039474	9	11.5982855	19	9.05967354
6	5.20436176	9	9.28920605	0	0	13	13.9121346	1	2.34252559	0	0	2	3.35061581	2	1.2397448
1105	97.5541941	1090	114.50647	469	83.5995661	1236	134.628291	393	93.7010237	804	92.5025315	501	85.4279145	2858	180.315045
166	5.82355276	145	6.05295979	88	6.23318636	167	7.22820716	99	9.37957669	173	7.90933429	87	5.89491558	209	5.23977074
63	3.91726154	39	2.88553593	49	6.15156493	26	1.99457127	28	4.70184348	38	3.07921148	14	1.68131259	73	3.24377672
97	4.76697913	70	4.09344932	60	5.95347152	64	3.8804821	79	10.4849587	73	4.67528703	49	4.65099645	185	6.49724612
32	5.63585706	16	3.35312571	10	3.55596522	26	5.64959782	11	5.23203685	25	5.73804437	14	4.76229658	44	5.53794632
15	5.25693107	28	11.6766675	19	13.4444221	36	15.5660248	9	8.51827488	37	16.8988305	13	8.79959708	35	8.76587232
61	4.95653501	67	6.47803076	37	6.07012424	36	3.60898467	45	9.87481514	51	5.40048073	44	6.90525038	128	7.43266203
35	3.22109039	25	2.73775598	27	5.01702361	40	4.54181094	14	3.47961361	40	4.79743126	18	3.19952703	54	3.55152357
18	2.34783237	12	1.86249745	5	1.3167766	10	1.60926948	9	3.17033539	13	2.20979423	10	2.51926001	11	1.02535284
112	9.71480861	91	9.39241946	76	13.3099778	119	12.734954	67	15.6949215	106	11.9821843	59	9.88431664	164	10.1659074
9	5.20436176	0	0	2	2.33508383	11	7.84787082	1	1.56168373	2	1.50719299	0	0	2	0.82649653
124	5.77486226	149	8.25707205	140	13.164231	198	11.3767792	76	9.55876214	217	13.1702367	84	7.55575109	252	8.38699838
85	5.78262417	61	4.93805289	49	6.73053574	76	6.37901799	39	7.1653724	113	10.0184005	39	5.12447124	114	5.54238852
35	4.11644433	24	3.35880897	16	3.79945843	28	4.0629963	21	6.67024236	16	2.45238181	17	3.8617267	38	3.19391881
50	2.80709911	37	2.47177723	42	4.76085053	24	1.662391	35	5.30669228	46	3.36557658	24	2.60242005	71	2.84860456
26	2.76714531	18	2.27955977	14	3.00839021	15	1.96962737	6	1.72455872	12	1.6643849	6	1.23335551	37	2.81414464
23	3.4545547	15	2.68086755	8	2.42606112	28	5.18867492	14	5.67884992	17	3.32756894	12	3.48115928	30	3.22011636
19	2.69069043	19	3.20172182	5	1.42964316	9	1.57248618	48	18.3577516	5	0.92277122	11	3.00871624	29	2.93490606
12	1.86703561	14	2.59190602	6	1.88482103	16	3.07132327	15	6.30275944	9	1.8248525	6	1.80302196	16	1.77900599
58	3.08170477	39	2.46574127	27	2.89650521	46	3.01547034	55	7.89212297	33	2.28502459	19	1.94982237	81	3.07563029
112	4.20554485	70	3.12767881	58	4.39723578	87	4.03048856	75	7.60560257	83	4.06159149	47	3.40863513	101	2.71026461
22	5.82676634	7	2.20608795	6	3.20851213	6	1.96060617	10	7.1527499	9	3.1064283	8	4.09235519	33	6.2460425
51	21.8454691	60	30.5817483	16	13.8375338	80	42.278092	12	13.8816331	43	24.0034439	3	2.48193764	11	3.3672081
64	15.6375189	57	16.5722925	40	19.7331028	81	24.4178311	14	9.23812909	67	21.3342106	26	12.2698607	86	15.0166272
19	4.28064387	13	3.48512781	10	4.5488646	19	5.28132983	14	8.51827488	16	4.69774438	14	6.09202875	21	3.38112218
34	3.94533556	22	3.03771881	15	3.51434021	21	3.00648137	25	7.83453375	25	3.78058442	14	3.13770042	39	3.23411687
18	3.03166704	11	2.20455807	11	3.74066827	12	2.49358649	9	4.09373404	12	2.63392949	6	1.95181504	16	1.92581717
4	2.83230572	1	0.84255837	0	0	1	0.87360343	1	1.91226579	0	0	0	0	0	0
16	6.45502233	19	9.12118424	6	4.88738476	24	11.946019	12	13.0745614	13	6.83494495	3	2.33763894	27	7.78444409
12	3.01702131	8	2.39335422	2	1.01525384	13	4.03250279	11	7.46892218	8	2.6212052	3	1.45678948	14	2.51542423
38	4.39479437	21	2.88997522	14	3.26911736	28	3.99527969	24	7.49608189	31	4.67229826	25	5.58435968	45	3.7192344
44	3.4695745	29	2.72108056	22	3.50262574	17	1.65389013	26	5.53687867	25	2.56907896	17	2.58911222	29	1.63420906
56	4.34667052	41	3.78680038	24	3.76120885	32	3.0644523	29	6.07903733	30	3.03461676	15	2.24873544	59	3.27270439
19	4.39479437	9	2.47712161	10	4.67016766	6	1.71226273	8	4.99738793	1	0.3014386	3	1.34024632	18	2.97538752
26	2.41200367	30	3.31165991	12	2.24767427	17	1.9457531	15	3.75806245	14	1.69256967	14	2.50848242	28	1.85630237
4	3.55853795	8	8.46879184	4	7.18487332	8	8.78083449	3	7.20777105	6	6.95627533	2	3.43652904	12	7.62919877
43	2.90822034	16	1.28765256	10	1.3655461	18	1.50198485	20	3.65306135	22	1.9390787	9	1.17565467	41	1.98165836
21	5.16745139	6	1.75682384	2	0.99365269	5	1.51796341	3	1.9936388	4	1.28271744	5	2.37632327	10	1.75850326
47	3.18496097	46	3.70923158	30	4.10463954	30	2.50819735	42	7.6864121	34	3.00261103	24	3.14120232	80	3.8742025
39	3.09641661	22	2.07843919	21	3.36636799	43	4.21208794	24	5.14605164	31	3.20752741	7	1.07342383	43	2.43977238
29	3.21462174	15	1.97853164	18	4.02857913	20	2.73524397	17	5.08919298	20	2.88918784	8	1.71277486	30	2.3765076
30	2.29773146	18	1.64047789	12	1.85569576	22	2.07890618	26	5.3779837	16	1.59702568	13	1.92309075	43	2.3535994
24	3.44090033	12	2.04720795	7	2.02631241	11	1.9457531	11	4.25913744	8	1.49473685	8	2.21528318	20	2.04916496
19	2.15431097	12	1.61903374	6	1.37357872	12	1.67868895	26	7.96152489	5	0.73882009	8	1.75195598	10	0.81029072
62	4.05874753	58	4.51802056	37	4.89045859	50	4.03835548	40	7.07177537	50	4.26564053	24	3.03451998	69	3.22801476
84	7.00587159	61	6.05386292	45	7.57779608	85	8.74653435	31	6.9825282	71	7.71711794	25	4.02718246	87	5.18547104
30	2.95702372	18	2.11118319	11	2.18914109	25	3.04023921	21	5.59011789	17	2.18371711	9	1.71338308	36	2.53584164
32	2.63720627	23	2.25549474	22	3.66070149	27	2.74531435	25	5.5641938	26	2.79242406	11	1.75091563	44	2.59139056
20	2.20290445	13	1.70384026	4	0.88955574	11	1.49483254	11	3.27209924	9	1.2918797	4	0.85095005	15	1.18070933
32	5.00118847	18	3.34746164	18	5.67993364	36	6.94160564	16	6.75322693	25	5.0918682	15	4.5278592	54	6.03119092
79	4.35765319	59	3.87255366	30	3.34113743	47	3.19858299	43	6.40563437	42	3.01917832	33	3.5157495	104	4.09963304
18	4.69566474	5	1.55208121	4	2.10684255	12	3.86224675	3	2.11355692	8	2.71974675	2	1.007704	12	2.23713347
4	2.6185468	6	4.67381437	0	0	1	0.8076711	2	3.53588769	2	1.70625621	0	0	3	1.40348468
25	7.95773969	16	6.06023637	10	6.42683623	23	9.03257859	8	6.87713935	27	11.2002415	4	2.45916757	20	4.5495222
74	2.98544783	50	2.40031164	32	2.6066052	53	2.6380792	40	4.35818715	73	3.83808447	35	2.72724543	108	3.11377764
19	4.33696813	16	4.34582739	3	1.38261543	12	3.3794659	8	4.93163282	6	1.7848338	3	1.3226115	13	2.12061611
35	15.1793885	30	15.4820101	23	20.140098	19	10.1665599	8	9.37010237	26	14.6951316	8	6.70123162	12	3.7192344
0	0	1	1.03213401	0	0	3	3.21049261	0	0	0	0	0	0	0	0
15	5.42121016	6	2.58033502	2	1.45942739	6	2.67541051	4	3.90420932	3	1.41299343	2	1.39608992	8	2.06624133
22	3.36258322	22	4.00122434	11	3.39461526	22	4.14865418	32	13.2089549	13	2.58945051	10	2.95208441	27	2.94917265
47	4.26884821	32	3.4584595	17	3.1175203	23	2.57735881	23	5.64168467	30	3.55097824	8	1.40339929	51	3.31031334
38	10.1418332	32	10.1625502	22	11.855041	24	7.90275104	49	35.3180781	15	5.2172065	18	9.2786284	36	6.86627889
22	5.53120573	23	6.88089337	12	6.09152303	17	5.27327288	11	7.46892218	17	5.57006104	7	3.39917546	35	6.28856058
33	14.6789691	14	7.41019286	10	8.98109165	26	14.268856	11	13.2142469	21	12.1734818	6	5.15479355	12	3.81459939
25	7.0519807	7	2.34957335	13	7.40392434	26	9.04854286	5	3.8089847	23	8.45498506	4	2.17926232	17	3.42693685
113	10.5110434	113	12.5073612	55	10.3294593	291	33.3960089	45	11.304413	220	26.6688304	61	10.9591187	202	13.4277989
460	228.00061	603	355.643889	138	138.103529	805	492.275533	80	107.086884	225	145.336467	74	70.8415914	425	150.54044
1281	753.309312	1451	1015.33996	395	468.99565	2074	1504.7597	315	500.268177	612	469.018021	343	389.580076	1782	748.88991
99	9.01542981	68	7.36851574	58	10.6641624	138	15.5047412	57	14.0182634	167	19.8189944	45	7.9148405	179	11.6490456
285	10.0592954	258	10.8358321	214	15.2504966	395	17.2010116	137	13.059044	376	17.2951545	124	8.45323216	453	11.4263356
34	4.73757161	18	2.98448387	15	4.22003102	20	3.43827856	27	10.160352	24	4.3581484	17	4.57513805	34	3.38564845
24	7.71016556	22	8.40998079	18	11.6754191	25	9.90892781	10	8.67602071	13	5.44264135	9	5.58435968	40	9.18329482
68	4.15371596	51	3.70696016	28	3.45329299	49	3.69282014	18	2.96939864	21	1.67171053	13	1.53373259	40	1.74611944
9	4.39805219	4	2.32593579	4	3.94662056	5	3.01454705	3	3.95919818	5	3.18421054	3	2.83150632	5	1.74611944
2	0.81637047	0	0	1	0.82414723	3	1.51082005	1	1.10236498	0	0	1	0.78838019	2	0.58340932
25	2.5892347	18	2.21831786	8	1.67289588	14	1.78893121	9	2.51734093	7	0.94480755	4	0.80014706	19	1.40627768
13	7.04757321	16	10.3213401	5	5.47285272	11	7.3573789	0	0	11	7.77146385	4	4.18826976	3	1.16226075
47	4.9868502	31	3.91390265	15	3.21341811	19	2.48723179	42	12.0349939	16	2.21239338	18	3.68875135	45	3.41214165
0	0	4	3.44044669	0	0	1	0.8918035	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	2	0.44155466	0	0	1	0.22891213	1	0.50107499	1	0.24179567	0	0	0	0
35	2.22816711	27	2.04532977	15	1.92805087	27	2.12069237	24	4.12628361	15	1.24447128	10	1.22958378	42	1.91079933
13	3.06833119	7	1.96596954	8	3.81238176	12	3.49441372	7	4.46195351	10	3.07590406	3	1.36759829	17	2.86743695
5	1.99400834	6	2.84726622	1	0.80520132	8	3.93623615	3	3.23106978	3	1.55916516	0	0	3	0.85499641
11	3.12830488	11	3.72245051	3	1.72260283	6	2.10524106	1	0.76804118	1	0.37062123	1	0.54928128	5	1.01618426
12	4.73123796	9	4.22236639	13	10.348667	14	6.81013584	7	7.45349052	14	7.19342108	6	4.56902156	19	5.35344346
15	5.53655506	2	0.87841192	0	0	3	1.36616707	8	7.9745552	2	0.96203808	2	1.42579396	4	1.05510196
200	7.2509394	162	6.98874437	160	11.7120192	192	8.5881516	142	13.9033912	235	11.1031458	115	8.05268167	375	9.71586834
36	5.89173029	45	8.76340194	31	10.2435281	68	13.7304086	117	51.7123574	43	9.17112715	45	14.2243124	58	6.78350928
95	5.37699148	88	5.92677276	50	5.71390823	80	5.58650155	104	15.8970742	93	6.85981801	36	3.93547045	132	5.33919457
7	3.28202994	8	4.46328219	6	5.67993364	11	6.3631385	1	1.26623005	6	3.66614511	1	0.90557184	3	1.00519849
46	3.82734837	38	3.76221508	24	4.03179942	41	4.20879926	35	7.86459431	47	5.09626406	16	2.57121597	62	3.6865313
253	52.5630149	296	73.1764469	159	66.6967058	251	64.3380156	85	47.6921378	215	58.2119448	98	39.3245927	459	68.1488459
37	13.5130796	14	6.08415835	15	11.0609234	37	16.6720318	13	12.8222453	20	9.51911361	12	8.46471362	36	9.39596059
67	8.70642291	59	9.12298223	42	11.0194967	62	9.94010196	32	11.2300852	77	13.0397596	30	7.52947373	102	9.47220746

gsyne_1901	Synechococcus_assembled_mapped	serine O-acetyltransferase	cysE	2.3.1.30	GO:0006535,GO:0009001	TIGR01172	1682792	1683545	-1	75	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis
gsyne_1902	Synechococcus_assembled_mapped	antidote-toxin recognition MazE family protein				PF04014.13	1683629	1683863	1	185	fig|1129.58.peg.1906			
gsyne_1903	Synechococcus_assembled_mapped	tRNA(fMet)-specific endonuclease Vap(	vapC	3.1.-.-	GO:0046872,GO:0004519	UniRef100_C	1683859	1684261	1	141,703	fig|1129.58.peg.1907			
gsyne_1904	Synechococcus_assembled_mapped	bacterial regulatory s, gntR family protein				PF00392.16	1684280	1685270	-1	261	fig|1129.58.peg.1908			
gsyne_1905	Synechococcus_assembled_mapped	dienelactone hydrolase family protein				PF01738.13	1685485	1686223	1	96,184	fig|1129.58.peg.1909			
gsyne_1906	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1686253	1686532	-1	156	fig|1129.58.p	Regulation and Cell signaling	Programmed Cell Death and T	Phd-Doc, YdcE-YdcD toxin-antitc
gsyne_1907	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1686500	1686641	1	856	fig|1129.58.p	Regulation and Cell signaling	Programmed Cell Death and T	Phd-Doc, YdcE-YdcD toxin-antitc
gsyne_1908	Synechococcus_assembled_mapped	prevent-host-death family protein			GO:0008219	TIGR01552	1686648	1686882	-1	94,708				
gsyne_1909	Synechococcus_assembled_mapped	translation initiation factor IF-3	infC		GO:0003743,GO:0006413	TIGR00168	1686960	1687572	-1	169	fig|1129.58.p	Virulence, Disease and Defense	Invasion and intracellular resis	Mycobacterium virulence operon
gsyne_1910	Synechococcus_assembled_mapped	tRNA dimethylallyltransferase	miaA	2.5.1.75	GO:0005737,GO:0006400	TIGR00174	1687653	1688589	-1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA processing
gsyne_1911	Synechococcus_assembled_mapped	DNA gyrase, B subunit	gyrB	5.99.1.3	GO:0003918,GO:0006265,G(	TIGR01059	1688786	1690748	1	132	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Resistance to fluoroquinolones
gsyne_1912	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1690778	1691087	-1	856	fig|1129.58.peg.1915			
gsyne_1913	Synechococcus_assembled_mapped	crcB-like family protein				PF02537.10	1691103	1691448	1	185	fig|1129.58.peg.1916			
gsyne_1914	Synechococcus_assembled_mapped	crcB-like family protein				PF02537.10	1691440	1691857	1	185	fig|1129.58.peg.1917			
gsyne_1915	Synechococcus_assembled_mapped	glutathione peroxidase family protein				PF00255.14	1691868	1692339	-1	185	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Redox cycle
gsyne_1916	Synechococcus_assembled_mapped	acyltransferase family protein				PF01757.17	1692406	1693534	1	703	fig|1129.58.peg.1919			
gsyne_1917	Synechococcus_assembled_mapped	magnesium transporter	mgtE		GO:0015095,GO:0015693	TIGR00400	1693569	1694979	1	145	fig|1129.58.peg.1920			
gsyne_1918	Synechococcus_assembled_mapped	RNA polymerase sigma factor rpoD2	rpoD2		GO:0003677,GO:0016987,G(	UniRef100_C	1695078	1696068	1	92,141,165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription factors cyanobacte
gsyne_1919	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1696082	1696685	-1	856	fig|1129.58.peg.1922			
gsyne_192	Synechococcus_assembled_mapped	transaldolase family protein				PF00923.14	151159	151855	1	703	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway
gsyne_1920	Synechococcus_assembled_mapped	A/G-specific adenine glycosylase	mutY	3.2.2.-	GO:0004844,GO:0006260,G(	TIGR01084	1696776	1697889	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_1921	Synechococcus_assembled_mapped	pfkB carbohydrate kinase family protein				PF00294.19	1697926	1698913	1	703	fig|1129.58.peg.1924			
gsyne_1922	Synechococcus_assembled_mapped	tRNA threonylcarbamoyl adenosine modification protein YjeE			GO:0005737,GO:0006400,G(	TIGR00150	1698924	1699425	-1	156	fig|1129.58.p	Cell Wall and Capsule	Cell Wall and Capsule - no sut	YjeE
gsyne_1923	Synechococcus_assembled_mapped	adenosylhomocysteinase	ahcY	3.3.1.1	GO:0004013,GO:0006730	TIGR00936	1699502	1700930	1	109	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis
gsyne_1924	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09335.6	1701068	1701728	1	156	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_1925	Synechococcus_assembled_mapped	single-stranded DNA-binding family prc	ssb		GO:0003697,GO:0006260,G(	TIGR00621	1701743	1702133	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa
gsyne_1926	Synechococcus_assembled_mapped	cell shape determining , MreB/Mrl family protein			GO:0008360	TIGR00904	1702269	1703316	1	89	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1927	Synechococcus_assembled_mapped	rod shape-determining MreC family protein				PF04085.9	1703321	1704059	1	89	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1928	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1704061	1704565	1	88	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_1929	Synechococcus_assembled_mapped	bacterial extracellular solute-binding family protein				PF13416.1	1704564	1705965	1	185	fig|1129.58.peg.1932			
gsyne_193	Synechococcus_assembled_mapped	L-asparaginase II family protein				PF06089.7	151974	152955	-1	109	fig|1129.58.peg.191			
gsyne_1930	Synechococcus_assembled_mapped	response regulator				PF00072.19	1706059	1706869	1	699	fig|1129.58.peg.1933			
gsyne_1931	Synechococcus_assembled_mapped	lysine--tRNA ligase	lysS	6.1.1.6	GO:0004824,GO:0005737,G(	TIGR00499	1706936	1708445	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Lys
gsyne_1932	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1708494	1708758	1	156	fig|1129.58.peg.1935			
gsyne_1933	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF02698.12	1708762	1709569	-1	156	fig|1129.58.peg.1936			
gsyne_1934	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1709594	1710074	-1	156	fig|1129.58.peg.1937			
gsyne_1935	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1710070	1710301	-1	156	fig|1129.58.peg.1938			
gsyne_1936	Synechococcus_assembled_mapped	dimethylhistidine N-methyltransferase	egtD	2.1.1.44	GO:0030745	TIGR03438	1710321	1711272	-1	703	fig|1129.58.peg.1939			
gsyne_1937	Synechococcus_assembled_mapped	formylglycine-generating sulfatase enzyme family protein				PF03781.11	1711304	1711832	-1	703	fig|1129.58.peg.1940			
gsyne_1938	Synechococcus_assembled_mapped	dinB superfamily protein				PF12867.2	1711828	1712503	-1	185	fig|1129.58.peg.1941			
gsyne_1939	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1712559	1713279	-1	856	fig|1129.58.peg.1942			
gsyne_194	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF06799.6	152976	153486	-1	156	fig|1129.58.peg.192			
gsyne_1940	Synechococcus_assembled_mapped	pyridoxal-phosphate dependent enzyme family protein				PF00291.20	1713547	1714537	1	185	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis
gsyne_1941	Synechococcus_assembled_mapped	phosphotransferase enzyme family protein				PF01636.18	1714549	1716463	1	703	fig|1129.58.peg.1945			
gsyne_1942	Synechococcus_assembled_mapped	ssrA-binding protein	smpB		GO:0003723,GO:0006450	TIGR00086	1716504	1717002	-1	136	fig|1129.58.p	Stress Response	Heat shock	Heat shock dnaK gene cluster ex
gsyne_1943	Synechococcus_assembled_mapped	holliday junction DNA helicase RuvB	ruvB	3.6.4.12	GO:0006310,GO:0009378,G(	TIGR00635	1717071	1718160	1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication
gsyne_1944	Synechococcus_assembled_mapped	tetratricopeptide repeat family protein				PF13371.1	1718164	1718935	1	157	fig|1129.58.peg.1948			
gsyne_1945	Synechococcus_assembled_mapped	amidohydrolase family protein			GO:0004180	TIGR01891	1718958	1720107	1	138	fig|1129.58.peg.1949			
gsyne_1946	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11384.3	1720106	1720331	1	156	fig|1129.58.peg.1950			
gsyne_1947	Synechococcus_assembled_mapped	HEAT repeats family protein				PF13646.1	1720373	1720964	1	185	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_1948	Synechococcus_assembled_mapped	ureidoglycolate hydrolase family protein				PF04115.7	1722511	1722994	-1	122	fig|1129.58.peg.1953			
gsyne_1949	Synechococcus_assembled_mapped	thiamine biosynthesis protein ThiC	thiC		GO:0003824,GO:0009228	TIGR00190	1721142	1722522	1	162	fig|1129.58.peg.1952			
gsyne_195	Synechococcus_assembled_mapped	oligomerisation domain protein				PF02410.10	153498	153933	-1	157	fig|1129.58.peg.193			
gsyne_1950	Synechococcus_assembled_mapped	transketolase	tkt	2.2.1.1	GO:0004802,GO:0005737,G(	TIGR00232	1723071	1725087	-1	117	fig|1129.58.p	Carbohydrates	CO2 fixation	Calvin-Benson cycle
gsyne_1951	Synechococcus_assembled_mapped	beta-ketoacyl-acyl-carrier-protein synth	fabF	2.3.1.179	GO:0006633,GO:0033817	TIGR03150	1725132	1726380	-1	176	fig|1129.58.peg.1955			
gsyne_1952	Synechococcus_assembled_mapped	acyl carrier protein	acpP		GO:0000036,GO:0006633	TIGR00517	1726387	1726630	-1	176	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophosphc
gsyne_1953	Synechococcus_assembled_mapped	photosystem I iron-sulfur protein PsaC	psaC		GO:0009055,GO:0009538,G(	TIGR03048	1726759	1727005	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_1954	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1727764	1727878	-1	856				
gsyne_1955	Synechococcus_assembled_mapped	glutamine amidotransferase domain protein				PF13537.1	1727086	1727782	1	703	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular pol	Sialic Acid Metabolism
gsyne_1956	Synechococcus_assembled_mapped	glutamine-fructose-6-phosphate transa	glmS	2.6.1.16	GO:0008152,GO:0016051,G(	UniRef100_B	1728215	1728584	1	119,141,703	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular pol	Sialic Acid Metabolism
gsyne_1957	Synechococcus_assembled_mapped	glutamine-fructose-6-phosphate transa	glmS	2.6.1.16	GO:0008152,GO:0016051,G(	UniRef100_B	1728709	1728856	1	119,141,703	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular pol	Sialic Acid Metabolism
gsyne_1958	Synechococcus_assembled_mapped	mannose-1-phosphate guanylyltransferase/mannose		5.3.1.8	GO:0004476,GO:0008905,G(	TIGR01479	1728942	1730388	-1	90	fig|1129.58.peg.1961			
gsyne_1959	Synechococcus_assembled_mapped	16S rRNA processing protein RimM	rimM		GO:0003723,GO:0006364	TIGR02273	1730513	1731131	-1	166	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome biogenesis bacterial
gsyne_196	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11780.3	153925	154561	-1	156	fig|1129.58.peg.194			
gsyne_1960	Synechococcus_assembled_mapped	ribonuclease III	rnc	3.1.26.3	GO:0004525,GO:0006396	TIGR02191	1731345	1732074	-1	166	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA processing and degradation
gsyne_1961	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11623.3	1731185	1731368	1	156	fig|1129.58.peg.1963			
gsyne_1962	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09852.4	1732094	1733516	-1	156	fig|1129.58.peg.1965			
gsyne_1964	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1734167	1734449	1	156	fig|1129.58.peg.1966			
gsyne_1965	Synechococcus_assembled_mapped	acetokinase family protein				PF00871.12	1734894	1735929	-1	114	fig|1129.58.p	Carbohydrates	Fermentation	Fermentations: Lactate
gsyne_1966	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_D	1734485	1734935	1	156	fig|1129.58.peg.1967			
gsyne_1967	Synechococcus_assembled_mapped	glycogen/starch/alpha-glucan phospho	glgP	2.4.1.1	GO:0004645,GO:0005977	TIGR02093	1735936	1738462	-1	105	fig|1129.58.p	Carbohydrates	Polysaccharides	Glycogen metabolism
gsyne_1968	Synechococcus_assembled_mapped	D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase family protein				PF03894.10	1738461	1740882	-1	119	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway
gsyne_1969	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein				PF00999.16	1740978	1742316	1	145	fig|1129.58.peg.1971			
gsyne_197	Synechococcus_assembled_mapped	carbamoyl-phosphate synthase, large s	carB	6.3.5.5	GO:0004088,GO:0005951,G(	TIGR01369	154643	157937	1	126	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis
gsyne_1970	Synechococcus_assembled_mapped	isoprenylcysteine carboxyl methyltransferase family protein				PF04140.9	1742275	1742827	1	703	fig|1129.58.peg.1972			
gsyne_1971	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1742830	1743151	-1	88	fig|1129.58.peg.1973			
gsyne_1972	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	1743198	1744077	1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_1973	Synechococcus_assembled_mapped	FAD binding domain protein				PF01565.18	1744903	1746097	-1	157	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Glycolate, glyoxylate interconvers
gsyne_1974	Synechococcus_assembled_mapped	aldose 1-epimerase family protein				PF01263.15	1744055	1744925	1	703	fig|1129.58.peg.1975			
gsyne_1975	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF07005.6	1746249	1747461	1	156	fig|1129.58.peg.1977			
gsyne_1976	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1748426	1748555	-1	856				
gsyne_1977	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1748880	1749015	-1	856	fig|1129.58.peg.1981			
gsyne_1978	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1749188	1750427	-1	856	fig|1129.58.peg.1982			
gsyne_1979	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1750626	1751454	-1	856	fig|1129.58.peg.1983			
gsyne_198	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11866.3	158013	158667	1	156	fig|1129.58.peg.196			
gsyne_1980	Synechococcus_assembled_mapped	amino acid permease family protein				PF00324.16	1751754	1753125	-1	142	fig|1129.58.peg.1984			
gsyne_1981	Synechococcus_assembled_mapped	4Fe-4S dicluster domain protein				PF13183.1	1753121	1754477	-1	157	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Glycolate, glyoxylate interconvers
gsyne_1982	Synechococcus_assembled_mapped	isocitrate dehydrogenase, NADP-depen	icd	1.1.1.42	GO:0004450,GO:0006099	TIGR00183	1754496	1755927	-1	120	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	TCA Cycle
gsyne_1983	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1756038	1756476	1	156	fig|1129.58.peg.1987			
gsyne_1984	Synechococcus_assembled_mapped	heme oxygenase 1	pbsA1	1.14.99.3	GO:0046872,GO:0006788,G(	UniRef100_P	1756559	1757273	1	92,141,703	fig|1129.58.p	Iron acquisition and metabolism	Iron acquisition and metabolis	Heme, hemin uptake and utilizati
gsyne_1985	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1757302	1758358	1	90	fig|1129.58.peg.1989			
gsyne_1986	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	1758382	1760200	1	141	fig|1129.58.peg.1990			
gsyne_1987	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	1760284	1762144	1	141	fig|1129.58.peg.1991			
gsyne_1988	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein				PF00534.15	1762185	1763358	1	90	fig|1129.58.peg.1992			
gsyne_1989	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1763368	1764514	1	856	fig|1129.58.peg.1993			
gsyne_199	Synechococcus_assembled_mapped	amino acid carrier family protein	agcS		GO:0005416,GO:0006865,G(	TIGR00835	158716	160063	1	141	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine cleavage system
gsyne_1990	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1764564	1765644	1	856	fig|1129.58.peg.1994			
gsyne_1991	Synechococcus_assembled_mapped	sulfotransferase domain protein				PF00685.22	1765659	1766604	1	703	fig|1129.58.peg.1995			
gsyne_1992	Synechococcus_assembled_mapped	uvrD/REP helicase N-terminal domain protein				PF00580.16	1766649	1769058	1	132	fig|1129.58.peg.1996			
gsyne_1993	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1769054	1770152	1	856	fig|1129.58.peg.1997			
gsyne_1994	Synechococcus_assembled_mapped	poly A polymerase head domain protein				PF01743.15	1770173	1771400	1	166	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA nucleotidyltransferase
gsyne_1995	Synechococcus_assembled_mapped	O-Antigen ligase family protein				PF04932.10	1772228	1773437	-1	90	fig|1129.58.peg.2000			
gsyne_1996	Synechococcus_assembled_mapped	UDP-glucose 4-epimerase GalE	galE	5.1.3.2	GO:0003978,GO:0006012	TIGR01179	1773433	1774480	-1	119	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular pol	Rhamnose containing glycans
gsyne_1997	Synechococcus_assembled_mapped	histidine--tRNA ligase	hisS	6.1.1.21	GO:0004821,GO:0005737,G(	TIGR00442	1774564	1775827	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, His
gsyne_1998	Synechococcus_assembled_mapped	UDP-glucose 6-dehydrogenase	sgl	1.1.1.22	GO:0007507,GO:0003979,G(	UniRef100_C	1775923	1777288	1	92,141,703	fig|1129.58.p	Cell Wall and Capsule	Gram-Negative cell wall comp	Lipid A-Ara4N pathway (Polymy)
gsyne_1999	Synechococcus_assembled_mapped	polysaccharide biosynthesis family protein				PF02719.10	1777304	1778252	1	90	fig|1129.58.peg.2004			
gsyne_2	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF06803.7	1026	1386	1	156	fig|1129.58.peg.2			
gsyne_20	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09990.4	12027	12648	1	156	fig|1129.58.peg.19			
gsyne_200	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	160115	161159	1	156	fig|1129.58.peg.198			
gsyne_2000	Synechococcus_assembled_mapped	polysaccharide biosynthesis family protein				PF02719.10	1778254	1779289	1	90	fig|1129.58.peg.2005			
gsyne_2001	Synechococcus_assembled_mapped	photosystem II reaction center J domai	psbJ		GO:0009539,GO:0016021,G(	UniRef100_P	1779412	1779613	-1	92	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2002	Synechococcus_assembled_mapped	psbL family protein				PF02419.12	1779628	1779748	-1	185	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2003	Synechococcus_assembled_mapped	cytochrome b559, beta subunit	psbF		GO:0009055,GO:0009538	TIGR01333	1779759	1779897	-1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2004	Synechococcus_assembled_mapped	cytochrome b559, alpha subunit	psbE		GO:0009055,GO:0009538	TIGR01332	1779900	1780149	-1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2005	Synechococcus_assembled_mapped	photosystem II stability/assembly facto	HCF136		GO:0009657,GO:0009535,G(	UniRef100_C	1780233	1781229	-1	92	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2006	Synechococcus_assembled_mapped	rubredoxin family protein				PF00301.15	1781236	1781512	-1	112	fig|1129.58.p	Stress Response	Oxidative stress	Rubrerythrin
gsyne_2007	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhC	1.6.5.-	GO:0006810,GO:0016021,G(	UniRef100_P	1781761	1782124	1	141,703	fig|1129.58.peg.2012			
gsyne_2008	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhK1	1.6.5.-	GO:0006810,GO:0046872,G(	UniRef100_P	1782157	1782883	1	141,703	fig|1129.58.peg.2013			
gsyne_2009	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR01826	1783434	1784805	-1	156	fig|1129.58.peg.2015			
gsyne_201	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF13787.1	161187	161670	1	156	fig|1129.58.peg.199			
gsyne_2010	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhJ	1.6.5.-	GO:0006810,GO:0048038,G(	UniRef100_P	1782886	1783441	1	141,703	fig|1129.58.peg.2014			
gsyne_2011	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	1784944	1785709	1	141	fig|1129.58.peg.2016			
gsyne_2012	Synechococcus_assembled_mapped	magnesium chelatase ATPase subunit D	bchD	6.6.1.1	GO:0010007,GO:0015995,G(	TIGR02031	1786609	1788733	-1	191	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis
gsyne_2013	Synechococcus_assembled_mapped	mce related family protein				PF02470.15	1785726	1786623	1	185	fig|1129.58.peg.2017			
gsyne_2014	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1788836	1790345	1	88	fig|1129.58.peg.2019			
gsyne_2015	Synechococcus_assembled_mapped	2-amino-4-hydroxy-6-hydroxymethyldil	folK	2.7.6.3	GO:0003848,GO:0009396	TIGR01498	1790314	1790890	1	78	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_2016	Synechococcus_assembled_mapped	PIN domain protein				PF01850.16	1790894	1791293	-1	157	fig|1129.58.peg.2021			
gsyne_2017	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1791431	1791746	-1	856	fig|1129.58.peg.2022			
gsyne_2018	Synechococcus_assembled_mapped	NUDIX domain protein				PF00293.23	1791710	1792274	1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynt
gsyne_2019	Synechococcus_assembled_mapped	cys/Met metabolism PLP-dependent enzyme family protein				PF01053.15	1793799	1795023	-1	185	fig|1129.58.peg.2025			
gsyne_202	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	161680	162406	-1	703	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_2020	Synechococcus_assembled_mapped	deoxyribodipyrimidine photo-lyase	phr	4.1.99.3	GO:0003904,GO:0003677,G(	UniRef100_P	1792270	1793803	1	92,141,703	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial photolyase
gsyne_2021	Synechococcus_assembled_mapped	thioredoxin family protein				PF00085.15	1795061	1795631	-1	112	fig|1129.58.peg.2026			
gsyne_2022	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1795614	1796247	1	156	fig|1129.58.peg.2027			
gsyne_2023	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1796259	1796733	-1	92,703	fig|1129.58.peg.2028			
gsyne_2024	Synechococcus_assembled_mapped	FAD binding domain of DNA photolyase family protein				PF03441.9	1796739	1797672	-1	132	fig|1129.58.peg.2029			
gsyne_2025	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	1797760	1798543	1	703	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_2026	Synechococcus_assembled_mapped	imidazoleglycerol-phosphate dehydratase family protein				PF00475.13	1798572	1799175	1	161	fig|1129.58.p	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_2027	Synechococcus_assembled_mapped	apocarotenoid-15,15'-oxygenase			GO:0016702,GO:0046872	UniRef100_P	1799367	1800834	1	141,703	fig|1129.58.peg.2032			
gsyne_2028	Synechococcus_assembled_mapped	YCII-related domain protein				PF03795.9	1800833	1801130	1	157	fig|1129.58.peg.2033			
gsyne_2029	Synechococcus_assembled_mapped	non-canonical purine NTP pyrophospha	rdgB	3.6.1.-	GO:0006281,GO:0016462	TIGR00042	1801902	1802505	-1	132	fig|1129.58.p	Stress Response	Heat shock	Heat shock dnaK gene cluster ex
gsyne_203	Synechococcus_assembled_mapped	pyridine nucleotide-disulfide oxidoreductase family protein				PF07992.9	162405	163767	-1	157	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Redox cycle
gsyne_2030	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04402.9	1801237	1801918	1	156	fig|1129.58.peg.2034			





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0.94779469	-1.0373675	0.23574635	1.63777604	0.80015175	-1.1133744	0.13509865	-1.8234579
0.10048777	-4.5131118	1	-1.4815021	0.44692995	-2.6833571	0.66815797	-1.8112408
0.6023342	1.25803958	0.56971842	1.38036428	0.11727378	2.06849011	0.38075158	1.49851031
0.84096352	-1.0870991	0.00965601	2.73910685	0.01171274	2.69301235	1	-1.0171163
1	-1.0748719	0.06706987	2.79073881	0.21277261	2.14156287	0.61594648	-1.3031319

21	2.90283126	11	1.80931858	11	3.07003053	24	4.09305831	18	6.71959532	28	5.04399247	14	3.73773875	27	2.66718005
4	1.77926898	9	4.76369541	2	1.79621833	7	3.84161509	4	4.8051807	2	1.15937922	1	0.85913226	4	1.27153313
7	1.81246429	11	3.38909674	2	1.04555992	2	0.638904	5	3.49630685	12	4.04917519	4	2.00036765	10	1.85036537
115	12.0909415	63	7.88175059	60	12.7368209	60	7.78301239	48	13.6292398	76	10.4133334	67	13.6055309	133	9.99309445
10	1.41039614	11	1.84609334	4	1.13906528	7	1.21807308	9	3.42808623	5	0.91902012	3	0.81722337	17	1.71346842
11	4.1037978	11	4.88321465	2	1.5065057	10	4.60285679	7	7.05276522	3	1.45857386	4	2.88225016	11	2.93272963
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17	7.56189315	9	4.76369541	6	5.38865499	8	4.39041724	4	4.8051807	6	3.47813767	1	0.85913226	8	2.54306626
483	82.1472787	559	113.129982	181	62.1544372	559	117.29839	106	48.6877868	354	78.4626938	118	38.762026	561	68.185964
29	3.22492502	8	1.05859898	3	0.67358187	11	1.50920593	13	3.90420932	9	1.30430162	4	0.85913226	15	1.19206231
250	13.2628995	214	13.5092769	157	16.8168881	326	21.3378306	129	18.482312	318	21.9856592	96	9.83667027	422	15.9991531
12	4.04222272	10	4.0082874	2	1.36024301	22	9.14315047	1	0.90971868	20	8.77976498	2	1.30121002	7	1.68509002
15	4.52553196	10	3.59003133	4	2.43660921	14	5.21123438	2	1.62958302	6	2.35908468	3	1.74814738	6	1.29364675
10	2.49609677	12	3.56420376	6	3.02384956	8	2.46368737	1	0.67410808	5	1.62646725	4	1.92841198	10	1.78380547
15	3.3148801	12	3.15556894	4	1.78477745	18	4.9077594	8	4.77457445	7	2.01599062	0	0	20	3.15858548
47	4.33696813	44	4.83126556	21	3.91250748	30	3.41541767	43	10.7158086	40	4.81019039	18	3.20803641	59	3.89068847
63	4.65070625	48	4.21637722	44	6.55810778	34	3.09664535	57	11.3637412	46	4.42537516	25	3.5644849	51	2.69050999
34	3.57471312	17	2.12682159	4	0.84912139	17	2.20518684	13	3.69125245	16	2.19228071	14	2.84294675	35	2.6297617
24	4.14277553	12	2.46479763	15	5.22779962	12	2.55561601	13	6.06026521	16	3.59926684	8	2.66715686	33	4.07080382
23	3.43966438	9	1.60158725	8	2.41560396	7	1.29157749	13	5.25048839	8	1.55916516	7	2.02192333	9	0.96187097
29	2.71206632	18	2.0030633	12	2.26584954	7	0.8076711	30	7.57690218	24	2.92501065	12	2.16751427	31	2.07181072
18	1.89824745	15	1.88231126	11	2.34218135	8	1.04088919	22	6.26572195	11	1.51177412	13	2.64790307	31	2.33629719
31	6.44052752	17	4.20270134	23	9.64795115	12	3.07592106	7	3.92758782	21	5.68581786	6	2.40762813	37	5.49347995
124	9.03838736	149	12.9233586	110	16.1886064	421	37.8604311	76	14.9606676	361	34.2918069	91	12.8111781	395	20.5755965
49	7.72768867	35	6.56812549	44	14.010503	94	18.2900791	25	10.6478436	67	13.7702632	23	7.00583306	91	10.2560706
6	1.60134208	6	1.90547817	4	2.155462	18	5.92706328	8	5.76621684	5	1.73906883	4	2.06191742	11	2.09802966
70	6.95903196	67	7.9258428	52	10.437624	90	11.0389431	34	9.12846649	65	8.42127887	38	7.29646996	89	6.32305371
24	3.38495074	36	6.04176004	18	5.12579377	24	4.17625055	38	14.4741419	19	3.49227644	8	2.17926232	31	3.12456007
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42	3.1203882	50	4.42027412	24	3.60012924	37	3.39152681	36	7.22320525	50	4.84109097	15	2.15242986	60	3.18563974
51	5.41126299	27	3.40888296	27	5.7841526	37	4.84355664	23	6.59059188	43	5.9458072	19	3.89368198	52	3.94291924
81	10.4087235	64	9.78615946	40	10.3781504	62	9.82965638	22	7.63489822	65	10.8852827	34	8.43858797	97	8.90779597
59	4.06967984	51	4.1859908	64	8.91324245	80	6.80820169	55	10.2456388	91	8.18019256	30	3.99675842	146	7.19692806
90	35.4842847	57	26.7416538	75	59.7038479	133	64.6962905	42	44.7209431	177	90.9453951	39	29.6986401	140	39.4464255
26	3.35349209	18	2.76258916	11	2.86460098	16	2.54611558	16	5.57329509	18	3.02559187	9	2.24204775	29	2.6730557
15	3.2527261	22	5.67673703	9	3.94045396	28	7.49114942	2	1.1712628	12	3.39118422	3	1.25648093	16	2.4794896
20	9.01188183	17	9.11494966	10	9.0977292	6	3.33557674	6	7.30137847	15	8.80827071	5	4.3514491	18	5.79620946
19	2.0795557	21	2.73499232	7	1.54690096	22	2.97080284	11	3.25145508	14	1.99691185	9	1.90255787	24	1.8772161
23	4.53410304	27	6.33354958	12	4.77630783	43	10.4584229	16	8.51827488	35	8.99177635	9	3.42676617	37	5.21256336
19	2.92986291	11	2.01839539	5	1.55672255	9	1.71226273	14	5.83028592	8	1.60767252	1	0.29783252	8	0.8815963
26	3.75870571	23	3.95651369	9	2.62696931	12	2.14032841	17	6.63715584	15	2.82598685	7	1.95452589	15	1.549681
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45	2.44719205	34	2.20016026	22	2.41560396	34	2.28122777	27	3.96540382	28	1.98439202	18	1.89062961	43	1.67112935
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47	4.49228655	43	4.89055232	49	9.4561246	38	4.48112834	26	6.71136809	58	7.22456143	19	3.5075317	86	5.87427288
23	3.10506668	24	3.8554422	24	6.54186909	19	3.16468792	13	4.7397405	30	5.27810774	7	1.82523818	42	4.05208417
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37	7.97355631	23	5.89790861	11	4.78619667	27	7.17874124	21	12.2218727	18	5.05518145	10	4.16225566	20	3.0801113
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25	4.21064867	11	2.20455807	12	4.08072902	17	3.53258086	17	7.73260875	8	1.755953	7	2.27711754	27	3.24981647
132	21.6030111	105	20.4479379	65	21.4783654	92	18.5764352	49	21.6573121	118	25.1672791	33	10.4311624	160	18.7131291
48	6.8534805	37	6.28624827	3	0.86484586	41	7.22250738	11	4.24161012	15	2.79109813	9	2.48193764	22	2.2448054
24	13.6507849	36	24.3651306	18	20.6712339	58	40.7013271	7	10.7525765	19	14.0836066	11	12.0841882	16	6.50357928
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47	17.3478725	41	18.0074444	16	11.9238323	39	17.7601719	9	8.9713746	19	9.13936174	8	5.70317585	40	10.5510196
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76	5.91227942	78	7.22030964	36	5.65446308	52	4.99090032	40	8.40367925	44	4.46075055	31	4.65780673	74	4.11395135
147	4.64505876	102	3.83525204	114	7.27321193	169	6.58862478	123	10.4965628	194	7.98894644	51	3.11259392	229	5.1712488
40	7.54255327	32	7.18006265	33	12.5637663	37	8.6078425	15	7.63867041	34	8.35509156	9	3.27777634	40	5.39019478
9	2.91833369	16	6.17351181	4	2.6187856	24	9.60147322	2	1.751421	17	7.18381705	3	1.87884999	21	4.866288
22	2.60514127	31	4.36807566	19	4.54265455	24	3.50634005	25	7.99496789	21	3.24072213	9	2.05839879	24	2.03098124
32	2.78960764	39	4.04555038	35	6.16039704	32	3.44173412	18	4.23773474	36	4.08987042	20	3.36745308	62	3.86252149
47	5.62310351	25	3.55908278	30	7.24681188	28	4.13304796	19	6.13903258	31	4.833412	22	5.08369295	49	4.18948243
35	3.0058195	34	3.47451052	16	2.77435702	34	3.60253296	36	8.34959617	17	1.90264461	9	1.49284863	40	2.4549402
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164	13.7774871	140	13.9950374	66	11.1948329	205	21.2478123	110	24.9566891	156	17.0790876	100	16.2257424	327	19.6317942
95	11.942376	79	11.8171865	53	13.4521134	107	16.5953	45	15.2773408	82	13.4336766	35	8.49793865	237	21.2912694
72	11.4591452	62	11.741708	53	17.031116	67	13.1561471	58	24.9296301	69	14.3114197	40	12.2958378	137	15.5821135
64	4.85892272	33	2.98121857	41	6.28479893	34	3.18473373	35	7.17622719	46	4.5512611	26	3.8125169	68	3.68939372
28	2.14929394	25	2.28348231	14	2.16976816	24	2.27291512	21	4.35336614	29	2.90101305	11	1.6308307	30	1.64567894
69	5.01888136	49	4.24105378	25	3.67151545	60	5.38447398	42	8.2504046	45	4.26564053	19	2.66925369	87	4.52233952
35	8.31747312	28	7.91774032	14	6.71736444	26	7.62308747	8	5.13430267	18	5.57454941	10	4.58988467	23	3.90604526
183	26.6778208	184	31.9180936	82	24.1357404	212	38.1302203	43	16.9291765	236	44.835825	90	25.3407918	242	25.2116169
35	3.44986101	30	3.51863866	19	3.7812437	42	5.10760188	13	3.46054917	33	4.23898028	8	1.52300719	34	2.39496155
60	3.43522228	29	1.97570206	34	3.93033912	55	3.88508457	31	4.79328669	76	5.67062708	22	2.43279036	58	2.37310886
135	7.55471868	106	7.05846482	69	7.79616698	111	7.66375655	80	12.0904547	155	11.3039474	50	5.40421905	190	7.59843587
31	2.75081355	30	3.1676747	13	2.32911175	41	4.48866827	43	10.3047162	30	3.46924217	21	3.59912696	46	2.91704659
137	12.4432384	147	15.8872983	75	13.753766	163	18.2656299	100	24.5290638	131	15.5059383	50	8.77124558	244	15.8375776
210	16.2274086	222	20.4128062	166	25.899148	290	27.6478948	95	19.8253836	382	38.4686674	75	11.193594	203	11.2101646
82	7.9029197	77	8.83047983	40	7.78361276	68	8.08568509	43	11.1920667	68	8.54076027	24	4.46748775	82	5.64772631
34	3.74493756	20	2.62129271	13	2.89105617	20	2.71787734	31	9.22137058	26	3.73209692	13	2.76558765	37	2.91241636
97	4.1911423	79	4.06169796	58	5.05983295	81	4.31797263	110	12.8357567	63	3.54744053	55	4.58988467	149	4.60079639
21	1.99073947	23	2.59443521	9	1.72260283	17	1.98828322	10	2.56013726	17	2.10018695	10	1.8309376	24	1.62589482
41	3.47805757	22	2.22072842	15	2.56916314	25	2.61653839	25	5.72744643	21	2.32159311	10	1.63844294	38	2.30368227
45	3.87421471	24	2.4586815	24	4.17186193	21	2.23061521	22	5.11519236	20	2.24395978	5	0.83141832	52	3.19934142
22	2.18712433	26	3.07570019	15	3.01085308	12	1.47185908	12	3.2218117	7	0.90690696	6	1.1520742	24	1.70509314
28	2.30755549	9	0.8825849	17	2.82872388	26	2.64363604	11	2.44824527	9	0.96660833	8	1.27339318	40	2.3558096
35	2.66890346	47	4.26464161	33	5.08073185	28	2.63425035	38	7.82558	34	3.3787623	15	2.20919724	49	2.67021957
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17	4.91523055	34	11.6975187	7	4.0863967	18	6.42098522	11	8.5892605	19	7.15916669	7	3.90905178	28	5.78547573
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24	2.39281	18	2.13544967	19	3.82470627	24	2.95217711	30	8.07767445	11	1.42923473	12	2.31076952	23	1.63874313
31	3.11758868	23	2.75235735	15	3.04576152	23	2.85377121	30	8.1479151	18	2.35908468	11	2.13662457	40	2.87477055
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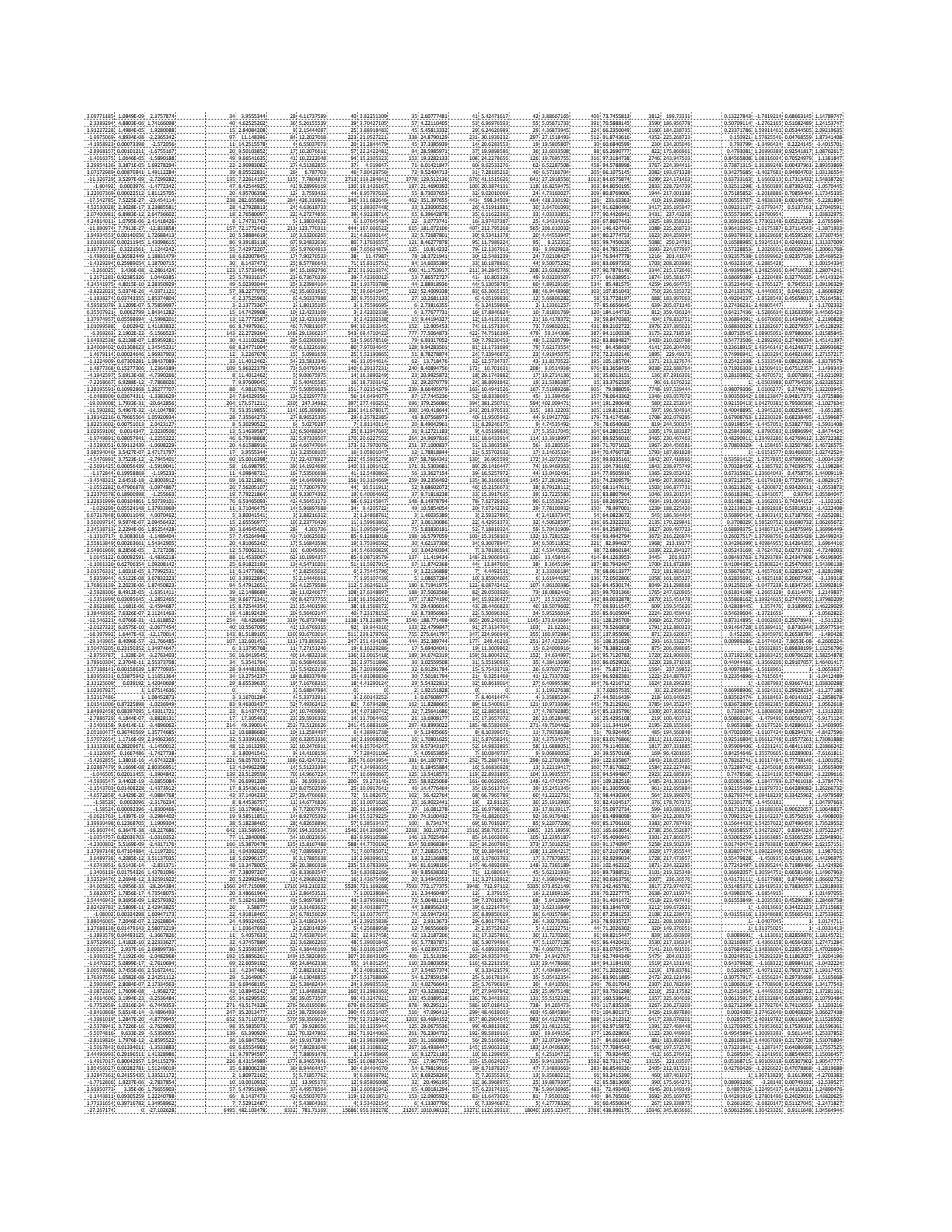
25	21.6848406	22	22.7069481	2	3.50262574	18	19.2629557	1	2.34252559	5	5.65197371	3	5.02592372	9	5.5788516
16	12.0680852	28	25.1302193	3	4.56864227	43	40.0148354	5	10.1848939	9	8.84656754	7	10.1975264	12	6.46823374
221	92.3826464	214	106.446592	102	86.0886327	269	138.73454	57	64.3488958	271	147.632277	86	69.4344481	234	69.9036827
63	6.58383114	36	4.47672581	22	4.64203412	69	8.89654578	29	8.18472797	52	7.08199115	31	6.2571741	121	9.03669402
21	7.91968093	7	3.14127741	1	0.76144038	9	4.18759906	6	6.11093633	6	2.94885585	5	3.64197371	14	3.77313635
114	32.6885532	75	25.5900993	51	29.5262666	113	39.9763818	34	26.3292133	146	54.5578949	30	16.6146239	108	22.1309816
60	8.60225083	50	8.53003311	21	6.07893724	66	11.6745186	27	10.4542464	40	7.47368424	22	6.09202875	78	7.99174334
82	6.22549473	65	5.87209719	45	6.89795004	64	5.99479291	43	8.8165077	65	6.43112982	36	5.27886955	116	6.29367163
6	1.29300913	6	1.53858485	1	0.43510879	6	1.59527583	6	3.49196361	6	1.68506048	3	1.2486767	7	1.07803896
43	8.06441641	43	9.5960567	40	15.1464897	48	11.106569	27	13.6752845	53	12.9537127	14	5.07120231	65	8.71172022
20	2.7212349	14	2.26664723	7	1.92301021	16	2.68590231	23	8.45146488	8	1.41853458	12	3.15352076	31	3.01428148
97	4.75351309	57	3.32382138	46	4.55143458	53	3.20444648	51	6.74965001	72	4.5982159	43	4.06995706	94	3.29197772
75	8.70294608	62	8.56084393	31	7.26296977	58	8.30361522	26	8.1479151	40	6.04893507	31	6.94776522	90	7.46334662
44	3.03501547	30	2.46234753	11	1.53196355	17	1.44674286	27	5.02967721	20	1.79784452	13	1.73192865	39	1.92246709
17	3.07201909	12	2.58033502	6	2.18914109	15	3.34426313	13	6.34434014	11	2.59048795	12	4.18826976	16	2.06624133
15	3.91305395	8	2.48332994	3	1.58013191	3	0.96556169	8	5.6361518	7	2.3797784	0	0	7	1.30499453
10	3.30435667	4	1.57277563	4	2.66866723	8	3.26145281	6	5.35434421	0	0	3	1.91463761	8	1.88913493
14	2.58372569	10	2.1960298	4	1.49047904	13	2.96002865	14	6.9777358	13	3.12662375	5	1.78224245	16	2.11020392
75	6.37789431	57	5.76780768	36	6.18110425	56	5.87541131	34	7.80841864	74	8.20090302	43	7.06257254	91	5.53023416
21	3.01078779	11	1.87660728	2	0.5789464	10	1.76886645	10	3.87194313	8	1.49473685	2	0.5538208	3	0.30737474
31	2.10482993	26	2.10062498	12	1.64506884	25	2.0942548	17	3.11725519	26	2.30060769	13	1.70481431	46	2.23202586
7	1.27826429	6	1.30374822	0	0	2	0.45059545	4	1.97265313	2	0.47595568	4	1.4107856	13	1.69649288
16	2.63095697	9	1.76098693	6	1.99201464	7	1.42012311	10	4.44080681	4	0.85717137	8	2.54075133	16	1.88018169
3	0.65877997	6	1.56779849	4	1.77348139	6	1.62556588	7	4.15131117	2	0.57235177	1	0.42412858	7	1.09850805
17	1.89655198	9	1.19475319	5	1.12624622	8	1.10113359	9	2.71160519	8	1.16310713	5	1.07736843	8	0.63781083
34	4.51975223	16	2.53090331	11	2.95240484	9	1.47608856	12	4.30809304	18	3.11833032	10	2.56752169	30	2.84998805
65	11.2200171	63	12.9401875	62	21.6082384	85	18.1022801	24	11.1881819	86	19.3460593	17	5.66770834	137	16.9000037
32	2.2704782	17	1.43527837	12	1.71908012	27	2.36355284	37	7.08985251	16	1.47945324	7	0.95927651	37	1.87609643
8	2.80369657	3	1.25107152	0	0	5	2.16194789	0	0	3	1.37017544	0	0	2	0.50090699
19	3.27969729	9	1.84859822	6	2.09111985	6	1.277808	6	2.79704548	10	2.24954177	8	2.66715686	22	2.71386921
36	2.75120445	29	2.63717059	7	1.08010486	9	0.84858836	20	4.1277984	21	2.09147926	13	1.91885487	39	2.12995803
16	2.44551507	21	3.81935051	8	2.4688111	3	0.56572557	17	7.01725728	13	2.58945051	9	2.65687597	20	2.18457234

gsyne_2031	Synechococcus_assembled_mapped	phosphoglucomutase/phosphomannomutase, C-terminal domain protein				PF00408.15	1802504	1803974	-1	119	fig|1129.58.peg.2036			
gsyne_2032	Synechococcus_assembled_mapped	recB nuclease, TM0106 family domain protein				TIGR03491	1804077	1805556	1	157	fig|1129.58.peg.2037			
gsyne_2033	Synechococcus_assembled_mapped	glycine cleavage T-C-terminal barrel domain protein				PF08669.6	1805562	1806465	-1	157	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Iron-sulfur cluster assembly
gsyne_2034	Synechococcus_assembled_mapped	orotate phosphoribosyltransferase	pyrE	2.4.2.10	GO:0004588,GO:0009220	TIGR00336	1806461	1807055	-1	126	fig|1129.58.peg.2039			
gsyne_2035	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1807126	1807258	1	856				
gsyne_2036	Synechococcus_assembled_mapped	occludin/ELL family protein				UniRef100_B	1807296	1807656	1	185	fig|1129.58.peg.2040			
gsyne_2038	Synechococcus_assembled_mapped	FKBP-type peptidyl-prolyl cis-trans isomerase family protein				PF00254.23	1807823	1808690	1	95	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_2039	Synechococcus_assembled_mapped	transporter associated domain protein				PF03471.12	1808746	1810039	1	141	fig|1129.58.peg.2042			
gsyne_204	Synechococcus_assembled_mapped	shikimate / quinate 5-dehydrogenase family protein				PF01488.15	163861	164689	-1	703	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_2040	Synechococcus_assembled_mapped	glycosyl hydrolases 15 family protein				PF00723.16	1811092	1814287	-1	105	fig|1129.58.peg.2044			
gsyne_2041	Synechococcus_assembled_mapped	oxidoreductase , NAD-binding Rossmann fold family protein				PF01408.17	1810142	1811096	1	703	fig|1129.58.peg.2043			
gsyne_2042	Synechococcus_assembled_mapped	glycosyltransferase, WecB/TagA/CpsF family protein		2.4.1.-	GO:0016757,GO:0043163	TIGR00696	1814424	1815114	1	90	fig|1129.58.peg.2045			
gsyne_2043	Synechococcus_assembled_mapped	photosystem II 4 kDa reaction centre component family protein				PF02533.10	1815228	1815372	-1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2044	Synechococcus_assembled_mapped	queuine tRNA-ribosyltransferase	tgt	2.4.2.29	GO:0005737,GO:0006400,G(	TIGR00430	1815402	1816521	-1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_2045	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	1817307	1818420	-1	699	fig|1129.58.peg.2049			
gsyne_2046	Synechococcus_assembled_mapped	cobalamin-5-phosphate synthase family protein				PF02654.10	1816553	1817336	1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis
gsyne_2047	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11352.3	1818763	1819135	1	156	fig|1129.58.peg.2050			
gsyne_2048	Synechococcus_assembled_mapped	phospholipase/Carboxylesterase family protein				PF02230.11	1819232	1819844	-1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_2049	Synechococcus_assembled_mapped	phosphoribosylaminoimidazolecarboxa	purH	2.1.2.3	GO:0003937,GO:0004643,G(	TIGR00355	1819899	1821465	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_205	Synechococcus_assembled_mapped	glutaredoxin family protein				PF00462.19	164832	166098	1	112	fig|1129.58.peg.203			
gsyne_2050	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF13301.1	1821503	1821968	1	156	fig|1129.58.peg.2053			
gsyne_2051	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09366.5	1821980	1822610	-1	156	fig|1129.58.peg.2054			
gsyne_2052	Synechococcus_assembled_mapped	4-hydroxy-3-methylbut-2-enyl diphospl	ispH	1.17.1.2	GO:0009240,GO:0015968,G(	TIGR00216	1822714	1823911	-1	76	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis
gsyne_2053	Synechococcus_assembled_mapped	sugar fermentation stimulation protein	sfsA		GO:0000023,GO:0003677	TIGR00230	1823952	1824690	-1	119,129	fig|1129.58.peg.2056			
gsyne_2054	Synechococcus_assembled_mapped	integral membrane protein MviN	mviN			TIGR01695	1824782	1826450	1	157	fig|1129.58.peg.2057			
gsyne_2055	Synechococcus_assembled_mapped	putative cytochrome c oxidase subunit Va			GO:0009536	UniRef100_B	1826488	1826743	-1	112	fig|1129.58.peg.2058			
gsyne_2056	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11378.3	1826767	1827055	-1	156	fig|1129.58.peg.2059			
gsyne_2057	Synechococcus_assembled_mapped	2TM domain protein				PF13239.1	1827077	1827317	-1	157	fig|1129.58.peg.2060			
gsyne_2058	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1827405	1827579	-1	856				
gsyne_206	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	166101	166275	-1	156	fig|1129.58.peg.204			
gsyne_2060	Synechococcus_assembled_mapped	serine hydroxymethyltransferase family protein				PF00464.14	1827594	1828884	1	75,78,125	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Glycine Biosynthesis
gsyne_2061	Synechococcus_assembled_mapped	glycosyl transferase 4 family protein				PF00953.16	1828949	1830047	1	89	fig|1129.58.peg.2062			
gsyne_2062	Synechococcus_assembled_mapped	competence/damage-inducible CinA C-terminal domain protein				TIGR00199	1830036	1831284	1	132	fig|1129.58.peg.2063			
gsyne_2063	Synechococcus_assembled_mapped	3-isopropylmalate dehydratase, large s	leuC	4.2.1.33	GO:0003861,GO:0009098,G(	TIGR00170	1831339	1832749	1	74	fig|1129.58.p	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios
gsyne_2064	Synechococcus_assembled_mapped	aconitase C-terminal domain protein				PF00694.14	1832753	1833389	1	157	fig|1129.58.p	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios
gsyne_2065	Synechococcus_assembled_mapped	pentapeptide repeats family protein				PF13599.1	1833460	1833955	1	185	fig|1129.58.peg.2066			
gsyne_2066	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF12600.3	1833957	1837083	-1	156	fig|1129.58.peg.2067			
gsyne_2067	Synechococcus_assembled_mapped	photosystem II reaction centre I family protein				PF02532.9	1837181	1837301	-1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2068	Synechococcus_assembled_mapped	photosystem II reaction centre N family protein				PF02468.10	1840409	1840529	-1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2069	Synechococcus_assembled_mapped	alpha mannosidase, middle domain protein				PF09261.6	1837401	1840422	1	157	fig|1129.58.peg.2069			
gsyne_207	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF10989.3	166353	166890	1	156	fig|1129.58.peg.205			
gsyne_2070	Synechococcus_assembled_mapped	photosystem II reaction center protein	psbH		GO:0042301,GO:0009523,G(	UniRef100_C	1840635	1840836	1	92,141	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2071	Synechococcus_assembled_mapped	twin arginine-targeting translocase, Tat	tatA		GO:0008565,GO:0015628	TIGR01411	1840870	1841104	1	97	fig|1129.58.p	Membrane Transport	Protein translocation across cy	Twin-arginine translocation syste
gsyne_2072	Synechococcus_assembled_mapped	peptidyl-tRNA hydrolase	pth	3.1.1.29	GO:0004045,GO:0006412	TIGR00447	1841123	1841774	1	136	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba
gsyne_2073	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11344.3	1841785	1842043	1	156	fig|1129.58.peg.2074			
gsyne_2074	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1842051	1842483	-1	141	fig|1129.58.peg.2075			
gsyne_2075	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11283.3	1842479	1843637	-1	156	fig|1129.58.peg.2076			
gsyne_2076	Synechococcus_assembled_mapped	global nitrogen regulator NtcA	ntcA		GO:0003677,GO:0003700,G(	TIGR03697	1843675	1844416	-1	129	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation
gsyne_2077	Synechococcus_assembled_mapped	ribonuclease PH	rph	2.7.7.56	GO:0004549,GO:0008033	TIGR01966	1844480	1845215	-1	166	fig|1129.58.p	Stress Response	Heat shock	Heat shock dnaK gene cluster ex
gsyne_2078	Synechococcus_assembled_mapped	ATP:corrinoid adenosyltransferase BtuR/CobO/CobP family protein				PF02572.10	1845277	1845961	1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis
gsyne_2079	Synechococcus_assembled_mapped	deoxycytidine triphosphate deaminase	dcd	3.5.4.13	GO:0008829,GO:0009394	TIGR02274	1845960	1846554	1	123	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	pyrimidine conversions
gsyne_208	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR02246	167433	167892	-1	185	fig|1129.58.peg.207			
gsyne_2080	Synechococcus_assembled_mapped	thymidylate synthase, flavin-dependen	thyX	2.1.1.148	GO:0009265,GO:0050797	TIGR02170	1846557	1847280	-1	123	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate Biosynthesis
gsyne_2081	Synechococcus_assembled_mapped	thioredoxin family protein				PF00085.15	1847340	1847928	-1	112	fig|1129.58.peg.2082			
gsyne_2082	Synechococcus_assembled_mapped	4Fe-4S binding domain protein				PF00037.22	1847979	1848396	1	157	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_2083	Synechococcus_assembled_mapped	transglycosylase SLT domain protein				PF01464.15	1848895	1850884	-1	703	fig|1129.58.p	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Murein Hydrolases
gsyne_2084	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1848392	1848899	1	88	fig|1129.58.peg.2084			
gsyne_2085	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1850933	1851158	1	856	fig|1129.58.peg.2086			
gsyne_2086	Synechococcus_assembled_mapped	badF/BadG/BcrA/BcrD ATPase family protein				PF01869.15	1852594	1853560	-1	185	fig|1129.58.p	Carbohydrates	Aminosugars	Chitin and N-acetylglucosamine u
gsyne_2087	Synechococcus_assembled_mapped	phosphoglucosamine mutase	glmM	5.4.2.10	GO:0008966,GO:0009103,G(	TIGR01455	1851201	1852608	1	89,100	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Sialic Acid Metabolism
gsyne_2088	Synechococcus_assembled_mapped	bicarbonate transporter, IctB family	ictB			TIGR00947	1853552	1854860	-1	144	fig|1129.58.peg.2089			
gsyne_2089	Synechococcus_assembled_mapped	tRNA (guanine-N(7)-)-methyltransferas	trmB	2.1.1.33	GO:0006400,GO:0008176	TIGR00091	1854871	1855582	-1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_209	Synechococcus_assembled_mapped	bacterial regulatory helix-turn-helix s, AraC family protein				PF00165.18	167077	167437	1	261	fig|1129.58.peg.206			
gsyne_2090	Synechococcus_assembled_mapped	FIST N domain protein				PF08495.5	1855590	1856904	-1	157	fig|1129.58.peg.2091			
gsyne_2091	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11375.3	1856973	1857591	1	156	fig|1129.58.peg.2092			
gsyne_2092	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1857580	1857886	1	156	fig|1129.58.peg.2093			
gsyne_2093	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF06172.6	1857889	1858393	-1	156	fig|1129.58.peg.2094			
gsyne_2094	Synechococcus_assembled_mapped	isoleucine--tRNA ligase	ileS	6.1.1.5	GO:0004822,GO:0005737,G(	TIGR00392	1858371	1861305	-1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Ile
gsyne_2095	Synechococcus_assembled_mapped	putative isoleucyl-tRNA synthetase			GO:0004812	UniRef100_D	1861329	1861878	-1	703	fig|1129.58.peg.2096			
gsyne_2097	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	1862070	1863096	1	121	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Myxoxanthophyll biosynthesis in
gsyne_2098	Synechococcus_assembled_mapped	aspartyl/glutamyl-tRNA(Asn/Gln) amid	gatC	6.3.5.-	GO:0006424,GO:0030956,G(	TIGR00135	1863096	1863390	-1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Asp and As
gsyne_2099	Synechococcus_assembled_mapped	creatininase			GO:0046872	UniRef100_B	1863399	1864176	-1	141	fig|1129.58.p	Amino Acids and Derivatives	Amino Acids and Derivatives -	Creatine and Creatinine Degrada
gsyne_21	Synechococcus_assembled_mapped	cytochrome C oxidase subunit II, periplasmic domain protein				PF00116.15	12695	13592	1	112	fig|1129.58.p	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_210	Synechococcus_assembled_mapped	parB-like nuclease family protein				PF08857.6	167910	168558	1	185	fig|1129.58.peg.208			
gsyne_2100	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1864245	1864545	1	156	fig|1129.58.peg.2100			
gsyne_2101	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G(	TMHMM	1864562	1864700	-1	88	fig|1129.58.peg.2101			
gsyne_2102	Synechococcus_assembled_mapped	methylpurine-DNA glycosylase family protein				PF02245.11	1864774	1865101	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_2103	Synechococcus_assembled_mapped	bbp50 domain protein			GO:0015074,GO:0003677,G(	UniRef100_C	1865276	1865873	1	92,141	fig|1129.58.peg.2104			
gsyne_2104	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	1865888	1866974	-1	157	fig|1129.58.peg.2105			
gsyne_2105	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	1866970	1867477	-1	154	fig|1129.58.peg.2106			
gsyne_2106	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1867603	1868041	1	132,152	fig|1129.58.peg.2107			
gsyne_2107	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1868041	1868614	-1	856	fig|1129.58.peg.2108			
gsyne_2108	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1869227	1869341	1	856	fig|1129.58.peg.2109			
gsyne_2109	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1869337	1869499	1	856	fig|1129.58.peg.2110			
gsyne_211	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	169065	170565	-1	141	fig|1129.58.peg.210			
gsyne_2110	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1869516	1869999	1	856	fig|1129.58.peg.2111			
gsyne_2111	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1870864	1871032	-1	156	fig|1129.58.peg.2113			
gsyne_2112	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1871091	1871832	-1	856	fig|1129.58.peg.2114			
gsyne_2113	Synechococcus_assembled_mapped	methylpurine-DNA glycosylase family protein				PF02245.11	1872040	1872232	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_2114	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	1872486	1873512	1	132,152	fig|1129.58.peg.2116			
gsyne_2115	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1873591	1874266	-1	856	fig|1129.58.peg.2117			
gsyne_2116	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1874819	1874954	1	856	fig|1129.58.peg.2118			
gsyne_2117	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1875087	1875738	1	856	fig|1129.58.peg.2119			
gsyne_2118	Synechococcus_assembled_mapped	methylpurine-DNA glycosylase family protein				PF02245.11	1878249	1878798	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_2119	Synechococcus_assembled_mapped	aspartate carbamoyltransferase	pyrB	2.1.3.2	GO:0004070,GO:0009220	TIGR00670	1878824	1879835	1	126	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis
gsyne_212	Synechococcus_assembled_mapped	universal stress family protein				PF00582.21	168595	169069	1	149	fig|1129.58.peg.209			
gsyne_2120	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04483.7	1879841	1880189	-1	156	fig|1129.58.peg.2123			
gsyne_2121	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1880196	1880394	-1	156	fig|1129.58.peg.2124			
gsyne_2122	Synechococcus_assembled_mapped	proto-chlorophyllide reductase 57 kD subunit				PF08369.5	1880509	1880671	-1	703	fig|1129.58.peg.2125			
gsyne_2124	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF10742.4	1880816	1881068	1	156	fig|1129.58.peg.2126			
gsyne_2125	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	1882307	1882646	-1	156	fig|1129.58.peg.2128			
gsyne_2126	Synechococcus_assembled_mapped	phosphopantothenoylcysteine decarbo	coaBC	4.1.1.36	GO:0004632,GO:0004633,G(	TIGR00521	1881057	1882311	1	83	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Coenzyme A	Coenzyme A Biosynthesis
gsyne_2127	Synechococcus_assembled_mapped	photosystem II manganese-stabilizing p	psbO		GO:0042549,GO:0005509,G(	UniRef100_P	1882785	1883607	1	92,141	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2128	Synechococcus_assembled_mapped	sulfate adenylyltransferase	sat	2.7.7.4	GO:0004781	TIGR00339	1883763	1884930	1	106	fig|1129.58.peg.2130			
gsyne_2129	Synechococcus_assembled_mapped	ATP-dependent zinc metalloprotease F	ftsH3	3.4.24.-	GO:0004222,GO:0005524,G(	UniRef100_P	1884967	1886812	1	141,189,703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_213	Synechococcus_assembled_mapped	carbohydrate-selective porin, OprB family protein				PF04966.7	170764	172075	-1	144,182	fig|1129.58.peg.212			
gsyne_2130	Synechococcus_assembled_mapped	KDPG and KHG aldolase family protein				PF01081.14	1886822	1887434	1	703	fig|1129.58.peg.2132			
gsyne_2131	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_C	1887453	1888068	1	156	fig|1129.58.peg.2133			
gsyne_2132	Synechococcus_assembled_mapped	chorismate synthase	aroC	4.2.3.5	GO:0004107,GO:0009423	TIGR00033	1888091	1889180	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_2133	Synechococcus_assembled_mapped	endonuclease III	nth	4.2.99.18	GO:0003906,GO:0006281	TIGR01083	1889239	1889893	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_2134	Synechococcus_assembled_mapped	photosystem II q(b) protein	psbA	1.10.3.9	GO:0009055,GO:0009538,G(	TIGR01151	1890001	1891081	-1	112,164	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem II
gsyne_2135	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	1891282	1892263	1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Coenzyme F420	Coenzyme F420 synthesis
gsyne_2136	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	1892299	1893856	1	703	fig|1129.58.peg.2138			
gsyne_2137	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	1893856	1895095	-1	699	fig|1129.58.peg.2139			
gsyne_2138	Synechococcus_assembled_mapped	response regulator				PF00072.19	1895165	1895930	-1	699	fig|1129.58.peg.2140			
gsyne_2139	Synechococcus_assembled_mapped	CAAX protease self-immunity family protein				PF02517.11	1895926	1896748	-1	157	fig|1129.58.peg.2141			
gsyne_214	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	170610	170775	1	856	fig|1129.58.peg.211			
gsyne_2140	Synechococcus_assembled_mapped	ATP-dependent Clp protease adaptor ClpS family protein				PF02617.12	1896747	1897095	-1	138	fig|1129.58.p	Protein Metabolism	Protein degradation	Proteolysis in bacteria, ATP-depe
gsyne_2141	Synechococcus_assembled_mapped	LL-diaminopimelate aminotransferase		2.6.1.83		TIGR03542	1897139	1898390	-1	703	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa
gsyne_2142	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	1898527	1901140	1	703	fig|1129.58.peg.2144			
gsyne_2143	Synechococcus_assembled_mapped	ribonuclease, Rne/Rng family domain protein		3.1.4.-	GO:0004540,GO:0006401	TIGR00757	1901524	1903591	1	134	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA processing and degradation
gsyne_2144	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09366.5	1904186	1904708	-1	156	fig|1129.58.peg.2147			
gsyne_2145	Synechococcus_assembled_mapped	ribonuclease HII family protein				PF01351.13	1903665	1904190	1	134	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	Ribonuclease H
gsyne_2146	Synechococcus_assembled_mapped	ubiE/COQ5 methyltransferase family protein				PF01209.13	1905600	1906542	-1	703	fig|1129.58.peg.2149			
gsyne_2147	Synechococcus_assembled_mapped	prephenate dehydratase family protein				PF00800.13	1904761	1905604	1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate Synthesis
gsyne_2148	Synechococcus_assembled_mapped	ATP-dependent protease La domain protein				PF02190.11	1906597	1907272	-1	138	fig|1129.58.peg.2150			
gsyne_2149	Synechococcus_assembled_mapped	ribosomal protein S10	rpsJ		GO:0000314,GO:0003735,G(	TIGR01049	1907429	1907750	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_215	Synechococcus_assembled_mapped	phycobilisome 32.1 kDa linker polypept	cpcC		GO:0030089,GO:0015979	UniRef100_P	172123	173188	-1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2150	Synechococcus_assembled_mapped	translation elongation factor Tu	tuf		GO:0003746,GO:0006414	TIGR00485	1907912	1909112	-1	169	fig|1129.58.p	Virulence, Disease and Defense	Invasion and intracellular resis	Mycobacterium virulence operon
gsyne_2151	Synechococcus_assembled_mapped	translation elongation factor G	fusA		GO:0003746,GO:0006414	TIGR00484	1909151	1911227	-1	169	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation elongation factors ba
gsyne_2152	Synechococcus_assembled_mapped	ribosomal protein S7	rpsG		GO:0000314,GO:0003735,G(	TIGR01029	1911311	1911782	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2153	Synechococcus_assembled_mapped	ribosomal protein S12	rpsL		GO:0000314,GO:0003735,G(	TIGR00981	1911828	1912203	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2154	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1912257	1912626	-1	156	fig|1129.58.peg.2156			
gsyne_2155	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF09992.4	1912671	1914444	-1	156	fig|1129.58.peg.2157			
gsyne_2156	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1914471	1914663	-1	856				
gsyne_2157	Synechococcus_assembled_mapped	ferredoxin-dependent glutamate synth	gltS	1.4.7.1	GO:0006541,GO:0046872,G(	UniRef100_P	1914630	1919214	1	92,141,703	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation
gsyne_2158	Synechococcus_assembled_mapped	lipoyl synthase	lipA	2.8.1.8	GO:0009107,GO:0017140,G(	TIGR00510	1919526	1920396	-1	80	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Lipoic acid	Lipoic acid metabolism
gsyne_2159	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1919341	1919530	1	856	fig|1129.58.peg.2159			
gsyne_216	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	173291	173462	-1	856	fig|1129.58.peg.214			
gsyne_2161	Synechococcus_assembled_mapped	precorrin-3B C17-methyltransferase	cobJ	2.1.1.131	GO:0009236,GO:0030789	TIGR01466	1920597	1922376	-1	79	fig|1129.58.peg.2161			
gsyne_2162	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	1922372	1923758	-1	156	fig|1129.58.peg.2162			
gsyne_2163	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	1923756	1923915	1	856				
gsyne_2164	Synechococcus_assembled_mapped	photosystem I core protein PsaA	psaA		GO:0009538,GO:0016168	TIGR01335	1924224	1926528	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopł	Photosystem I



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1	-1.0508618	0.64212082	1.29379747	0.80985947	1.16523587	0.91220041	-1.110331
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24	4.65194347	16	3.69031153	17	6.65303214	12	2.86971406	17	8.8989799	6	1.51561306	2	0.74874096	27	3.74001225
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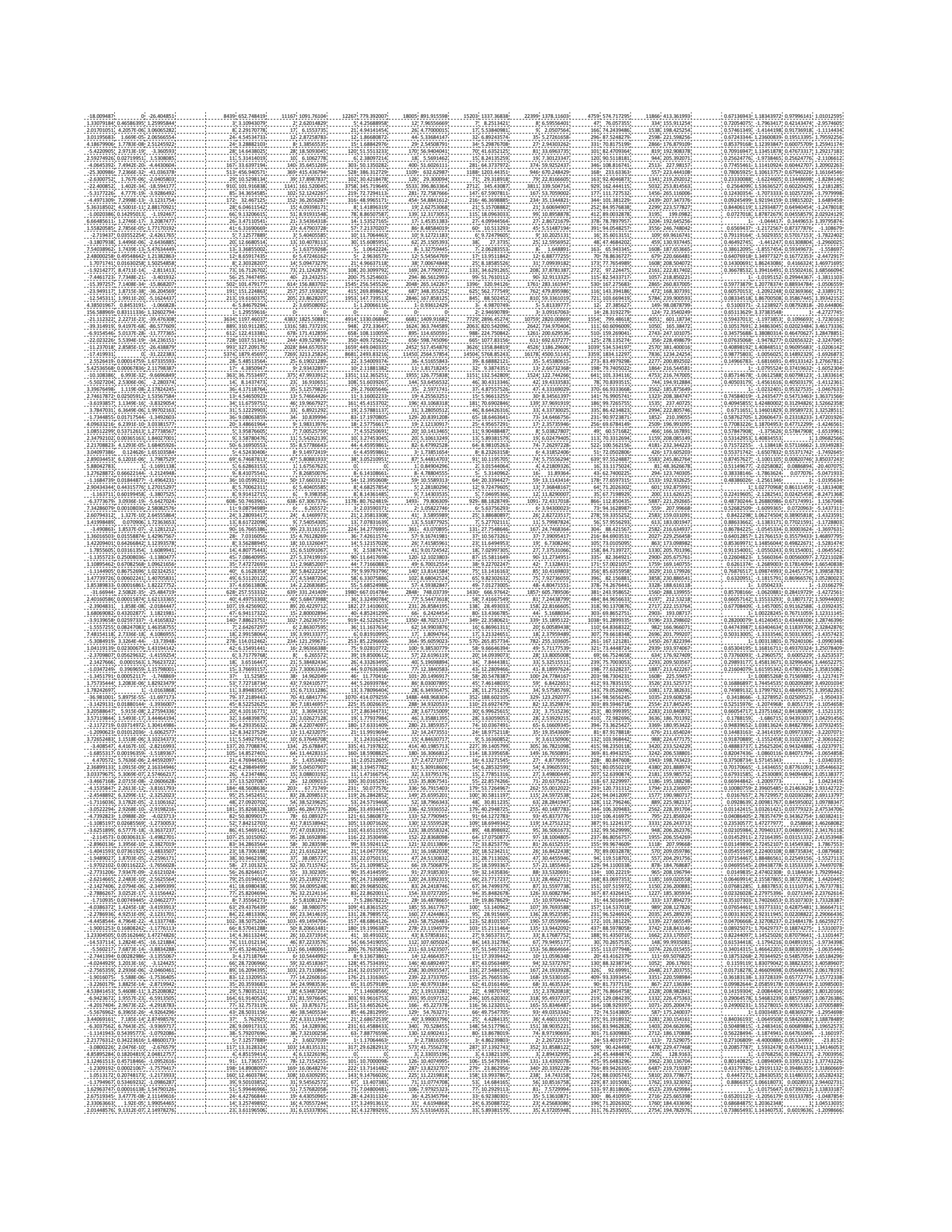
10	2.06522292	5	1.22873096	0	0	8	2.03840801	2	1.11548838	1	0.26914161	3	1.1966485	4	0.59035467
94	3.33476486	57	2.40620198	38	2.72187686	67	2.9325563	74	7.08985251	79	3.65240019	55	3.76858629	109	2.76343933
39	7.39417517	29	6.54248878	20	7.65601255	17	3.97656644	35	17.9209608	17	4.2003739	22	8.05612544	70	9.48438645
58	5.88407372	45	5.43228424	33	6.75945319	58	7.25959342	46	12.6030617	49	6.47828565	26	5.09450357	106	7.68496777
15	5.31057322	21	8.84686291	18	12.8667885	17	7.42562916	18	17.2103921	18	8.30494096	8	5.47039316	27	6.83124686
19	2.54524771	20	3.18805871	11	2.97520333	9	1.48748692	16	5.78848023	8	1.39662671	10	2.58734812	43	4.11652714
254	29.4739774	338	46.6704072	150	35.1434021	275	39.3705894	83	26.0106521	207	31.303239	96	21.5156601	534	44.2825233
40	6.42513797	43	8.21884486	24	7.78361276	41	8.1253208	25	10.8450259	36	7.53596494	18	5.58435968	65	7.46142704
143	49.6149154	133	54.9095291	54	37.828358	105	44.9468965	30	28.1103071	109	49.2852107	31	20.773818	149	36.944395
107	80.70532	111	99.6233693	18	27.4118536	62	57.6958092	10	20.3697878	14	13.7613273	3	4.37036845	5	2.69509739
6	1.90985753	11	4.1664125	3	1.92805087	11	4.31992889	8	6.87713935	5	2.07411879	2	1.22958378	7	1.59233277
56	9.76362674	41	8.50602899	35	12.3207941	56	12.0460694	43	20.2469549	62	14.0873315	23	7.74514207	67	8.34803031
34	3.25871638	34	3.87763052	14	2.70921328	23	2.71975433	41	10.6125469	23	2.87282641	20	3.70233791	46	3.15073264
28	5.74840746	13	3.17579694	10	4.14511922	8	2.02634642	14	7.76221498	11	2.94303956	8	3.17218065	23	3.3744533
34	8.07983104	19	5.37275236	10	4.79811746	11	3.22515239	21	13.4775445	11	3.40666908	14	6.42583854	18	3.05690499
29	5.26794035	21	4.53922809	14	5.13473931	21	4.70648131	17	8.33988169	18	4.26117389	17	5.96444699	47	6.10136184
0	0	3	3.25937055	0	0	1	1.12648864	0	0	0	0	0	0	0	0
3	1.92754139	4	3.05817483	0	0	8	6.3417138	1	1.73520414	1	0.83732944	0	0	0	0
83	5.75949368	56	4.62396035	54	7.56567161	46	3.93820427	43	8.05828803	56	5.06416844	29	3.88671434	88	4.3639017
23	4.95653501	27	6.92363184	8	3.4808703	25	6.64698263	15	8.72990904	15	4.21265121	17	7.07583463	19	2.92610574
17	10.5326369	25	18.4309644	2	2.50187553	22	16.8168661	1	1.67323257	4	3.22969926	0	0	5	2.21383
214	30.0602811	266	44.4611572	91	25.8088213	290	50.2587237	66	25.0375205	203	37.1611551	86	23.3322235	311	31.2194844
12	6.50545219	11	7.09592129	0	0	12	8.02623152	2	2.92815699	1	0.70649671	4	4.18826976	3	1.16226075
32	3.2463855	31	3.74224026	14	2.86764681	38	4.75628535	48	13.1510209	20	2.64419823	28	5.48638846	39	2.82748814
48	7.40175894	37	6.78914813	20	6.22689021	42	7.99055938	30	12.4934698	42	8.44028073	30	8.93497549	52	5.73037597
3	2.31304967	9	8.25707205	0	0	15	14.268856	0	0	1	1.00479533	1	1.48916258	0	0
221	35.3352979	203	38.6217886	101	32.6050876	262	51.6835062	112	48.3618187	152	31.6718895	95	29.3371891	335	38.2778348
13	2.46472506	15	3.38404592	6	2.29680377	11	2.5730724	11	5.63230197	9	2.22372736	5	1.8309376	19	2.57433347
139	14.3107079	74	9.06562807	64	13.3037417	65	8.25645973	53	14.7363628	62	8.31863192	41	8.15283372	114	8.38759093
74	16.2499059	82	21.4265794	44	19.5082953	50	13.5463823	29	17.1982892	51	14.5949701	17	7.21018592	156	24.4810366
17	5.08472126	13	4.62680761	5	3.01950495	21	7.74946492	7	5.65437212	20	7.7958258	11	6.35461619	26	5.55747669
43	22.6048036	27	16.8894656	26	27.5964453	27	17.5117779	6	8.51827488	28	19.1824562	6	6.09202875	67	25.1705762
8	5.14011038	11	8.40998079	2	2.59453759	8	6.3417138	5	8.67602071	9	7.53596494	1	1.24096882	7	3.21415319
15	6.19566876	9	4.42343145	4	3.33583404	18	9.17283603	8	8.92390701	10	5.3828321	4	3.19106268	12	3.542128
19	5.83379784	15	5.48035755	9	5.57940384	22	8.33402211	4	3.3168504	12	4.80167678	6	3.55817608	19	4.16905331
38	3.15415864	30	2.96306413	29	4.86010271	48	4.91558677	22	4.93163282	63	6.81481997	17	2.72538128	46	2.72862492
642	81.2944099	791	119.185109	463	118.37341	1033	161.383886	325	111.141725	815	134.492221	393	96.1162053	1422	128.680081
77	6.86779529	58	6.15565783	51	9.18426288	66	7.26281104	38	9.15331336	79	9.18264108	46	7.92433559	162	10.325895
166	9.36503037	143	9.59968539	204	23.2369318	285	19.8371901	183	27.881768	397	29.1880788	144	15.6906887	463	18.6667266
31	2.46125422	45	4.25135289	19	3.04576152	45	4.40799901	23	4.93163282	42	4.3456823	23	3.52696401	51	2.89368352
18	3.06138927	10	2.02379217	5	1.7169734	9	1.88852506	13	5.97114366	14	3.10304439	7	2.29944222	6	0.72926165
48	8.12388176	61	12.2849121	42	14.3522226	43	8.97893868	32	14.6265013	33	7.27863931	25	8.17223368	89	10.7646134
47	4.49228655	44	5.00428609	43	8.29823179	40	4.7169772	33	8.51827488	38	4.73333335	29	5.35360102	75	5.1229124
20	3.18309587	13	2.46197102	8	2.57073449	6	1.17816243	16	6.87713935	6	1.24447128	5	1.53697973	16	1.81980888
1196	115.588053	1497	172.156502	1225	239.037133	1144	136.408674	740	193.144171	1458	183.634043	1235	230.529834	3333	230.198853
20	2.12206392	13	1.64131402	9	1.92805087	4	0.52362775	15	4.29821209	6	0.82964752	7	1.43451441	26	1.97145962
47	3.14200389	44	3.50010761	25	3.3743986	29	2.39188916	45	8.12436621	31	2.70075044	29	3.74442615	55	2.62759014
26	2.18423577	19	1.8993265	12	2.03542416	21	2.17660516	22	4.99133782	19	2.08014529	17	2.75837621	41	2.46147878
22	2.9933584	24	3.88568096	21	5.76903064	23	3.86098458	12	4.40945994	30	5.31950466	14	3.67910756	47	4.57003966
24	3.03904336	14	2.10947096	14	3.57932558	11	1.71851186	15	5.12961808	10	1.6502113	10	2.44570497	19	1.7193541
1	0.63083173	2	1.50128583	1	1.27368209	2	1.55660248	1	1.70365498	1	0.82210527	0	0	0	0
11	3.29011375	14	4.98271589	5	3.01950495	12	4.42826567	11	8.8854419	9	3.50812161	8	4.62153905	16	3.41998566
32	2.66250322	22	2.17812452	8	1.34393314	20	2.05307281	23	5.16816198	23	2.49391646	12	1.92841198	38	2.25948693
80	3.18675041	56	2.65439744	48	3.86052895	63	3.09622709	72	7.74566441	57	2.95901264	36	2.76973982	78	2.22043845
192	9.66848047	159	9.52739083	98	9.96392809	386	23.9816187	85	11.5596328	432	28.3501032	75	7.29451918	248	8.92472309
69	13.7586575	60	14.2363311	27	10.8702178	56	13.7768265	20	10.7702326	71	18.4501211	9	3.46615429	59	8.40746474
13	2.5773982	8	1.88733075	3	1.20090026	8	1.95687169	8	4.28347537	9	2.32538347	2	0.76585504	5	0.7084256
29	3.2043841	19	2.49815874	11	2.45406899	9	1.22693985	22	6.56503987	27	3.88798191	2	0.42683004	34	2.68479766
33	4.07458927	21	3.08538279	12	2.99156647	9	1.37102887	27	9.0033012	20	3.21820567	10	2.38477994	29	2.55890386
43	6.63074238	39	7.15612911	12	3.73613413	31	5.89779383	25	10.4112249	55	11.0527486	19	5.65881781	44	4.84877966
65	21.0768545	65	25.0798917	39	25.5331596	181	72.4111106	63	55.1697616	134	56.6253814	33	20.6673499	153	35.454384
271	26.4860476	290	33.7260689	217	42.820833	253	30.5072162	170	44.8709127	271	34.5168422	227	42.850129	599	41.8370217
247	21.4246226	240	24.7712161	385	67.4255456	836	89.4657274	219	51.3013105	922	104.222395	287	48.0813369	1022	63.3509593
652	32.6902106	606	36.1545207	768	77.7461437	1521	94.087847	376	50.9126949	1661	108.530963	352	34.0871897	1878	67.2901946
98	21.6572166	96	25.2445515	63	28.1102448	203	55.3486199	66	39.3902392	162	46.6557829	54	23.0488221	210	33.1651475
139	38.5816685	128	42.2762089	63	35.3064675	215	73.6272972	52	38.9796258	200	72.3452634	61	32.7020103	211	41.8537845
36	10.1548522	34	11.4122134	27	15.3773813	48	16.7050022	17	12.950548	62	22.7916988	20	10.8963116	44	8.86971889
70	4.10947911	67	4.68040463	37	4.38569044	51	3.69396781	32	5.07349028	85	6.50311695	48	5.44262467	94	3.94368904
11	5.96333118	7	4.51558628	3	3.28371163	3	2.00655788	7	10.2485495	7	4.94547699	3	3.14120232	5	1.93710125
226	5.13170051	185	4.99855474	228	10.4528622	337	9.44097739	171	10.4861748	391	11.5702708	125	5.48202848	508	8.2433293
35	4.1874175	36	5.1250792	14	3.38184555	27	3.9854391	17	5.49281863	21	3.27424684	14	3.23507733	36	3.07798709
2	1.10145222	5	3.27661589	2	2.22388936	5	3.39734668	0	0	1	0.71771095	1	1.06368756	3	1.18070933
10	6.08697281	11	7.96735022	0	0	5	3.75496212	0	0	1	0.79325947	3	3.52696401	0	0
57	3.33500416	39	2.71522605	34	4.0165017	51	3.68150923	30	4.74035533	53	4.04120886	21	2.37311744	97	4.05582616
67	5.03163402	44	3.93193907	45	6.8232969	55	5.09602001	41	8.31545881	69	6.75300754	22	3.19106268	126	6.76224436
7	4.58245689	4	3.11587625	0	0	3	2.42301329	3	5.30383153	0	0	0	0	0	0
6498	293.55853	9167	492.790231	4436	404.626245	11929	664.895249	2566	313.068785	10146	597.342971	4701	410.18867	16047	518.077729

gsyne_2165	Synechococcus_assembled_mapped	photosystem I core protein PsaB	psaB		GO:0009522,GO:0009538,G	TIGR01336	1926547	1928758	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_2166	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1928862	1929027	-1	88	fig|1129.58.peg.2165			
gsyne_2167	Synechococcus_assembled_mapped	telomere recombination family protein				PF01300.13	1929033	1929630	-1	185	fig|1129.58.peg.2166			
gsyne_2168	Synechococcus_assembled_mapped	protein-(glutamine-N5) methyltransfera	prmC	2.1.1.-	GO:0006412,GO:0008757,G	TIGR03534	1929649	1930552	-1	703	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba
gsyne_2169	Synechococcus_assembled_mapped	DNA recombination-mediator A family protein				PF02481.10	1930577	1931825	-1	185	fig|1129.58.peg.2168			
gsyne_217	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	173541	173868	-1	856	fig|1129.58.peg.215			
gsyne_2170	Synechococcus_assembled_mapped	thioesterase superfamily protein				PF03061.17	1931873	1932227	-1	703	fig|1129.58.peg.2169			
gsyne_2171	Synechococcus_assembled_mapped	universal stress family protein				PF00582.21	1932390	1933239	1	149	fig|1129.58.peg.2170			
gsyne_2172	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1933341	1933533	1	856				
gsyne_2173	Synechococcus_assembled_mapped	2Fe-2S iron-sulfur cluster binding domain protein				PF00111.22	1933566	1934037	-1	112	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_2174	Synechococcus_assembled_mapped	photosystem II chlorophyll-binding prot	psbB		GO:0009769,GO:0016168,G	TIGR03039	1934338	1935865	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2175	Synechococcus_assembled_mapped	transcriptional regulator NrdR	nrdR		GO:0030528,GO:0045449	TIGR00244	1936246	1936669	1	261	fig|1129.58.p	Nucleosides and Nucleotides	Nucleosides and Nucleotides -	Ribonucleotide reduction
gsyne_2176	Synechococcus_assembled_mapped	30S ribosomal protein S1	rpsA		GO:0005840,GO:0003723,G	UniRef100_P	1936935	1937841	1	92,141	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2177	Synechococcus_assembled_mapped	HAD hydrolase, IA, variant 1 family protein			GO:0008152,GO:0016787	TIGR01549	1937848	1938640	1	703	fig|1129.58.peg.2177			
gsyne_2178	Synechococcus_assembled_mapped	methionine adenosyltransferase	metK	2.5.1.6	GO:0004478,GO:0006556	TIGR01034	1938705	1939941	1	102	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis
gsyne_2179	Synechococcus_assembled_mapped	carbohydrate kinase, FGGY family				PF02782.11	1939930	1941211	1	703	fig|1129.58.peg.2179			
gsyne_218	Synechococcus_assembled_mapped	dihydroorotase, homodimeric type	pyrC	3.5.2.3	GO:0004151,GO:0009220	TIGR00856	173960	175070	-1	126	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis
gsyne_2180	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	1941207	1941327	1	88	fig|1129.58.peg.2180			
gsyne_2181	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10615.4	1941363	1941633	1	156	fig|1129.58.peg.2181			
gsyne_2182	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1941685	1942345	1	92,703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Biotin	Biotin biosynthesis Experimental
gsyne_2184	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1942484	1942721	1	156	fig|1129.58.peg.2183			
gsyne_2185	Synechococcus_assembled_mapped	phycocyanobilin lyase CpcT	cpcT1	4.-.-.-	GO:0016829,GO:0017009	UniRef100_C	1942762	1943356	1	92,703	fig|1129.58.peg.2184			
gsyne_2186	Synechococcus_assembled_mapped	phycobilisome Linker polypeptide family protein				PF00427.16	1943442	1944189	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2187	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1944192	1944564	-1	856	fig|1129.58.peg.2186			
gsyne_2188	Synechococcus_assembled_mapped	phycobilisome 31.8 kDa linker polypept	cpeC		GO:0030089,GO:0015979	UniRef100_P	1944813	1945659	1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2189	Synechococcus_assembled_mapped	cpcD/allophycocyanin linker domain protein				PF01383.16	1945695	1945911	1	164	fig|1129.58.peg.2188			
gsyne_219	Synechococcus_assembled_mapped	EAL domain protein				PF00563.15	175367	177224	-1	264,710	fig|1129.58.peg.217			
gsyne_2190	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1946107	1946224	-1	856	fig|1129.58.peg.2189			
gsyne_2191	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1945991	1946123	1	856				
gsyne_2192	Synechococcus_assembled_mapped	phycocyanin, beta subunit			GO:0009055,GO:0015979,G	TIGR01339	1946263	1946782	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2193	Synechococcus_assembled_mapped	phycocyanin, alpha subunit	cpcA		GO:0009055,GO:0015979,G	TIGR01338	1946836	1947325	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2194	Synechococcus_assembled_mapped	phycobilisome 31.8 kDa linker polypept	cpeC		GO:0030089,GO:0015979	UniRef100_P	1947565	1948420	1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2195	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1948618	1948738	-1	856	fig|1129.58.peg.2193			
gsyne_2196	Synechococcus_assembled_mapped	phycocyanin, beta subunit			GO:0009055,GO:0015979,G	TIGR01339	1948776	1949295	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2197	Synechococcus_assembled_mapped	phycocyanin, alpha subunit	cpcA		GO:0009055,GO:0015979,G	TIGR01338	1949349	1949838	1	164	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2198	Synechococcus_assembled_mapped	phycocyanobilin lyase subunit alpha	cpcE	4.-.-.-	GO:0016829,GO:0030089,G	UniRef100_P	1949963	1950836	1	141,703	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_2199	Synechococcus_assembled_mapped	phycocyanobilin lyase subunit beta don	cpcF	4.-.-.-	GO:0016829,GO:0030089,G	UniRef100_P	1950847	1951510	1	141,703	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome
gsyne_22	Synechococcus_assembled_mapped	cytochrome C and Quinol oxidase polypeptide I family protein				PF00115.15	13598	15287	1	112	fig|1129.58.p	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_220	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02594.11	175105	175399	1	156				
gsyne_2200	Synechococcus_assembled_mapped	cytidylate kinase	cmk	2.7.4.14	GO:0004127,GO:0015949	TIGR00017	1951987	1953463	-1	124	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_2201	Synechococcus_assembled_mapped	low molecular weight phosphotyrosine phosphatase family protein				PF01451.16	1951502	1951991	1	703	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Protein deglycation
gsyne_2202	Synechococcus_assembled_mapped	rare lipoA family protein	rlpA			TIGR00413	1953634	1954132	-1	88	fig|1129.58.peg.2200			
gsyne_2203	Synechococcus_assembled_mapped	phosphoribosylformylglycinamidine cyc	purM	6.3.3.1	GO:0004641,GO:0006189,G	TIGR00878	1954581	1955616	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis
gsyne_2204	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1955788	1956466	1	156	fig|1129.58.peg.2202			
gsyne_2205	Synechococcus_assembled_mapped	aldo/keto reductase family protein				PF00248.16	1956466	1957447	-1	703				
gsyne_2206	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1957445	1957661	1	156	fig|1129.58.peg.2204			
gsyne_2207	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1957747	1958176	1	856	fig|1129.58.peg.2205			
gsyne_2208	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_D	1958374	1959760	1	92,141	fig|1129.58.peg.2206			
gsyne_2209	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1959864	1960053	-1	856	fig|1129.58.peg.2207			
gsyne_221	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	177279	179028	-1	264,710	fig|1129.58.peg.218			
gsyne_2210	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1960036	1960165	-1	856	fig|1129.58.peg.2208			
gsyne_2211	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1960167	1960350	-1	856	fig|1129.58.peg.2209			
gsyne_2212	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1960380	1960992	-1	856	fig|1129.58.peg.2210			
gsyne_2213	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1961700	1961940	1	856	fig|1129.58.peg.2211			
gsyne_2214	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1962001	1962139	-1	856	fig|1129.58.peg.2212			
gsyne_2215	Synechococcus_assembled_mapped	acyltransferase family protein				PF01757.17	1962184	1964233	-1	703	fig|1129.58.peg.2213			
gsyne_2216	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	1964363	1964570	-1	856				
gsyne_2218	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	1964893	1966144	1	92,703	fig|1129.58.peg.2215			
gsyne_2219	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1966169	1966427	1	156	fig|1129.58.peg.2216			
gsyne_222	Synechococcus_assembled_mapped	NMT1-like family protein				PF13379.1	179202	180120	1	185	fig|1129.58.peg.219			
gsyne_2220	Synechococcus_assembled_mapped	3'-5' exonuclease family protein				PF01612.15	1966435	1967116	-1	703	fig|1129.58.peg.2217			
gsyne_2221	Synechococcus_assembled_mapped	pex protein	pex			UniRef100_C	1967337	1967721	1	185	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_2222	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12046.3	1967695	1968193	1	156	fig|1129.58.peg.2219			
gsyne_2223	Synechococcus_assembled_mapped	coproporphyrinogen III oxidase family protein				PF01218.13	1969017	1970103	-1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi
gsyne_2224	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	1968258	1969059	1	156	fig|1129.58.peg.2220			
gsyne_2225	Synechococcus_assembled_mapped	cobQ/CobB/MinD/ParA nucleotide binding domain protein				PF01656.18	1970280	1971390	1	157	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Scaffold proteins for [4Fe-4S] clu
gsyne_2226	Synechococcus_assembled_mapped	rod shape-determining protein RodA	mrdB		GO:0008360	TIGR02210	1971386	1972673	1	89,93	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_2227	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	1972687	1974046	1	699	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton
gsyne_2228	Synechococcus_assembled_mapped	photosystem I reaction center subunit I	psaD		GO:0009538,GO:0015979	UniRef100_P	1974173	1974590	1	92	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_2229	Synechococcus_assembled_mapped	chorismate binding enzyme family protein				PF00425.13	1974685	1976206	1	185	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn
gsyne_223	Synechococcus_assembled_mapped	NMT1-like family protein				PF13379.1	180146	181088	1	185	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Urea decomposition
gsyne_2230	Synechococcus_assembled_mapped	putative glutamate--cysteine ligase			GO:0004357,GO:0006750	TIGR02048	1976202	1977360	1	86	fig|1129.58.peg.2227			
gsyne_2231	Synechococcus_assembled_mapped	phosphoenolpyruvate carboxylase family protein				PF00311.12	1977356	1980392	1	184	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism I: anaplerot
gsyne_2232	Synechococcus_assembled_mapped	gnat family acetyltransferase			GO:0016740	UniRef100_B	1980416	1980869	1	703	fig|1129.58.peg.2229			
gsyne_2234	Synechococcus_assembled_mapped	DNA replication and repair RecF family	recF		GO:0003697,GO:0005524,G	TIGR00611	1981141	1982170	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa
gsyne_2235	Synechococcus_assembled_mapped	S-adenosylmethionine decarboxylase p	speD	4.1.1.50	GO:0004014,GO:0008295	TIGR03330	1982197	1982674	1	104	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Polyamine Metabolism
gsyne_2236	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein				PF00999.16	1983021	1984188	-1	145	fig|1129.58.peg.2233			
gsyne_2237	Synechococcus_assembled_mapped	rho termination factor, N-terminal domain protein				PF07498.7	1982774	1983050	1	165	fig|1129.58.peg.2232			
gsyne_2238	Synechococcus_assembled_mapped	asparagine synthase family protein				PF00733.16	1984204	1985047	-1	703	fig|1129.58.peg.2234			
gsyne_2239	Synechococcus_assembled_mapped	cob(I)yrinic acid a,c-diamide adenosyltr	cobO	2.5.1.17	GO:0008817,GO:0009236	TIGR00708	1985138	1986338	1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis
gsyne_224	Synechococcus_assembled_mapped	ion channel family protein				PF07885.11	182289	182838	-1	141	fig|1129.58.peg.222			
gsyne_2240	Synechococcus_assembled_mapped	thiF family protein				PF00899.16	1986396	1987569	-1	185	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Cofactors, Vitamins, Prosthetic	Thiamin biosynthesis
gsyne_2241	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14464.1	1987596	1988079	-1	156	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Protein deglycation
gsyne_2242	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14159.1	1988132	1988495	1	156	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Protein deglycation
gsyne_2243	Synechococcus_assembled_mapped	phosphotransferase enzyme family protein				PF01636.18	1988520	1989423	-1	703	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Protein deglycation
gsyne_2244	Synechococcus_assembled_mapped	prephenate dehydrogenase family protein				PF02153.12	1990958	1991792	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate Synthesis
gsyne_2245	Synechococcus_assembled_mapped	C-3',4' desaturase CrtD	crtD	1.-.-.-	GO:0016117,GO:0016491	TIGR02733	1989462	1990962	1	76	fig|1129.58.peg.2240			
gsyne_2246	Synechococcus_assembled_mapped	putative carboxyl-terminal protease			GO:0008233	UniRef100_B	1991890	1993324	1	703	fig|1129.58.peg.2242			
gsyne_2247	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10999.3	1993360	1993606	1	156	fig|1129.58.peg.2243			
gsyne_2248	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08844.5	1993720	1994059	1	156	fig|1129.58.peg.2244			
gsyne_2249	Synechococcus_assembled_mapped	protein RecA	recA		GO:0003677,GO:0005737,G	TIGR02012	1994165	1995293	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair system including Rec
gsyne_225	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	181084	182293	1	264,710	fig|1129.58.peg.221			
gsyne_2250	Synechococcus_assembled_mapped	haloacid dehalogenase-like hydrolase family protein				PF13419.1	1995449	1996202	-1	703	fig|1129.58.peg.2246			
gsyne_2252	Synechococcus_assembled_mapped	AAA domain family protein				PF07728.9	1996399	1998070	-1	157	fig|1129.58.peg.2247			
gsyne_2253	Synechococcus_assembled_mapped	iron-Sulfur binding C terminal family protein				PF12617.3	1998125	1999175	-1	185	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_2254	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhN	1.6.5.-	GO:0006810,GO:0048038,G	UniRef100_P	1999171	1999639	-1	141,703	fig|1129.58.peg.2249			
gsyne_2255	Synechococcus_assembled_mapped	50S ribosomal protein L3	rplC			TIGR03625	2000036	2000684	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2256	Synechococcus_assembled_mapped	50S ribosomal protein L4	rplD		GO:0003735,GO:0006412,G	TIGR03953	2000695	2001331	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2257	Synechococcus_assembled_mapped	50S ribosomal protein L23	rplW		GO:0005840,GO:0000166,G	UniRef100_C	2001323	2001626	1	92,141	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2258	Synechococcus_assembled_mapped	ribosomal protein L2	rplB		GO:0000315,GO:0003735,G	TIGR01171	2001641	2002505	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2259	Synechococcus_assembled_mapped	ribosomal protein S19	rpsS		GO:0000314,GO:0003735,G	TIGR01050	2002540	2002816	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_226	Synechococcus_assembled_mapped	fusaric acid resistance -like family protein				PF13515.1	182834	183968	-1	94	fig|1129.58.peg.223			
gsyne_2260	Synechococcus_assembled_mapped	ribosomal protein L22	rplV		GO:0000311,GO:0003735,G	TIGR01044	2002820	2003174	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2261	Synechococcus_assembled_mapped	ribosomal protein S3	rpsC		GO:0000312,GO:0003735,G	TIGR01009	2003193	2003922	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2262	Synechococcus_assembled_mapped	ribosomal protein L16	rplP		GO:0000315,GO:0003735,G	TIGR01164	2003986	2004400	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2263	Synechococcus_assembled_mapped	ribosomal protein L29	rpmC		GO:0000315,GO:0003735,G	TIGR00012	2004402	2004612	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2264	Synechococcus_assembled_mapped	30S ribosomal protein S17	rpsQ		GO:0003735,GO:0006412,G	TIGR03635	2004671	2004881	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2265	Synechococcus_assembled_mapped	ribosomal protein L14	rplN		GO:0000315,GO:0003735,G	TIGR01067	2004893	2005259	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2266	Synechococcus_assembled_mapped	ribosomal protein L24	rplX		GO:0000315,GO:0003735,G	TIGR01079	2005260	2005617	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2267	Synechococcus_assembled_mapped	ribosomal L5 family protein				PF00281.14	2005683	2006223	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2268	Synechococcus_assembled_mapped	ribosomal S8 family protein				PF00410.14	2006269	2006644	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2269	Synechococcus_assembled_mapped	ribosomal protein L6	rplF		GO:0003735,GO:0006412,G	TIGR03654	2006690	2007200	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_227	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	183957	184143	-1	856	fig|1129.58.peg.224			
gsyne_2270	Synechococcus_assembled_mapped	ribosomal protein L18	rplR		GO:0000315,GO:0003735,G	TIGR00060	2007232	2007598	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2271	Synechococcus_assembled_mapped	ribosomal protein S5	rpsE		GO:0000312,GO:0003735,G	TIGR01021	2007612	2008251	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2272	Synechococcus_assembled_mapped	ribosomal protein L15	rplO		GO:0000315,GO:0003735,G	TIGR01071	2008259	2008712	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2273	Synechococcus_assembled_mapped	preprotein translocase, SecY subunit	secY		GO:0005887,GO:0015450,G	TIGR00967	2008817	2010134	1	97	fig|1129.58.p	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_2274	Synechococcus_assembled_mapped	adenylate kinase	adk	2.7.4.3	GO:0005524,GO:0009165,G	UniRef100_C	2010191	2010740	1	92,141,703	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2275	Synechococcus_assembled_mapped	ribosomal protein L36	rpmJ		GO:0000315,GO:0003735,G	TIGR01022	2010786	2010900	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2276	Synechococcus_assembled_mapped	30S ribosomal protein S13	rpsM		GO:0003735,GO:0006412,G	TIGR03631	2010968	2011334	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2277	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2011343	2011466	-1	856				
gsyne_2278	Synechococcus_assembled_mapped	30S ribosomal protein S11	rpsK		GO:0003735,GO:0006412,G	TIGR03632	2011464	2011857	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2279	Synechococcus_assembled_mapped	DNA-directed RNA polymerase, alpha s	rpoA	2.7.7.6	GO:0000345,GO:0003899,G	TIGR02027	2011914	2012853	1	135	fig|1129.58.peg.2273			
gsyne_228	Synechococcus_assembled_mapped	biotin-lipoyl like family protein				PF13533.1	184139	185309	-1	185	fig|1129.58.peg.225			
gsyne_2280	Synechococcus_assembled_mapped	ribosomal protein L17	rplQ		GO:0003735,GO:0005762,G	TIGR00059	2012961	2013255	1	158	fig|1129.58.peg.2274			
gsyne_2281	Synechococcus_assembled_mapped	tRNA pseudouridine(38-40) synthase	truA	5.4.99.12	GO:0006400,GO:0009982	TIGR00071	2013339	2014197	1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_2282	Synechococcus_assembled_mapped	ribosomal protein L13	rplM		GO:0000315,GO:0003735,G	TIGR01066	2014374	2014827	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2283	Synechococcus_assembled_mapped	ribosomal S9/S16 family protein				PF00380.14	2014823	2015225	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial
gsyne_2284	Synechococcus_assembled_mapped	ribosomal protein L31	rpmE		GO:0000315,GO:0003735,G	TIGR00105	2015256	2015514	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_2285	Synechococcus_assembled_mapped	peptide chain release factor 1	prfA		GO:0003747,GO:0006415	TIGR00019	2015627	2016725	1	169	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba
gsyne_2286	Synechococcus_assembled_mapped	HNH endonuclease family protein				PF01844.18	2016732	2017260	-1	157	fig|1129.58.peg.2280			
gsyne_2287	Synechococcus_assembled_mapped	alanine racemase	alr	5.1.1.1	GO:0008784,GO:0009252	TIGR00492	2017428	2018550	1	89	fig|1129.58.p	Amino Acids and Derivatives	Alanine, serine, and glycine	Alanine biosynthesis
gsyne_2289	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2018836	2018956	-1	856				
gsyne_229	Synechococcus_assembled_mapped	outer membrane efflux family protein				PF02321.13	185374	186877	1	141	fig|1129.58.peg.226			
gsyne_2290	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2018735	2018876	1	856	fig|1129.58.peg.2282			
gsyne_2291	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2019089	2020415	1	856	fig|1129.58.peg.2283			
gsyne_2292	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2020416	2022690	1	141	fig|1129.58.peg.2284			
gsyne_2293	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2022692	2024888	1	141	fig|1129.58.peg.2285			
gsyne_2294	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein				PF00486.23	2024889	2025591	-1	261	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_2295	Synechococcus_assembled_mapped	HAMP domain protein				PF00672.20	2025587	2027042	-1	129	fig|1129.58.peg.2287			
gsyne_2296	Synechococcus_assembled_mapped	beta-lactamase enzyme family protein				PF13354.1	2027038	2027965	-1	185	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Beta-lactamase
gsyne_2297	Synechococcus_assembled_mapped	NLP/P60				UniRef100_C	2028000	2028735	1	185	fig|1129.58.peg.2289			
gsyne_2298	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF05684.7	2028740	2029829	1	156	fig|1129.58.peg.2290			



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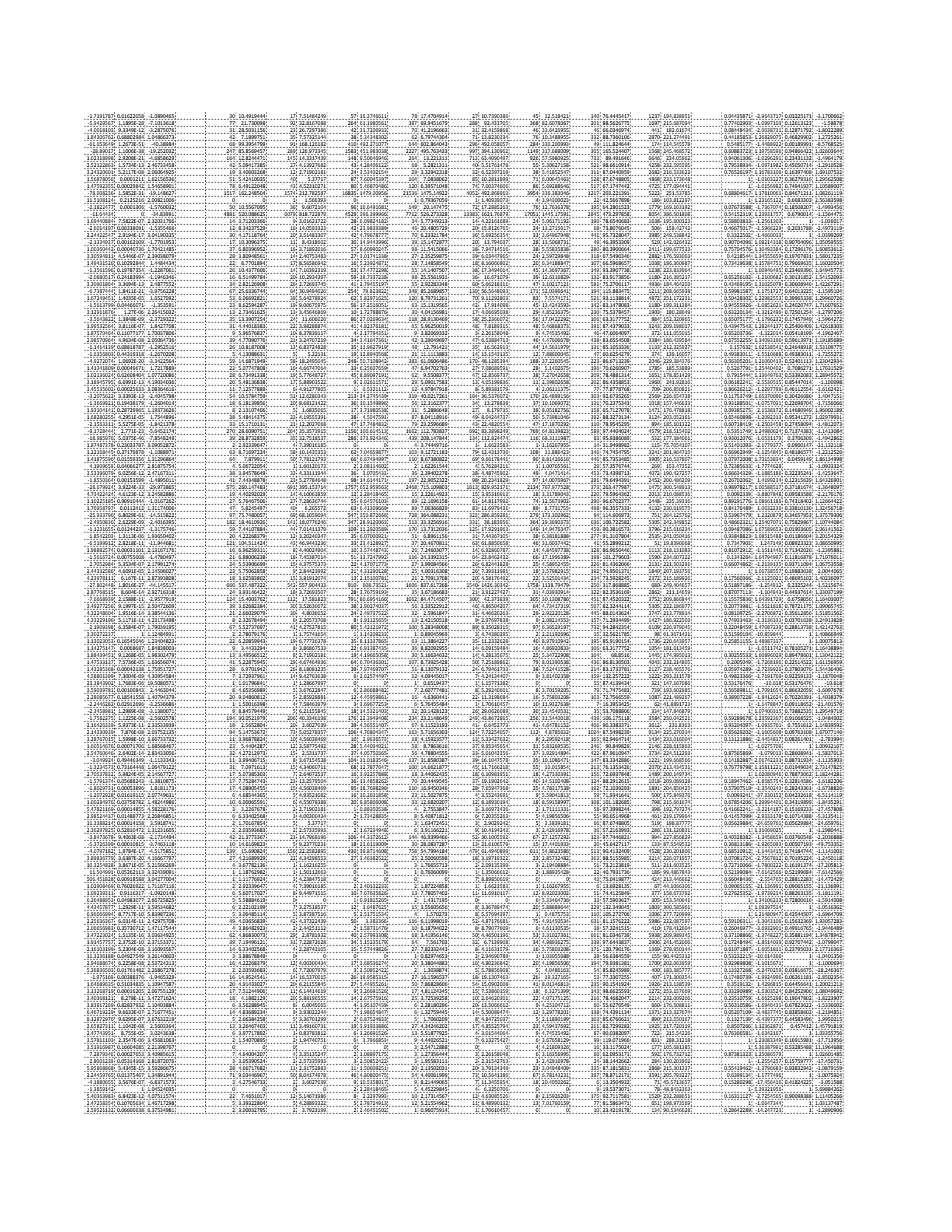
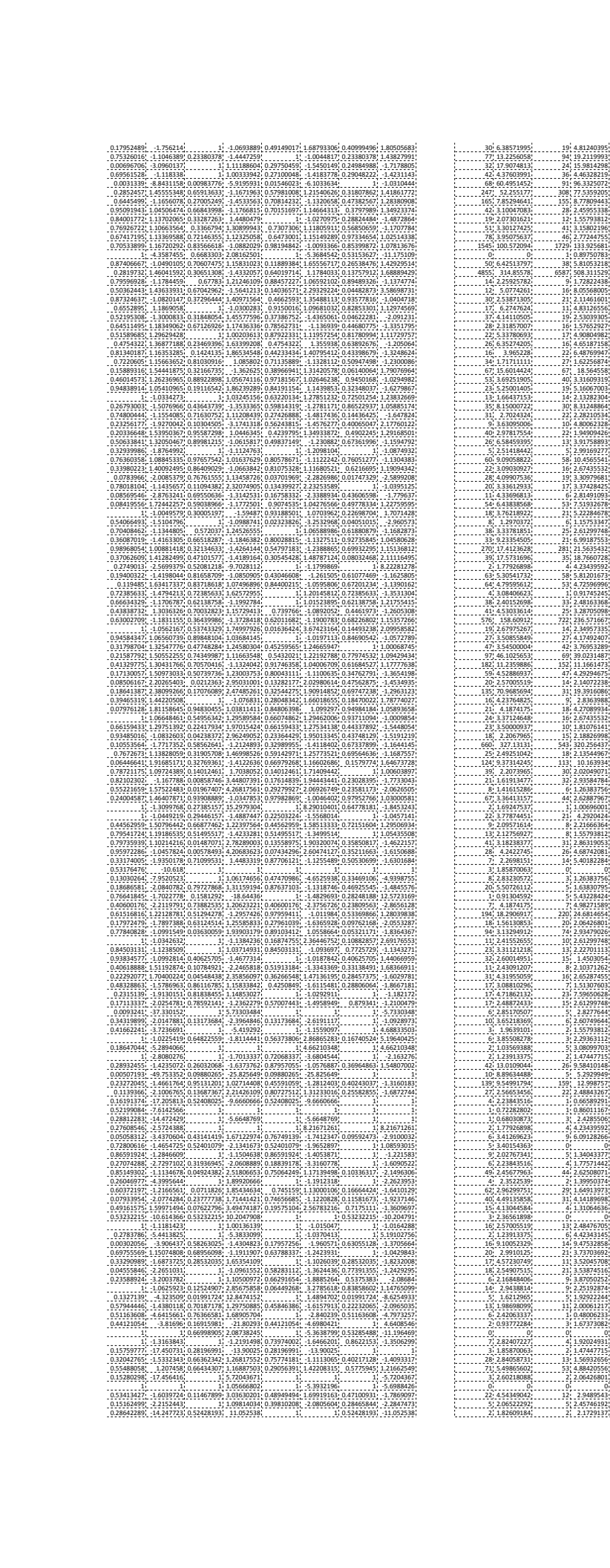
5	4.33696813	3	3.09640202	0	0	4	4.28065681	1	2.34252559	2	2.26078948	1	1.67530791	0	0
20	7.71016556	16	7.3396196	8	6.22689021	10	4.75628535	8	8.32897988	11	5.52637429	5	3.72290646	32	8.81596302
13	2.05020312	5	0.93830364	2	0.63684104	5	0.97287655	6	2.55548246	1	0.20552632	2	0.60920287	1	0.11270407
12	5.27023975	6	3.13559698	3	2.66022208	16	8.66968468	1	1.18608891	4	2.28940707	0	0	5	1.56929722
8	1.40184828	14	2.91916689	11	3.89180638	20	4.32389577	8	3.78589995	15	3.42543861	8	2.70756833	22	2.75498844
73	10.1718449	78	12.9327635	58	16.3174533	99	17.0194789	74	27.8468906	102	18.5221307	96	25.8360737	121	12.0489254
56	15.6690461	41	13.6508046	34	19.2079476	32	11.0468563	13	9.82349442	37	13.4918082	24	12.9701257	59	11.7975715
502	61.7633475	675	98.821341	304	75.5176047	833	126.446352	266	88.3846535	551	88.3471635	398	94.5776661	1136	99.8829853
191	92.0401014	257	147.3658	58	56.4311925	251	149.228453	54	70.2757677	81	50.8677634	35	32.5754315	107	36.8479705
213	11.9389236	210	14.0063419	300	33.9511381	231	15.9746644	176	26.6419712	227	16.5815578	149	16.1305898	590	23.6332611
4	3.55853795	2	2.11719796	0	0	2	2.19520862	0	0	0	0	0	0	0	0
1	0.78853966	0	0	1	1.59210261	2	1.9457531	0	0	0	0	0	0	1	0.56352036
3620	726.003451	3956	944.07448	1538	622.779005	3336	825.449198	1095	593.078734	2047	535.00995	1999	774.321503	5082	728.367985
911	193.913029	1417	358.904021	2770	1190.46298	530	139.187001	2038	1171.55022	3829	1062.15496	3088	1269.53394	10576	1608.77804
612	74.5045472	711	102.996109	604	148.462172	698	104.838542	451	148.27776	753	119.464876	698	164.121392	1817	158.078337
730	633.197347	246	253.904966	101	176.8826	272	291.084663	116	271.732969	158	178.602369	88	147.427096	194	120.255246
1008	202.157867	3110	742.18191	1606	650.314098	2991	740.083499	1057	572.497006	1965	513.578189	1955	757.277908	5131	735.390817
5354	1139.63815	7848	1987.77612	2776	1193.0416	7815	2052.35172	1939	1114.63978	3737	1036.63439	3104	1276.11184	10767	1637.83218
28	3.3384222	26	3.68872634	7	1.68511204	17	2.50072735	18	5.79593961	30	4.66142161	10	2.30282874	35	2.98220399
17	2.66890346	9	1.68130426	8	2.53583764	9	1.74325391	4	1.69594613	7	1.43217433	10	3.0322315	11	1.2341351
363	22.370436	400	29.3324051	184	22.8946052	363	27.599972	169	28.1269503	287	23.0496121	154	18.3301895	554	24.39853
14	4.95653501	23	9.68942128	4	2.85928632	16	6.98882745	5	4.78066447	14	6.45939852	7	4.78659401	19	4.80717371
36	2.53871305	36	3.02088002	25	3.55957901	25	2.17513049	18	3.42808623	30	2.75706034	14	1.90685453	43	2.16703359
13	2.76714531	13	3.29269744	4	1.71908012	12	3.15140379	15	8.62279359	8	2.21917986	10	4.11118504	11	1.67327519
34	7.10635742	49	12.1866425	16	6.75204963	83	21.4032841	19	10.724816	78	21.2459735	28	11.3032823	104	15.5341517
31	3.11758868	37	4.4277053	29	5.88847226	26	3.22600224	28	7.60472076	34	4.45604883	19	3.69053336	42	3.01850908
36	5.52675585	34	6.2110719	17	5.26943696	48	9.09166049	21	8.70673229	53	10.6037029	20	5.93029347	65	7.1312754
20	2.12206392	9	1.13629432	9	1.92805087	16	2.09451098	4	1.14618989	10	1.38274586	7	1.43451441	9	0.68242833
5	2.40942674	7	4.01385447	0	0	7	4.16174968	2	2.60280621	3	1.88399124	3	2.79217984	4	1.37749422
9	2.18364829	12	3.46450575	6	2.93926636	17	5.08889271	3	1.96575574	14	4.42672066	8	3.74894077	10	1.73390881
50	3.75495076	59	5.27237285	32	4.85212224	37	3.42823165	44	8.92390701	44	4.30626568	29	4.2064008	87	4.66916873
5	2.75363056	8	5.24258543	1	1.11194468	5	3.39734668	3	4.46195351	2	1.43542189	3	3.19106268	3	1.18070933
69	4.10635747	51	3.61158383	26	3.12412588	56	4.11178013	214	34.3945438	57	4.42075473	76	8.73573933	72	3.06214839
5	4.03438896	1	0.96012466	1	1.62912825	1	0.99550158	0	0	0	0	1	1.55842596	1	0.57662549
9	5.11904435	7	4.73766429	0	0	7	4.91222913	1	1.53608236	1	0.74124245	2	2.19712512	3	1.21942112
36	6.12277854	51	10.3213401	12	4.12073617	43	9.02295308	27	12.4016061	32	7.09267289	25	8.21229365	73	8.87268337
8	3.4695745	6	3.09640202	2	1.75131287	9	4.81573891	4	4.68505118	4	2.26078948	0	0	6	1.8596172
8	6.03404261	6	5.38504699	0	0	5	4.65288784	0	0	1	0.98295195	0	0	0	0
609	30.936616	682	41.2249132	372	38.1545176	909	56.9709669	378	51.8579604	687	45.4805966	367	36.0080821	1462	53.0748726
11	5.53120573	6	3.59003133	1	1.01525384	7	4.34269532	2	2.7159717	0	0	0	0	2	0.71869264
24	1.99687741	24	2.37613584	21	3.52782449	14	1.43715097	10	2.24702695	13	1.40960495	13	2.08911298	24	1.42704437
13	5.24470564	9	4.32056096	6	4.88738476	8	3.98200634	4	4.35818715	9	4.73188496	4	3.11685192	10	2.88312744
90	10.2046309	100	13.4919478	45	10.3018404	92	12.8699486	33	10.1050124	66	9.75242522	26	5.69385693	81	6.56335482
28	4.27965137	16	2.90998134	19	5.86342636	18	3.39435342	12	4.95335808	34	6.77240902	4	1.18083377	40	4.36914467
8	2.16848406	18	5.80575378	13	7.11470854	8	2.67541051	5	3.66019624	7	2.4727385	5	2.6176686	20	3.8742025
14	2.92614717	15	3.73060484	5	2.11001551	16	4.12593428	7	3.95124799	12	3.2686113	4	1.61475461	11	1.64303528
45	4.31300698	30	3.42143869	37	7.16006367	46	5.43950866	81	20.9662512	47	5.87055832	48	8.88561099	101	6.91791297
35	4.54813137	11	1.70089499	6	1.57421382	21	3.36680873	24	8.42256392	26	4.4030357	13	3.26277195	32	2.97167293
40	3.75089136	32	3.57062575	22	4.16528467	36	4.16496339	32	8.10387232	36	4.39937413	18	3.26005863	74	4.9589792
49	3.96291727	30	2.88708813	17	2.77597378	32	3.19303072	25	5.46043261	31	3.26734144	12	1.87447038	52	3.00544194
38	2.91045985	16	1.45820257	12	1.85569576	30	2.83487206	17	3.51637396	18	1.79665389	9	1.33137052	42	2.29886453
629	157.004487	675	200.486462	310	156.232227	626	192.783537	221	148.977887	434	141.177358	303	146.077207	883	157.510023
40	2.73733689	40	3.25722763	22	3.0397541	48	4.05269284	44	8.13184426	36	3.21058861	17	2.24696129	59	2.8854021
107	11.8230724	92	12.0963476	53	11.8241506	72	9.81551881	46	13.7269016	89	12.8159404	17	3.62805534	83	6.55406487
47	4.22461144	16	1.71131027	17	3.08521439	28	3.10513966	20	4.85497532	27	3.16276249	11	1.9096774	32	2.05553542
140	4.79980663	107	4.36515173	101	6.99140712	151	6.38714603	75	6.94424582	149	6.65726547	60	3.97306223	237	5.80670983
7	1.60841202	6	1.64047789	5	2.3196197	11	3.11835927	5	3.1026829	17	5.09051936	4	1.77516069	6	0.98522766
18	1.82076796	19	2.28694415	6	1.22540842	15	1.87200735	11	3.0049891	6	0.79094676	5	0.97685592	20	1.44576653
278	69.3914901	240	71.2840752	144	72.5723895	238	73.2946994	89	59.9956195	257	83.6004168	80	38.5682395	482	85.9794235
42	3.74607016	17	1.80424454	20	3.60167172	29	3.19123516	19	4.57665668	31	3.60331486	15	2.58402248	50	3.18700463
6	2.26276598	8	3.59003133	3	2.28432114	5	2.32644392	2	2.03697878	4	1.9659039	6	4.37036845	3	0.80852922
18	2.22250324	21	3.08538279	22	5.48453853	18	2.74205774	17	5.6687452	22	3.54002624	8	1.90782395	32	2.82361805
15	2.29267038	23	4.18309817	15	4.62902081	32	6.03440608	12	4.95335808	25	4.97971252	5	1.47604221	27	2.94917265
37	7.0149867	38	8.57291633	21	8.03881318	35	8.18704855	20	10.240549	26	6.42410126	10	3.6618752	39	5.28415816
53	4.7030038	46	4.85710121	63	11.2872339	55	6.02138426	143	34.2691723	72	8.32618121	50	8.5693499	156	9.89259278
11	2.37051674	15	3.84646213	5	2.17554394	19	5.0517068	8	4.65595149	18	5.05518145	7	2.91357897	18	2.77210017
79	22.6525939	73	24.9076967	37	21.4210169	45	15.9197981	21	16.2621611	33	12.331579	31	17.1684446	99	20.2867331
45	5.18707152	31	4.25198062	17	3.95645433	29	4.12422085	19	5.91468256	28	4.20611997	13	2.89421964	41	3.37737786
20	2.49609677	14	2.07911886	11	2.7718621	20	3.07960922	9	3.03348638	11	1.78911398	13	3.13366946	18	1.60542492
32	2.22052768	23	1.89912657	12	1.68126036	11	0.9417445	17	3.1858348	22	1.98949474	11	1.47427096	26	1.28933459
36	2.61306866	30	2.5911314	17	2.49140743	34	3.04481865	20	3.92054492	29	2.74321736	15	2.10289695	60	3.11233004
12	5.0774261	13	6.54524004	2	1.70859792	6	3.13218791	4	4.57078164	1	0.55141207	6	4.90334021	6	1.81426068
11	3.37746191	11	4.01892887	8	4.95947008	5	1.89409594	5	4.14606299	1	0.40013973	7	4.15120543	5	1.09711929
137	12.6418007	139	15.2624071	100	18.630988	155	17.6463246	57	14.2046765	139	16.7154116	69	12.2974729	278	18.3323965
105	9.03983431	67	6.8638192	43	7.47458595	72	7.64782359	27	6.27773608	90	10.097819	29	4.82222623	85	5.22969271
21	2.90283126	6	0.98690104	12	3.34912422	18	3.06979373	12	4.47973021	4	0.72057035	7	1.86886938	18	1.77812003
42	2.61619621	42	3.11307923	24	3.01842075	29	2.22870822	26	4.37383593	35	2.84120761	12	1.44371238	50	2.22575368
26	2.5773982	15	1.76937258	8	1.60120034	16	1.95687169	16	4.28347537	12	1.55025565	1	0.19146376	18	1.27516608
37	8.22911901	28	7.41019286	19	8.53203707	19	5.21362048	11	6.60712346	38	11.0141026	19	8.16175646	41	6.51660728
184	29.5556347	217	41.4764962	117	37.9451122	707	140.112239	58	25.1604601	570	119.319445	105	32.5754315	553	63.4795254
95	15.5476216	88	17.1373193	105	34.695821	293	59.1619078	54	23.8672419	330	70.3830688	59	18.649654	256	29.9410065
48	16.489067	58	23.7084247	27	18.7269099	153	64.8455933	16	14.8437265	73	32.6807193	18	11.942789	55	13.5021711
181	21.805312	197	28.2403332	265	64.4580432	627	93.193466	102	33.1857792	636	99.8515355	114	26.5257085	588	50.6229127
82	30.9244684	79	35.4515593	40	30.4576152	349	162.385786	29	29.5361922	172	84.5338676	39	28.4073949	166	44.7386167
52	4.77295963	45	4.91492384	38	7.04231631	68	7.70065247	22	5.45349873	83	9.92833476	24	4.25475024	65	4.26367259
86	25.2867294	83	29.0397025	69	40.9629112	309	112.095166	53	42.086053	251	96.1793492	61	34.6419601	297	62.4074925
107	15.2775503	101	17.1597588	112	32.2875789	337	59.3654875	66	25.4496607	320	59.5434267	69	19.0281886	333	33.9781908
83	20.8677307	63	18.8476645	73	37.0567651	242	75.0665905	37	25.1227382	159	52.0964533	42	20.3950528	188	33.778554
23	11.4000305	22	12.9753989	15	15.0112532	66	40.3604785	7	9.37010237	23	14.8566166	18	17.2317385	27	9.5637456
38	18.834833	37	21.8222618	24	24.0180051	89	54.4254938	8	10.7086884	27	17.440376	16	15.3171008	35	12.397448
58	16.4946985	57	19.2890618	50	28.7100471	139	48.7714178	31	23.8092765	120	44.4745472	47	25.8162202	178	36.1761597
56	16.3274094	55	19.081469	47	27.6678	175	62.9508355	43	33.8583531	101	38.3764265	40	22.5251483	198	41.2553732
79	15.227577	66	15.1379654	46	17.9023094	210	49.9409961	29	15.096276	129	32.4046492	54	20.1036949	146	20.1114156
41	11.3802044	61	20.1472558	34	19.054284	123	42.121663	41	30.7339358	91	32.9170949	35	18.7634485	133	26.3817693
77	15.7151316	79	19.1855498	79	32.5538157	198	49.8570617	59	32.519767	203	53.9929723	45	17.7385543	179	26.107567
8	4.47687033	5	3.32946454	5	5.64939636	12	8.28514222	4	6.04522733	12	8.75144316	2	2.16168762	8	3.19934142
63	17.9166552	67	22.6731077	42	24.1164395	163	57.192382	34	26.1134	97	35.950259	37	20.3234074	165	33.5340807
84	13.682829	78	15.1185826	110	36.1773551	254	51.0463301	61	26.8345655	217	46.0649125	86	27.0566159	294	34.223941
102	23.4368609	104	28.4349501	111	51.4955573	260	73.7066736	43	26.683073	222	66.476194	46	20.414348	341	55.9937718
66	5.21621679	52	4.89029324	51	8.13821927	99	9.65341741	34	7.25702689	97	9.99073256	31	4.732077	126	7.11653052
14	2.65431929	27	6.09128266	12	4.59360753	24	5.61397615	11	5.63230197	15	3.70621227	5	1.8309376	23	3.1162984
74	67.5653982	46	49.977015	17	31.339283	62	69.8422954	11	27.1239805	32	38.0764544	6	10.580892	15	9.78745895
97	27.5859612	128	43.3157878	53	30.4326499	221	77.5430455	41	31.4896883	117	43.3626835	39	21.4219699	214	43.4926864
3	2.53871305	6	6.04176004	2	3.41719585	19	19.8371901	3	6.85617246	8	8.8225931	0	0	8	4.83802849
66	17.480299	62	19.5396361	43	22.9943369	144	47.0545482	30	21.4582497	104	35.8965048	31	15.8578764	191	36.1513369
89	9.86556328	112	14.7730363	121	27.0810042	263	35.9684582	68	20.3567719	248	35.8259292	57	12.2035208	279	22.1015207
83	7.38396625	80	8.46879184	73	13.1123938	81	8.89059492	52	12.4934698	79	9.15909585	38	6.52940517	131	8.32854199
35	12.3913375	34	14.3234923	35	25.0187553	73	31.8865252	11	10.5174618	104	47.9841033	12	8.20558974	81	20.4937406
29	3.51810002	18	2.59837932	3	0.73481659	15	2.24509973	37	12.1221604	15	2.3714575	8	1.87447038	28	2.42747234
164	37.6827959	191	52.2218795	86	39.8974588	370	104.890266	58	35.9911217	232	69.4706172	80	35.5032139	363	59.6062732
77	19.9371072	67	20.6426801	50	26.1389981	122	38.9731441	17	11.8874433	101	34.0805579	33	16.5030331	123	22.7594941
43	17.3478725	46	22.0828671	12	9.77476952	63	31.3582999	13	14.1641082	37	19.4533049	9	7.01291681	24	6.91950586
37	3.50749335	24	2.70723674	12	2.29680377	31	3.62569293	25	6.40034315	23	2.8414294	13	2.38021888	37	2.50658785
28	5.51977762	36	8.44473278	15	5.97038479	23	5.59404015	17	9.05066706	38	9.76250004	9	3.42676617	40	5.63520364
38	3.52523613	43	4.74671254	18	3.37151141	33	3.77705013	18	4.50967494	31	3.74783283	12	2.15012779	35	2.32037797
5	4.33696813	2	2.06426801	0	0	1	1.0701642	0	0	0	0	0	0	0	0
117	8.10259914	108	8.89983814	116	16.219744	138	11.7910307	45	8.41625961	183	16.5159471	64	8.56045556	234	11.5808496
4	2.95282936	4	3.51364768	0	0	6	5.46466827	0	0	2	1.92407616	2	2.85158792	1	0.52755098
91	7.14324162	85	7.93949235	40	6.33959411	82	7.94149001	84	17.8074344	76	7.77466066	42	6.36768615	172	9.64869256
199	9.10877739	179	9.74944523	123	11.3673606	245	13.835896	127	15.699248	223	13.3022706	123	10.8740302	276	9.02822071
160	7.58376941	116	6.54248878	87	8.32591365	178	10.4092474	137	17.5369402	169	10.4391646	65	5.9505472	254	8.60369342
39	5.78262417	31	5.46942807	20	5.98739443	35	6.40269181	87	34.8375601	41	7.92242468	26	7.44581291	65	6.88747111
51	3.64841855	51	4.34134716	33	4.76645978	39	3.44217764	31	5.98913759	50	4.66142161	31	4.28326145	95	4.85673221
24	2.69481515	21	2.80580118	12	2.72048601	15	2.07798874	10	3.03239559	20	2.92658833	17	3.68676173	39	3.12945289
14	1.982614	16	2.69618679	17	4.86078675	7	1.2230448	5	1.91226579	18	3.32197638	7	1.91463761	21	2.1252768
23	2.19835299	32	3.63948079	15	2.89473202	33	3.89150619	12	3.0975545	20	2.49122808	10	1.84606932	32	2.18577596

gsyne_2299	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2030842	2031331	-1	141				
gsyne_23	Synechococcus_assembled_mapped	cytochrome c oxidase subunit III family protein				PF00510.13	15290	15896	1	112	fig|1129.58.j	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_230	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	186886	187072	1	856	fig|1129.58.peg.227			
gsyne_2300	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	2029892	2030891	1	90	fig|1129.58.peg.2291			
gsyne_2301	Synechococcus_assembled_mapped	photosystem I reaction center subunit '	psaI		GO:0003674,GO:0009538,G	TIGR03052	2031426	2031543	1	164	fig|1129.58.j	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_2302	Synechococcus_assembled_mapped	photosystem I reaction center subunit ;	psaL		GO:0009538,GO:0016021,G	UniRef100_P	2031585	2032077	1	92	fig|1129.58.j	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_2303	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2032100	2034287	-1	856	fig|1129.58.j	Membrane Transport	Cation transporters	Copper Transport System
gsyne_2304	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09852.4	2034610	2036020	-1	156	fig|1129.58.peg.2296			
gsyne_2305	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	2037286	2038240	-1	90				
gsyne_2306	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11204.3	2039053	2040661	-1	156	fig|1129.58.peg.2298			
gsyne_2307	Synechococcus_assembled_mapped	dolichyl-phosphate-mannose-mannosyltransferase family protein				PF02366.13	2040657	2042712	-1	90	fig|1129.58.peg.2299			
gsyne_2308	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2042895	2044494	1	141	fig|1129.58.peg.2300			
gsyne_2309	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2044555	2044693	-1	856	fig|1129.58.peg.2301			
gsyne_231	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	189168	189978	-1	156	fig|1129.58.peg.229			
gsyne_2310	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF00395.15	2044737	2046342	1	91	fig|1129.58.peg.2302			
gsyne_2311	Synechococcus_assembled_mapped	dnaJ domain protein				PF00226.26	2046533	2047178	1	95	fig|1129.58.peg.2303			
gsyne_2312	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhO	1.6.5.-	GO:0006810,GO:0048038,G	UniRef100_P	2047181	2047427	-1	141,703	fig|1129.58.peg.2304			
gsyne_2313	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein				PF00999.16	2047481	2048711	1	145	fig|1129.58.peg.2305			
gsyne_2314	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2049637	2049919	-1	156	fig|1129.58.peg.2307			
gsyne_2315	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein				PF01370.16	2048739	2049669	1	119	fig|1129.58.j	Dormancy and Sporulation	Dormancy and Sporulation - n	Persister Cells
gsyne_2316	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2049911	2051168	-1	92,703	fig|1129.58.peg.2308			
gsyne_2317	Synechococcus_assembled_mapped	tetratricopeptide repeat family protein				PF13429.1	2051125	2051554	-1	157	fig|1129.58.peg.2309			
gsyne_2318	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01934.12	2051581	2052007	-1	156	fig|1129.58.peg.2310			
gsyne_2319	Synechococcus_assembled_mapped	nucleotidyltransferase domain protein				PF01909.18	2052003	2052423	-1	703	fig|1129.58.peg.2311			
gsyne_232	Synechococcus_assembled_mapped	selenide, water dikinase	selD	2.7.9.3	GO:0001887,GO:0004756	TIGR00476	187111	189172	1	137	fig|1129.58.j	Protein Metabolism	Selenoproteins	Selenocysteine metabolism
gsyne_2320	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_P	2052423	2052870	-1	92,141	fig|1129.58.j	Miscellaneous	Plant-Prokaryote DOE project	Iron-sulfur cluster assembly
gsyne_2321	Synechococcus_assembled_mapped	9,9'-di-cis-zeta-carotene desaturase	zds			TIGR02732	2052946	2054440	1	185	fig|1129.58.peg.2313			
gsyne_2322	Synechococcus_assembled_mapped	polyketide cyclase / dehydrase and lipid transport family protein				PF03364.15	2054473	2054929	1	706	fig|1129.58.peg.2314			
gsyne_2323	Synechococcus_assembled_mapped	uroporphyrinogen-III synthase HemD family protein				PF02602.10	2055447	2056260	-1	79	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi
gsyne_2324	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2055011	2055458	1	156	fig|1129.58.peg.2315			
gsyne_2325	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	2056265	2057459	-1	90	fig|1129.58.peg.2317			
gsyne_2326	Synechococcus_assembled_mapped	putative beta-glucosidase			GO:0004553,GO:0005975	UniRef100_B	2057512	2057770	-1	119,703	fig|1129.58.j	Carbohydrates	Aminosugars	Chitin and N-acetylglucosamine u
gsyne_2327	Synechococcus_assembled_mapped	glycosyl hydrolase family 3 N terminal domain protein				PF00933.16	2057729	2059127	-1	105	fig|1129.58.j	Carbohydrates	Aminosugars	Chitin and N-acetylglucosamine u
gsyne_2328	Synechococcus_assembled_mapped	ribosome-binding factor A	rbfA		GO:0006396,GO:0019843	TIGR00082	2059113	2059524	-1	166	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Translation initiation factors bacte
gsyne_2329	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF05421.6	2059526	2059733	-1	156	fig|1129.58.j	Carbohydrates	CO2 fixation	Photorespiration (oxidative C2 cy
gsyne_233	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	190030	190717	-1	261	fig|1129.58.peg.230			
gsyne_2330	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2060480	2061221	-1	156	fig|1129.58.peg.2323			
gsyne_2331	Synechococcus_assembled_mapped	glutaredoxin family protein				PF00462.19	2059788	2060499	1	112	fig|1129.58.j	Stress Response	Oxidative stress	Glutathione: Non-redox reactions
gsyne_2332	Synechococcus_assembled_mapped	shikimate kinase family protein				PF01202.17	2061479	2062103	1	70	fig|1129.58.j	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_2333	Synechococcus_assembled_mapped	asl3597 protein				UniRef100_C	2061219	2061483	1	185	fig|1129.58.peg.2324			
gsyne_2334	Synechococcus_assembled_mapped	queuosine biosynthesis protein	QueD	queD	GO:0003824,GO:0008616	TIGR03367	2062264	2063137	1	168	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Pterin synthesis related cluster
gsyne_2335	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2063754	2064252	-1	156	fig|1129.58.peg.2328			
gsyne_2336	Synechococcus_assembled_mapped	ribD C-terminal domain protein				PF01872.12	2063123	2063765	1	85	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metabo
gsyne_2337	Synechococcus_assembled_mapped	acetyltransferase domain protein				PF13480.1	2064225	2065410	1	703	fig|1129.58.peg.2329			
gsyne_2338	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14251.1	2065434	2065806	1	156	fig|1129.58.peg.2330			
gsyne_2339	Synechococcus_assembled_mapped	radical SAM superfamily protein				PF04055.16	2065812	2067426	1	703	fig|1129.58.peg.2331			
gsyne_234	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11334.3	190769	191000	-1	156	fig|1129.58.peg.231			
gsyne_2340	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2067547	2067664	1	88	fig|1129.58.peg.2332			
gsyne_2341	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	2067684	2068920	-1	141	fig|1129.58.peg.2333			
gsyne_2342	Synechococcus_assembled_mapped	ribosomal protein S12 methylthiotransl	rimO		GO:0008172,GO:0016782,G	TIGR01125	2068916	2070305	-1	168	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	Methylthiotransferases
gsyne_2343	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2070279	2070414	1	856				
gsyne_2344	Synechococcus_assembled_mapped	L-aspartate oxidase	nadB	1.4.3.16	GO:0008734,GO:0019363,G	TIGR00551	2071348	2072995	-1	163	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynt
gsyne_2345	Synechococcus_assembled_mapped	vitamin K epoxide reductase family protein				PF07884.9	2070414	2071356	1	703	fig|1129.58.peg.2335			
gsyne_2346	Synechococcus_assembled_mapped	photosystem II 12 kDa extrinsic protein	psbU		GO:0006810,GO:0042549,G	UniRef100_C	2073095	2073473	-1	92	fig|1129.58.j	Photosynthesis	Electron transport and photopl	Photosystem II
gsyne_2347	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11318.3	2073580	2074318	-1	156	fig|1129.58.peg.2338			
gsyne_2348	Synechococcus_assembled_mapped	undecaprenyl-diphosphatase	UppP	uppP	3.6.1.27	GO:0009252,GO:0030288,G	TIGR00753	2074489	2075290	1	89	fig|1129.58.peg.2339			
gsyne_2349	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04459.7	2075331	2076711	1	156	fig|1129.58.peg.2340			
gsyne_235	Synechococcus_assembled_mapped	CP12 domain protein				PF02672.10	191004	191223	-1	157	fig|1129.58.peg.232			
gsyne_2350	Synechococcus_assembled_mapped	outer membrane efflux family protein				PF02321.13	2076758	2078444	1	141	fig|1129.58.peg.2341			
gsyne_2351	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	2078515	2079871	1	141	fig|1129.58.peg.2342			
gsyne_2352	Synechococcus_assembled_mapped	inositol monophosphatase family protein				PF00459.20	2079867	2080677	1	703	fig|1129.58.j	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_2353	Synechococcus_assembled_mapped	putative pG1 protein				UniRef100_C	2081523	2081721	-1	185	fig|1129.58.j	Carbohydrates	Monosaccharides	Deoxyribose and Deoxynucleosic
gsyne_2359	Synechococcus_assembled_mapped	snoaL-like domain protein				PF13474.1	2087053	2087446	-1	157	fig|1129.58.peg.2346			
gsyne_236	Synechococcus_assembled_mapped	putative lipoprotein			GO:0008150,GO:0003674,G	lipoP	191346	191868	1	88	fig|1129.58.peg.233			
gsyne_2360	Synechococcus_assembled_mapped	2,3-diketo-5-methylthio-1-phosphopen	mtnC	3.1.3.77	GO:0016791,GO:0016862,G	TIGR01691	2087432	2088173	-1	106	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Salvage
gsyne_2361	Synechococcus_assembled_mapped	methylthioribulose-1-phosphate dehyd	mtnB	4.2.-.-	GO:0016835,GO:0019509	TIGR03328	2088169	2088853	-1	71	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Salvage
gsyne_2362	Synechococcus_assembled_mapped	formamidopyrimidine-DNA glycosylase	mutM	3.2.2.23	GO:0005737,GO:0006281,G	TIGR00577	2088874	2089723	-1	132	fig|1129.58.j	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_2363	Synechococcus_assembled_mapped	photosystem I reaction center subunit I	psaE		GO:0009538,GO:0003824,G	UniRef100_C	2089846	2090056	-1	92,703	fig|1129.58.j	Photosynthesis	Electron transport and photopl	Photosystem I
gsyne_2364	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2090166	2091210	1	156	fig|1129.58.peg.2351			
gsyne_2365	Synechococcus_assembled_mapped	spore coat assembly SafA domain prote	safA		GO:0003674,GO:0030436	TIGR02899	2092705	2094082	-1	705	fig|1129.58.peg.2353			
gsyne_2366	Synechococcus_assembled_mapped	ATP-dependent DNA helicase	recQ	recQ	3.6.4.12	GO:0003677,GO:0006281,G	UniRef100_P	2091220	2092705	1	92,141,703	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa
gsyne_2367	Synechococcus_assembled_mapped	aldehyde dehydrogenase family protein				PF00171.17	2094170	2095520	-1	703	fig|1129.58.j	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-C
gsyne_2368	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2095558	2096146	-1	856	fig|1129.58.peg.2355			
gsyne_2369	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	2096195	2098268	-1	699	fig|1129.58.j	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria
gsyne_237	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	192211	192334	-1	856				
gsyne_2370	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	2098271	2098877	-1	261	fig|1129.58.peg.2357			
gsyne_2373	Synechococcus_assembled_mapped	3-dehydroquinate dehydratase, type II	aroQ	4.2.1.10	GO:0003855,GO:0009423	TIGR01088	2099212	2099659	1	70	fig|1129.58.j	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_2374	Synechococcus_assembled_mapped	tRNA-(Ms(2)io(6)a)-hydroxylase, putative			GO:0046914,GO:0016491	UniRef100_C	2099655	2100291	1	141,703	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_2375	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	2100434	2101775	1	132,152	fig|1129.58.peg.2360			
gsyne_2376	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2103231	2103918	1	856	fig|1129.58.peg.2362			
gsyne_2377	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2103928	2104249	-1	856				
gsyne_2378	Synechococcus_assembled_mapped	putative kelch motif protein				UniRef100_A	2104247	2104415	1	185	fig|1129.58.peg.2363			
gsyne_2379	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07864.6	2104418	2104712	1	156	fig|1129.58.peg.2364			
gsyne_238	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	191864	192242	1	856	fig|1129.58.peg.234			
gsyne_2380	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2105099	2105213	-1	856	fig|1129.58.peg.2366			
gsyne_2381	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2104937	2105111	-1	856				
gsyne_2382	Synechococcus_assembled_mapped	eamA-like transporter family protein				PF00892.15	2106001	2107105	-1	141	fig|1129.58.peg.2367			
gsyne_2383	Synechococcus_assembled_mapped	efflux transporter, RND family, MFP subunit			GO:0005215,GO:0006810	TIGR01730	2107088	2108288	-1	141	fig|1129.58.peg.2368			
gsyne_2384	Synechococcus_assembled_mapped	heavy metal efflux pump, CzcA family protein			GO:0016021,GO:0030001,G	TIGR00914	2108294	2111417	-1	96,145	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Cobalt-zinc-cadmium resistance
gsyne_2385	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2111413	2111887	-1	156	fig|1129.58.peg.2370			
gsyne_2386	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein				PF00486.23	2112073	2112796	1	261	fig|1129.58.peg.2371			
gsyne_2387	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	2112795	2114076	1	699	fig|1129.58.peg.2372			
gsyne_2388	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04214.8	2114121	2114592	1	156	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Copper homeostasis
gsyne_2389	Synechococcus_assembled_mapped	glutaredoxin family protein				PF00462.19	2114591	2115338	1	112	fig|1129.58.peg.2374			
gsyne_239	Synechococcus_assembled_mapped	lipase family protein		3.1.1.3	GO:0016787,GO:0004806	UniRef100_B	192346	192919	1	703	fig|1129.58.j	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_2390	Synechococcus_assembled_mapped	merR regulatory family protein				PF00376.18	2115406	2115781	-1	261	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Copper homeostasis
gsyne_2391	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03713.8	2115849	2116560	1	156	fig|1129.58.peg.2376			
gsyne_2392	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12518.3	2116568	2116787	1	156	fig|1129.58.peg.2377			
gsyne_2393	Synechococcus_assembled_mapped	pepSY-associated TM helix family protein				PF03929.11	2116792	2117077	1	185	fig|1129.58.peg.2378			
gsyne_2394	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2117441	2117600	-1	856	fig|1129.58.peg.2379			
gsyne_2395	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2117728	2117890	-1	856	fig|1129.58.peg.2380			
gsyne_2396	Synechococcus_assembled_mapped	lysozyme domain protein		3.2.1.17		UniRef100_F	2118673	2118874	1	157	fig|1129.58.peg.2382			
gsyne_2397	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2118919	2119087	1	856	fig|1129.58.peg.2383			
gsyne_2398	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	2119288	2119624	1	165	fig|1129.58.peg.2384			
gsyne_2399	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2119959	2120076	1	856	fig|1129.58.peg.2385			
gsyne_24	Synechococcus_assembled_mapped	GMC oxidoreductase family protein				PF05199.8	15899	17414	1	703	fig|1129.58.j	Respiration	Electron donating reactions	Respiratory dehydrogenases 1
gsyne_240	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	192981	194076	1	90	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Polyprenyl Diphosphate Biosynth
gsyne_2400	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2120378	2120564	1	856	fig|1129.58.peg.2386			
gsyne_2401	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2120595	2120739	-1	856				
gsyne_2402	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2121031	2121184	-1	856	fig|1129.58.peg.2388			
gsyne_2403	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2121425	2121542	1	856	fig|1129.58.peg.2389			
gsyne_2404	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	2121538	2121721	1	261	fig|1129.58.peg.2390			
gsyne_2405	Synechococcus_assembled_mapped	cation-transporting ATPase, E1-E2 ATPase domain protein			GO:0016020,GO:0015662,G	UniRef100_A	2122602	2122755	-1	92,141,703	fig|1129.58.peg.2393			
gsyne_2406	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	2123130	2123592	-1	157	fig|1129.58.peg.2394			
gsyne_2407	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	2123959	2124238	-1	154	fig|1129.58.peg.2395			
gsyne_2408	Synechococcus_assembled_mapped	putative cation-transporting ATPase F			GO:0006754,GO:0046872,G	UniRef100_P	2124280	2126356	-1	92,141,703	fig|1129.58.peg.2396			
gsyne_2409	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2126641	2126818	-1	856	fig|1129.58.peg.2397			
gsyne_241	Synechococcus_assembled_mapped	glycosyl hydrolase family 3 C-terminal domain protein				PF01915.17	194535	196713	-1	105	fig|1129.58.peg.238			
gsyne_2410	Synechococcus_assembled_mapped	penicillin binding transpeptidase domain protein				PF00905.17	2126879	2127806	-1	89	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Beta-lactamase
gsyne_2411	Synechococcus_assembled_mapped	large conductance mechanosensitive ch	mscL		GO:0006810,GO:0022833	TIGR00220	2127816	2128194	-1	149	fig|1129.58.j	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis
gsyne_2412	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2128277	2128409	1	856				
gsyne_2413	Synechococcus_assembled_mapped	HD domain protein				PF13328.1	2128365	2129013	1	157	fig|1129.58.peg.2400			
gsyne_2414	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2129087	2129255	-1	856	fig|1129.58.peg.2401			
gsyne_2415	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2129412	2129595	1	856				
gsyne_2416	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	2129629	2130325	1	261	fig|1129.58.peg.2403			
gsyne_2417	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2130660	2131047	1	856	fig|1129.58.peg.2404			
gsyne_2418	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2131436	2132171	1	856	fig|1129.58.peg.2406			
gsyne_2419	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2132606	2132894	1	856	fig|1129.58.peg.2408			
gsyne_242	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	194072	194567	1	156	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Polyprenyl Diphosphate Biosynth
gsyne_2420	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2134570	2134891	-1	856	fig|1129.58.peg.2411			
gsyne_2421	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2135404	2136085	1	856	fig|1129.58.peg.2412			
gsyne_2422	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2138806	2139064	1	856	fig|1129.58.peg.2417			
gsyne_2423	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2139258	2139480	1	856	fig|1129.58.peg.2418			
gsyne_2424	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2140110	2140239	1	856	fig|1129.58.peg.2420			
gsyne_2425	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2142908	2143166	1	156	fig|1129.58.peg.2426			
gsyne_2426	Synechococcus_assembled_mapped	putative tRNA-(MS(2)IO(6)A)-hydroxylase-like protein			GO:0046914,GO:0055114,G	UniRef100_C	2143337	2143505	1	141,703	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria
gsyne_2427	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	2143518	2144544	-1	157	fig|1129.58.peg.2428			
gsyne_2428	Synechococcus_assembled_mapped	transposase IS116/IS110/IS902 family protein				PF02371.11	2144601	2145945	-1	154	fig|1129.58.peg.2429			
gsyne_2429	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2146010	2146130	-1	856	fig|1129.58.peg.2430			
gsyne_243	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	196680	196803	1	856				
gsyne_2430	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	2146148	2146652	-1	157	fig|1129.58.peg.2431			
gsyne_2431	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2146793	2147045	-1	856	fig|1129.58.peg.2432			
gsyne_2432	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2147007	2147121	1	88				





gsyne_2433	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2147236	2147455	-1	856					
gsyne_2434	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2147161	2147281	1	856	fig|1129.58.peg.2433				
gsyne_2435	Synechococcus_assembled_mapped	acireductone dioxygenase	mtnD	1.13.11.53	GO:0010309,GO:0005506,G	UniRef100_C	2147606	2148152	-1	92,141,703	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionin	Methionine Salvage	
gsyne_2436	Synechococcus_assembled_mapped	precorrin-2 C20-methyltransferase	cobI	2.1.1.130	GO:0009236,GO:0030788	TIGR01467	2148258	2148984	-1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic	Tetrapyrroles	Cobalamin synthesis	
gsyne_2437	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	2149631	2151713	-1	90	fig|1129.58.peg.2438				
gsyne_2438	Synechococcus_assembled_mapped	TIM-barrel , nifR3 family protein				TIGR00737	2151709	2152705	-1	157	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_2439	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2152763	2153213	1	156	fig|1129.58.peg.2440				
gsyne_244	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	196925	197066	1	856	fig|1129.58.peg.239				
gsyne_2440	Synechococcus_assembled_mapped	L,D-transpeptidase catalytic domain protein				PF03734.9	2153219	2153603	-1	138	fig|1129.58.peg.2441				
gsyne_2441	Synechococcus_assembled_mapped	ribosome-associated GTPase EngA	engA		GO:0003924,GO:0005525,G	TIGR03594	2153743	2155108	1	185	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Universal GTPases	
gsyne_2442	Synechococcus_assembled_mapped	cobalt transport family protein				PF02361.11	2155144	2156053	1	141	fig|1129.58.peg.2443				
gsyne_2443	Synechococcus_assembled_mapped	pipX				UniRef100_C	2156089	2156356	1	185	fig|1129.58.peg.2444				
gsyne_2444	Synechococcus_assembled_mapped	alanine racemase, N-terminal domain protein				PF01168.15	2156365	2157037	1	157	fig|1129.58.p	Amino Acids and Derivatives	Proline and 4-hydroxyproline	A Hypothetical Protein Related to	
gsyne_2445	Synechococcus_assembled_mapped	cell division protein sepF	sepF		GO:0007049,GO:0000917,G	UniRef100_C	2157065	2157620	1	92	fig|1129.58.peg.2446				
gsyne_2446	Synechococcus_assembled_mapped	pyrroline-5-carboxylate reductase	proC	1.5.1.2	GO:0004735,GO:0006561	TIGR00112	2157685	2158453	1	73	fig|1129.58.p	Amino Acids and Derivatives	Proline and 4-hydroxyproline	Proline Synthesis	
gsyne_2447	Synechococcus_assembled_mapped	acyl-phosphate glycerol 3-phosphate a	plsY	2.3.1.-	GO:0005886,GO:0006654,G	TIGR00023	2158464	2159109	-1	156	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho	
gsyne_2448	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11285.3	2159105	2160026	-1	156	fig|1129.58.peg.2449				
gsyne_2449	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11317.3	2160022	2160418	-1	156	fig|1129.58.peg.2450				
gsyne_245	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	197479	197638	-1	261	fig|1129.58.peg.241				
gsyne_2450	Synechococcus_assembled_mapped	conserved hypothetical family protein				TIGR00056	2160414	2161200	-1	156	fig|1129.58.peg.2451				
gsyne_2451	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	2161209	2162622	-1	141	fig|1129.58.peg.2452				
gsyne_2452	Synechococcus_assembled_mapped	alpha amylase, catalytic domain protein				PF00128.19	2162788	2164867	-1	105	fig|1129.58.rna.31				
gsyne_2454	Synechococcus_assembled_mapped	metallo-beta-lactamase superfamily hy	gloB		GO:0016787	UniRef100_C	2164971	2165613	1	703	fig|1129.58.peg.2454				
gsyne_2455	Synechococcus_assembled_mapped	DNA-binding protein HU 1	hupA		GO:0030261,GO:0003677	UniRef100_P	2165796	2166072	1	92,141	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	DNA structural proteins, bacterial	
gsyne_2456	Synechococcus_assembled_mapped	glutamyl-queuosine tRNA(Asp) synthet	gluQ	6.1.1.-	GO:0006400,GO:0016876	TIGR03838	2166130	2167102	-1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth	
gsyne_2457	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2167396	2167522	-1	88					
gsyne_2458	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2167239	2167425	1	856	fig|1129.58.peg.2457				
gsyne_2459	Synechococcus_assembled_mapped	putative d-lactate dehydrogenase			GO:0050578,GO:0055114,G	UniRef100_A	2167600	2167807	1	703	fig|1129.58.peg.2458				
gsyne_246	Synechococcus_assembled_mapped	putative alkaline phosphatase				UniRef100_C	198224	199847	-1	703	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2460	Synechococcus_assembled_mapped	ferrous iron transport protein B	feoB		GO:0015639,GO:0015684	TIGR00437	2167828	2169628	-1	145	fig|1129.58.peg.2459				
gsyne_2461	Synechococcus_assembled_mapped	feoA domain protein				PF04023.9	2169624	2169858	-1	157	fig|1129.58.peg.2460				
gsyne_2462	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2169936	2170224	-1	156	fig|1129.58.peg.2461				
gsyne_2463	Synechococcus_assembled_mapped	delta-aminolevulinic acid dehydratase,	HEMB	4.2.1.24	GO:0046872,GO:0004655,G	UniRef100_P	2170276	2171278	1	92,141,703	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling	Zinc regulated enzymes	
gsyne_2464	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2171359	2171605	1	88	fig|1129.58.peg.2463				
gsyne_2465	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2171616	2171859	1	88	fig|1129.58.peg.2464				
gsyne_2466	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2173512	2173716	-1	856	fig|1129.58.peg.2466				
gsyne_2467	Synechococcus_assembled_mapped	outer membrane efflux family protein				PF02321.13	2171855	2173559	1	141	fig|1129.58.peg.2465				
gsyne_2468	Synechococcus_assembled_mapped	NHLM bacteriocin system secretion protein				TIGR03794	2173712	2175044	-1	185					
gsyne_2469	Synechococcus_assembled_mapped	glycosalase/Bleomycin resistance /Dioxygenase superfamily protein				PF00903.20	2175122	2175530	1	703	fig|1129.58.peg.2467				
gsyne_247	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	199948	201217	-1	141	fig|1129.58.peg.244				
gsyne_2470	Synechococcus_assembled_mapped	mutS2 family protein			GO:0006259,GO:0030983	TIGR01069	2175595	2178112	1	130	fig|1129.58.peg.2468				
gsyne_2471	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2178139	2179384	-1	141	fig|1129.58.peg.2469				
gsyne_2472	Synechococcus_assembled_mapped	obg family GTPase CgtA	cgtA		GO:0005525,GO:0042254	TIGR02729	2179423	2180413	1	136	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Universal GTPases	
gsyne_2473	Synechococcus_assembled_mapped	CP12 domain protein				PF02672.10	2180448	2180667	-1	157	fig|1129.58.peg.2471				
gsyne_2474	Synechococcus_assembled_mapped	heme ABC exporter, ATP-binding protei	ccmA	3.6.3.41	GO:0015439,GO:0015886,G	TIGR01189	2181307	2183266	-1	97,147	fig|1129.58.peg.2473				
gsyne_2475	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2180832	2181327	-1	156	fig|1129.58.peg.2472				
gsyne_2476	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	2183803	2185429	-1	157	fig|1129.58.peg.2474				
gsyne_2477	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	2185495	2186287	1	132,152	fig|1129.58.peg.2475				
gsyne_2478	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2186582	2186759	1	856	fig|1129.58.peg.2476				
gsyne_2479	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2186834	2187008	-1	156	fig|1129.58.peg.2477				
gsyne_248	Synechococcus_assembled_mapped	glyceraldehyde-3-phosphate dehydrog	gap	1.2.1.-	GO:0006094,GO:0006096,G	TIGR01534	201216	202242	-1	116	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine		Pyridoxin (Vitamin B6) Biosynthe
gsyne_2480	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2187182	2187335	-1	856	fig|1129.58.peg.2478				
gsyne_2481	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2187512	2187647	-1	856	fig|1129.58.peg.2479				
gsyne_2482	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	2187668	2188649	1	154	fig|1129.58.peg.2480				
gsyne_2483	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2188702	2188846	1	856	fig|1129.58.peg.2481				
gsyne_2484	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10063.4	2189614	2190256	-1	156	fig|1129.58.peg.2483				
gsyne_2485	Synechococcus_assembled_mapped	glutathione S-transferase, C-terminal domain protein				PF00043.20	2190252	2191218	-1	703	fig|1129.58.peg.2484				
gsyne_2486	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2192194	2192518	-1	156	fig|1129.58.peg.2486				
gsyne_2487	Synechococcus_assembled_mapped	succinylglutamate desuccinylase / Aspartoacylase family protein				PF04952.9	2191274	2192216	1	185	fig|1129.58.peg.2485				
gsyne_2488	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2192623	2192947	-1	156	fig|1129.58.peg.2487				
gsyne_2489	Synechococcus_assembled_mapped	photosystem II q(b) protein	psbA	1.10.3.9	GO:0009055,GO:0009538,G	TIGR01151	2193166	2194225	1	112,164	fig|1129.58.p	Photosynthesis	Electron transport and photop	Photosystem II	
gsyne_249	Synechococcus_assembled_mapped	S-adenosylmethionine decarboxylase p	speD	4.1.1.50	GO:0004014,GO:0008295	TIGR03330	202716	203133	-1	104	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Polyamine Metabolism	
gsyne_2490	Synechococcus_assembled_mapped	cytidine and deoxycytidylate deaminase zinc-binding region family protein				PF00383.17	2194342	2194777	-1	703	fig|1129.58.p	Amino Acids and Derivatives	Amino Acids and Derivatives -	Creatine and Creatinine Degrada	
gsyne_2491	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11103.3	2195557	2196103	1	156	fig|1129.58.peg.2490				
gsyne_2492	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2196130	2197582	-1	156	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Biotin		Biotin biosynthesis
gsyne_2493	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2197663	2197870	1	156	fig|1129.58.peg.2492				
gsyne_2494	Synechococcus_assembled_mapped	helix-turn-helix , CopG family protein			GO:0006355	UniRef100_A	2197901	2198159	-1	185	fig|1129.58.peg.2493				
gsyne_2495	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04365.8	2198145	2198409	-1	156	fig|1129.58.peg.2494				
gsyne_2496	Synechococcus_assembled_mapped	DEAD/DEAH box helicase family protein				PF00270.24	2199517	2201863	-1	703	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	Type I Restriction-Modification	
gsyne_2497	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08401.6	2198603	2199521	1	156	fig|1129.58.peg.2496				
gsyne_2498	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2201880	2202621	1	856					
gsyne_2499	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2202675	2202849	-1	856	fig|1129.58.peg.2500				
gsyne_25	Synechococcus_assembled_mapped	mannosyl oligosaccharide glucosidase family protein				PF03200.11	17467	20110	1	185	fig|1129.58.peg.24				
gsyne_250	Synechococcus_assembled_mapped	bacterial regulatory , arsR family protein				PF01022.15	202387	202720	1	261	fig|1129.58.peg.246				
gsyne_2500	Synechococcus_assembled_mapped	type I restriction modification DNA specificity domain protein				PF01420.14	2203361	2204369	-1	183	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	Restriction-Modification System	
gsyne_2501	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2204566	2204692	1	856	fig|1129.58.peg.2503				
gsyne_2502	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2204968	2205130	1	856					
gsyne_2503	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein				TIGR02937	2205355	2206288	1	135	fig|1129.58.p	RNA Metabolism	Transcription	Transcription initiation, bacterial s	
gsyne_2504	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	2206387	2207203	1	261	fig|1129.58.peg.2506				
gsyne_2505	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04255.9	2207265	2207496	1	156	fig|1129.58.peg.2507				
gsyne_2506	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_D	2207492	2207840	1	156	fig|1129.58.peg.2508				
gsyne_2507	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2207876	2208332	-1	856	fig|1129.58.peg.2509				
gsyne_2508	Synechococcus_assembled_mapped	putative lipoprotein			GO:0008150,GO:0003674,G	lipoP	2208637	2208856	1	88	fig|1129.58.peg.2510				
gsyne_2509	Synechococcus_assembled_mapped	outer membrane beta-barrel domain protein				PF13505.1	2208916	2209564	-1	88	fig|1129.58.peg.2511				
gsyne_251	Synechococcus_assembled_mapped	phosphate ABC transporter, phosphate	pstS		GO:0006817,GO:0015415,G	TIGR00975	203350	204328	1	143	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2510	Synechococcus_assembled_mapped	sigma-70 region 2 family protein				PF04542.9	2209840	2210263	1	165	fig|1129.58.peg.2512				
gsyne_2511	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase superfamily domain protein				PF12850.2	2211261	2212482	1	157	fig|1129.58.peg.2513				
gsyne_2512	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	2212465	2214166	1	157	fig|1129.58.peg.2514				
gsyne_2513	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	2214207	2215026	1	154	fig|1129.58.peg.2515				
gsyne_2514	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2215091	2215265	1	856	fig|1129.58.peg.2516				
gsyne_2515	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2215497	2215800	1	856	fig|1129.58.peg.2517				
gsyne_2516	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2216589	2216745	1	856	fig|1129.58.peg.2519				
gsyne_2517	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2216802	2216940	-1	856	fig|1129.58.peg.2520				
gsyne_2518	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	216993	2217974	-1	154	fig|1129.58.peg.2521				
gsyne_2519	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2218818	2218992	-1	856	fig|1129.58.peg.2522				
gsyne_252	Synechococcus_assembled_mapped	alkaline phosphatase synthesis transcri	sphR		GO:0006817,GO:0003677,G	UniRef100_P	204345	205152	1	92,141	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2520	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07864.6	2219217	2219511	-1	156	fig|1129.58.peg.2523				
gsyne_2521	Synechococcus_assembled_mapped	putative kelch motif protein				UniRef100_A	2219514	2219715	-1	185	fig|1129.58.peg.2524				
gsyne_2522	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2219838	2220291	1	856	fig|1129.58.peg.2525				
gsyne_2523	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2220295	2220469	-1	856					
gsyne_2524	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2220742	2221144	-1	856	fig|1129.58.peg.2527				
gsyne_2525	Synechococcus_assembled_mapped	transposase, Mutator family protein				PF00872.13	2221272	2221668	1	154	fig|1129.58.peg.2528				
gsyne_2526	Synechococcus_assembled_mapped	putative Protein kinase C terminal domain protein			GO:0016310,GO:0016301	UniRef100_C	2221774	2222728	1	92,703	fig|1129.58.peg.2529				
gsyne_2527	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2222786	2223029	-1	856					
gsyne_2528	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2223005	2223197	1	856	fig|1129.58.peg.2530				
gsyne_2529	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2223201	2223375	-1	856					
gsyne_253	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	205214	205376	-1	856					
gsyne_2530	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2223470	2223671	1	856	fig|1129.58.peg.2532				
gsyne_2531	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2223726	2225100	-1	856	fig|1129.58.peg.2533				
gsyne_2532	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2225547	2225898	-1	856	fig|1129.58.peg.2534				
gsyne_2533	Synechococcus_assembled_mapped	phage lysozyme family protein				PF00959.14	2225969	2227202	1	152	fig|1129.58.peg.2535				
gsyne_2534	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2227247	2227415	1	856	fig|1129.58.peg.2536				
gsyne_2535	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	2228529	2228895	1	165	fig|1129.58.peg.2539				
gsyne_2536	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2229221	2229338	1	856					
gsyne_2537	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2229664	2229826	1	856	fig|1129.58.peg.2540				
gsyne_2538	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2229835	2230147	-1	856	fig|1129.58.peg.2541				
gsyne_2539	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2230464	2230581	1	856	fig|1129.58.peg.2542				
gsyne_254	Synechococcus_assembled_mapped	protein sphX	sphX		GO:0005886,GO:0005215	UniRef100_P	205485	206538	-1	141	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2540	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	2230577	2230760	1	261	fig|1129.58.peg.2543				
gsyne_2541	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2230827	2230998	-1	856	fig|1129.58.peg.2544				
gsyne_2542	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2231173	2231296	-1	856					
gsyne_2543	Synechococcus_assembled_mapped	large conductance mechanosensitive ch	mscL		GO:0006810,GO:0022833	TIGR00220	2231270	2231648	-1	149	fig|1129.58.p	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis	
gsyne_2544	Synechococcus_assembled_mapped	HD domain protein				PF13328.1	2231819	2232467	-1	157	fig|1129.58.peg.2546				
gsyne_2545	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	2232477	2232681	-1	157	fig|1129.58.peg.2547				
gsyne_2546	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2232826	2233000	-1	156	fig|1129.58.peg.2548				
gsyne_2547	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2233081	2233366	1	856					
gsyne_2548	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2233510	2233786	1	156	fig|1129.58.peg.2549				
gsyne_2549	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2233982	2234183	1	88	fig|1129.58.peg.2550				
gsyne_255	Synechococcus_assembled_mapped	phosphate ABC transporter, permease	pstC		GO:0005887,GO:0006817,G	TIGR02138	206762	207656	1	143	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2550	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2234733	2235054	-1	156	fig|1129.58.peg.2552				
gsyne_2551	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04255.9	2235053	2235293	-1	156	fig|1129.58.peg.2553				
gsyne_2552	Synechococcus_assembled_mapped	rad52/22 double-strand break repair family protein				PF04098.10	2235340	2236003	-1	185	fig|1129.58.peg.2554				
gsyne_2553	Synechococcus_assembled_mapped	siphovirus Gp157 family protein				PF05565.6	2236291	2236945	-1	185	fig|1129.58.peg.2555				
gsyne_2554	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10686.4	2236983	2237472	-1	156	fig|1129.58.peg.2556				
gsyne_2555	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2237986	2238193	-1	856					
gsyne_2556	Synechococcus_assembled_mapped	glycine zipper 2TM domain protein				PF05433.10	2238173	2238533	1	157	fig|1129.58.peg.2557				
gsyne_2557	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11334.3	2239096	2239348	1	156	fig|1129.58.peg.2558				
gsyne_2558	Synechococcus_assembled_mapped	response regulator				PF00072.19	2239393	2240158	1	699	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2559	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2240501	2240645	-1	856					
gsyne_256	Synechococcus_assembled_mapped	phosphate ABC transporter, permease	pstA		GO:0005887,GO:0006817,G	TIGR00974	207682	208576	1	143	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2560	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2240982	2241096	-1	856	fig|1129.58.peg.2562				
gsyne_2561	Synechococcus_assembled_mapped	response regulator				PF00072.19	2242064	2242739	1	699	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2562	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2243729	2243900	-1	856	fig|1129.58.peg.2565				

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0.0907915	-21.138051	1	1.0936875	1	-5.40488	1	-5.9112497
0.00016459	-76.798381	0.51456017	-10.336596	0.51456017	-10.336596	1	1
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0.11340264	1.74522712	0.87954522	-1.0548224	0.47018688	1.28965812	0.37998897	1.36036027
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1	1	0.30178309	11.2230825	1	1	0.53452206	-11.223082
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0.39826446	-1.3971881	0.90250693	-1.0859109	0.52349791	1.35086513	0.37990179	1.46691915
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0.17921691	-1.6056297	0.3743159	-1.4218917	0.3302719	-1.4049899	1	1.01202988
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1	1.01623446	0.04773919	2.03345529	0.67366408	-1.2778653	0.01367881	-2.5984819
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1	-1.0146596	0.81797361	-1.0951101	0.42881275	1.32097718	0.27394741	1.44661551
0.82197635	-1.1325344	1	-1.0015252	0.61330348	-1.2564946	0.61330348	-1.2545811
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51	24.2394931	53	29.9743026	42	40.3041866	33	19.3509144	20	25.6715133	37	22.917592	28	25.7033542	136	46.1932309
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13	3.00696457	11	3.02759308	2	0.93403353	5	1.4268856	3	1.87402047	4	1.20575439	1	0.44674878	6	0.99179584
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88	16.503922	50	11.1582055	61	23.0983968	37	8.56131362	29	14.6882686	56	13.6869417	43	15.5758357	160	21.4442344
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5	2.94031738	4	2.79900747	2	2.37466152	6	4.35321032	1	1.58815294	1	0.76636932	3	3.40740591	0	0
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24	9.46247592	33	15.4820101	9	7.16446175	15	7.29657411	8	8.51827488	17	8.73486845	5	3.80751797	18	5.07168327
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17	1.92754139	3	0.40475843	3	0.68678936	9	1.25901671	23	7.0428874	2	0.29552804	10	2.18994497	17	1.37749422
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15	8.97303751	13	9.25361523	0	0	10	7.38044278	2	3.23106978	2	1.55916516	1	1.15538476	4	1.70999283
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31	9.68980267	18	6.69492328	5	3.15551869	40	15.4257903	3	2.5324601	25	10.1837364	10	6.0371456	33	7.37145557
13	1.3423949	6	0.73723858	6	1.25093777	15	1.91100751	56	15.6168373	6	0.80742482	14	2.79217984	9	0.664149
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19	2.11967574	5	0.66375177	6	1.35149546	7	0.96349189	8	2.41031572	2	0.29077678	1	0.21547369	8	0.63781083
9	1.14802098	7	1.06249089	2	0.51509202	3	0.47213127	6	2.06693435	2	0.33246904	2	0.49273762	7	0.63810394
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12	3.589215	9	3.2031745	5	3.01950495	9	3.32119925	2	1.61553489	9	3.50812161	5	2.88846191	8	1.70999283
9	2.05435332	10	2.71614212	4	1.84348723	1	0.28162216	4	2.46581641	2	0.5949446	1	0.4408705	3	0.48937295
2	0.95056836	9	5.08997592	5	4.79811746	8	4.69113075	5	6.41787833	1	0.61939438	3	2.7539308	4	1.35862444
28	4.49759658	9	1.72022334	6	1.94590319	10	1.98178556	36	15.6168373	10	2.0933236	14	4.34339086	23	2.64019726
38	3.95927421	22	2.72756134	29	6.10066946	43	5.52757486	23	6.47184247	30	4.07349456	21	4.22600192	78	5.80781348
12	2.95282936	10	2.92803973	3	1.49047904	13	3.94670486	6	3.9872776	10	3.20679359	4	1.90105862	9	1.58265294
32	2.72792099	11	1.11582055	5	0.86059601	10	1.05175843	33	7.5973803	6	0.66657184	6	0.98789655	21	1.27934353
89	5.44606933	56	4.07756644	8	0.98839527	16	1.20794549	155	25.6149183	18	1.43542189	18	2.12737512	81	3.542128
16	2.03345026	9	1.36105583	4	1.02641047	6	0.9408037	8	2.74581754	5	0.82812802	4	0.98186544	10	0.90823795
8	4.78562	2	1.42363311	0	0	1	0.73804428	0	0	0	0	0	0	0	0
5	1.71761114	9	3.67889349	1	0.69358926	1	0.42382741	3	2.78319872	1	0.44768109	2	1.32697656	6	1.47296412
2	1.33445173	4	3.17579694	0	0	1	0.82320323	1	1.80194276	0	0	0	0	0	0
13	9.80531925	10	8.97507831	2	3.04576152	0	0	0	0	0	0	0	0	0	0
145	15.3849634	284	35.8563985	0	0	456	59.6935629	0	0	0	0	0	0	0	0
24	14.35686	19	13.5245146	1	1.20780198	13	9.59457561	15	24.2330234	8	6.23666064	3	3.46615429	7	2.99248745
61	7.86780835	35	5.37170115	11	2.86460098	52	8.27487562	24	8.35994263	42	7.05971437	18	4.48409551	53	4.88523973
9	3.18634393	8	3.37023349	0	0	7	3.05761201	3	2.86839868	2	0.92277122	2	1.36759829	9	2.27708229
0	0	0	0	0	0	0	0	0	0	0	0	1	1.00018382	0	0
11	2.52750461	10	2.73412982	2	0.92784788	9	2.55138486	15	9.30804871	8	2.39553852	1	0.44379017	6	0.98522766
2	1.196405	0	0	1	1.20780198	3	2.21413283	0	0	0	0	0	0	0	0
18	4.66062247	15	4.62149555	4	2.09111985	15	4.79178001	20	13.9852274	4	1.34972506	7	3.50064338	8	1.4802923
31	8.14824315	43	13.4490189	8	4.24560696	54	17.5117779	8	5.67884992	28	9.59122811	7	3.55368344	32	6.01088388
257	28.0402719	292	37.9098276	164	36.1277121	420	56.5369768	158	46.5558545	355	50.4767463	168	35.4027331	764	59.5701275
20	8.56685063	9	4.58726225	2	1.72969173	19	10.0410468	1	1.15680276	6	3.34931775	1	0.82731255	7	2.14276879
2	1.08424203	0	0	0	0	2	1.33770525	1	1.46407849	1	0.70649671	1	1.04706744	1	0.38742025
3	1.7946075	3	2.13544967	0	0	0	0	1	1.61553489	1	0.77958258	0	0	0	0
208	133.64287	112	85.6288953	35	45.4044078	90	71.3442802	20	34.7040828	40	33.4931775	56	69.4942538	102	46.8348036
2	1.03569388	2	1.23239881	0	0	3	1.91671201	1	1.39852274	0	0	1	1.00018382	0	0
20	1.51509804	9	0.81128437	8	1.22362471	14	1.30849772	12	2.45504865	6	0.59234659	6	0.87789061	21	1.13688388
7	2.07581381	8	2.82293062	0	0	1	0.3658681	1	0.80086345	6	2.31875844	0	0	4	0.84768875
17	1.43510381	9	0.90405898	2	0.34088815	4	0.41660894	9	2.05184723	4	0.44005635	0	0	13	0.78426678
2	1.23913375	1	0.73723858	0	0	2	1.528806	1	1.67323257	0	0	0	0	0	0
30	8.53174058	28	9.47532858	10	5.74200942	33	11.5788258	7	5.37628824	25	9.26553067	6	3.29568768	44	8.94242151
3	2.66890346	2	2.11719796	0	0	2	2.19520862	0	0	0	0	0	0	1	0.63576656
1	0.6425138	1	0.76454371	0	0	2	1.58542845	0	0	0	0	1	1.24096882	0	0
6	2.0016776	12	4.76369541	0	0	4	1.64640647	9	8.10874243	1	0.43476721	0	0	5	1.19206231
0	0	0	0	0	0	0	0	2	4.8051807	0	0	0	0	0	0
108	10.6756139	122	14.3498973	93	18.5609227	122	14.8786362	72	19.2207228	118	15.2007498	48	9.16407743	241	17.0244158
9	5.11904435	3	2.03042755	0	0	3	2.10524106	0	0	2	1.48248491	1	1.09856256	2	0.81294741
8	4.86957825	4	2.89721826	4	4.91596596	4	3.00396969	2	3.28775522	3	2.3797784	5	5.87827335	5	2.17499088
7	5.92366379	5	5.03480003	0	0	5	5.22031319	3	6.85617246	2	2.20564828	0	0	1	0.60475356
11	3.02899361	7	2.29363112	4	2.22388936	12	4.07681601	7	5.20561243	6	2.15313284	11	5.85028157	12	2.36141867
21	3.37319743	16	3.05817483	11	3.56748918	10	1.98178556	10	4.33801035	11	2.30265595	9	2.79217984	31	3.55852674
27	13.7762517	23	13.964166	9	9.27165638	10	6.29508355	5	6.88978115	12	7.979257	8	7.88380191	23	8.38650894
2	1.196405	3	2.13544967	2	2.41560396	0	0	2	3.23106978	1	0.77958258	1	1.15538476	0	0
11	4.01740206	8	3.47666192	3	2.21218468	3	1.35178636	2	1.97265313	6	2.85573408	3	2.11617841	2	0.52199781
6	2.26276598	9	4.03878524	0	0	3	1.39586635	2	2.03697878	3	1.47442792	0	0	7	1.88656817
28	14.4997143	35	21.5669792	21	21.9567584	18	11.500272	11	15.3837502	16	10.7978005	7	7.00128677	29	10.7321192
183	21.3064475	369	51.1218051	152	35.7314841	497	71.3921623	123	38.6752547	322	48.8573298	162	36.4295142	630	52.4187399
9	2.91833369	4	1.54337795	3	1.9640892	12	4.80073661	6	5.25426301	3	1.26773242	7	4.3839833	8	1.853824
18	7.80654263	16	8.25707205	11	9.63222079	22	11.7718062	34	39.8229351	25	14.1299343	9	7.53888557	20	6.198724
33	5.18081261	18	3.36260853	8	2.53583764	11	2.13064366	21	8.90371718	9	1.841367	8	2.4257852	17	1.90729969
62	9.86759721	51	9.65850171	12	3.85610174	19	3.73084768	86	36.964624	11	2.28153067	37	11.37365	45	5.11821248
40	8.51429326	21	5.31897279	11	4.72747033	14	3.67663775	7	4.02397034	10	2.77397483	4	1.64447402	15	2.2817389
2	1.00567377	2	1.19667711	0	0	0	0	0	0	0	0	1	0.97119299	0	0
12	3.4695745	7	2.40831268	3	1.75131287	5	1.78360701	9	7.02757677	2	0.75359649	3	1.67530791	6	1.2397448
47	19.4130954	25	12.2873096	14	11.6754191	25	12.74005	10	11.1548838	24	12.918797	16	12.7642507	44	12.9878027
32	4.35397585	21	3.39997084	13	3.57130468	31	5.20393573	13	4.77691493	28	4.96487102	13	3.41631416	25	2.43087216
4	2.89131209	3	2.58033502	3	4.37828218	1	0.8918035	0	0	1	0.94199562	0	0	1	0.51656033
138	16.0671571	174	24.1062171	135	31.7351997	346	49.7015858	100	31.4432965	277	42.0294421	119	26.7599518	476	39.6052701
4	3.65218369	1	1.08645685	0	0	1	1.12648864	1	2.46581641	0	0	0	0	0	0
38	5.85972583	23	4.22028127	14	4.35882315	33	6.27829666	50	20.8224497	8	1.60767252	18	5.3609853	31	3.41618567
5	3.04348641	1	0.72430457	1	1.22899149	3	2.25297727	1	1.64387761	1	0.79325947	1	1.17565467	2	0.86999635

gsyne_2563	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2244408	2244723	-1	156	fig|1129.58.peg.2566				
gsyne_2564	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2244233	2244419	1	856					
gsyne_2565	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04472.7	2244790	2245051	1	156	fig|1129.58.peg.2567				
gsyne_2566	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2245122	2245482	1	856	fig|1129.58.peg.2568				
gsyne_2567	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10929.3	2245874	2246108	1	156	fig|1129.58.peg.2569				
gsyne_2568	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2246206	2247319	1	92	fig|1129.58.peg.2570				
gsyne_2569	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2247338	2247557	-1	856	fig|1129.58.peg.2571				
gsyne_257	Synechococcus_assembled_mapped	phosphate ABC transporter, ATP-bindin	pstB	3.6.3.27	GO:0005524,GO:0006817,G	TIGR00972	208672	209440	1	143	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2570	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2247680	2248097	-1	156	fig|1129.58.peg.2572				
gsyne_2571	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2248197	2248326	-1	856					
gsyne_2572	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2248483	2248657	-1	156	fig|1129.58.peg.2574				
gsyne_2573	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2248858	2249050	-1	156	fig|1129.58.peg.2575				
gsyne_2574	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2249472	2249691	1	856	fig|1129.58.peg.2577				
gsyne_2575	Synechococcus_assembled_mapped	DNA primase	dnaG	2.7.7.-	GO:0003896,GO:0006269	TIGR01391	2249847	2251500	-1	132	fig|1129.58.j	DNA Metabolism	DNA replication	DNA-replication	
gsyne_2576	Synechococcus_assembled_mapped	dnaB-like helicase C terminal domain protein				PF03796.10	2251622	2253332	-1	157	fig|1129.58.peg.2579				
gsyne_2577	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2253394	2254489	-1	856	fig|1129.58.peg.2580				
gsyne_2578	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2254560	2254797	-1	856	fig|1129.58.peg.2581				
gsyne_2579	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein				TIGR02937	2254782	2255715	1	135	fig|1129.58.j	RNA Metabolism	Transcription	Transcription initiation, bacterial s	
gsyne_258	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	209641	209761	1	856	fig|1129.58.peg.255				
gsyne_2580	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	2255814	2256630	1	261					
gsyne_2581	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2256592	2257018	1	856					
gsyne_2582	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2257253	2257412	-1	856	fig|1129.58.peg.2584				
gsyne_2583	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2257558	2259196	1	141	fig|1129.58.peg.2585				
gsyne_2584	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	2259300	2259762	-1	157	fig|1129.58.peg.2586				
gsyne_2585	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	2260130	2260409	-1	154	fig|1129.58.peg.2587				
gsyne_2586	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2260451	2260667	-1	856	fig|1129.58.peg.2588				
gsyne_2587	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12518.3	2260671	2261076	-1	156	fig|1129.58.peg.2589				
gsyne_2588	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12518.3	2261084	2261342	-1	156	fig|1129.58.peg.2590				
gsyne_2589	Synechococcus_assembled_mapped	merR regulatory family protein				PF00376.18	2261475	2261886	1	261	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Cobalt-zinc-cadmium resistance	
gsyne_259	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	209928	210909	-1	154	fig|1129.58.repeat.8				
gsyne_2590	Synechococcus_assembled_mapped	putative lipoprotein			GO:0008150,GO:0003674,G	lipoP	2261948	2262164	1	88	fig|1129.58.peg.2592				
gsyne_2591	Synechococcus_assembled_mapped	sigma-70 region 2 family protein				PF04542.9	2262126	2262348	1	165	fig|1129.58.peg.2593				
gsyne_2592	Synechococcus_assembled_mapped	group 3 sigma-70 RNA polymerase sigm	sigJ		GO:0003677,GO:0006355,G	UniRef100_B	2262344	2262575	1	92,141,165	fig|1129.58.peg.2594				
gsyne_2593	Synechococcus_assembled_mapped	transposase DDE domain protein				PF01609.16	2262891	2263872	1	154	fig|1129.58.peg.2595				
gsyne_2594	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2263925	2264102	1	856					
gsyne_2595	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase superfamily domain protein				PF12850.2	2264794	2266000	1	157	fig|1129.58.peg.2596				
gsyne_2596	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2265999	2266386	1	856	fig|1129.58.peg.2597				
gsyne_2597	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2266447	2266921	1	856	fig|1129.58.peg.2598				
gsyne_2598	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2267268	2268309	1	156	fig|1129.58.peg.2599				
gsyne_2599	Synechococcus_assembled_mapped	periplasmic solute binding family protein				PF01297.12	2268290	2269172	-1	185	fig|1129.58.peg.2600				
gsyne_26	Synechococcus_assembled_mapped	GMC oxidoreductase family protein				PF05199.8	20167	21766	1	703	fig|1129.58.j	Respiration	Electron donating reactions	Respiratory dehydrogenases 1	
gsyne_260	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	211071	211218	1	856	fig|1129.58.peg.257				
gsyne_2600	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2270243	2270417	-1	856					
gsyne_2601	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07864.6	2270642	2270936	-1	156	fig|1129.58.peg.2603				
gsyne_2602	Synechococcus_assembled_mapped	putative kelch motif protein				UniRef100_A	2270939	2271107	-1	185	fig|1129.58.peg.2604				
gsyne_2603	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2271351	2271717	1	856	fig|1129.58.peg.2605				
gsyne_2604	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2271786	2271984	1	856	fig|1129.58.peg.2606				
gsyne_2605	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2272170	2273559	-1	856	fig|1129.58.peg.2607				
gsyne_2606	Synechococcus_assembled_mapped	helix-turn-helix domain protein				PF12728.2	2271983	2272202	1	157					
gsyne_2608	Synechococcus_assembled_mapped	bacterial transferase hexapeptide family protein				PF00132.19	2273992	2274517	1	703	fig|1129.58.j	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Cyanate hydrolysis	
gsyne_2609	Synechococcus_assembled_mapped	photosystem II Y family protein				PF06298.6	2274610	2274733	1	164	fig|1129.58.j	Photosynthesis	Electron transport and photop	Photosystem II	
gsyne_261	Synechococcus_assembled_mapped	polyphosphate kinase 1	ppk1	2.7.4.1	GO:0006799,GO:0008976,G	TIGR03705	212843	215096	-1	703	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Polyphosphate	
gsyne_2610	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2274852	2275335	-1	92,141,165	fig|1129.58.peg.2610				
gsyne_2611	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2275298	2275589	-1	856	fig|1129.58.peg.2611				
gsyne_2612	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	2275597	2276035	-1	156	fig|1129.58.peg.2612				
gsyne_2613	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2276012	2276681	1	856	fig|1129.58.peg.2613				
gsyne_2614	Synechococcus_assembled_mapped	m(5)U-54 methyltransferase	trmFO	2.1.1.74	GO:0006400,GO:0016740	TIGR00137	2276766	2278128	1	168	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_2615	Synechococcus_assembled_mapped	ribbon-helix-helix , copG family protein				PF01402.16	2278168	2278390	1	261	fig|1129.58.peg.2615				
gsyne_2616	Synechococcus_assembled_mapped	toxin-antitoxin system toxin component, PIN family			GO:0004521,GO:0005515	TIGR00305	2278395	2278797	1	156	fig|1129.58.peg.2616				
gsyne_2617	Synechococcus_assembled_mapped	cation efflux family protein				PF01545.16	2278821	2279766	-1	145	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Cobalt-zinc-cadmium resistance	
gsyne_2618	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11455.3	2279929	2280058	1	156	fig|1129.58.peg.2618				
gsyne_2619	Synechococcus_assembled_mapped	pemK-like family protein				PF02452.12	2280120	2280387	1	261	fig|1129.58.peg.2619				
gsyne_262	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	215146	215287	-1	856	fig|1129.58.peg.260				
gsyne_2620	Synechococcus_assembled_mapped	carotene isomerase	crtH	5.-.-.-	GO:0016117,GO:0046608	TIGR02730	2280416	2281988	1	76	fig|1129.58.peg.2620				
gsyne_2621	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2282396	2282510	-1	856	fig|1129.58.peg.2621				
gsyne_2622	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2282796	2283147	1	856	fig|1129.58.peg.2622				
gsyne_2623	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2283292	2283604	1	856					
gsyne_2624	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2284542	2284713	-1	856					
gsyne_2625	Synechococcus_assembled_mapped	histidine kinase family protein				PF06580.8	2284719	2285376	1	703	fig|1129.58.peg.2625				
gsyne_2626	Synechococcus_assembled_mapped	homeo-like domain protein				PF13384.1	2285345	2285999	1	157	fig|1129.58.peg.2626				
gsyne_2627	Synechococcus_assembled_mapped	ID514 domain protein	id514		GO:0015074,GO:0003677	UniRef100_C	2285956	2286715	1	92,141	fig|1129.58.peg.2627				
gsyne_2628	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	2286756	2287794	1	154	fig|1129.58.peg.2628				
gsyne_2629	Synechococcus_assembled_mapped	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein				PF02518.21	2287816	2288113	1	703	fig|1129.58.peg.2629				
gsyne_263	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	215275	215401	1	856					
gsyne_2630	Synechococcus_assembled_mapped	response regulator				PF00072.19	2288109	2288442	1	699	fig|1129.58.peg.2630				
gsyne_2631	Synechococcus_assembled_mapped	lytTr DNA-binding domain protein				PF04397.10	2288540	2288855	1	261	fig|1129.58.peg.2631				
gsyne_2632	Synechococcus_assembled_mapped	EAL domain protein				PF00563.15	2288851	2290591	1	264,710	fig|1129.58.peg.2632				
gsyne_2633	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2290599	2290803	-1	856					
gsyne_2634	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2291039	2291456	-1	856					
gsyne_2635	Synechococcus_assembled_mapped	alpha amylase, catalytic region		3.2.1.54	GO:0043169,GO:0005975,G	UniRef100_B	2293207	2294632	-1	119,141,703	fig|1129.58.j	Carbohydrates	Di- and oligosaccharides	Maltose and Maltodextrin Utilizati	
gsyne_2636	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2294731	2295022	1	156	fig|1129.58.peg.2638				
gsyne_2637	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_P	2295018	2295558	1		fig|1129.58.peg.2639				
gsyne_2638	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2295765	2295879	-1	856					
gsyne_2639	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2296061	2296247	1	856	fig|1129.58.peg.2640				
gsyne_264	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	215673	216210	1	156	fig|1129.58.peg.261				
gsyne_2640	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2296262	2298218	1	141	fig|1129.58.peg.2641				
gsyne_2641	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2298232	2298883	-1	156	fig|1129.58.peg.2642				
gsyne_2642	Synechococcus_assembled_mapped	response regulator				PF00072.19	2298914	2299628	1	699	fig|1129.58.peg.2643				
gsyne_2643	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2299778	2300045	1	156	fig|1129.58.peg.2644				
gsyne_2644	Synechococcus_assembled_mapped	monothiol glutaredoxin, Grx4 family	grxD		GO:0009055,GO:0030508	TIGR00365	2300073	2300394	-1	157	fig|1129.58.j	Stress Response	Oxidative stress	Glutathione: Redox cycle	
gsyne_2645	Synechococcus_assembled_mapped	bolA-like family protein				PF01722.13	2300397	2300616	-1	92,149	fig|1129.58.j	Miscellaneous	Miscellaneous - no subcategor	Broadly distributed proteins not ir	
gsyne_2646	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2300683	2301211	-1	141	fig|1129.58.peg.2647				
gsyne_2647	Synechococcus_assembled_mapped	acyltransferase family protein				PF01553.16	2301220	2301961	-1	703	fig|1129.58.peg.2648				
gsyne_2648	Synechococcus_assembled_mapped	pyridoxine 5'-phosphate synthase	pdxJ	2.6.99.2	GO:0008615,GO:0033856	TIGR00559	2302108	2302858	1	84	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthe	
gsyne_2649	Synechococcus_assembled_mapped	ycf54 protein	ycf54			UniRef100_C	2302854	2303175	1	185	fig|1129.58.peg.2650				
gsyne_265	Synechococcus_assembled_mapped	PAP2 superfamily protein				PF01569.16	216263	216968	1	185	fig|1129.58.peg.262				
gsyne_2650	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2303304	2303658	-1	156	fig|1129.58.peg.2651				
gsyne_2651	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	2303783	2304428	1	703	fig|1129.58.peg.2652				
gsyne_2652	Synechococcus_assembled_mapped	exodeoxyribonuclease V, gamma subunit				PF04257.9	2304431	2307689	1	166	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, bacterial RecBCD pa	
gsyne_2653	Synechococcus_assembled_mapped	uvrD/REP helicase N-terminal domain protein				PF00580.16	2307685	2311300	1	132	fig|1129.58.j	DNA Metabolism	DNA replication	DNA-replication	
gsyne_2654	Synechococcus_assembled_mapped	AAA domain protein				PF13604.1	2311296	2312463	1	157	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, bacterial RecBCD pa	
gsyne_2655	Synechococcus_assembled_mapped	description family protein				PF13538.1	2312490	2312865	1	185	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, bacterial RecBCD pa	
gsyne_2656	Synechococcus_assembled_mapped	cupin domain protein				PF07883.6	2312887	2313247	1	157	fig|1129.58.peg.2657				
gsyne_2657	Synechococcus_assembled_mapped	helicase conserved C-terminal domain protein				PF00271.26	2313396	2315283	1	703	fig|1129.58.peg.2658				
gsyne_2658	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2315301	2315502	-1	156	fig|1129.58.peg.2659				
gsyne_2659	Synechococcus_assembled_mapped	RNA recognition motif family protein				PF14259.1	2315753	2316185	1	185	fig|1129.58.peg.2660				
gsyne_266	Synechococcus_assembled_mapped	pyridine nucleotide-disulfide oxidoreductase family protein				PF07992.9	217050	218508	1	157	fig|1129.58.j	Respiration	Electron donating reactions	Respiratory dehydrogenases 1	
gsyne_2660	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2316319	2316526	-1	156	fig|1129.58.peg.2661				
gsyne_2661	Synechococcus_assembled_mapped	2,3-dimethylmalate lyase	Dml	4.1.3.32	GO:0046872,GO:0051187,G	UniRef100_C	2316592	2317492	-1	92,141,703	fig|1129.58.peg.2662				
gsyne_2662	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2317557	2319348	1	141	fig|1129.58.peg.2663				
gsyne_2663	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2320344	2320581	-1	88	fig|1129.58.peg.2665				
gsyne_2664	Synechococcus_assembled_mapped	cell envelope-related function transcriptional attenuator common domain protein				TIGR00350	2319436	2320363	1	129	fig|1129.58.j	Regulation and Cell signaling	Regulation and Cell signaling -	Cell envelope-associated LytR-C	
gsyne_2665	Synechococcus_assembled_mapped	mgtC family protein				PF02308.11	2320573	2321020	-1	157	fig|1129.58.peg.2666				
gsyne_2666	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF06081.6	2321071	2322055	1	156	fig|1129.58.peg.2667				
gsyne_2667	Synechococcus_assembled_mapped	fusaric acid resistance -like family protein				PF13515.1	2322051	2323110	1	94	fig|1129.58.peg.2668				
gsyne_2668	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	2323117	2323954	1	88	fig|1129.58.peg.2669				
gsyne_2669	Synechococcus_assembled_mapped	outer membrane efflux family protein				PF02321.13	2323910	2325797	1	141	fig|1129.58.peg.2670				
gsyne_267	Synechococcus_assembled_mapped	sugar (and other) transporter family protein				PF00083.19	218568	220005	1	141	fig|1129.58.peg.264				
gsyne_2670	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2325811	2326831	1	856	fig|1129.58.peg.2671				
gsyne_2671	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF06081.6	2326834	2327878	1	156	fig|1129.58.peg.2672				
gsyne_2672	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	2327881	2328073	-1	156	fig|1129.58.peg.2673				
gsyne_2673	Synechococcus_assembled_mapped	NHLM bacteriocin system secretion protein				TIGR03794	2328069	2329410	-1	185	fig|1129.58.peg.2674				
gsyne_2674	Synechococcus_assembled_mapped	pyridine nucleotide-disulfide oxidoreductase family protein				PF07992.9	2329442	2330528	-1	157	fig|1129.58.peg.2675				
gsyne_2675	Synechococcus_assembled_mapped	psbP protein	psbP		GO:0005509,GO:0019898,G	UniRef100_C	2330527	2331100	-1	92,141	fig|1129.58.j	Photosynthesis	Electron transport and photop	Photosystem II	
gsyne_2676	Synechococcus_assembled_mapped	recombination protein RecR	recR		GO:0006281,GO:0006310	TIGR00615	2331345	2331783	1	132	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa	
gsyne_2677	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2332695	2333208	-1	156	fig|1129.58.peg.2679				
gsyne_2678	Synechococcus_assembled_mapped	lipoyl synthase	lipA	2.8.1.8	GO:0009107,GO:0017140,G	TIGR00510	2331790	2332717	1	80	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Lipoic acid	Lipoic acid metabolism	
gsyne_2679	Synechococcus_assembled_mapped	glutathione S-transferase, C-terminal domain protein				PF00043.20	2333204	2334140	-1	703	fig|1129.58.j	Miscellaneous	Plant-Prokaryote DOE project	Single-Rhodanese-domain protei	
gsyne_268	Synechococcus_assembled_mapped	glycogen/starch/alpha-glucan phospho	glgP	2.4.1.1	GO:0004645,GO:0005977	TIGR02093	220042	222580	1	105	fig|1129.58.j	Carbohydrates	Polysaccharides	Glycogen metabolism	
gsyne_2680	Synechococcus_assembled_mapped	rhodanese-like domain protein				PF00581.15	2334162	2335092	-1	157	fig|1129.58.j	Miscellaneous	Plant-Prokaryote DOE project	Single-Rhodanese-domain protei	
gsyne_2681	Synechococcus_assembled_mapped	biotin synthase	bioB	2.8.1.6	GO:0004076,GO:0009102,G	TIGR00433	2335100	2336078	-1	77	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Biotin	Biotin biosynthesis	
gsyne_2682	Synechococcus_assembled_mapped	di-trans,poly-cis-decaprenylcistransfera	uppS	2.5.1.31	GO:0005737,GO:0008834,G	TIGR00055	2336092	2336830	-1	90	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis	
gsyne_2683	Synechococcus_assembled_mapped	disA bacterial checkpoint controller nucleotide-binding family protein				PF02457.11	2336883	2337684	-1	185	fig|1129.58.j	Cell Division and Cell Cycle	Checkpoint control	Bacterial checkpoint-control-relati	
gsyne_2684	Synechococcus_assembled_mapped	diaminopimelate decarboxylase	lysA	4.1.1.20	GO:0008836,GO:0009089	TIGR01048	2337745	2339071	-1	71	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa	
gsyne_2685	Synechococcus_assembled_mapped	ribosomal-protein-alanine acetyltransfe	rimI	2.3.1.128	GO:0006464,GO:0008999,G	TIGR01575	2339180	2339684	1	158	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Ribosome biogenesis bacterial	
gsyne_2686	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	2339834	2342396	1	154	fig|1129.58.j	Protein Metabolism	Protein degradation	Proteolysis in bacteria, ATP-depe	
gsyne_2687	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2342607	2342733	-1	856	fig|1129.58.peg.2688				
gsyne_2688	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2343633	2345967	-1	856	fig|1129.58.peg.2690				
gsyne_2689	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	2346014	2346152	-1	856	fig|1129.58.peg.2691				
gsyne_269	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein				TIGR02937	222590	223430	1	135	fig|1129.58.j	RNA Metabolism	Transcription	Transcription factors cyanobacter	
gsyne_2695	Synechococcus_assembled_mapped	putative pG1 protein				UniRef100_C	2351446	2351644	1	185	fig|1129.58.j	Carbohydrates	Monosaccharides	Deoxyribose and Deoxynucleosic	
gsyne_2696	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	2352486	2352795	-1	156	fig|1129.58.peg.2694				
gsyne_2697	Synechococcus_assembled_mapped	glyceraldehyde-3-phosphate dehydrogi	gap	1.2.1.-	GO:0006094,GO:0006096,G	TIGR01534	2353743	2354745	-1	116	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthe	

0.71710108	-1.2351374	1	1.06136415	1	-1.0480874	1	-1.1124024
0.91343968	1.1297251	0.18804643	-2.9548613	0.24279913	1.9940472	0.00922681	5.89213293
0.0361802	-4.4343277	0.7479077	1.4053912	0.64052753	-1.7254995	0.24815159	-2.4250018
0.14817841	-2.4547399	0.21318066	-2.3485595	0.40932089	-1.7909621	0.82452456	1.31133956
0.65021932	1.34129247	0.25480758	2.10833472	0.50634823	1.60665688	0.72753026	-1.3122495
0.56494997	1.20644109	0.87106586	1.05739173	0.49682942	1.25140905	0.6148386	1.1834867
0.01027044	-3.8548522	0.13247982	-2.6910557	0.13247982	-2.4498067	1	1.09847673
0.23029692	1.49881673	0.91998102	-1.0388447	0.9019332	-1.045186	0.99090246	-1.0061041
0.10948351	-2.0994793	0.14319769	2.01979638	1	1.02550822	0.14319769	-1.9695565
0.16890659	-2.9368994	1	5.72539119	1	8.27745209	1	1.44574437
0.00122626	-16.666407	0.05921062	-4.7556572	0.02136811	-10.50305	1	-2.208538
0.00925073	-2.345955	0.2293088	-1.6854012	0.89600851	1.09054887	0.16203602	1.83801239
0.52345581	-1.3158889	0.55729178	-1.3730787	0.8999385	1.0512959	0.43717631	1.44351204
0.79207549	1.10073952	0.91090513	-1.0402834	1	1.03231759	0.88194232	1.07390289
0.28878321	-1.9535121	0.03733117	3.85940758	0.63105998	1.48461668	0.12066903	-2.5995987
0.75781838	-1.2189011	0.00939974	5.16178209	0.13970924	2.64169332	0.2455634	-1.9539672
0.68687053	1.86477597	0.06434705	7.52095206	0.68687053	1.8063125	0.22365392	-4.1637048
0.41776759	-1.5889253	0.12342136	2.70702746	0.19397648	2.44592435	1	-1.1067503
0.37669753	-2.3254282	0.19522343	-6.5300008	0.19522343	-3.3486763	1	1.95002449
0.16924907	-2.5201139	0.79847746	1.36677043	0.49444931	1.72608023	0.83876138	1.26288965
1	-1.101295	0.09994738	4.02692516	1	1.10401387	0.17152772	-3.6475313
1	-2.1444988	1	1	1	5.13744365	1	5.13744365
0.39796364	-1.3203188	0.04117205	2.12753664	0.14509428	1.75051482	0.55949005	-1.2153777
0.01077683	-3.0163735	0.06144663	4.50444947	0.04030705	4.91500903	1	1.09114534
0.41109332	-1.9314114	1	-1.0688013	1	-1.3297938	1	-1.2441919
0.01237927	-6.1839531	0.00969723	-40.245381	0.04361116	-4.8507974	1	8.2966526
0.79131844	1.14812546	0.1191455	1.85341419	0.27683693	1.55160405	0.69532746	-1.1945149
0.01299698	-3.2943284	0.60009127	-1.3105154	0.03495243	-2.9347439	0.09767192	-2.2393815
0.94545081	-1.0424964	0.17939021	-1.6882835	0.33928048	-1.4031433	0.70943509	1.20321531
0.063009	-27.201227	0.10188853	-25.72371	0.10188853	-25.72371	1	1
1	-4.2559815	0.29584805	-13.717022	0.29584805	-13.717022	1	1
0.52023388	-11.002655	0.28035083	15.7300942	1	1	0.28035083	-15.730094
0.53876071	-10.574668	0.18509214	-17.551997	0.18509214	-17.551997	1	1
1	-1.4829666	1	1	1	5.13507745	1	5.13507745
0.0919259	-3.9151086	0.46472597	-1.9231054	0.10573029	-3.9005377	0.42748566	-2.0282496
0.4002667	-1.5409027	0.06907182	2.52133343	1	1.07946958	0.0856867	-2.3357151
0.39860481	-1.7502615	0.05954673	3.74663433	0.85003464	1.26824011	0.08801417	-2.9541995
0.75630515	1.2499151	0.04198675	6.3696584	0.11754815	4.63859515	0.74914382	-1.373187
0.47147508	1.47563603	0.01198165	4.31273843	0.12384639	2.43018132	0.32263352	-1.7746571
0.20754138	-1.9761692	0.03103656	3.95081122	0.12616985	2.85402294	0.59522593	-1.3842955
0.60904741	1.19697511	0.96563987	1.01768546	0.40660679	1.34550042	0.43120668	1.32211815
0.33482263	-1.7611337	0.29025275	-1.9044382	0.69717253	-1.3674679	0.61881859	1.3926749
0.06444397	-4.307246	0.55100836	1.53865258	0.46288439	-2.0373947	0.15992806	-3.1348426
0.02388975	-27.487465	1	-1.5088484	0.07713432	-23.513577	0.26700775	-15.58379
0.52314021	-7.6148324	1	-5.6496823	1	-5.6496823	1	1
0.07285149	-3.2198685	0.57037925	1.87516719	1	1.40327838	0.7913107	-1.336276
0.08783277	-21.114807	0.27885326	15.7147244	1	1	0.27885326	-15.714724
0.45814757	-1.657673	0.41542461	1.70984941	0.41542461	1.77508671	1	1.03815383
1	-2.2928303	0.52950553	-9.6081566	1	-2.0718242	1	4.63753464
0.51816889	-1.3045891	1	1.00806212	1	-1.0123506	0.88723656	-1.0205123
0.00040982	-14.069372	0.00031492	-14.74519	0.00263547	-10.10155	0.78129431	1.45969578
0.80617276	1.09757899	0.01529718	2.34569091	0.16285981	1.64100527	0.29034725	-1.4294231
0.93580446	1.06570972	0.14612571	2.76698594	0.56665036	1.64024476	0.43112774	-1.6869348
0.5953349	1.52859075	1	-1.0211318	0.87000672	1.22513344	0.87000672	1.25102269
1	-1.0489262	0.49349926	-1.79267	1	-1.0701027	0.57094034	1.67523169
0.01097551	2.63686257	0.16252359	1.7717731	0.05721674	2.14733152	0.65079041	1.21196756
0.60997793	1.21071656	0.20732294	1.55750942	0.35015141	1.4252543	0.77495441	-1.092794
0.04043005	-2.4022367	0.94633078	1.11186511	0.22985536	-1.7594177	0.16007529	-1.9562352
1	1.02400391	0.53100035	-1.2584463	0.71588636	-1.1568882	0.84248697	1.08778557
0.7799964	-1.0634435	0.22055972	1.51903172	0.7799964	-1.077603	0.10233963	-1.6369131
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0.50655801	1.41935788	0.04852546	3.377089	0.0184336	4.19398545	0.69445347	1.24189367
0.67075948	-1.7979104	0.76994888	-2.060321	1	-1.1966911	0.76994888	1.72168166
0.35275427	1.35418577	0.13237845	1.65065747	0.46377351	1.27450602	0.46320713	-1.2951351
1	-4.2608681	1	-1.6215817	0.52691875	-9.6353076	1	-5.9419194
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0.8274433	1.10872559	0.3943091	-1.4899171	0.99743046	1.00287913	0.39160332	1.49420678
0.11755448	-3.6948852	0.65422836	1.95066419	1	1.46008189	0.65422836	-1.3359964
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37	2.25217994	14	1.01402639	3	0.36869745	10	0.75099242	34	5.58918387	4	0.31730379	3	0.3526964	22	0.95699599
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13	7.77663251	26	18.5072305	1	1.20780198	15	11.0706642	16	25.8485583	1	0.77958258	2	2.31076952	6	2.56498924
4	1.41615286	4	1.68511674	2	1.42964316	3	1.31040515	2	1.91226579	1	0.46138561	0	0	0	0
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34	2.54785169	21	1.87255414	6	0.90780797	7	0.64718354	18	3.64280438	0	0	8	1.15788019	19	1.01750113
3	1.42585254	0	0	0	0	2	1.17278269	0	0	0	0	0	0	1	0.33965611
12	2.3791368	12	2.83099613	4	1.60120034	10	2.44608961	5	2.6771721	8	2.06700753	1	0.38292752	17	2.40864704
40	33.8495074	49	49.3410403	2	3.41719585	55	57.423445	0	0	3	3.30847241	2	3.26889347	3	1.81426068
86	4.18490052	64	3.70583879	28	2.7510104	45	2.70167681	93	12.2218727	55	3.48789401	32	3.00756538	116	4.03395222
10	2.15501522	14	3.59003133	6	2.61065273	5	1.32939653	23	13.3858605	3	0.84253024	7	2.91357897	14	2.15607791
6	2.14612856	3	1.27686681	4	2.8887635	4	1.7652193	6	5.79593961	1	0.46614216	3	2.07254586	9	2.30055736
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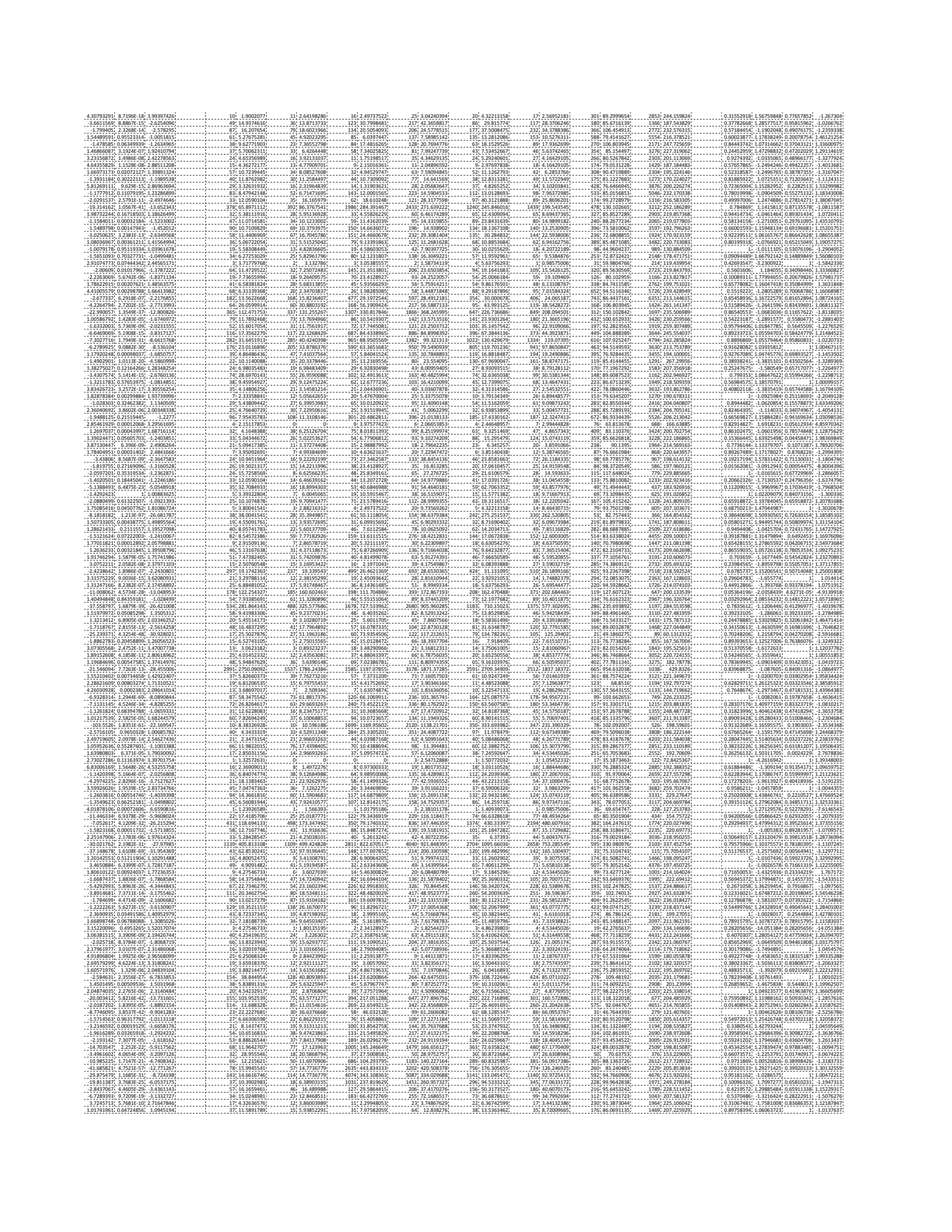
39	2.98047149	36	3.27372901	20	3.08601387	26	2.45147747	40	8.2555968	24	2.39026201	17	2.50927175	66	3.60454435
30	14.0658426	33	18.411039	16	15.1464897	17	9.83394133	7	8.86361035	31	18.9417497	7	6.33900288	15	5.02599243
34	8.80339799	28	8.62679169	15	7.84169943	41	13.097532	13	9.09039782	28	9.44807545	12	6.00110294	45	8.32664418
32	3.52464711	28	3.6698098	19	4.22538979	25	3.39734668	25	7.43658918	39	5.59814538	8	1.70190009	45	3.542128
4	3.22751117	2	1.92024931	0	0	1	0.99550158	0	0	1	1.05152999	0	0	0	0
17	6.62727714	8	3.71104362	2	1.57421382	4	1.9238907	12	12.6338459	6	3.04825548	12	9.03536848	13	3.62172638
5	3.69103671	5	4.3920596	1	1.49047904	4	3.64311218	2	3.9872776	0	0	3	4.27738189	1	0.52755098
83	5.49570007	52	4.09702048	41	5.48120822	62	5.06489928	82	14.6631373	71	6.12656692	48	6.13853278	94	4.44793936
1	0.91304592	0	0	0	0	2	2.25297727	1	2.46581641	0	0	0	0	0	0
10	2.96544829	10	3.52866327	3	1.79621833	8	2.92694483	12	9.6103614	4	1.54583896	4	2.29101936	7	1.48345532
789	263.220604	912	362.040851	393	264.717676	1105	454.819786	135	121.631137	866	376.508402	223	143.68987	1848	440.586229
6	3.65218369	3	2.1729137	1	1.22899149	0	0	2	3.28775522	0	0	0	0	2	0.86999635
26	4.11912955	7	1.31962339	4	1.27949799	11	2.1501016	16	6.84573689	9	1.85818314	5	1.52996156	16	1.81149925
0	0	1	0.18938239	3	0.96402543	1	0.1963604	1	0.42982121	1	0.20741188	3	0.92218784	3	0.34121417
13	2.63768822	8	1.93147884	5	2.04831915	8	2.00264646	20	10.9591841	6	1.58651894	9	3.52696401	10	1.44999392
27	2.70747143	9	1.07389665	13	2.63203091	12	1.48462086	18	4.87461973	10	1.30681473	7	1.3557405	41	2.93812351
5	1.75231036	5	2.0851192	2	1.41520232	1	0.43238958	0	0	1	0.45672515	0	0	1	0.2504535
2	1.65217834	2	1.96596954	0	0	4	4.07681601	0	0	1	1.07656642	0	0	1	0.59035467
6	1.87544568	2	0.74388037	1	0.63110374	3	1.15693427	7	5.90907356	2	0.81469891	0	0	3	0.67013232
11	3.63479234	4	1.57277563	1	0.66716681	1	0.4076816	5	4.46195351	3	1.2918797	1	0.63821254	0	0
70	4.1874175	46	3.27435616	43	5.19354852	51	3.76402582	44	7.10835352	62	4.833412	21	2.426308	83	3.54823512
12	6.12277854	7	4.24996355	1	1.03018404	7	4.40655848	0	0	1	0.66493808	1	0.98547524	4	1.45852329
23	5.74102256	25	7.4254245	8	4.03179942	14	4.3114529	5	3.37054042	4	1.3011738	4	1.92841198	12	2.14056656
53	3.87131471	20	1.73833096	16	2.35966366	23	2.07273909	31	6.1152247	14	1.33267591	12	1.69294273	37	1.9313919
11	3.93456902	7	2.97935589	2	1.44438175	7	3.08913378	2	1.93197987	3	1.39842648	3	2.07254586	8	2.04493988
13	2.50580381	11	2.52299424	9	3.50262574	9	2.14032841	7	3.6439287	6	1.50719299	4	1.48916258	15	2.06624133
5	4.56522961	3	3.25937055	0	0	4	4.50595454	0	0	2	2.3797784	0	0	0	0
11	6.1556967	7	4.66125035	1	1.12987927	12	8.28514222	1	1.51130683	5	3.64643465	3	3.24253143	3	1.19975303
43	8.33473205	38	8.76448988	17	6.65303214	24	5.73942813	26	13.6102046	12	3.03122612	16	5.9899277	40	5.54075888
114	6.06643395	81	5.12900948	43	4.62002782	128	8.40374344	67	9.62878617	119	8.2525751	55	5.65287943	208	7.91002817
74	11.8317287	52	9.89326605	45	14.5270192	64	12.6249786	33	14.2494644	53	11.0434878	23	7.10268789	117	13.3686767
65	9.47572869	67	11.6223493	33	9.71316383	61	10.9714313	32	12.598457	40	7.59929238	12	3.37877225	64	6.66753506
22	8.5764763	21	9.7414895	4	3.14842764	27	12.9862622	7	7.36974343	12	6.09651096	9	6.77652636	17	4.73610373
23	7.45796389	27	10.4178012	18	11.7845352	29	11.6017801	16	14.011368	14	5.91608463	11	6.88911662	45	10.42776
50	23.7642089	54	30.5398555	31	29.7483282	51	29.9059586	11	14.1193323	28	17.3430426	21	19.2775156	74	25.1345521
28	5.51977762	20	4.69151821	19	7.5624874	23	5.59404015	6	3.19435308	24	6.1657895	15	5.71127695	37	5.21256336
50	7.02343017	43	7.18732992	29	8.2247892	44	7.62546153	9	3.41420734	38	6.95627533	10	2.71304924	48	4.81844133
14	1.94296172	10	1.65141441	12	3.36252071	3	0.51367882	8	2.99843276	12	2.1703579	4	1.07219706	12	1.19015501
19	6.16092669	23	8.87442323	18	11.7845352	22	8.80135046	5	4.37855251	16	6.76123957	13	8.14168328	43	9.964304
36	5.31509286	31	5.4461539	7	2.08667066	21	3.82526779	10	3.9872776	15	2.88611423	9	2.56642913	32	3.37632626
21	6.17466649	12	4.19851121	3	1.78099614	8	2.90214021	9	7.14668824	3	1.14955397	4	2.27160394	15	3.15189356
77	12.425918	94	18.0503436	31	10.1005952	81	16.1271257	16	6.97309943	57	11.9874419	23	7.16875941	106	12.2244604
69	2.20442579	61	2.31897512	21	1.35460664	48	1.89200301	36	3.10611128	43	1.79031211	16	0.98729011	58	1.32422097
87	2.505004	63	2.15848771	31	1.80218088	52	1.84725439	57	4.43233058	41	1.53846255	37	2.05763958	93	1.91363098
28	2.49738011	13	1.37971641	9	1.62075227	15	1.65063887	16	3.85402668	11	1.27859559	13	2.23948615	21	1.33854194
9	2.49809364	5	1.65141441	6	3.36252071	6	2.05471527	8	5.99686551	9	3.25553685	3	1.60829559	5	0.99179584
28	8.09567384	25	8.60111672	12	7.00525149	26	9.27475643	14	10.9317861	15	5.65197371	13	7.25966759	34	7.02522053
181	9.98399022	187	12.274026	115	12.8076935	627	42.6704582	78	11.6195228	591	42.4841521	65	6.92496113	331	13.0478706
90	46.6062247	120	73.9439288	32	33.4579176	118	75.3906722	16	22.3763639	73	49.2649648	10	10.0018382	64	23.6846768
267	64.3316939	214	61.3546326	57	27.7291205	400	118.907134	40	26.0280621	161	50.5537648	46	21.4067121	138	23.7617753
65	4.64037742	79	6.71099477	46	6.63048495	51	4.49204727	127	24.4856584	36	3.34931775	57	7.85946918	98	4.99979384
678	340.923408	779	466.105734	54	54.8237073	392	243.190938	40	54.319434	48	31.4544624	33	32.0493686	76	27.3103202
21	2.42870215	13	1.78903228	11	2.56859221	11	1.56957416	9	2.81103071	11	1.65791229	12	2.68049265	15	1.2397448
61	3.54512638	43	2.97365241	39	4.57629494	66	4.73238442	38	5.96421926	51	3.8626554	26	2.91845933	90	3.73792402
8	3.51349317	4	2.09039799	1	0.8867407	3	1.62556588	7	8.30262235	3	1.7170553	2	1.69651433	3	0.94157833
37	4.15450669	39	5.21077362	14	3.17390035	27	3.74037974	20	6.06479118	40	5.85317665	8	1.7349467	49	3.93187671
18	4.19143229	20	5.54165909	11	5.17166217	20	5.74584807	11	6.91752524	16	4.85538681	11	4.94721797	8	1.33126958
49	5.18320581	35	4.40545003	15	3.20362111	30	3.91523489	29	8.28454173	23	3.1706194	16	3.26889347	46	3.47733298
31	3.04693512	17	1.98824681	7	1.38914335	27	3.27415677	20	5.30883987	16	2.04944089	6	1.13901954	25	1.75601247
23	2.86022271	29	4.29130985	16	4.01734852	34	5.21657103	18	6.04522733	25	4.05159405	12	2.88225016	61	5.42110629
50	2.75800835	41	2.69109661	18	2.00468246	28	1.9055388	32	4.76698372	32	2.30032634	14	1.49153009	53	2.08923607
148	10.7201884	199	17.1519555	114	16.672206	144	12.8687804	154	30.1251725	127	11.98832	135	18.8865609	355	18.3761755
25	2.55115772	9	1.09284777	10	2.06036808	19	2.39213175	13	3.5826862	17	2.26078948	7	1.37966533	33	2.40656344
23	2.29310959	17	2.01681358	16	3.22080528	20	2.46014759	15	4.03883723	30	3.8979129	4	0.77025651	35	2.49373954
3	1.62636305	4	2.58033502	0	0	5	3.34426313	2	2.92815699	4	2.82598685	2	2.09413488	5	1.93710125
69	5.35571903	53	4.8951322	48	7.5224177	77	7.37383836	69	14.4639164	64	6.47384908	44	6.59629063	124	6.87822618
23	2.20442579	7	0.7983357	12	2.32218281	13	1.53725245	15	3.8826391	20	2.49810993	9	1.66605206	20	1.36988376
24	4.35967477	13	2.80999834	4	1.46706837	20	4.48236315	11	5.39639403	12	2.8407826	15	5.26274735	30	3.89448628
20	4.75284179	16	4.52442304	8	3.83849397	18	5.2775221	6	3.850727	9	2.7872747	7	3.21291927	16	2.71724888
12	2.43478913	9	2.1729137	6	2.45798298	3	0.75099242	2	1.09591841	9	2.3797784	6	2.35130934	9	1.30499453
33	3.70537083	26	3.47384908	12	2.72048601	23	3.18624941	16	4.85183294	26	3.80456482	8	1.7349467	34	2.72824098
12	1.33445173	11	1.4555736	4	0.89810917	13	1.78360701	9	2.70291414	7	1.01445682	6	1.28869839	10	0.79470821
160	6.79476035	102	5.15435342	19	1.62912825	63	3.30087367	49	5.61976764	63	3.48665208	32	2.6247174	83	2.51894292
26	2.90996571	16	2.1308573	11	2.4857344	30	4.14257111	38	11.4859319	14	2.0420034	11	2.37785638	28	2.23953899
52	5.53429062	41	5.19233058	26	5.58701039	50	6.56542456	18	5.17367615	49	6.79623832	21	4.3167443	74	5.62828928
75	10.5779711	56	9.39829339	43	12.2449518	68	11.8327099	24	9.14156328	50	9.19020115	29	7.89982589	82	8.26496533
28	3.6385051	32	4.94805816	26	6.82159321	57	9.13848084	37	12.9847861	56	9.4834615	19	4.7686667	56	5.20042763
69	5.41630409	60	5.60434754	36	5.7056347	74	7.1667105	79	16.747468	86	8.79764233	49	7.42896718	131	7.34871352
20	4.13044584	18	4.42343145	14	5.83770957	24	6.11522402	7	3.90420932	14	3.76798247	7	2.79217984	24	3.542128
377	15.3165057	347	16.7751991	272	22.311808	655	32.8317355	234	25.6745194	660	34.9442871	225	17.6554697	883	25.6368773
5	4.13044584	3	2.9489543	2	3.33583404	4	4.07681601	3	6.69293026	1	1.07656642	0	0	1	0.59035467
151	6.73400707	92	4.88207345	75	6.75313447	107	5.88727865	221	26.6168718	98	5.69556219	99	8.52727417	178	5.67286824
6	4.52553196	2	1.79501566	2	3.04576152	1	0.93057757	0	0	0	0	0	0	0	0
62	7.68262926	85	12.5330558	27	6.75506393	69	10.5487614	24	8.03151631	25	4.03712408	28	6.70123162	58	5.1360856
124	65.1859452	35	21.8937516	100	106.140174	24	15.5660248	209	296.719908	95	65.0833336	124	125.901927	70	26.297617
16	5.3896303	18	7.21491732	17	11.5620656	5	2.07798874	8	7.27774941	2	0.8779765	7	4.55423508	27	6.49963293
52	5.40173276	47	5.80961656	51	10.6966415	43	5.51102524	32	8.97734358	72	9.74711633	41	8.22606277	127	9.42799938

gsyne_2698	Synechococcus_assembled_mapped	membrane transport family protein				PF03547.13	2352865	2353765	1	141	fig|1129.58.peg.2695			
gsyne_2699	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2354810	2355371	-1	856	fig|1129.58.peg.2697			
gsyne_27	Synechococcus_assembled_mapped	ABC transporter, phosphonate, periplasmic substrate-binding family protein				PF12974.2	21762	22680	1	141	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter alkylphosphonat
gsyne_270	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF05787.8	223475	225452	-1	156	fig|1129.58.peg.267			
gsyne_2700	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF01169.14	2355440	2356115	-1	156	fig|1129.58.peg.2698			
gsyne_2701	Synechococcus_assembled_mapped	iron-containing alcohol dehydrogenase family protein				PF13685.1	2356199	2357309	1	703	fig|1129.58.peg.2699			
gsyne_2702	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	2357315	2358197	1	703	fig|1129.58.(	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_2703	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11209.3	2358225	2358813	1	156	fig|1129.58.peg.2701			
gsyne_2704	Synechococcus_assembled_mapped	cytidylyltransferase family protein				PF01148.15	2358819	2359728	-1	176	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho
gsyne_2705	Synechococcus_assembled_mapped	precorrin-6Y C5,15-methyltransferase (	cbiT	2.1.1.132	GO:0046025,GO:0046140	TIGR02469	2359724	2360300	-1	79	fig|1129.58.peg.2703			
gsyne_2706	Synechococcus_assembled_mapped	orn/Lys/Arg decarboxylase, major domain protein				PF01276.15	2360265	2361756	-1	703	fig|1129.58.(	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine degradation
gsyne_2707	Synechococcus_assembled_mapped	ABC1 family protein				PF03109.11	2361809	2363483	1	185	fig|1129.58.peg.2705			
gsyne_2708	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	2363509	2363977	1	156	fig|1129.58.peg.2706			
gsyne_2709	Synechococcus_assembled_mapped	RNA polymerase sigma factor rpoD2	rpoD2		GO:0003677,GO:0016987,G(	UniRef100_C	2364000	2364981	-1	92,141,165	fig|1129.58.(	RNA Metabolism	Transcription	Transcription factors cyanobacte
gsyne_271	Synechococcus_assembled_mapped	esterase-like activity of phytase family protein				PF13449.1	225583	226600	-1	185	fig|1129.58.peg.268			
gsyne_2710	Synechococcus_assembled_mapped	pseudouridine synthase family protein		5.4.99.-	GO:0001522,GO:0009982	TIGR00093	2365080	2365806	1	168	fig|1129.58.peg.2708			
gsyne_2711	Synechococcus_assembled_mapped	4-alpha-glucanotransferase	malQ	2.4.1.25	GO:0004134,GO:0005980	TIGR00217	2366718	2368155	-1	105	fig|1129.58.(	Carbohydrates	Polysaccharides	Glycogen metabolism
gsyne_2712	Synechococcus_assembled_mapped	helix-turn-helix family protein				PF01381.17	2365892	2366759	1	261	fig|1129.58.peg.2709			
gsyne_2713	Synechococcus_assembled_mapped	coenzyme F420 hydrogenase/dehydrogenase, beta subunit C terminus family protein				PF04432.8	2368205	2369420	-1	703	fig|1129.58.peg.2711			
gsyne_2714	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2370418	2371000	-1	856	fig|1129.58.peg.2713			
gsyne_2715	Synechococcus_assembled_mapped	cell envelope-related function transcriptional attenuator common domain protein				TIGR00350	2369535	2370462	1	129				
gsyne_2716	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2370974	2371112	-1	856				
gsyne_2717	Synechococcus_assembled_mapped	ribose-phosphate pyrophosphokinase 2	PRS2	2.7.6.1	GO:0000287,GO:0004749,G(	UniRef100_C	2371112	2372066	1	92,141,703	fig|1129.58.(	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway
gsyne_2718	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11940.3	2373219	2373639	-1	156	fig|1129.58.(	Protein Metabolism	Protein degradation	Aminopeptidases (EC 3.4.11.-)
gsyne_2719	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF02638.10	2372158	2373223	1	156	fig|1129.58.peg.2715			
gsyne_272	Synechococcus_assembled_mapped	trkA-C domain protein				PF02080.16	226592	228434	-1	157	fig|1129.58.peg.269			
gsyne_2720	Synechococcus_assembled_mapped	aminopeptidase N	pepN	3.4.11.2	GO:0004177,GO:0006508,G(	TIGR02414	2373622	2375917	-1	138	fig|1129.58.(	Protein Metabolism	Protein degradation	Aminopeptidases (EC 3.4.11.-)
gsyne_2721	Synechococcus_assembled_mapped	putative cAMP phosphodiesterases class-II				UniRef100_B	2375939	2376359	-1	185	fig|1129.58.peg.2718			
gsyne_2722	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_D	2376409	2376964	-1	141	fig|1129.58.peg.2719			
gsyne_2723	Synechococcus_assembled_mapped	adaptive-response sensory-kinase sasA	sasA	2.7.13.3	GO:0018106,GO:0000155,G(	UniRef100_C	2377189	2378335	1	92,141,703	fig|1129.58.(	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Cyanobacterial Circadian Clock
gsyne_2725	Synechococcus_assembled_mapped	polyketide cyclase / dehydrase and lipid transport family protein				PF03364.15	2378672	2379242	-1	706	fig|1129.58.peg.2721			
gsyne_2726	Synechococcus_assembled_mapped	ferredoxin--NADP reductase	petH	1.18.1.2	GO:0050661,GO:0030089,G(	UniRef100_C	2379384	2380527	1	141,703	fig|1129.58.(	Respiration	Respiration - no subcategory	Cytochrome B6-F complex
gsyne_2727	Synechococcus_assembled_mapped	glucose-6-phosphate dehydrogenase	zwf	1.1.1.49	GO:0004345,GO:0006098	TIGR00871	2380636	2382160	1	117	fig|1129.58.(	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway
gsyne_2728	Synechococcus_assembled_mapped	glucose-6-phosphate dehydrogenase subunit				PF10128.4	2382205	2383513	1	703	fig|1129.58.peg.2724			
gsyne_2729	Synechococcus_assembled_mapped	cobyrinic acid a,c-diamide synthase	cobB	6.3.1.-	GO:0005737,GO:0009236,G(	TIGR00379	2383522	2384893	1	79	fig|1129.58.peg.2725			
gsyne_273	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	228538	228910	1	157	fig|1129.58.(	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria
gsyne_2730	Synechococcus_assembled_mapped	histidine phosphatase super family protein				PF00300.17	2384908	2385496	1	703	fig|1129.58.peg.2726			
gsyne_2731	Synechococcus_assembled_mapped	acylphosphatase domain protein	acyP	3.6.1.7	GO:0003998	UniRef100_P	2385552	2385993	1	703	fig|1129.58.(	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-C(
gsyne_2732	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11139.3	2386003	2386690	1	156	fig|1129.58.peg.2728			
gsyne_2733	Synechococcus_assembled_mapped	AAA domain protein				PF13086.1	2386692	2388135	-1	157	fig|1129.58.peg.2729			
gsyne_2734	Synechococcus_assembled_mapped	divergent PAP2 family protein				PF02681.9	2388127	2388640	-1	185	fig|1129.58.peg.2730			
gsyne_2735	Synechococcus_assembled_mapped	geranylgeranyl pyrophosphate synthas(	GGPS	2.5.1.10	GO:0046872,GO:0004337,G(	UniRef100_C	2388636	2389548	-1	92,141,703	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Polyprenyl Diphosphate Biosynth
gsyne_2736	Synechococcus_assembled_mapped	tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain protein				PF00763.18	2389621	2390518	-1	78	fig|1129.58.(	Carbohydrates	One-carbon Metabolism	One-carbon metabolism by tetrah
gsyne_2737	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	TIGR00277	2390631	2392695	1	156	fig|1129.58.peg.2733			
gsyne_2738	Synechococcus_assembled_mapped	PQ loop repeat family protein				PF04193.9	2393974	2394292	-1	185	fig|1129.58.peg.2735			
gsyne_2739	Synechococcus_assembled_mapped	rieske [2Fe-2S] domain protein				PF00355.21	2392694	2394008	1	112	fig|1129.58.peg.2734			
gsyne_274	Synechococcus_assembled_mapped	magnesium and cobalt transport protei	corA		GO:0006824,GO:0015087,G(	TIGR00383	228922	230041	-1	145	fig|1129.58.(	Membrane Transport	Cation transporters	Magnesium transport
gsyne_2740	Synechococcus_assembled_mapped	RNA pseudouridylate synthase family protein				PF00849.17	2394288	2394993	-1	168	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	RNA pseudouridine syntheses
gsyne_2741	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2395386	2395689	-1	156	fig|1129.58.peg.2738			
gsyne_2742	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2395015	2395390	1	156	fig|1129.58.peg.2737			
gsyne_2743	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04472.7	2395723	2395951	-1	156	fig|1129.58.peg.2739			
gsyne_2744	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2396055	2396316	-1	156	fig|1129.58.peg.2740			
gsyne_2745	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF04248.7	2396612	2397080	-1	156	fig|1129.58.peg.2742			
gsyne_2746	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2396429	2396612	1	156	fig|1129.58.peg.2741			
gsyne_2747	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	2397093	2397345	-1	157	fig|1129.58.peg.2743			
gsyne_2748	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	2397426	2397849	1	156	fig|1129.58.(	DNA Metabolism	DNA repair	DNA repair, bacterial
gsyne_2749	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_B	2397845	2398070	1	156	fig|1129.58.(	Amino Acids and Derivatives	Glutamine, glutamate, asparta	Glutamine, Glutamate, Aspartate
gsyne_275	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	230196	230367	1	856	fig|1129.58.peg.273			
gsyne_2750	Synechococcus_assembled_mapped	2OG-Fe(II) oxygenase family protein				PF13759.1	2398086	2398800	-1	185	fig|1129.58.peg.2746			
gsyne_2751	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	2398865	2399714	-1	141	fig|1129.58.peg.2747			
gsyne_2752	Synechococcus_assembled_mapped	2-isopropylmalate synthase	leuA	2.3.3.13	GO:0003852,GO:0009098	TIGR00973	2399713	2401354	-1	74	fig|1129.58.(	Amino Acids and Derivatives	Branched-chain amino acids	Leucine Biosynthesis
gsyne_2753	Synechococcus_assembled_mapped	NYN domain protein				PF01936.13	2401407	2401935	-1	157	fig|1129.58.peg.2749			
gsyne_2754	Synechococcus_assembled_mapped	glycosyl hydrolase 57 family protein				PF03065.10	2402079	2403612	1	105	fig|1129.58.(	Carbohydrates	Polysaccharides	Glycogen metabolism
gsyne_2755	Synechococcus_assembled_mapped	lycopene cyclase family protein				TIGR01790	2404638	2405805	-1	185	fig|1129.58.peg.2752			
gsyne_2756	Synechococcus_assembled_mapped	radical SAM/Cys-rich domain family protein				TIGR04167	2403626	2404649	1	157	fig|1129.58.peg.2751			
gsyne_2757	Synechococcus_assembled_mapped	DNA gyrase, A subunit	gyrA	5.99.1.3	GO:0003916,GO:0003918,G(	TIGR01063	2405887	2408536	-1	132	fig|1129.58.(	Virulence, Disease and Defense	Resistance to antibiotics and t(	Resistance to fluoroquinolones
gsyne_2758	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF01837.11	2408635	2409724	1	156	fig|1129.58.(	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_2759	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF14159.1	2409777	2410398	1	156	fig|1129.58.peg.2755			
gsyne_276	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	230535	230784	-1	856	fig|1129.58.peg.275			
gsyne_2760	Synechococcus_assembled_mapped	nitronate monooxygenase family protein				PF03060.10	2410465	2411629	1	703	fig|1129.58.(	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_2761	Synechococcus_assembled_mapped	thioredoxin	trxA		GO:0005737,GO:0015036,G(	TIGR01068	2411812	2412136	1	112	fig|1129.58.peg.2757			
gsyne_2762	Synechococcus_assembled_mapped	putative lysine decarboxylase family protein				PF03641.9	2412237	2413290	1	703	fig|1129.58.peg.2758			
gsyne_2763	Synechococcus_assembled_mapped	imidazole glycerol phosphate synthase,	hisH	2.4.2.-	GO:0000105,GO:0000107,G(	TIGR01855	2413286	2413913	1	161	fig|1129.58.(	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_2764	Synechococcus_assembled_mapped	ribosomal L11 methyltransferase family protein				PF06325.8	2413984	2414482	1	158	fig|1129.58.peg.2760			
gsyne_2765	Synechococcus_assembled_mapped	cytochrome b6-f complex subunit 5	petG		GO:0006810,GO:0022900,G(	UniRef100_C	2414501	2414615	-1	92	fig|1129.58.(	Respiration	Respiration - no subcategory	Cytochrome B6-F complex
gsyne_2766	Synechococcus_assembled_mapped	cytochrome c family protein				PF00034.16	2414688	2415081	1	112	fig|1129.58.peg.2762			
gsyne_2767	Synechococcus_assembled_mapped	RNA methyltransferase, TrmH , group 1 family protei		2.1.1.-	GO:0008173,GO:0009451	TIGR00050	2415077	2415803	1	168	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	RNA methylation
gsyne_2768	Synechococcus_assembled_mapped	tll2115 protein				UniRef100_C	2415875	2416940	1	185	fig|1129.58.(	Virulence, Disease and Defense	Resistance to antibiotics and t(	Beta-lactamase
gsyne_2769	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11850.3	2416936	2418316	1	156	fig|1129.58.peg.2765			
gsyne_277	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	230359	230545	1	856	fig|1129.58.peg.274			
gsyne_2770	Synechococcus_assembled_mapped	magnesium chelatase ATPase subunit I	bchI	6.6.1.1	GO:0010007,GO:0015995,G(	TIGR02030	2418315	2419401	1	191	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr(	Tetrapyrroles	Chlorophyll Biosynthesis
gsyne_2771	Synechococcus_assembled_mapped	crossover junction endodeoxyribonuclease RuvC family protein				PF02075.12	2419418	2419895	1	166	fig|1129.58.(	DNA Metabolism	DNA replication	DNA-replication
gsyne_2772	Synechococcus_assembled_mapped	5-formyltetrahydrofolate cyclo-ligase		6.3.3.2	GO:0006730,GO:0030272	TIGR02727	2419891	2420494	1	698	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr(	Folate and pterines	Folate Biosynthesis
gsyne_2773	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2420501	2420756	1	856	fig|1129.58.peg.2769			
gsyne_2774	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2420792	2421251	1	156	fig|1129.58.peg.2770			
gsyne_2775	Synechococcus_assembled_mapped	fe-S metabolism associated domain protein				PF02657.10	2421250	2421670	1	76	fig|1129.58.(	Miscellaneous	Plant-Prokaryote DOE project	Iron-sulfur cluster assembly
gsyne_2776	Synechococcus_assembled_mapped	homoserine dehydrogenase	hom	1.1.1.3	GO:0050661,GO:0016597,G(	UniRef100_P	2421732	2423043	1	92,141,703	fig|1129.58.(	Amino Acids and Derivatives	Lysine, threonine, methionine,	Threonine and Homoserine Biosy
gsyne_2777	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2423226	2423430	1	156	fig|1129.58.peg.2773			
gsyne_2778	Synechococcus_assembled_mapped	bacterial extracellular solute-binding s, 5 Middle family protein				PF00496.17	2423452	2425027	1	141	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter oligopeptide (TC
gsyne_2779	Synechococcus_assembled_mapped	alpha/beta hydrolase family protein				PF12697.2	2426032	2427562	-1	703	fig|1129.58.(	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental
gsyne_278	Synechococcus_assembled_mapped	CHAD domain protein				PF05235.9	230879	231821	1	157	fig|1129.58.(	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria
gsyne_2780	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	2425023	2426043	1	141	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter dipeptide (TC 3.
gsyne_2781	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2428767	2428896	-1	856				
gsyne_2782	Synechococcus_assembled_mapped	major Facilitator Superfamily protein				PF07690.11	2427657	2428812	1	141	fig|1129.58.peg.2777			
gsyne_2783	Synechococcus_assembled_mapped	cation diffusion facilitator transporter family protein			GO:0006812,GO:0008324,G(	TIGR01297	2428866	2429766	1	145	fig|1129.58.(	Virulence, Disease and Defense	Resistance to antibiotics and t(	Cobalt-zinc-cadmium resistance
gsyne_2784	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2429778	2429976	-1	856	fig|1129.58.peg.2779			
gsyne_2785	Synechococcus_assembled_mapped	50S ribosome-binding GTPase family protein				PF01926.18	2430034	2431126	-1	157	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	Universal GTPases
gsyne_2786	Synechococcus_assembled_mapped	UDP-N-acetylglucosamine 2-epimerase		5.1.3.14	GO:0008761,GO:0009103	TIGR00236	2432412	2433531	-1	90	fig|1129.58.(	Cell Wall and Capsule	Capsular and extracellular pol(	Sialic Acid Metabolism
gsyne_2787	Synechococcus_assembled_mapped	efflux transporter, RND family, MFP subunit			GO:0005215,GO:0006810	TIGR01730	2431239	2432412	1	141	fig|1129.58.peg.2781			
gsyne_2788	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2433596	2433734	-1	856	fig|1129.58.peg.2783			
gsyne_2789	Synechococcus_assembled_mapped	putative high light inducible protein				UniRef100_B	2434821	2435037	-1	185	fig|1129.58.peg.2785			
gsyne_279	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	231910	232531	1	157	fig|1129.58.peg.277			
gsyne_2790	Synechococcus_assembled_mapped	twitching motility family protein			GO:0005524,GO:0043107	TIGR01420	2434045	2434825	1	91,188	fig|1129.58.(	Membrane Transport	Protein and nucleoprotein sec(	Type IV pilus
gsyne_2791	Synechococcus_assembled_mapped	tRNA threonylcarbamoyl adenosine modification protein YgjD				TIGR03723	2435050	2436118	-1	145	fig|1129.58.peg.2786			
gsyne_2792	Synechococcus_assembled_mapped	photosystem I reaction center subunit I	psaF		GO:0009538,GO:0015979	UniRef100_P	2436180	2436660	1	92	fig|1129.58.(	Photosynthesis	Electron transport and photop(	Photosystem I
gsyne_2793	Synechococcus_assembled_mapped	photosystem I reaction center subunit I	psaJ		GO:0016021,GO:0015979,G(	UniRef100_P	2436709	2436826	1	92	fig|1129.58.(	Photosynthesis	Electron transport and photop(	Photosystem I
gsyne_2794	Synechococcus_assembled_mapped	guanylate kinase	gmk	2.7.4.8	GO:0004385,GO:0015949	TIGR03263	2436879	2437449	-1	124	fig|1129.58.(	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_2795	Synechococcus_assembled_mapped	fibronectin-binding A family protein				PF05833.6	2437532	2439239	1	185	fig|1129.58.peg.2790			
gsyne_2796	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF11267.3	2440047	2440407	-1	156	fig|1129.58.peg.2792			
gsyne_2797	Synechococcus_assembled_mapped	twin arginine-targeting protein transloc	tatC		GO:0005887,GO:0008565,G(	TIGR00945	2439361	2440051	1	97	fig|1129.58.(	Membrane Transport	Protein translocation across c(	Twin-arginine translocation syste
gsyne_2798	Synechococcus_assembled_mapped	cytochrome b6-f complex iron-sulfur su	petC1		GO:0051537,GO:0008121,G(	UniRef100_C	2440551	2441055	1	92,141,703	fig|1129.58.(	Respiration	Respiration - no subcategory	Cytochrome B6-F complex
gsyne_2799	Synechococcus_assembled_mapped	apocytochrome f	petA		GO:0006810,GO:0009055,G(	UniRef100_P	2441093	2442026	1	92,141	fig|1129.58.(	Respiration	Respiration - no subcategory	Cytochrome B6-F complex
gsyne_28	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	22683	23865	1	264,710				
gsyne_280	Synechococcus_assembled_mapped	his Kinase A domain protein				PF00512.20	232535	233675	-1	699	fig|1129.58.(	Phosphorus Metabolism	Phosphorus Metabolism - no s	High affinity phosphate transport(
gsyne_2800	Synechococcus_assembled_mapped	prolipoprotein diacylglyceryl transferas	lgt	2.4.99.-	GO:0008961,GO:0009249,G(	TIGR00544	2442037	2442880	1	140	fig|1129.58.(	Protein Metabolism	Protein processing and modific	Lipoprotein Biosynthesis
gsyne_2801	Synechococcus_assembled_mapped	precorrin-4 C11-methyltransferase	cobM	2.1.1.133	GO:0005737,GO:0009236,G(	TIGR01465	2442876	2443638	1	79	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr(	Tetrapyrroles	Cobalamin synthesis
gsyne_2803	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2443800	2443920	1	856	fig|1129.58.peg.2797			
gsyne_2804	Synechococcus_assembled_mapped	ppx/GppA phosphatase family protein				PF02541.11	2444756	2446364	-1	703	fig|1129.58.(	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_2805	Synechococcus_assembled_mapped	helix-turn-helix family protein				PF01381.17	2443960	2444776	1	261	fig|1129.58.peg.2798			
gsyne_2806	Synechococcus_assembled_mapped	ubiA prenyltransferase family protein				PF01040.13	2446440	2447346	1	76	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr(	Quinone cofactors	Ubiquinone Biosynthesis
gsyne_2807	Synechococcus_assembled_mapped	2-C-methyl-D-erythritol 4-phosphate cy	ispD	2.7.7.60	GO:0019288,GO:0050518	TIGR00453	2448220	2448904	-1	76	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis
gsyne_2808	Synechococcus_assembled_mapped	LD-carboxypeptidase family protein				PF02016.10	2447342	2448230	1	138	fig|1129.58.(	Cell Wall and Capsule	Cell Wall and Capsule - no sul	Murein Hydrolases
gsyne_2809	Synechococcus_assembled_mapped	putative aDP-heptose:LPS heptosyltransferase			GO:0016740	UniRef100_A	2448965	2449802	1	703	fig|1129.58.peg.2803			
gsyne_281	Synechococcus_assembled_mapped	alkaline phosphatase synthesis transcri	sphR		GO:0006817,GO:0003677,G(	UniRef100_P	233678	234356	-1	92,141	fig|1129.58.(	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_2810	Synechococcus_assembled_mapped	trkA-C domain protein				PF02080.16	2449798	2450911	1	157	fig|1129.58.peg.2804			
gsyne_2811	Synechococcus_assembled_mapped	3-oxoacyl-[acyl-carrier-protein] reducta	fabG	1.1.1.100	GO:0004316,GO:0006633	TIGR01830	2450967	2451720	1	176	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_2812	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2451724	2451979	-1	156	fig|1129.58.peg.2806			
gsyne_2813	Synechococcus_assembled_mapped	chaperonin GroL	groL		GO:0005515,GO:0006457,G(	TIGR02348	2452104	2453772	1	95	fig|1129.58.(	Protein Metabolism	Protein folding	GroEL GroES
gsyne_2814	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	UniRef100_A	2453788	2453965	-1	156	fig|1129.58.peg.2808			
gsyne_2815	Synechococcus_assembled_mapped	pcrB family protein				PF01884.12	2454049	2454742	-1	157	fig|1129.58.(	Cell Wall and Capsule	Capsular and extracellular pol(	Sialic Acid Metabolism
gsyne_2816	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	2454731	2455172	-1	856	fig|1129.58.peg.2810			
gsyne_2817	Synechococcus_assembled_mapped	ABC-2 type transporter family protein				PF01061.19	2455182	2456049	-1	141	fig|1129.58.peg.2811			
gsyne_2818	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2456096	2457116	-1	141	fig|1129.58.peg.2812			
gsyne_2819	Synechococcus_assembled_mapped	protoheme IX farnesyltransferase	cyoE	2.5.1.-	GO:0006783,GO:0008495	TIGR01473	2457185	2458157	-1	79	fig|1129.58.(	Respiration	Respiration - no subcategory	Biogenesis of cytochrome c oxid(
gsyne_282	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G(	default	234450	234639	-1	856	fig|1129.58.peg.280			
gsyne_2820	Synechococcus_assembled_mapped	cytochrome oxidase assembly family protein				PF02628.10	2458197	2459121	-1	95,112	fig|1129.58.(	Respiration	Respiration - no subcategory	Biogenesis of cytochrome c oxid(
gsyne_2821	Synechococcus_assembled_mapped	cytochrome c oxidase, subunit II	coxB	1.9.3.1	GO:0004129,GO:0055114	TIGR02866	2459306	2460140	1	112	fig|1129.58.(	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_2822	Synechococcus_assembled_mapped	cytochrome c oxidase, subunit I	ctaD	1.9.3.1	GO:0004129,GO:0055114	TIGR02891	2460136	2461804	1	112	fig|1129.58.(	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_2823	Synechococcus_assembled_mapped	cytochrome c oxidase subunit III family protein				PF00510.13	2461800	2462409	1	112	fig|1129.58.(	Respiration	Electron accepting reactions	Terminal cytochrome C oxidases
gsyne_2824	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G(	PF03729.8	2462897	2463500	-1	156	fig|1129.58.peg.2819			
gsyne_2825	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	2462523	2462910	1	165	fig|1129.58.peg.2818			
gsyne_2826	Synechococcus_assembled_mapped	riboflavin synthase, alpha subunit	ribE	2.5.1.9	GO:0004746,GO:0009231	TIGR00187	2463545	2464217	-1	85	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr(	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metab(
gsyne_2827	Synechococcus_assembled_mapped	bifunctional nuclease family protein				PF02577.9	2464287	2464833	1	185	fig|1129.58.peg.2821			



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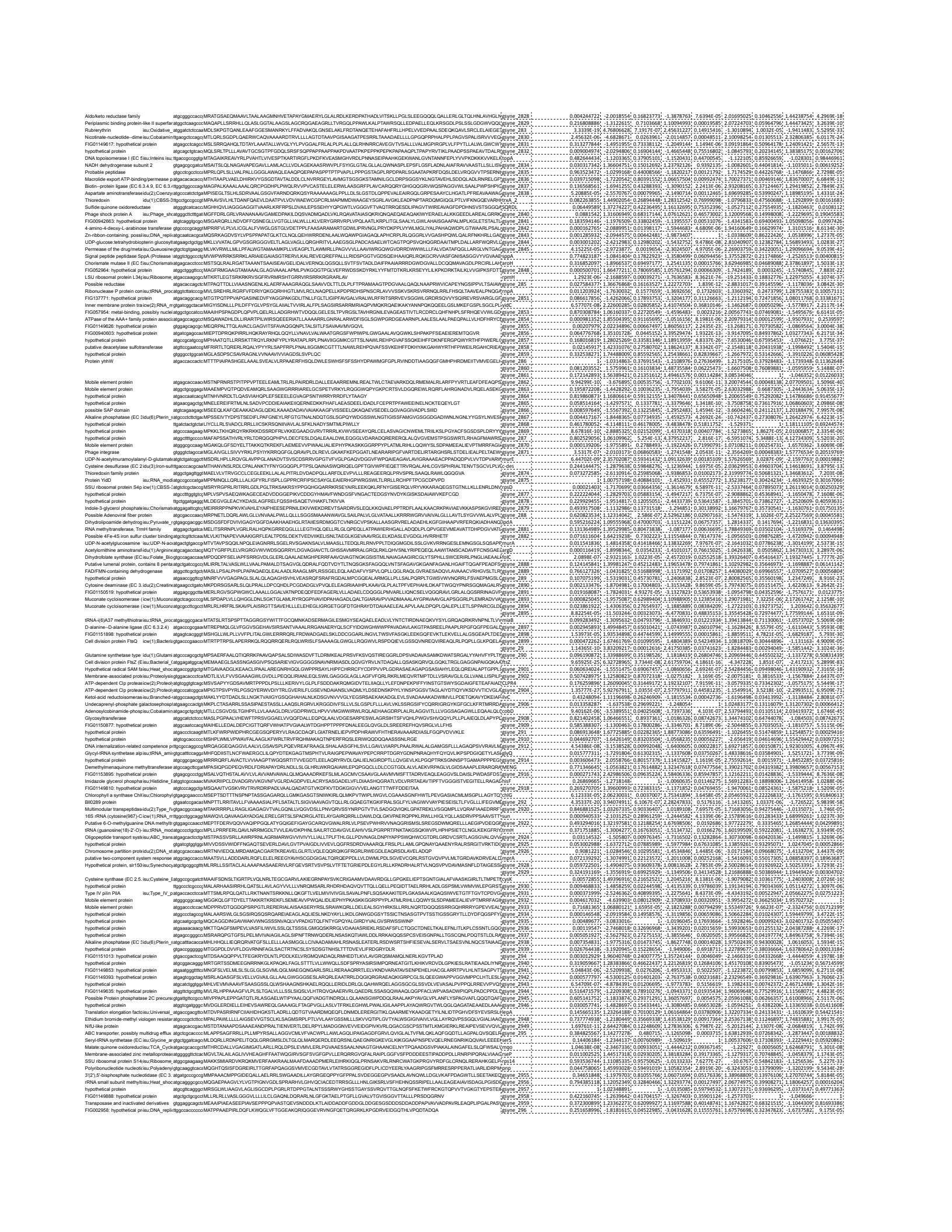
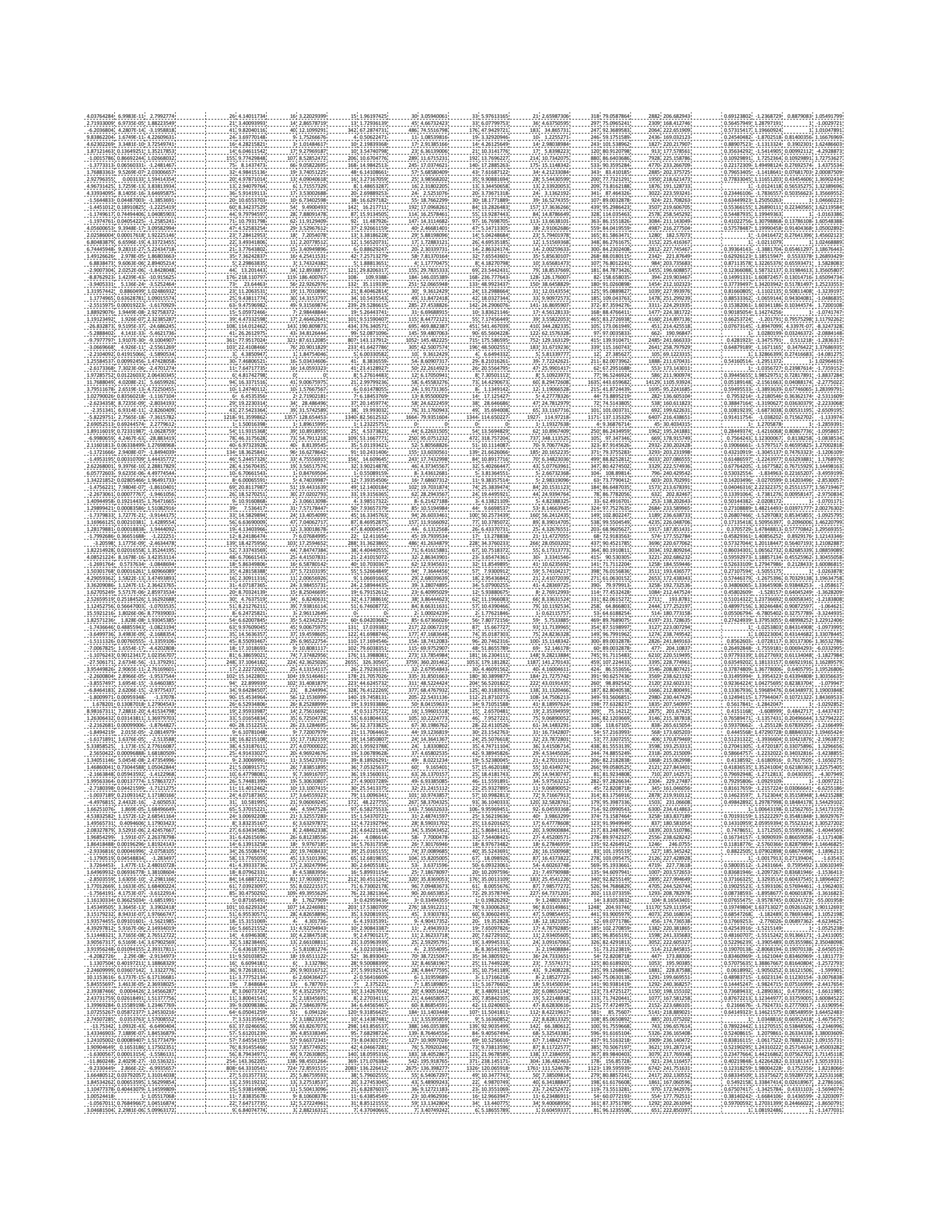
61	3.211594	45	2.81918241	35	3.72054328	56	3.63758394	53	7.53589416	49	3.36202381	21	2.13544558	86	3.23575274
38	5.85972583	23	4.22028127	14	4.35882315	35	6.65879949	21	8.74542887	35	7.03356728	19	5.65881781	43	4.73858013
37	3.4695745	33	3.68220781	41	7.76257597	29	3.35510939	18	4.55842818	47	5.74362733	23	4.16563047	72	4.82495274
24	2.83230572	16	2.24682233	8	1.90619088	21	3.05761201	6	1.91226579	15	2.30692804	11	2.50726353	32	2.69876419
15	2.65528661	14	2.9489543	3	1.07223237	15	3.27601287	7	3.34646513	7	1.61484963	8	2.73519658	16	2.02407314
57	6.52692233	35	4.768936	24	5.54871405	28	3.95572247	21	6.49413035	26	3.87990274	15	3.3174414	55	4.5007237
40	7.22828022	33	7.09592129	23	8.39170751	34	7.58032977	15	7.32039247	31	7.30046604	6	2.09413488	29	3.74506242
30	2.09431057	17	1.4121753	21	2.95996542	16	1.37807865	23	4.33626468	25	2.2744361	18	2.42700542	41	2.0454542
83	5.16083663	54	3.99535744	35	4.39397495	56	4.29599967	38	6.3810733	75	6.07739108	23	2.7621564	82	3.64369439
33	7.33948453	37	9.79204057	24	10.77731	41	11.2504442	28	16.8181325	39	11.3039474	13	5.58435968	48	7.62919877
376	39.8948016	430	54.2896174	105	22.4939268	687	89.9330651	84	24.0699877	504	69.6903914	197	40.3713342	599	45.4193967
32	3.27511458	29	3.53178598	16	3.30631339	27	3.40937268	15	4.14606299	31	4.13477722	14	2.76747029	52	3.80334688
47	6.73842982	34	5.80042251	21	6.07893724	24	4.24527948	46	17.8109384	28	5.23157897	11	3.04601437	56	5.73766188
90	6.51903351	74	6.37811411	50	7.31237107	91	8.13235428	34	6.65101212	104	9.81720694	32	4.47681444	96	4.96933198
58	6.9631599	69	9.85705833	22	5.3327174	88	13.0345259	16	5.18759993	91	14.2374978	22	5.10128359	52	4.46136537
36	3.08406623	31	3.16011399	11	1.9026609	37	3.91072351	19	4.39585049	37	4.13082523	13	2.15101262	40	2.44887862
19	3.39803689	13	2.76654476	9	3.24985894	14	3.08913378	2	0.96598993	16	3.72913729	8	2.76339448	32	4.08987975
34	3.81765479	25	3.3402395	25	5.6676792	48	6.64956398	23	6.97450985	41	5.99950607	14	3.03615672	55	4.413331
3	2.26276598	2	1.79501566	0	0	1	0.93057757	2	4.07395755	0	0	1	1.45678948	0	0
64	6.98279145	36	4.67381437	36	7.93047338	48	6.46136877	35	10.3130058	56	7.96252899	31	6.53264718	88	6.86148065
19	4.70870825	18	5.30811775	15	7.50562659	35	10.701642	11	7.36222329	31	10.0120677	8	3.82927521	26	4.6047664
41	4.00711422	28	3.2563101	28	5.52526878	28	3.3762927	21	5.54287746	45	5.73157897	13	2.45397214	56	3.91130754
68	3.84252551	20	1.34480001	17	1.93956474	32	2.23096121	36	5.49387109	28	2.06195783	14	1.52796812	77	3.10945764
182	8.25441254	177	9.55229904	126	11.5380613	178	9.96022108	82	10.0437699	202	11.9393327	63	5.51866133	327	10.5986026
64	15.860912	62	18.2835167	27	13.5101279	47	14.3707764	55	36.8111164	31	10.0120677	24	11.4878256	69	12.2203416
365	68.4537672	344	76.7684536	231	87.470978	228	52.7562029	79	40.0128696	207	50.5928025	77	27.8916127	521	69.8277882
79	7.17529806	82	8.86230246	9	1.65045192	99	11.0938488	26	6.37755658	65	7.6937862	23	4.03477297	45	2.92086471
52	9.49567759	31	6.73603246	24	8.84873872	37	8.3360159	22	10.8495922	23	5.47349033	13	4.58505321	47	6.13347427
117	10.6545989	124	13.4367052	55	10.1125678	144	16.1788604	59	14.5101323	156	18.5135517	68	11.9602034	167	10.868104
282	19.2602364	296	24.0560367	247	34.0609669	155	13.0610592	196	36.1523635	178	15.8433279	178	23.4806935	690	33.6781068
176	14.0056219	219	20.7373713	132	21.2085596	165	16.1997334	111	23.8550771	168	17.4225978	125	19.2122466	388	22.0651827
39	2.96090603	49	4.42665788	21	3.21904335	50	4.68343196	27	5.53594669	25	2.47351147	13	1.90625845	58	3.14683582
23	6.4355011	35	11.6531259	10	5.64939636	22	7.5947137	11	8.31218758	20	7.2928693	12	6.48506286	25	4.99897097
24	4.24845858	19	4.00215227	7	2.50187553	13	2.83921115	10	4.78066447	14	3.22969926	4	1.36759829	29	3.66863257
74	17.4658853	56	15.7277563	54	25.7335769	41	11.9392469	20	12.7484386	56	17.2250627	21	9.57318803	96	16.1925851
38	5.75737254	31	5.58884789	28	8.565373	30	5.60784735	21	8.59267029	26	5.13367044	17	4.97471343	54	5.84683137
35	2.52463841	22	1.8883117	11	1.60203257	19	1.69090394	23	4.48050633	21	1.97407813	13	1.81114368	24	1.23716737
7	1.42029366	12	2.89721826	5	2.04831915	8	2.00264646	2	1.09591841	4	1.05767929	6	2.35130934	6	0.86999635
29	3.30979147	27	3.66679186	17	3.91741037	21	2.95703267	32	9.86326565	29	4.31334835	23	5.07001077	38	3.099362
25	2.90098203	30	4.14234384	16	3.74862956	20	2.86331559	12	3.7605762	15	2.26835065	11	2.46533605	42	3.48289509
96	4.84126675	114	6.84088818	63	6.4146925	122	7.59069958	49	6.67347407	108	7.09782744	58	5.6492941	181	6.52307584
4	1.3092734	1	0.38948453	0	0	7	2.82684884	12	10.6076631	3	1.27969216	1	0.63219166	2	0.46782823
32	2.53484895	40	3.77035253	18	2.87887047	33	3.22515239	19	4.06465628	39	4.02606346	16	2.44793849	36	2.03793666
33	3.06959675	26	2.87779991	33	6.19767558	35	4.0167021	44	11.0532039	32	3.8791026	14	2.51520758	76	5.05204315
22	3.2481123	11	1.93250622	14	4.17334131	12	2.18586731	17	6.77837192	23	4.42537516	12	3.42190551	31	3.27081607
7	2.4046556	7	2.8613616	8	5.54871405	3	1.27148222	5	4.63866454	2	0.89536217	4	2.65395312	6	1.47296412
24	6.66158305	16	5.28452611	23	12.8896627	21	7.19150344	10	7.49608189	13	4.70244212	8	4.28878824	31	6.14913421
26	11.869597	15	8.14842636	1	0.92174362	9	5.06919886	1	1.23290821	2	1.1898892	3	2.64522301	6	1.95749179
24	9.57124001	8	3.79635497	10	8.0520132	12	5.90435422	5	5.3851163	12	6.23666064	11	8.47282159	20	5.69997609
33	7.33948453	14	3.70509643	6	2.6943275	14	3.84161509	9	5.40582829	10	2.89844805	6	2.57739678	20	3.17883282
35	19.9073947	16	10.828947	8	9.18721507	10	7.01747018	8	12.2886588	11	8.15366699	8	8.78850048	16	6.50357928
5	2.06522292	8	3.93193907	3	2.50187553	7	3.56721401	2	2.23097675	5	2.69141605	3	2.39329701	9	2.656596
25	6.15172784	19	5.56327549	19	9.43970059	18	5.46466827	20	13.2909253	15	4.81019039	13	6.1784405	45	7.91326468
5	2.31304967	3	1.65141441	2	1.86806706	7	3.99527969	3	3.74804095	1	0.6028772	2	1.7869951	0	0
38	23.1304967	28	20.2805278	48	58.9915915	13	9.7629015	30	49.3163282	20	15.8651894	23	27.0400574	54	23.4899015
19	2.76982839	14	2.4285506	21	6.18110425	25	4.49648825	11	4.33071958	19	3.60966388	6	1.68938612	30	3.12540706
40	4.90399223	22	3.20946263	11	2.72288927	34	5.14283857	14	4.63538633	36	5.7518319	10	2.36792637	28	2.45320526
82	5.2011903	61	4.60403469	56	7.17173827	79	6.18230143	38	6.5093947	80	6.61291256	34	4.16529936	171	7.75123806
9	1.77421424	7	1.64203137	6	2.38815392	9	2.18897223	9	4.79152962	20	5.13815791	8	3.04601437	12	1.69056109
46	3.12329603	34	2.74697113	23	3.15304861	39	3.26703749	24	4.40083086	36	3.18545681	16	2.09823299	47	2.28054816
51	4.54879948	33	3.50235704	18	3.24150454	35	3.85149071	35	8.43068336	33	3.83578678	30	5.16804495	35	2.23090324
15	1.52620579	15	1.81607157	3	0.61629779	9	1.12979212	16	4.39652897	11	1.45857386	14	2.75123879	11	0.79983536
297	11.6700298	248	11.5954353	184	14.5975795	270	13.0892111	155	16.4480846	331	16.9495202	114	8.65164671	575	16.1461667
21	2.00719186	13	1.47853907	5	0.96491067	10	1.1792443	12	3.0975545	11	1.37017544	4	0.73842773	14	0.95627698
25	4.19030737	19	3.78947751	9	3.04576152	14	2.89513021	11	4.97928145	22	4.80554286	16	5.17969594	33	3.95280951
178	74.4077424	196	97.4931398	31	26.1641923	118	60.8575306	11	12.418208	46	25.0593533	19	15.3401688	41	12.2480812
54	4.82878926	61	6.49073963	75	13.5410789	99	10.9222944	47	11.3503817	89	10.3716631	42	7.25391052	221	14.122866
534	171.551184	518	198.01682	227	147.240008	491	194.611342	92	79.8193905	490	205.145712	109	67.6328006	639	146.703135
58	5.73320003	46	5.41061701	23	4.59033573	36	4.39041724	22	5.87299863	34	4.37987706	19	3.62744732	83	5.86318054
20	3.32016699	10	1.97537609	14	4.69251296	19	3.89150619	12	5.37996308	18	3.89418284	9	2.88569783	29	3.44044012
48	10.0325046	45	11.1918145	9	3.79802792	42	10.8305775	10	5.64463998	28	7.6267597	2	0.8073773	31	4.63037215
17	15.5217807	27	29.3343349	9	16.5913851	34	38.3006136	4	9.86326565	8	9.51911361	4	7.05392802	8	5.21997811
15	3.97279523	5	1.57577711	7	3.74326415	9	2.94090926	5	3.57637495	5	1.7257935	4	2.04617759	10	1.89274015
13	1.86382101	4	0.68240265	1	0.2894732	7	1.23820652	7	2.71036019	5	0.93421053	11	3.04601437	3	0.30737474
25	2.44336233	12	1.39556147	10	1.97331028	9	1.08523694	11	2.903412	14	1.7831579	7	1.32136962	21	1.46674033
48	3.62042557	37	3.32077898	19	2.89347344	39	3.62925252	26	5.29614482	29	2.85056065	18	2.62222107	51	2.74899934
2991	1673.78989	1540	1025.47508	1299	1467.71317	1562	1078.44935	549	829.707451	2561	1867.70383	385	416.124867	2020	807.833708
37	3.54625018	42	4.79001417	23	4.45085039	34	4.0205064	60	15.5305564	41	5.12112535	30	5.55350687	67	4.58911059
19	4.14603243	15	3.89484531	8	3.52465484	25	6.73059247	33	19.4473823	19	5.40314467	9	3.79314997	20	3.11885484
13	2.24400341	7	1.43779862	5	1.74259987	6	1.277808	11	5.12791672	8	1.79963342	2	0.66678922	7	0.86350384
87	35.5121155	73	35.4568388	45	37.0866255	71	35.7560746	28	30.8662196	48	25.5336224	28	22.0746453	63	18.3773935
72	16.3274094	65	17.5395321	70	32.0501702	63	17.6262339	34	20.8224497	54	15.958514	23	10.0737469	127	20.5813843
31	7.68262926	16	4.71832689	15	7.50562659	34	10.3958808	11	7.36222329	12	3.87563911	11	5.26525342	31	5.4902984
60	4.76371785	39	3.68450583	33	5.29000684	41	4.01617687	25	5.36047046	29	3.00059016	24	3.68031027	90	5.10650032
10	5.10231545	11	6.67851416	2	2.06036808	18	11.3311504	3	4.13386869	3	1.99481425	2	1.97095048	14	5.10483153
40	2.64348534	33	2.59507979	18	2.40180051	28	2.28301697	33	5.88977863	27	2.32538347	17	2.16992262	50	2.36141867
21	1.42864833	21	1.69998542	18	2.4724417	29	2.43409897	40	7.34909989	20	1.77316822	12	1.57676038	33	1.60437562
66	7.29273622	79	10.3870811	80	17.8477745	53	7.22531245	45	13.4284907	78	11.2319478	31	6.61586561	127	10.0285089
17	1.73478725	15	1.82141295	15	3.09055213	20	2.51803342	26	7.1653724	35	4.65456658	16	3.15352076	31	2.26071111
1	0.80687779	0	0	0	0	0	0	1	2.17909357	0	0	0	0	0	0
16	1.44190109	10	1.07234702	3	0.54586375	12	1.3342307	10	2.43379282	9	1.05699249	3	0.52217389	17	1.09483956
36	4.1634894	40	5.5047147	32	7.47226825	31	4.42334537	29	9.05776562	34	5.12445616	27	6.03110846	55	4.54573093
21	11.0395552	21	13.136251	5	5.3070087	11	7.13442802	12	17.0365498	6	4.11052633	4	4.0613525	5	1.87840121
45	4.28930914	37	4.19658882	28	5.38865499	27	3.17521247	20	5.14840789	37	4.59611049	13	2.39329701	63	4.29142431
94	8.74369982	61	6.75176133	66	12.3953512	93	10.6729513	71	17.8358517	81	9.81897845	34	6.10836126	130	8.64165276
45	3.99311644	43	4.54033374	34	6.09152303	48	5.25502627	26	6.23075861	57	6.59156013	22	3.77051396	85	5.39019478
1	0.75425533	1	0.89750783	0	0	2	1.86115514	0	0	0	0	0	0	3	1.61705844
22	10.6014777	25	14.3351945	11	10.7024676	27	16.052463	7	9.10982174	21	13.1879387	5	4.65363307	15	5.16560333
431	72.2408991	551	109.894848	340	115.062102	799	165.229217	264	119.502755	747	163.170024	332	107.478691	660	79.0561902
58	7.73982005	43	6.82796342	31	8.35241523	41	6.75026651	34	12.2532108	28	4.86939273	21	5.41253323	63	6.00799403
33	3.21617861	26	3.01522294	21	4.13231127	32	3.8477814	22	5.7905127	30	3.81031935	14	2.63531581	39	2.71629479
1140	247.207183	1184	305.511666	634	277.58309	1328	355.294515	311	182.131365	1292	365.117501	369	154.547154	1296	200.838658
43	38.254283	53	56.105746	13	23.3508383	48	52.6850069	10	24.0259035	11	12.7531714	13	22.3374387	17	10.8080316
16	2.92174695	9	1.95562233	3	1.10609234	16	3.60476363	8	3.94530626	15	3.5696676	6	2.11617841	15	1.95749179
49	2.98785854	43	3.11998329	33	4.06279963	31	2.33216804	40	6.58706669	27	2.14556471	20	2.35544169	68	2.96318617
9	2.60218088	7	2.40831268	4	2.33508383	4	1.4268856	6	4.68505118	14	5.27517546	5	2.79217984	8	1.65299307
58	8.74936179	51	9.15457988	35	10.6601653	60	11.1669308	15	6.11093633	35	6.88066364	13	3.78765265	76	8.19309607
67	13.8369936	58	14.2532791	42	17.5131287	86	21.9128861	33	18.4055582	45	12.1113722	30	11.966485	95	14.0209233
111	12.3833688	85	11.2837801	97	21.8491767	139	19.132196	58	17.474789	162	23.5529194	93	20.0390528	294	23.439548
90	7.92542399	90	9.43066605	34	6.04514088	49	5.32365949	23	5.46985671	52	5.96756615	19	3.2315584	88	5.53794632
129	11.7782924	142	15.4276873	66	12.1670157	203	22.8677193	67	16.52097	191	22.7268837	56	9.87549923	145	9.46121032
43	5.3093133	20	2.9384598	15	3.73945809	31	4.72243278	24	8.0029344	37	5.95368049	20	4.76955987	51	4.50014127
32	4.37111748	35	5.68892759	21	5.79174336	34	5.73001306	21	7.74693503	31	5.51846252	8	2.11062413	69	6.73562135
3	2.60218088	1	1.03213401	0	0	0	0	0	0	0	0	0	0	1	0.6198724
40	2.5892347	24	1.84859822	24	3.13667977	35	2.79520501	26	4.54519891	28	2.36201886	18	2.2504136	44	2.03540191
66	8.41882049	61	9.25884917	33	8.49901835	55	8.65573988	38	13.0905842	52	8.64419508	26	6.40558905	114	10.3919785
16	1.83818517	16	2.18730385	7	1.62373379	6	0.85046162	6	1.86160974	18	2.69498084	4	0.88758035	10	0.82102305
25	3.80435801	9	1.62968527	5	1.53623936	12	2.25297727	31	12.7400515	9	1.7848338	6	1.76348201	12	1.30499453
19	2.22709174	14	1.95268596	6	1.41998341	10	1.44616784	11	3.48213264	7	1.06929232	3	0.67917888	8	0.67013232
19	2.36279267	15	2.21964302	3	0.75325285	16	2.45485695	7	2.35092174	23	3.72746653	12	2.88225016	19	1.68854131
154	23.6422333	138	25.2096448	76	23.5574829	171	32.3890405	48	19.9011024	170	34.0118772	56	16.6048217	171	18.7607399
38	3.55374208	29	3.22715754	14	2.64349113	19	2.19225012	23	5.80895834	32	3.9000142	11	1.98688808	39	2.60647155
20	2.7646012	10	1.64483507	8	2.23274948	15	2.55816144	11	4.10641936	17	3.062424	9	2.40283206	32	3.16110228
155	63.2687115	76	36.9139692	86	70.8766621	89	44.8209949	28	30.8662196	102	54.2589476	24	18.9211246	118	34.4211497
114	7.11387578	87	6.46011932	102	12.8513606	254	19.5555185	93	15.673013	214	17.4031996	92	11.0883689	387	17.2583179
23	13.5254599	30	20.9925561	7	8.31131532	37	26.844797	1	1.58815294	15	11.4955397	5	5.67900985	8	3.3620198
28	4.20554485	23	4.11066357	10	3.0325764	40	7.41239275	20	8.11264274	26	5.08922308	12	3.48115928	37	3.97147685
21	4.95653501	22	6.1787614	16	7.62476352	30	8.73603431	6	3.82453158	27	8.30494096	10	4.55866097	36	6.07221943
54	6.48294198	39	5.57138079	27	6.54469862	64	9.47965522	14	4.53914993	34	5.31950466	15	3.4781479	70	6.00568415
53	5.40845437	41	4.97852874	22	4.53280979	63	7.93180527	34	9.37010237	47	6.25041798	22	4.33609105	68	4.9589792
68	7.28182303	83	10.576188	60	12.9726879	81	10.701642	32	9.25442209	77	10.7457278	45	9.30726614	147	11.2495362
32	17.6232356	18	11.7958172	7	7.78361276	24	16.3072641	4	5.94927134	7	5.02397663	2	2.12737512	17	6.69068622
66	7.43480251	52	6.97025563	45	10.2349454	36	5.00336511	23	6.99715436	39	5.72537596	15	3.26358683	64	5.15218618
78	9.73477738	62	9.20752638	53	13.3553356	78	12.010476	46	15.5044859	81	13.1743848	34	8.1957509	136	12.1298772
143	8.92354593	119	8.83625516	90	11.3394359	85	6.54416959	73	12.3024725	108	8.78292317	65	7.83417366	240	10.7028328
37	6.32385501	18	3.66077086	30	10.3525884	36	7.59131257	9	4.15423258	23	5.12297124	17	5.61186884	39	4.76355145
58	10.0117075	51	10.4753899	51	17.7745187	47	10.009496	44	20.5116669	39	8.77321292	44	14.6693628	138	17.0233614
34	9.14461497	26	8.32108036	16	8.68868402	16	5.30934178	12	8.71637429	15	5.25764996	7	3.63632724	48	9.22600781
17	2.63315922	13	2.39602537	7	2.18914109	5	0.95550375	10	4.18308141	13	2.62413065	6	1.79497276	24	2.656596
37	7.05353058	15	3.40263958	21	8.08298249	16	3.76321478	12	6.17808947	23	5.71408331	16	5.89119263	32	4.35954215

gsyne_2828	Synechococcus_assembled_mapped	aldo/keto reductase family protein					PF00248.16	2464885	2465959	1	703	fig|1129.58.peg.2822				
gsyne_2829	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_B	2465970	2467026	-1	156	fig|1129.58.peg.2823				
gsyne_283	Synechococcus_assembled_mapped	rubrerythrin family protein					PF02915.12	234719	235433	1	157	fig|1129.58.p	Stress Response	Oxidative stress	Oxidative stress	
gsyne_2830	Synechococcus_assembled_mapped	phosphoribosyltransferase family protein					PF02277.12	2467052	2468162	-1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Cobalamin synthesis	
gsyne_2831	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF09991.4	2468158	2468797	-1	156	fig|1129.58.peg.2825				
gsyne_2832	Synechococcus_assembled_mapped	putative translation initiation factor IF-2				GO:0006413,GO:0003743	UniRef100_B	2468793	2469189	-1	92,169	fig|1129.58.peg.2826				
gsyne_2833	Synechococcus_assembled_mapped	DNA topoisomerase I	topA	5.99.1.2		GO:0003677,GO:0003917,GO	TIGR01051	2469188	2471900	-1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA topoisomerases, Type I, ATI	
gsyne_2834	Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, chain N family protein					TIGR01770	2472018	2473593	1	112	fig|1129.58.peg.2828				
gsyne_2835	Synechococcus_assembled_mapped	peptidase M23 family protein					PF01551.17	2474299	2475397	-1	138	fig|1129.58.peg.2830				
gsyne_2836	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	2473616	2474303	1	141	fig|1129.58.peg.2829				
gsyne_2837	Synechococcus_assembled_mapped	biotin--[acetyl-CoA-carboxylase] ligase		6.3.4.15		GO:0004077,GO:0006464	TIGR00121	2475400	2476156	-1	140	fig|1129.58.peg.2831				
gsyne_2838	Synechococcus_assembled_mapped	putative N-succinyldiaminopimelate aminotransferase				GO:0009058,GO:0008483,GO	UniRef100_C	2476137	2477178	-1	141,703	fig|1129.58.p	Amino Acids and Derivatives	Glutamine, glutamate, aspartat	Glutamine, Glutamate, Aspartate	
gsyne_2839	Synechococcus_assembled_mapped	thioredoxin	trxA			GO:0005737,GO:0015036,GO	TIGR01068	2477344	2477665	-1	112	fig|1129.58.peg.2833				
gsyne_284	Synechococcus_assembled_mapped	sulfide:quinone oxidoreductase, mitoch	SQRDL	1.-.-.-		GO:0016491	UniRef100_C	235581	236811	1	703	fig|1129.58.peg.282				
gsyne_2840	Synechococcus_assembled_mapped	putative membrane-associated 30 kDa protein, chloroplastic				GO:0009508,GO:0016050,GO	UniRef100_C	2477697	2478465	-1	92	fig|1129.58.peg.2834				
gsyne_2841	Synechococcus_assembled_mapped	mechanosensitive ion channel family protein					PF00924.13	2478561	2479686	1	141	fig|1129.58.peg.2835				
gsyne_2842	Synechococcus_assembled_mapped	dolichyl-phosphate-mannose--mannosyltransferase family protein					PF13231.1	2480218	2481994	1	703	fig|1129.58.peg.2837				
gsyne_2843	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF05258.7	2479685	2480225	1	156	fig|1129.58.peg.2836				
gsyne_2844	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein					PF00534.15	2482042	2483119	-1	90	fig|1129.58.peg.2838				
gsyne_2845	Synechococcus_assembled_mapped	eamA-like transporter family protein					PF00892.15	2483115	2484066	-1	141	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth	
gsyne_2846	Synechococcus_assembled_mapped	signal peptide peptidase SppA, 36K type	sppA	3.4.-.-		GO:0006465,GO:0008981	TIGR00706	2484128	2484941	1	138	fig|1129.58.peg.2840				
gsyne_2847	Synechococcus_assembled_mapped	chorismate mutase	aroH	5.4.99.5		GO:0004106,GO:0009073	TIGR01796	2484937	2485309	1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate Synthesis	
gsyne_2848	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF10989.3	2485431	2486001	1	156	fig|1129.58.peg.2842				
gsyne_2849	Synechococcus_assembled_mapped	ribosomal protein L34	rpmH			GO:0000315,GO:0003735,GO	TIGR01030	2486058	2486196	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial	
gsyne_285	Synechococcus_assembled_mapped	NADPH-dependent FMN reductase family protein					PF03358.10	236870	237398	1	112	fig|1129.58.peg.283				
gsyne_2850	Synechococcus_assembled_mapped	ribonuclease P protein component	rnpA	3.1.26.5		GO:0004526,GO:0006396	TIGR00188	2486281	2486632	1	166	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA processing	
gsyne_2851	Synechococcus_assembled_mapped	bacterial PH domain protein					PF03703.9	2486628	2487081	1	157	fig|1129.58.peg.2845				
gsyne_2852	Synechococcus_assembled_mapped	membrane insertase, YidC/Oxa1 family	yidC			GO:0003674,GO:0031224,GO	TIGR03592	2487136	2488273	1	88	fig|1129.58.peg.2846				
gsyne_2853	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF02620.12	2488322	2488829	1	156	fig|1129.58.peg.2847				
gsyne_2854	Synechococcus_assembled_mapped	ATPase associated with various cellular activities family protein					PF00004.24	2488825	2490316	1	157	fig|1129.58.peg.2848				
gsyne_2855	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	2490409	2490571	1	88	fig|1129.58.peg.2849				
gsyne_2856	Synechococcus_assembled_mapped	2TM domain protein					PF13239.1	2490585	2490852	1	157	fig|1129.58.peg.2850				
gsyne_2857	Synechococcus_assembled_mapped	sulfotransferase domain protein					PF00685.22	2490992	2491784	1	703	fig|1129.58.peg.2851				
gsyne_2858	Synechococcus_assembled_mapped	sulfotransferase domain protein					PF00685.22	2491825	2492611	1	703	fig|1129.58.peg.2852				
gsyne_2859	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2493462	2493579	-1	856	fig|1129.58.peg.2853				
gsyne_286	Synechococcus_assembled_mapped	putative quercetin 2,3-dioxygenase	yhhW			GO:0046872,GO:0005515,GO	UniRef100_P	237484	238171	1	141,703	fig|1129.58.peg.284				
gsyne_2860	Synechococcus_assembled_mapped	transposase family protein					PF01527.15	2494179	2494425	-1	154					
gsyne_2861	Synechococcus_assembled_mapped	putative carbamoyl-phosphate synthase L chain domain protein				GO:0009279,GO:0016021	UniRef100_C	2493982	2494195	1	703					
gsyne_2862	Synechococcus_assembled_mapped	isftB-like ATP binding family protein					PF01695.12	2494491	2495475	-1	154	fig|1129.58.peg.2855				
gsyne_2863	Synechococcus_assembled_mapped	integrase core domain protein					PF00665.21	2495516	2496887	-1	157	fig|1129.58.peg.2856				
gsyne_2864	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2497204	2497363	1	856	fig|1129.58.peg.2857				
gsyne_2865	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2497822	2498080	-1	856	fig|1129.58.peg.2859				
gsyne_2866	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein					TIGR03798	2497559	2497826	1	157	fig|1129.58.peg.2858				
gsyne_2867	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2498197	2500477	-1	856	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2868	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	2501279	2501393	-1	88	fig|1129.58.peg.2861				
gsyne_2869	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2502125	2502899	-1	856	fig|1129.58.peg.2862				
gsyne_287	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_B	238250	238538	1	156	fig|1129.58.peg.285				
gsyne_2870	Synechococcus_assembled_mapped	transposase DDE domain protein					PF01609.16	2503126	2504107	1	154	fig|1129.58.peg.2863				
gsyne_2871	Synechococcus_assembled_mapped	phage integrase family protein					PF00589.17	2504599	2505847	-1	132,152	fig|1129.58.peg.2865				
gsyne_2872	Synechococcus_assembled_mapped	UDP-N-acetylmuramyl-tripeptide synth	murE				TIGR01085	2507077	2508577	-1	89	fig|1129.58.peg.2867				
gsyne_2873	Synechococcus_assembled_mapped	L-cysteine/cystine lyase C-DES	c-des			GO:0016829,GO:0030170	UniRef100_C	2505929	2507081	1	141,703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_2874	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF05768.9	2508698	2508953	-1	156	fig|1129.58.peg.2868				
gsyne_2875	Synechococcus_assembled_mapped	putative membrane protein insertion efficiency factor					TIGR00278	2508952	2509180	-1	156	fig|1129.58.peg.2869				
gsyne_2876	Synechococcus_assembled_mapped	ribosomal protein S4	rpsD			GO:0000314,GO:0003735,GO	TIGR01017	2509377	2509944	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial	
gsyne_2877	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2510024	2510264	-1	856	fig|1129.58.peg.2871				
gsyne_2878	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2510384	2510525	-1	856	fig|1129.58.peg.2872				
gsyne_2879	Synechococcus_assembled_mapped	indole-3-glycerol phosphate synthase family protein					PF00218.16	2510514	2511399	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn	
gsyne_288	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	238537	238924	1	88	fig|1129.58.peg.286				
gsyne_2880	Synechococcus_assembled_mapped	dihydrolipoyl dehydrogenase	lpdA	1.8.1.4		GO:0004148,GO:0005624,GO	TIGR01350	2511403	2512846	-1	703	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	TCA Cycle	
gsyne_2881	Synechococcus_assembled_mapped	RNA 2'-O ribose methyltransferase substrate binding family protein					PF08032.7	2512881	2513667	-1	168	fig|1129.58.peg.2875				
gsyne_2882	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_C	2513666	2513915	-1	156	fig|1129.58.peg.2876				
gsyne_2884	Synechococcus_assembled_mapped	UDP-N-acetylglucosamine 1-carboxyvin	murA	2.5.1.7		GO:0008760,GO:0009252	TIGR01072	2514295	2515585	1	89	fig|1129.58.p	Cell Wall and Capsule	Cell Wall and Capsule - no sut	UDP-N-acetylmuramate from Fru	
gsyne_2886	Synechococcus_assembled_mapped	transaminase, acetylornithine/succinyl	argD				TIGR00707	2515734	2516946	1	185	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis -- gjo	
gsyne_2887	Synechococcus_assembled_mapped	bifunctional FolC family protein	folC	6.3.2.-		GO:0004326,GO:0005737,GO	TIGR01499	2516915	2518139	1	78	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gro	Folate and pterines	Folate Biosynthesis	
gsyne_2888	Synechococcus_assembled_mapped	pentapeptide repeats family protein					PF13599.1	2518159	2518684	1	185	fig|1129.58.peg.2880				
gsyne_2889	Synechococcus_assembled_mapped	FAD binding domain protein					PF01565.18	2518696	2520094	-1	157	fig|1129.58.peg.2881				
gsyne_289	Synechococcus_assembled_mapped	FAD binding domain protein					PF01494.14	241192	242377	-1	157	fig|1129.58.peg.288				
gsyne_2890	Synechococcus_assembled_mapped	amidohydrolase family protein					PF07969.6	2520102	2521404	-1	703	fig|1129.58.p	Amino Acids and Derivatives	Amino Acids and Derivatives -	Creatine and Creatinine Degrada	
gsyne_2891	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF14271.1	2521393	2521786	-1	156	fig|1129.58.peg.2883				
gsyne_2893	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_C	2521961	2523038	-1	141	fig|1129.58.p	Miscellaneous	Miscellaneous - no subcategor	Muconate lactonizing enzyme far	
gsyne_2894	Synechococcus_assembled_mapped	mandelate racemase / muconate lactonizing enzyme, C-terminal domain protein					PF01188.16	2523037	2524099	-1	184	fig|1129.58.p	Miscellaneous	Miscellaneous - no subcategor	Muconate lactonizing enzyme far	
gsyne_2895	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2524081	2524300	1	856					
gsyne_2896	Synechococcus_assembled_mapped	N-(4-(6)A37 (6)isopentenyltransferase enzyme N-mia	miaB	2.-.-.-		GO:0006400,GO:0016782,GO	TIGR01574	2524299	2525694	1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA processing	
gsyne_2897	Synechococcus_assembled_mapped	D-alanine--D-alanine ligase family protein		6.3.2.4		GO:0008716,GO:0009252	TIGR01205	2525762	2526842	1	89	fig|1129.58.peg.2887				
gsyne_2898	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2526838	2527249	1	156	fig|1129.58.peg.2888				
gsyne_2899	Synechococcus_assembled_mapped	POTRA domain, FtsQ-type family protein					PF08478.5	2527245	2528145	1	157	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton	
gsyne_29	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	24004	24184	1	856					
gsyne_290	Synechococcus_assembled_mapped	glutamine synthetase, catalytic domain protein					PF00120.19	239027	241196	1	73	fig|1129.58.p	Amino Acids and Derivatives	Glutamine, glutamate, aspartat	Glutamine, Glutamate, Aspartate	
gsyne_2900	Synechococcus_assembled_mapped	cell division protein FtsZ	ftsZ			GO:0000910,GO:0003924	TIGR00065	2528275	2529418	1	93	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton	
gsyne_2901	Synechococcus_assembled_mapped	radical SAM superfamily protein					PF04055.16	2530375	2531683	-1	703	fig|1129.58.p	Stress Response	Heat shock	Heat shock dnaK gene cluster ex	
gsyne_2902	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_P	2531681	2532833	1	141	fig|1129.58.p	Protein Metabolism	Protein degradation	Proteolysis in bacteria, ATP-depe	
gsyne_2903	Synechococcus_assembled_mapped	ATP-dependent Clp protease proteolyti	CLPR4			GO:0004252,GO:0006508,GO	UniRef100_C	2532864	2533566	1	189,703	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria	
gsyne_2904	Synechococcus_assembled_mapped	clp protease family protein					PF00574.18	2533640	2534243	1	138	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria	
gsyne_2905	Synechococcus_assembled_mapped	ketol-acid reductoisomerase	ilvC	1.1.1.86		GO:0004455,GO:0009097,GO	TIGR00465	2534303	2535299	1	74	fig|1129.58.p	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios	
gsyne_2906	Synechococcus_assembled_mapped	bacterial sugar transferase family protein					PF02397.11	2536469	2537150	-1	90	fig|1129.58.peg.2899				
gsyne_2907	Synechococcus_assembled_mapped	cobalamin biosynthesis protein CobD	cobD	6.3.1.10		GO:0009236,GO:0016880	TIGR00380	2535378	2536476	1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Cobalamin synthesis	
gsyne_2908	Synechococcus_assembled_mapped	glycosyl transferases group 1 family protein					PF00534.15	2537225	2538350	-1	90	fig|1129.58.peg.2900				
gsyne_2909	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_D	2538538	2538781	1	156	fig|1129.58.peg.2901				
gsyne_291	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	242475	242727	1	156	fig|1129.58.peg.289				
gsyne_2910	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2538798	2538981	1	156	fig|1129.58.peg.2902				
gsyne_2912	Synechococcus_assembled_mapped	comEC/Rec2-related domain protein					TIGR00360	2539194	2540628	-1	157	fig|1129.58.peg.2903				
gsyne_2913	Synechococcus_assembled_mapped	glycine--tRNA ligase, alpha subunit	glyQ	6.1.1.14		GO:0004820,GO:0006426,GO	TIGR00388	2541925	2542795	-1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Glycyl-tRNA synthetase	
gsyne_2914	Synechococcus_assembled_mapped	lysM domain protein					PF01476.15	2541260	2541929	1	90	fig|1129.58.peg.2904				
gsyne_2915	Synechococcus_assembled_mapped	2-phytyl-1,4-naphtoquinone methyltra	MENG			GO:0042372,GO:0009507	UniRef100_C	2543038	2543755	-1	92,703	fig|1129.58.peg.2906				
gsyne_2916	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2543723	2543987	-1	156	fig|1129.58.peg.2907				
gsyne_2917	Synechococcus_assembled_mapped	imidazoleglycerol phosphate synthase,	hisF			GO:0000105,GO:0000107	TIGR00735	2544070	2544844	-1	161	fig|1129.58.p	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis	
gsyne_2918	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11061.3	2544971	2545136	1	156	fig|1129.58.peg.2909				
gsyne_2919	Synechococcus_assembled_mapped	chlorophyll synthase ChlG	chlG	2.5.1.62		GO:0016767,GO:0046408	TIGR02056	2545149	2546157	1	191	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_292	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF03729.8	242736	243237	-1	156	fig|1129.58.peg.290				
gsyne_2920	Synechococcus_assembled_mapped	penicillin-binding , 1A family protein					TIGR02074	2546153	2548223	1	89	fig|1129.58.p	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus	
gsyne_2921	Synechococcus_assembled_mapped	ribosomal RNA small subunit methyltra	sun	2.1.1.-		GO:0000154,GO:0016434	TIGR00563	2548233	2549598	-1	168	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation	
gsyne_2922	Synechococcus_assembled_mapped	6-O-methylguanine DNA methyltransferase, DNA binding domain protein					PF01035.15	2549594	2549951	-1	157	fig|1129.58.peg.2913				
gsyne_2923	Synechococcus_assembled_mapped	tRNA guanosine-2'-O-methyltransferas	trmH	2.1.1.34		GO:0003723,GO:0009020,GO	UniRef100_P	2550013	2550709	1	141,703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation	
gsyne_2924	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein					PF00528.17	2550712	2551537	-1	141	fig|1129.58.p	Membrane Transport	ABC transporters	ABC transporter oligopeptide (TC	
gsyne_2925	Synechococcus_assembled_mapped	PIN domain protein					PF01850.16	2551609	2551999	-1	157	fig|1129.58.peg.2916				
gsyne_2926	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF09957.4	2551995	2552214	-1	156	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	DNA structural proteins, bacterial	
gsyne_2927	Synechococcus_assembled_mapped	response regulator	mprA			GO:0003677,GO:0006355,GO	UniRef100_A	2552333	2553053	1	##########	fig|1129.58.peg.2918				
gsyne_2928	Synechococcus_assembled_mapped	alpha/beta hydrolase family protein					PF12697.7	2553392	2554988	-1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental	
gsyne_2929	Synechococcus_assembled_mapped	response regulator					PF00072.19	2553049	2553430	1	699					
gsyne_293	Synechococcus_assembled_mapped	cysteine synthase A	cysK	2.5.1.47		GO:0004124,GO:0006535	TIGR01139	243335	244313	1	75	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis	
gsyne_2930	Synechococcus_assembled_mapped	HAMP domain protein					PF00672.20	2555061	2556543	-1	129	fig|1129.58.peg.2920				
gsyne_2931	Synechococcus_assembled_mapped	prepilin-type N-terminal cleavage/methylation domain protein					TIGR02532	2556696	2557173	1	91,97	fig|1129.58.p	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus	
gsyne_2932	Synechococcus_assembled_mapped	transposase DDE domain protein					PF01609.16	2557330	2558311	1	154	fig|1129.58.peg.2922				
gsyne_2933	Synechococcus_assembled_mapped	integrase core domain protein					PF00665.21	2559610	2561236	-1	157	fig|1129.58.peg.2924				
gsyne_2934	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2558364	2559618	1	156	fig|1129.58.peg.2923				
gsyne_2935	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2561288	2561489	1	156	fig|1129.58.peg.2925				
gsyne_2936	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2561485	2561968	1	156	fig|1129.58.peg.2926				
gsyne_2937	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2561964	2562474	1	156	fig|1129.58.peg.2927				
gsyne_2938	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2562449	2563505	1	156	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_2939	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2563501	2563687	1	156	fig|1129.58.peg.2929				
gsyne_294	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_B	244337	244535	-1	156	fig|1129.58.peg.292				
gsyne_2940	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2563939	2564353	1	856	fig|1129.58.peg.2930				
gsyne_2941	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2564445	2565078	-1	156	fig|1129.58.peg.2931				
gsyne_2942	Synechococcus_assembled_mapped	prepilin-type N-terminal cleavage/methylation domain protein					TIGR02532	2565082	2565580	-1	91,97	fig|1129.58.peg.2932				
gsyne_2943	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2565576	2565990	-1	856	fig|1129.58.peg.2933				
gsyne_2944	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2565998	2566445	-1	856	fig|1129.58.peg.2934				
gsyne_2945	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF07176.6	2567243	2567738	-1	156	fig|1129.58.peg.2936				
gsyne_2946	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2566516	2567257	1	856	fig|1129.58.peg.2935				
gsyne_2947	Synechococcus_assembled_mapped	GTP-binding protein LepA	lepA	3.6.5.-		GO:0005525	TIGR01393	2567944	2569753	-1	157	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation elongation factors ba	
gsyne_2948	Synechococcus_assembled_mapped	small Multidrug Resistance family protein					PF00893.14	2569836	2570175	1	94,147	fig|1129.58.peg.2938				
gsyne_2949	Synechococcus_assembled_mapped	nifU-like domain protein					PF01106.12	2570211	2570502	1	157	fig|1129.58.peg.2939				
gsyne_295	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	244608	246345	-1	141	fig|1129.58.peg.293				
gsyne_2950	Synechococcus_assembled_mapped	serine--tRNA ligase	serS	6.1.1.11		GO:0004828,GO:0005737,GO	TIGR00414	2570543	2571818	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Ser	
gsyne_2951	Synechococcus_assembled_mapped	malate dehydrogenase	mqo	1.1.5.4		GO:0006099,GO:0008924	TIGR01320	2571958	2573416	-1	120	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	TCA Cycle	
gsyne_2952	Synechococcus_assembled_mapped	RIP metalloprotease RseP	rseP	3.4.24.-		GO:0004222,GO:0006508	TIGR00054	2573463	2574552	1	138	fig|1129.58.peg.2942				
gsyne_2953	Synechococcus_assembled_mapped	30S ribosomal protein S14, chloroplast	rps14			GO:0005840,GO:0006412,GO	UniRef100_C	2574604	2574907	1	92,141	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial	
gsyne_2954	Synechococcus_assembled_mapped	polyribonucleotide nucleotidyltransfer	pnp	2.7.7.8		GO:0004654,GO:0006402	TIGR03591	2575095	2577243	1	703	fig|1129.58.peg.2944				
gsyne_2955	Synechococcus_assembled_mapped	inositol monophosphatase family protein					PF00459.20	2577311	2578232	-1	703	fig|1129.58.peg.2945				
gsyne_2956	Synechococcus_assembled_mapped	tetrapyrrole (Corrin/Porphyrin) Methylases family protein					PF00590.15	2578255	2579113	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	16S rRNA modification within P s	
gsyne_2957	Synechococcus_assembled_mapped	putative lipoprotein				GO:0008150,GO:0003674,GO	lipoP	2579333	2579765	-1	88	fig|1129.58.peg.2948				
gsyne_2958	Synechococcus_assembled_mapped	putative membrane protein	mqo	1.1.5.4		GO:0008150,GO:0003674,GO	TMHMM	2579112	2579352	1	88	fig|1129.58.peg.2947				
gsyne_2959	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_C	2579795	2580287	-1	141	fig|1129.58.peg.2949				
gsyne_296	Synechococcus_assembled_mapped	S4 domain protein					PF13275.1	246368	246593	1	157	fig|1129.58.peg.294				





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44	8.03480411	34	7.38790657	38	14.010503	51	11.4901841	37	18.2470415	33	7.85326873	26	9.17010643	95	12.397448
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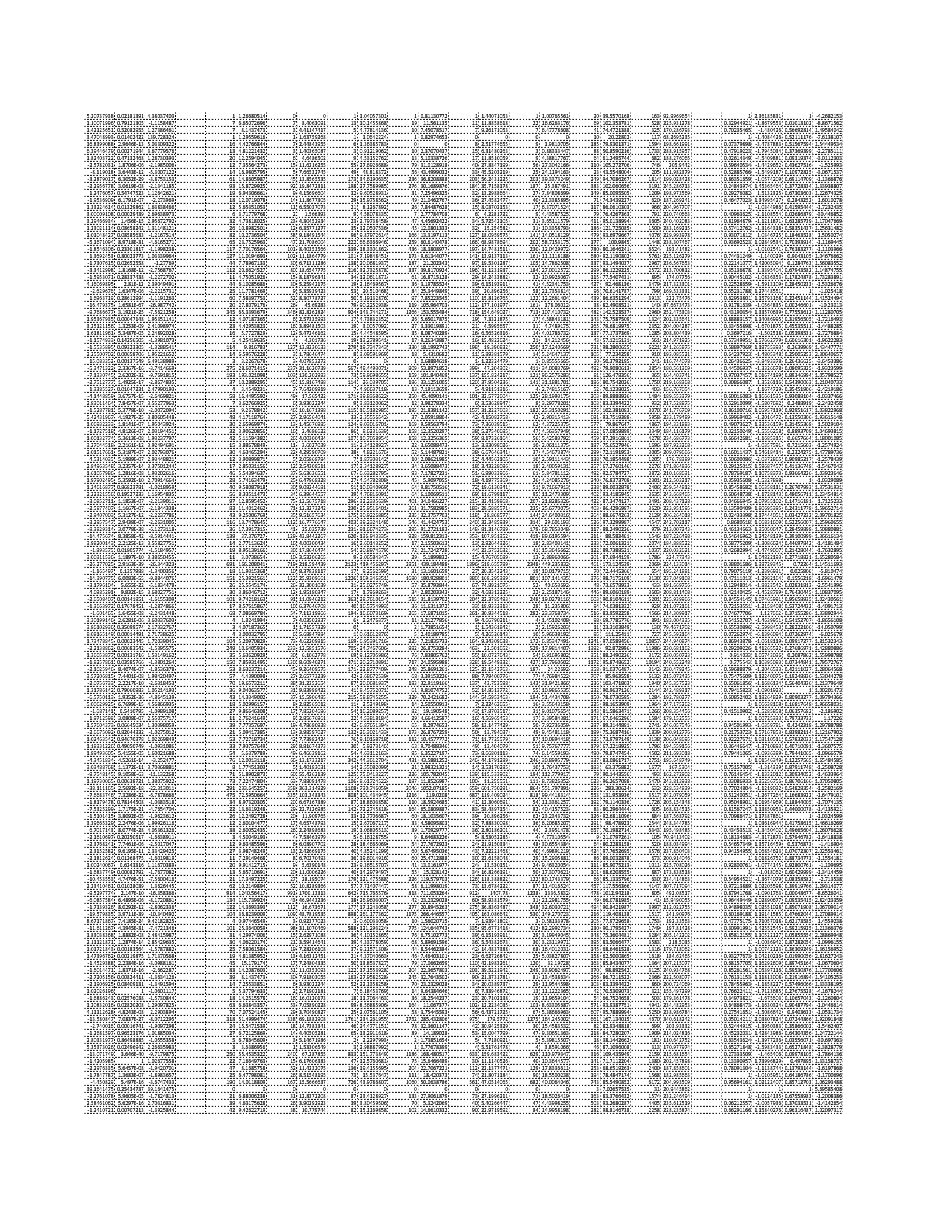
35	8.86387647	38	11.4514138	19	9.71531228	36	11.2484413	39	26.674014	24	7.92101424	27	13.2068068	39	7.05840105
45	5.20436176	32	4.40377176	21	4.90367604	31	4.42334537	26	8.12075538	47	7.08380704	16	3.5739902	47	3.88453371
18	10.4087235	10	6.88089337	2	2.33508383	10	7.13442802	1	1.56168373	2	1.50719299	1	1.11687194	7	2.89273787
81	3.88707517	76	4.33981657	43	4.16633214	75	4.44051537	39	5.05441206	52	3.25203466	52	4.81969632	145	4.97269699
248	22.584107	230	24.9229209	149	27.3958654	273	30.6724228	99	24.3475101	314	37.2644566	125	21.985668	372	24.2091898
17	1.35281575	25	2.36727983	19	3.05274721	23	2.25814465	15	3.22365907	20	2.07411879	15	2.30546959	32	1.81980888
102	9.21605727	106	11.3964797	85	15.5064161	128	14.268856	54	13.1767065	145	17.0736706	56	9.77262945	172	11.1060472
94	13.937607	107	18.8783485	54	16.165965	105	19.2080754	41	16.4177007	94	18.1636078	41	11.7414742	148	15.6822419
34	5.868932	24	4.92959525	25	8.71299936	43	9.15762403	13	6.06026521	36	8.09835038	17	5.66770834	50	6.16788458
90	9.40547305	60	7.46120968	89	18.779138	95	12.2488674	42	11.853744	163	22.1993184	58	11.7069709	272	20.3138907
26	3.97396199	27	4.91059351	16	4.93762219	13	2.45147747	10	4.1277984	27	5.37808952	7	2.06645909	27	2.94917265
19	1.80114523	14	1.57922143	9	1.72260283	5	0.58478918	9	2.30412353	6	0.74124245	4	0.73237504	17	1.1516755
33	3.05322556	35	3.85330029	15	2.8021006	30	3.42452545	38	9.49503706	31	3.73783861	18	3.21659118	37	2.44642974
40	17.1337013	27	13.7617868	22	19.026609	14	7.3986661	17	19.6656469	20	11.1643925	9	7.44581291	22	6.7344162
9	3.71740125	10	4.91492384	7	5.83770957	14	7.13442802	5	5.57744188	11	5.92111531	7	5.58435968	14	4.13248267
18	10.2380887	15	10.1521378	8	9.18721507	9	6.31572317	6	9.21649413	4	2.96496981	4	4.39425024	13	5.28415816
38	2.75823915	28	2.4183893	15	2.19830068	17	1.52240933	25	4.90068115	35	3.31077958	12	1.68231756	29	1.50429285
25	2.9910125	20	2.84726622	10	2.41560396	17	2.50935055	7	2.26174885	15	2.33874774	8	1.84861562	32	2.73598852
9	1.40027671	11	2.03649759	4	1.25654735	5	0.95978852	4	1.68073585	8	1.62209111	3	0.90151098	10	1.11187874
21	3.04858011	27	4.66403651	22	6.44834865	25	4.47767449	17	6.66492637	24	4.54049771	15	4.2057939	31	3.21607438
10	3.9426983	9	4.22236639	4	3.18420522	7	3.40506792	0	0	3	1.54144737	0	0	11	3.099362
26	3.49647043	20	3.20041552	11	2.98673513	20	3.31833861	14	5.08455167	17	2.97933498	11	2.85711426	29	2.78702319
11	6.93914901	10	7.50642914	1	1.27368209	13	10.1179161	1	1.70365498	1	0.82210527	1	1.21840575	0	0
24	2.4782675	18	2.21171573	17	3.54432367	37	4.71381851	9	2.50984885	35	4.70997809	16	3.19106268	40	2.95177333
31	6.44052752	21	5.19157225	14	5.87266592	37	9.48408994	19	10.6605955	37	10.0178696	22	8.8279698	49	7.27514913
65	3.26843975	45	2.69252349	32	3.24881228	48	2.97784822	44	5.97513774	73	4.78369948	25	2.42798247	75	2.69509739
24	1.83010523	23	2.08695228	12	1.84753885	29	2.72833072	20	4.11872631	24	2.38500868	13	1.91463761	28	1.52583975
8	2.33248706	6	2.0816148	6	3.53205957	16	5.75550496	3	2.36221068	10	3.79964619	6	3.37877225	9	1.87524424
27	4.03786688	8	1.42363311	14	4.22730693	14	2.58315497	9	3.6349535	7	1.36426952	6	1.73307714	28	2.99248745
31	3.91115671	26	3.90334315	5	1.27368209	18	2.80188446	23	7.83681289	9	1.47978948	7	1.70576805	17	1.53277539
14	3.73646485	18	5.7164345	4	2.155462	5	1.64640647	18	12.9739879	5	1.73906883	3	1.54643807	11	2.09802966
34	16.1596621	20	11.3110576	14	13.4347289	29	17.005349	12	15.402908	19	11.7684932	12	11.0157232	39	13.2465883
58	8.38480505	47	8.08504971	50	14.5942739	15	2.67541051	23	8.97968143	19	3.57958335	28	7.81810356	107	11.0543911
41	2.6739202	18	1.39687309	13	1.71180957	21	1.68973295	24	4.22711385	18	1.52985754	15	1.88944501	49	2.28374042
18	4.91750717	8	2.60065261	10	5.51594605	4	1.34823837	3	2.21341001	13	4.62838792	5	2.63828017	16	3.12376643
84	8.94000792	83	10.5113034	71	15.2568361	88	11.5551472	46	13.2216168	96	13.3150792	32	6.57789607	115	8.74666577
61	4.2842924	57	4.76369541	30	4.25420131	23	1.99301835	28	5.3109892	40	3.66119754	15	2.03478693	54	2.71037325
85	18.5480398	112	29.0815116	31	13.6580375	46	12.3842902	56	33.0016184	39	11.0906654	81	34.1383498	161	25.1067815
6	0.63661918	10	1.26254924	0	0	3	0.39272081	0	0	0	0	0	0	0	0
89	5.69727179	117	8.91215341	139	17.9654974	86	6.79218609	114	19.7083334	160	13.3478346	77	9.5201999	286	13.0836536
51	4.23321291	28	2.76552652	21	3.51938472	26	2.6626095	35	7.84577949	20	2.16343491	14	2.24443164	47	2.78794285
18	9.32124493	4	2.46479763	0	0	6	3.83342401	1	1.39852274	2	1.34972506	0	0	5	1.85036537
16	3.44802435	11	2.8207389	1	0.43510879	13	3.45643097	9	5.23794542	8	2.24674731	4	1.66490227	7	1.07803896
14	2.85729665	10	2.4285506	5	2.06036808	6	1.51082005	10	5.51182492	2	0.53195047	3	1.18257029	15	2.18778494
32	3.15415864	14	1.64203137	8	1.59210261	16	1.9457531	47	12.5112162	18	2.31217106	18	3.42676617	27	1.90188123
7	3.91726154	5	3.32946454	1	1.12987927	2	1.38085704	1	1.51130683	2	1.45857386	1	1.08084381	2	0.79983536
11	5.78262417	18	11.2596437	6	6.36841044	13	8.43159675	8	11.3576998	9	6.1657895	2	2.03067625	17	6.38656412
16	4.02269508	8	2.39335422	7	3.55338844	18	5.58346541	9	6.11093633	3	0.98295195	2	0.97119299	16	2.87477055
36	5.91965318	30	5.86995643	11	3.65202684	14	2.84024623	13	5.77304885	15	3.21439263	6	1.90556349	18	2.1152044
11	2.29911564	7	1.74094893	4	1.68801241	4	1.03148357	1	0.564464	3	0.81715283	4	1.61475461	8	1.19493475
19	4.7769504	14	4.18836988	5	2.5381346	7	2.17134766	5	3.39496463	4	1.3106026	6	2.91357897	11	1.97640475
8	1.86285879	9	2.49374659	2	0.94030221	8	2.29833923	3	1.88659779	4	1.2138467	1	0.44974709	8	1.33126958
11	2.31304967	6	1.50128583	5	2.12280348	9	2.33490372	6	3.40730995	13	3.56245615	3	1.21840575	11	1.65299307
39	5.47827553	26	4.34582739	16	4.53781473	8	1.38644755	12	4.55227645	15	2.74589816	7	1.89913447	60	6.02305166
64	3.68246713	52	3.56026324	42	4.87927964	53	3.76243468	51	7.9249622	81	6.07376279	36	4.0007353	110	4.52311536
7	2.14929394	6	2.19214302	3	1.85980128	7	2.65173431	3	2.4876378	3	1.20041919	1	0.59302935	5	1.09711929
63	22.5343499	61	25.9629585	31	22.3879171	75	33.097862	19	18.3538088	54	25.1716767	21	14.507821	130	33.230273
57	3.41564329	41	2.92348838	27	3.26669759	62	4.58377759	39	6.31146791	53	4.13892375	28	3.24066469	66	2.8263612
57	4.65331169	59	5.73137942	28	4.61522451	54	5.43895219	38	8.37797388	49	5.21311457	18	2.83816869	73	4.25888802
76	5.42567206	53	4.50231295	51	7.35118983	62	5.46092021	69	13.3032318	51	4.74486681	32	4.41233358	78	3.97942775
56	5.35251163	50	5.68668874	34	6.56139258	83	9.7877277	44	11.3576998	84	10.4631579	31	5.72281488	112	7.65021585
254	87.2546459	138	56.4097001	158	109.587103	238	100.870923	63	58.4471732	385	172.357218	66	43.7902264	306	75.1211701
808	39.1538575	782	45.090994	628	61.4427086	1874	112.03842	313	40.961481	1962	123.901368	420	39.3089006	2113	73.172647
27	3.05141732	26	3.49648002	23	5.24823401	20	2.78870151	18	5.49387109	27	3.97663297	13	2.83765508	34	2.74601454
13	1.57707932	15	2.1653161	10	2.44938863	18	2.69411967	23	7.53539701	20	3.16194333	6	1.40585279	25	2.16738601
15	3.61414011	13	3.72715058	10	4.86475798	4	1.18907134	6	3.90420932	6	1.88399124	2	0.93072661	9	1.549681
11	4.77066494	9	4.64460303	2	1.75131287	7	3.74557471	1	1.1712628	5	2.82598685	7	5.86357767	7	2.1695534
22	4.65430726	12	3.02088002	13	5.55294325	18	4.69828187	7	3.99943394	5	1.37853017	7	2.86028179	15	2.26782585
9	4.1634894	3	1.65141441	5	4.67016766	4	2.28301697	3	3.74804095	4	2.41150878	4	3.5739902	3	0.99179584

gsyne_2960	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2580549	2580684	1	856						
gsyne_2962	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2580971	2581151	1	856	fig|1129.58.peg.2950					
gsyne_2963	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2581438	2581585	1	856	fig|1129.58.peg.2951					
gsyne_2964	Synechococcus_assembled_mapped	integrase core domain protein				PF13683.1	2581771	2581903	-1	157	fig|1129.58.peg.2952					
gsyne_2965	Synechococcus_assembled_mapped	HTH-like domain protein				PF13276.1	2581911	2582529	-1	157						
gsyne_2966	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	2582620	2583082	-1	157	fig|1129.58.peg.2954					
gsyne_2967	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	2583449	2583728	-1	154	fig|1129.58.peg.2955					
gsyne_2968	Synechococcus_assembled_mapped	transposase family protein				PF01527.15	2583861	2584140	-1	154	fig|1129.58.peg.2956					
gsyne_2969	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2584679	2584820	1	856	fig|1129.58.peg.2957					
gsyne_297	Synechococcus_assembled_mapped	triose-phosphate isomerase	tpiA	5.3.1.1	GO:0004807,GO:0006096	TIGR00419	246676	247378	1	116	fig|1129.58.p	Carbohydrates	CO2 fixation	Calvin-Benson cycle		
gsyne_2970	Synechococcus_assembled_mapped	dnaJ C terminal domain protein				PF01556.13	2584827	2585829	-1	95	fig|1129.58.p	Protein Metabolism	Protein folding	Protein chaperones		
gsyne_2971	Synechococcus_assembled_mapped	putative vitamin K epoxide reductase			GO:0045454	UniRef100_B	2585961	2586429	1	92	fig|1129.58.peg.2959					
gsyne_2972	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	2586437	2586692	-1	157	fig|1129.58.peg.2960					
gsyne_2973	Synechococcus_assembled_mapped	heavy-metal-binding family protein				PF01906.12	2586724	2587087	-1	185	fig|1129.58.peg.2961					
gsyne_2974	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2587158	2587434	-1	156	fig|1129.58.peg.2962					
gsyne_2975	Synechococcus_assembled_mapped	methyltransferase domain protein				PF13659.1	2587822	2588977	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA methylation		
gsyne_2976	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	TIGR03132.6	2589339	2590747	-1	156	fig|1129.58.peg.2965					
gsyne_2977	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein				PF00999.16	2589009	2590374	-1	145	fig|1129.58.peg.2964					
gsyne_2978	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF05957.8	2590743	2591211	-1	156	fig|1129.58.peg.2966					
gsyne_2979	Synechococcus_assembled_mapped	recF/RecN/SMC N terminal domain protein				PF02463.14	2591369	2593967	1	93	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	DNA structural proteins, bacterial		
gsyne_298	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	248254	250225	-1	264,710	fig|1129.58.peg.297					
gsyne_2980	Synechococcus_assembled_mapped	recF/RecN/SMC N terminal domain protein				PF02463.14	2593963	2594929	1	93	fig|1129.58.p	DNA Metabolism	DNA Metabolism - no subcate	DNA structural proteins, bacterial		
gsyne_2981	Synechococcus_assembled_mapped	PRC-barrel domain protein				PF05239.11	2594963	2595890	1	157	fig|1129.58.peg.2969					
gsyne_2982	Synechococcus_assembled_mapped	methionine-R-sulfoxide reductase	msrB	1.8.4.-	GO:0000318,GO:0006979,GO	TIGR00357	2595914	2596310	-1	140,149	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Protein processing and modific	Peptide methionine sulfoxide redi		
gsyne_2983	Synechococcus_assembled_mapped	putative cyanobacteria-specific lipid A disaccharide synthetase-like			GO:0016757,GO:0008915,GO	UniRef100_A	2596350	2597583	-1	703	fig|1129.58.peg.2971					
gsyne_2985	Synechococcus_assembled_mapped	YGGT family protein				PF02325.12	2599323	2599686	-1	185	fig|1129.58.peg.2973					
gsyne_2986	Synechococcus_assembled_mapped	acetyl-CoA carboxylase, biotin carboxyl	accC	6.3.4.14	GO:0003989,GO:0004075,GO	TIGR00514	2597974	2599327	1	176	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII		
gsyne_2987	Synechococcus_assembled_mapped	photosystem II reaction centre X family protein				PF06596.6	2599763	2599886	1	164	fig|1129.58.p	Photosynthesis	Electron transport and photop	Photosystem II		
gsyne_2988	Synechococcus_assembled_mapped	ycf66 family protein				PF07444.6	2599961	2600864	1	185	fig|1129.58.peg.2975					
gsyne_2989	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2600901	2601405	1	156	fig|1129.58.peg.2976					
gsyne_299	Synechococcus_assembled_mapped	dihydropteroate synthase	folP	2.5.1.15	GO:0004156,GO:0009396	TIGR01496	247377	248265	1	78	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster		
gsyne_2990	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2601419	2601893	1	156	fig|1129.58.peg.2977					
gsyne_2991	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	2601922	2602123	-1	185	fig|1129.58.peg.2978					
gsyne_2992	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2602129	2604115	-1	141	fig|1129.58.peg.2979					
gsyne_2993	Synechococcus_assembled_mapped	histidine triad nucleotide-binding prote	HINT1	3.-.-.-	GO:0016787,GO:0005737	UniRef100_P	2604153	2604516	-1	703	fig|1129.58.peg.2980					
gsyne_2994	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2606192	2606351	-1	856						
gsyne_2995	Synechococcus_assembled_mapped	sigma-54 interaction domain protein				PF00158.21	2604591	2606235	1	263	fig|1129.58.peg.2981					
gsyne_2996	Synechococcus_assembled_mapped	ribosomal protein S21	rpsU		GO:0000314,GO:0003735,GO	TIGR00030	2606364	2606535	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial		
gsyne_2997	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF12565.3	2606591	2607206	-1	156	fig|1129.58.peg.2983					
gsyne_2998	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	2607262	2607460	-1	88	fig|1129.58.peg.2984					
gsyne_2999	Synechococcus_assembled_mapped	peptide deformylase	def	3.5.1.88	GO:0006464,GO:0042586	TIGR00079	2607472	2608075	-1	140	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation termination factors ba		
gsyne_3	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	1385	1715	1	156	fig|1129.58.peg.3					
gsyne_30	Synechococcus_assembled_mapped	glyoxalase/Bleomycin resistance /Dioxygenase superfamily protein				PF00903.20	24376	25354	-1	703	fig|1129.58.peg.29					
gsyne_300	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	250295	252263	-1	90	fig|1129.58.peg.298					
gsyne_3000	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF07859.8	2608140	2610069	1	703	fig|1129.58.peg.2986					
gsyne_3001	Synechococcus_assembled_mapped	sodium/glutamate symporter family protein				PF03616.9	2610079	2611480	1	185	fig|1129.58.peg.2987					
gsyne_3002	Synechococcus_assembled_mapped	sodium/glutamate symporter family protein				PF03616.9	2611476	2612880	1	185	fig|1129.58.peg.2988					
gsyne_3003	Synechococcus_assembled_mapped	class II Aldolase and Adducin N-terminal domain protein				PF00596.16	2612883	2613543	-1	703	fig|1129.58.peg.2989					
gsyne_3004	Synechococcus_assembled_mapped	S-methyl-5-thioribose-1-phosphate isor	mtnA	5.3.1.23	GO:0019509,GO:0046523	TIGR00512	2613554	2614661	-1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Salvage		
gsyne_3005	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	2615720	2616245	-1	156	fig|1129.58.peg.2992					
gsyne_3006	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	2614725	2615745	1	703	fig|1129.58.peg.2991					
gsyne_3007	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	2616308	2617727	1	157	fig|1129.58.peg.2993					
gsyne_3008	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	2617723	2618557	1	703	fig|1129.58.peg.2994					
gsyne_3009	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	2618562	2619276	1	703	fig|1129.58.peg.2995					
gsyne_301	Synechococcus_assembled_mapped	hlyD secretion family protein				PF13437.1	252268	253417	-1	185	fig|1129.58.peg.299					
gsyne_3010	Synechococcus_assembled_mapped	putative cysteine desulfurase			GO:0006534,GO:0030170,GO	UniRef100_C	2619292	2620582	-1	92,141,703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	mnm5U34 biosynthesis bacteria		
gsyne_3011	Synechococcus_assembled_mapped	feS assembly protein SufD	sufD		GO:0005198,GO:0016226	TIGR01981	2620578	2621823	-1	76	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria		
gsyne_3012	Synechococcus_assembled_mapped	feS assembly ATPase SufC	sufC		GO:0005524,GO:0016226	TIGR01978	2621822	2622617	-1	76	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria		
gsyne_3013	Synechococcus_assembled_mapped	feS assembly protein SufB	sufB		GO:0005198,GO:0016226	TIGR01980	2622697	2624140	-1	76	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria		
gsyne_3014	Synechococcus_assembled_mapped	ferredoxin thioredoxin reductase catalytic beta chain family protein				PF02943.10	2624150	2624504	-1	112	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio		
gsyne_3015	Synechococcus_assembled_mapped	iron-sulfur cluster biosynthesis transcri	sufR		GO:0016226,GO:0030528,GO	TIGR02702	2624703	2625339	1	76,261	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Iron-sulfur cluster assembly		
gsyne_3016	Synechococcus_assembled_mapped	eamA-like transporter family protein				PF00892.15	2625675	2626539	-1	141	fig|1129.58.peg.3003					
gsyne_3017	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2625332	2625695	1	156	fig|1129.58.peg.3002					
gsyne_3018	Synechococcus_assembled_mapped	phycocyanobilin lyase subunit CpcS	cpcS	4.-.-.-	GO:0016829,GO:0017009,GO	UniRef100_A	2626592	2627204	1	92,141,703	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome		
gsyne_3019	Synechococcus_assembled_mapped	phycobilisome rod-core linker polypept	cpcG		GO:0030089,GO:0015979	UniRef100_C	2627357	2628068	1	92	fig|1129.58.p	Photosynthesis	Light-harvesting complexes	Phycobilisome		
gsyne_302	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF07862.6	253491	253749	-1	156	fig|1129.58.peg.300					
gsyne_3020	Synechococcus_assembled_mapped	rho termination factor, N-terminal domain protein				PF07498.7	2628260	2629277	1	165	fig|1129.58.peg.3006					
gsyne_3021	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	2629287	2629461	1	88	fig|1129.58.peg.3007					
gsyne_3022	Synechococcus_assembled_mapped	phospholipase D family protein				PF00614.17	2629592	2630921	1	177	fig|1129.58.peg.3008					
gsyne_3023	Synechococcus_assembled_mapped	sulfotransferase domain protein				PF00685.22	2631138	2632911	1	703	fig|1129.58.peg.3009					
gsyne_3024	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	2633038	2633377	1	156	fig|1129.58.peg.3010					
gsyne_3025	Synechococcus_assembled_mapped	phosphoglucomutase/phosphomannomutase, C-terminal domain protein				PF00408.15	2633445	2635086	1	119	fig|1129.58.peg.3011					
gsyne_3026	Synechococcus_assembled_mapped	putative antibiotic biosynthesis monooxygenase			GO:0004497	UniRef100_B	2635300	2635675	1	703	fig|1129.58.peg.3012					
gsyne_3027	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2635733	2635859	-1	856						
gsyne_3028	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	2635845	2636073	-1	88	fig|1129.58.peg.3014					
gsyne_3029	Synechococcus_assembled_mapped	RND transporter, hydrophobe/amphiphile efflux-1 family protein			GO:0006810,GO:0015562,GO	TIGR00915	2636131	2639545	-1	94,141	fig|1129.58.peg.3015					
gsyne_303	Synechococcus_assembled_mapped	magnesium chelatase, H subunit	bchH	6.6.1.1	GO:0005488,GO:0010007,GO	TIGR02025	253762	257764	-1	191	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis		
gsyne_3030	Synechococcus_assembled_mapped	efflux transporter, RND family, MFP subunit			GO:0005215,GO:0006810	TIGR01730	2639554	2640616	-1	141	fig|1129.58.peg.3016					
gsyne_3031	Synechococcus_assembled_mapped	MMPL family protein				PF03176.10	2640660	2643924	-1	185	fig|1129.58.peg.3017					
gsyne_3032	Synechococcus_assembled_mapped	efflux transporter, RND family, MFP subunit			GO:0005215,GO:0006810	TIGR01730	2643932	2644982	-1	141	fig|1129.58.peg.3018					
gsyne_3033	Synechococcus_assembled_mapped	ATPase, AAA family domain protein	yrvN		GO:0006281,GO:0000166,GO	UniRef100_C	2645160	2647356	1	92,141,703	fig|1129.58.peg.3019					
gsyne_3034	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF07176.6	2647358	2647967	-1	156	fig|1129.58.peg.3020					
gsyne_3035	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	2648129	2648810	-1	156	fig|1129.58.peg.3021					
gsyne_3036	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2648926	2649439	-1	156	fig|1129.58.peg.3022					
gsyne_3037	Synechococcus_assembled_mapped	4'-phosphopantetheinyl transferase superfamily protein				PF01648.15	2649475	2650087	-1	140	fig|1129.58.peg.3023					
gsyne_3038	Synechococcus_assembled_mapped	ahpC/TSA family protein				PF00578.16	2650148	2650616	1	96,149	fig|1129.58.p	Sulfur Metabolism	Sulfur Metabolism - no subcate	Thioredoxin-disulfide reductase		
gsyne_3039	Synechococcus_assembled_mapped	pantothenate kinase, type III family proc	coaX	2.7.1.33	GO:0004594,GO:0015937	TIGR00671	2650618	2651299	-1	261	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Coenzyme A	Coenzyme A Biosynthesis		
gsyne_304	Synechococcus_assembled_mapped	dihydrodipicolinate reductase	dapB		GO:0008839,GO:0009089	TIGR00036	257887	258745	1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa		
gsyne_3040	Synechococcus_assembled_mapped	phosophoadenylyl-sulfate reductase fa	cysH	1.8.4.8	GO:0004604,GO:0019379	TIGR00434	2651299	2652004	-1	106	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis		
gsyne_3041	Synechococcus_assembled_mapped	pyridine nucleotide-disulfide oxidoreductase family protein				PF07992.9	2652125	2653298	1	157	fig|1129.58.p	Respiration	Electron donating reactions	Respiratory dehydrogenases 1		
gsyne_3042	Synechococcus_assembled_mapped	HAD hydrolase, IA, variant 1 family protein			GO:0008152,GO:0016787	TIGR01549	2653288	2653999	1	703	fig|1129.58.peg.3028					
gsyne_3043	Synechococcus_assembled_mapped	GTP-binding protein HflX	hflX		GO:0005525,GO:0008150	TIGR03156	2653995	2655633	1	157	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Universal GTPases		
gsyne_3044	Synechococcus_assembled_mapped	ahpC/TSA family protein				PF00578.16	2655686	2656769	1	96,149	fig|1129.58.p	Stress Response	Oxidative stress	Rubrerythrin		
gsyne_3045	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	TIGR03702.9	2656761	2657532	1	89,100	fig|1129.58.p	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Recycling of Peptidoglycan Amin		
gsyne_3046	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	2657612	2657846	1	156	fig|1129.58.peg.3032					
gsyne_3047	Synechococcus_assembled_mapped	heme ABC exporter, ATP-binding protei	ccmA	3.6.3.41	GO:0015439,GO:0015886,GO	TIGR01189	2658067	2659795	1	97,147	fig|1129.58.peg.3033					
gsyne_3048	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2659921	2660134	1	156	fig|1129.58.peg.3034					
gsyne_3049	Synechococcus_assembled_mapped	putative serine protease HhoA			GO:0004252,GO:0006508,GO	UniRef100_P	2660140	2661259	-1	189,703	fig|1129.58.peg.3035					
gsyne_305	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	258771	259419	1	156	fig|1129.58.peg.303					
gsyne_3050	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11189.3	2661426	2661702	1	156	fig|1129.58.peg.3036					
gsyne_3051	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	2661784	2662147	1	156	fig|1129.58.peg.3037					
gsyne_3052	Synechococcus_assembled_mapped	HAD hydrolase, IIB family protein			GO:0008152,GO:0016787	TIGR01484	2664653	2665442	1	703	fig|1129.58.p	Carbohydrates	Di- and oligosaccharides	Trehalose Biosynthesis		
gsyne_3053	Synechococcus_assembled_mapped	ATP-dependent helicase HrpB	hrpB	3.6.4.-	GO:0006139,GO:0008026	TIGR01970	2662170	2664669	1	703	fig|1129.58.peg.3038					
gsyne_3054	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	2665574	2665688	1	88	fig|1129.58.peg.3040					
gsyne_3055	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	2665750	2665963	1	156	fig|1129.58.peg.3041					
gsyne_3056	Synechococcus_assembled_mapped	exodeoxyribonuclease VII, large subuni	xseA	3.1.11.6	GO:0006308,GO:0008855,GO	TIGR00237	2665959	2667117	1	131	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial		
gsyne_3057	Synechococcus_assembled_mapped	exonuclease VII small subunit				PF02609.11	2667109	2667367	1	131	fig|1129.58.peg.3043					
gsyne_3058	Synechococcus_assembled_mapped	zinc-ribbon domain protein				PF13248.1	2667753	2668098	1	157	fig|1129.58.peg.3045					
gsyne_3059	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11196.3	2667375	2667768	1	156	fig|1129.58.peg.3044					
gsyne_306	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	259525	259732	1	185	fig|1129.58.peg.304					
gsyne_3060	Synechococcus_assembled_mapped	virulence factor BrkB family protein				PF03631.10	2668129	2669167	-1	185	fig|1129.58.peg.3046					
gsyne_3063	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2672449	2672575	-1	856						
gsyne_3067	Synechococcus_assembled_mapped	putative pG1 protein				UniRef100_C	2674307	2674505	1	185	fig|1129.58.p	Carbohydrates	Monosaccharides	Deoxyribose and Deoxynucleosic		
gsyne_3068	Synechococcus_assembled_mapped	alkaline and neutral invertase family protein				PF12899.2	2675413	2676865	1	185	fig|1129.58.peg.3049					
gsyne_3069	Synechococcus_assembled_mapped	cytB6/f complex subunit IV			GO:0009055,GO:0009512,GO	TIGR01156	2676945	2677428	-1	112,164	fig|1129.58.p	Respiration	Respiration - no subcategory	Cytochrome B6-F complex		
gsyne_307	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	260291	260993	1	157	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Quinone cofactors	Ubiquinone Biosynthesis		
gsyne_3070	Synechococcus_assembled_mapped	cytochrome b6	petB		GO:0006810,GO:0020037,GO	UniRef100_P	2677552	2678233	-1	92,141,703	fig|1129.58.p	Respiration	Respiration - no subcategory	Cytochrome B6-F complex		
gsyne_3071	Synechococcus_assembled_mapped	C-terminal processing peptidase family protein		3.4.21.-	GO:0006508,GO:0019132	TIGR00225	2678301	2679534	1	138,140	fig|1129.58.peg.3052					
gsyne_3072	Synechococcus_assembled_mapped	HD domain protein				PF01966.17	2679533	2680796	1	703	fig|1129.58.p	Nucleosides and Nucleotides	Purines	Purine conversions		
gsyne_3073	Synechococcus_assembled_mapped	chromate transporter family protein				PF02417.10	2681461	2682025	-1	143	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Resistance to chromium compou		
gsyne_3074	Synechococcus_assembled_mapped	septum formation inhibitor MinC, C-terminal domain protein				PF03775.11	2680797	2681472	1	157	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton		
gsyne_3075	Synechococcus_assembled_mapped	chromate transporter family protein				PF02417.10	2682060	2682567	-1	143	fig|1129.58.peg.3056					
gsyne_3076	Synechococcus_assembled_mapped	archaeal transcriptional regulator TrmB family protein				PF11495.3	2682614	2683613	-1	165	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho		
gsyne_3077	Synechococcus_assembled_mapped	septum site-determining protein MinD	minD		GO:0000918,GO:0016887	TIGR01968	2683730	2684549	1	93	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton		
gsyne_3078	Synechococcus_assembled_mapped	cell division topological specificity facto	minE		GO:0000910,GO:0000918	TIGR01215	2684553	2684883	1	93	fig|1129.58.p	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton		
gsyne_3079	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	2684962	2685121	1	261	fig|1129.58.peg.3060					
gsyne_308	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11165.3	261023	261239	1	156	fig|1129.58.peg.307					
gsyne_3081	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF09852.4	2686918	2688541	-1	156	fig|1129.58.peg.3062					
gsyne_3082	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF09852.4	2685236	2686928	1	156	fig|1129.58.peg.3061					
gsyne_3083	Synechococcus_assembled_mapped	photosystem II D2	psbD		GO:0009055,GO:0009538,GO	TIGR01152	2688592	2689648	-1	112,164	fig|1129.58.p	Photosynthesis	Electron transport and photop	Photosystem II		
gsyne_3084	Synechococcus_assembled_mapped	putative uPF0367 protein RS9916_35777				UniRef100_C	2689796	2690060	1	185	fig|1129.58.peg.3064					
gsyne_3085	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	2690052	2690739	1	141	fig|1129.58.peg.3065					
gsyne_3087	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2691001	2691127	-1	856	fig|1129.58.peg.3066					
gsyne_3088	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2690892	2691033	1	856						
gsyne_3089	Synechococcus_assembled_mapped	response regulator				PF00072.19	2691163	2691934	1	699	fig|1129.58.peg.3067					
gsyne_309	Synechococcus_assembled_mapped	adenine phosphoribosyltransferase	apt	2.4.2.7	GO:0003999,GO:0005737,GO	TIGR01090	261256	261781	-1	127	fig|1129.58.p	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria		
gsyne_3090	Synechococcus_assembled_mapped	DNA polymerase III, delta subunit				PF13177.1	2691944	2692928	-1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication		
gsyne_3091	Synechococcus_assembled_mapped	thymidylate kinase	tmk	2.7.4.9	GO:0004798,GO:0015949	TIGR00041	2692920	2693580	-1	124	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	pyrimidine conversions		
gsyne_3092	Synechococcus_assembled_mapped	copper-translocating P-type ATPase		3.6.3.4	GO:0004008,GO:0005375,GO	TIGR01511	2693572	2695891	-1	96,145	fig|1129.58.p	Membrane Transport	Cation transporters	Copper Transport System		
gsyne_3093	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	2695907	2696021	-1	856						
gsyne_3094	Synechococcus_assembled_mapped	TPR repeat family protein				PF13414.1	2696025	2696547	1	185	fig|1129.58.p	Photosynthesis	Electron transport and photop	Photosystem I		
gsyne_3095	Synechococcus_assembled_mapped	DNA repair protein RadA	radA		GO:0005524,GO:0006281	TIGR00416	2696557	2697997	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial		
gsyne_3096	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein				PF00486.23	2698095	2698857	1	261	fig|1129.58.peg.3073					



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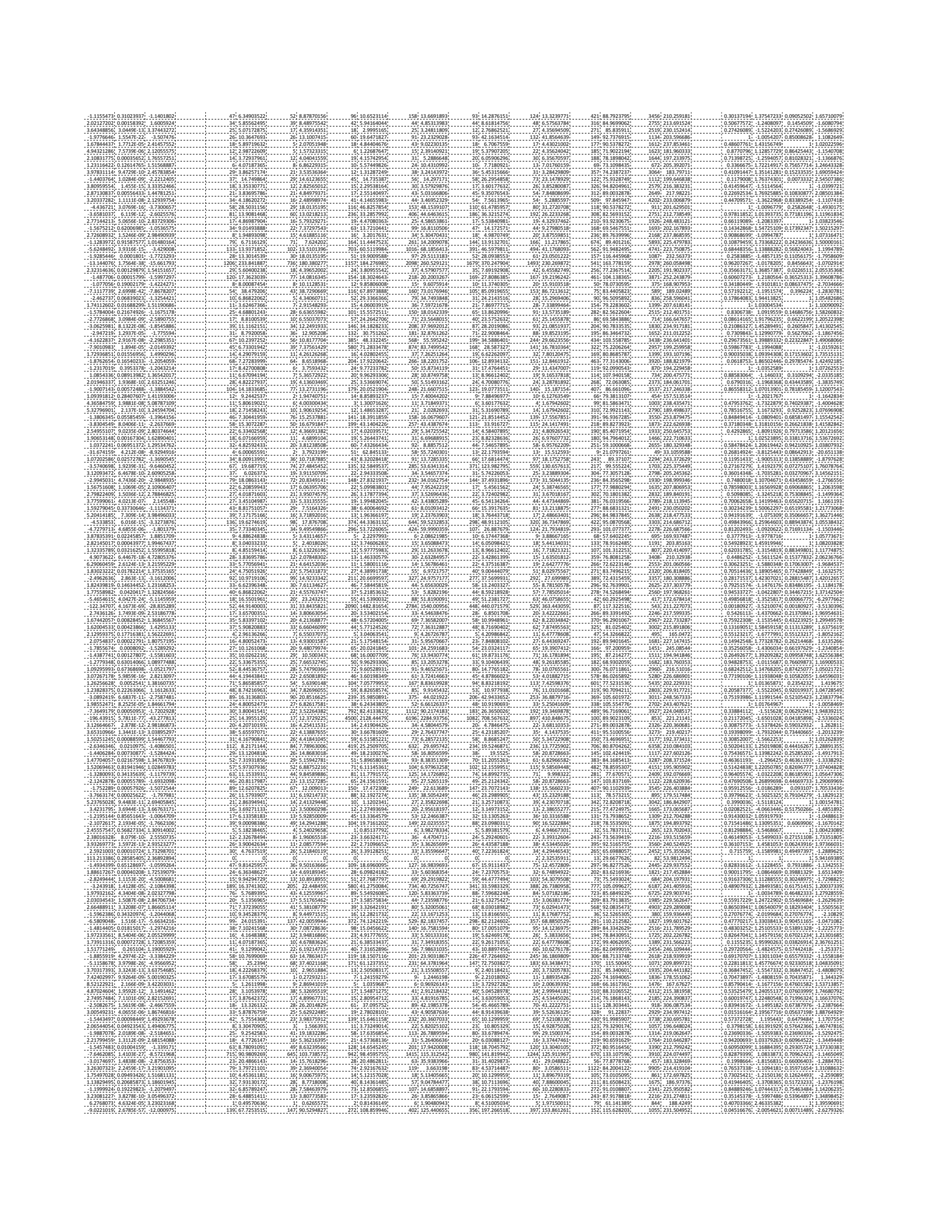
23	2.69595316	16	2.23164109	10	2.36663902	6	0.86770071	9	2.84901761	9	1.37480442	6	1.35835776	32	2.6805293
16	3.51349317	12	3.13559698	3	1.33011104	11	2.98020411	2	1.18608891	5	1.43087942	4	1.69651433	12	1.88315666
5	2.5892347	4	2.46479763	2	2.09111985	9	5.75013602	2	2.79704548	1	0.67486253	3	3.00055147	4	1.4802923
114	5.97479597	137	8.54394917	84	8.88883875	141	9.11741104	112	15.8527412	135	9.2207426	79	7.99693804	263	9.85054025
14	4.01438372	5	1.70600662	1	0.5789464	9	3.18395961	22	17.0365498	3	1.12105264	2	1.10764159	4	0.81966598
3	1.9639101	3	2.33690718	0	0	1	0.8076711	0	0	1	0.85312811	0	0	0	0
275	17.4111859	251	18.9099004	151	19.3027915	113	8.82690182	94	16.0728033	85	7.01339803	98	11.9839544	422	19.0938798
193	117.478575	104	75.3276748	96	117.983183	112	84.1111514	58	95.3449013	167	132.474331	71	83.4714816	144	62.6397373
37	6.26215886	47	9.46542406	36	12.3019051	47	9.81418879	32	14.6265013	38	8.38146345	17	5.5571189	71	8.58750057
4	2.10277243	7	4.37875033	2	2.12280348	8	5.18867492	2	2.83942496	1	0.68508772	2	2.03067625	3	1.12704073
58	10.0117075	50	10.2699901	32	11.1526392	62	13.204016	29	13.5190532	43	9.67302963	25	8.3348652	95	11.7189807
7	2.20791105	6	2.25192874	2	1.27368209	4	1.55660248	0	0	4	1.64421053	2	1.21840575	5	1.12704073
53	5.64071928	49	6.20546826	27	5.8018954	54	7.09065852	24	6.89823487	51	7.0736358	25	5.1389813	91	6.92127465
48	2.53871305	27	1.69924501	15	1.60181055	31	2.02287136	66	9.42723714	20	1.37853017	30	3.06458763	41	1.549681
30	1.61877504	15	0.96311105	15	1.63419553	29	1.93062282	29	4.22601817	13	0.9141606	10	1.04218221	38	1.46532822
32	2.37743863	16	1.41448772	9	1.35004847	13	1.19161753	17	3.41095803	16	1.54914911	16	2.29592518	24	1.2742559
42	3.11372071	27	2.38184771	16	2.39495777	27	2.4696097	21	4.20453311	35	3.38152273	23	3.29334033	35	1.85431915
15	2.36561898	13	2.43958947	7	2.22894366	13	2.52947903	8	3.40730995	7	1.43868422	7	2.13221006	13	1.46515295
30	2.82079228	24	2.68522668	29	5.5054822	30	3.48020879	22	5.5865109	33	4.04368851	13	2.36086751	56	3.76291105
12	2.3791368	5	1.17958172	5	2.00150043	0	0	7	3.74804095	1	0.25837594	4	1.53171008	11	1.55853632
17	1.73478725	12	1.45713036	20	4.12073617	11	1.38491838	4	1.10236498	9	1.19688855	8	1.57676038	29	2.11485878
46	3.37421622	38	3.31679427	36	5.33169246	27	2.44350389	37	7.32967838	18	1.72068544	16	2.26680139	67	3.51217343
28	3.49453547	25	3.71271225	14	3.52782449	10	1.53980461	19	6.4040268	15	2.43970088	9	2.16946347	33	2.94327902
40	5.83121765	30	5.20403701	22	6.47544255	32	5.75550496	27	10.6299481	39	7.40931007	12	3.37877225	47	4.89647106
56	5.07300711	34	3.66501893	15	2.74357108	43	4.80595935	35	8.56275673	39	4.60421879	14	2.44953636	39	2.52480664
97	7.82671458	77	7.39295986	80	13.033026	198	19.7109314	45	9.80592108	178	18.7172339	47	7.324602	157	9.05302017
83	6.93914901	77	7.66017527	64	10.8032794	160	16.5037371	30	6.77356797	167	18.1952696	36	5.81311659	123	7.34884869
43	5.62987561	36	5.60857724	43	11.3670119	86	13.8919429	26	9.19330798	97	16.5506853	28	7.08054662	50	4.67828226
116	8.36737302	116	9.95655257	41	5.97121229	160	14.2391911	65	12.6623005	146	13.7245432	58	8.08048719	187	9.63959574
36	10.5851426	46	16.094293	20	11.8733076	69	25.0309593	16	12.7052236	79	30.271588	25	14.1975246	63	13.237953
139	22.7486253	134	26.0954636	102	33.7045119	144	29.0761595	63	27.8451155	216	46.0689178	46	14.5404082	213	24.9118531
14	1.68659872	17	2.43698307	5	1.21618949	13	1.93224092	7	2.27745544	8	1.25599416	7	1.62877157	9	0.7748405
19	5.4480922	30	10.2360397	12	6.94735685	12	4.24527948	6	4.64633175	14	5.23157897	2	1.10764159	21	4.30324641
11	1.870849	10	2.02379217	7	2.40376277	9	1.88852506	14	6.43046241	9	1.99481425	7	2.29944222	20	2.43087216
691	101.159324	755	131.520873	470	138.922709	1087	196.332234	259	102.399009	1006	191.928626	361	102.073612	1256	131.402487
18	7.26190012	10	4.80062328	2	1.62912825	16	7.96401267	2	2.17909357	1	0.525765	0	0	11	3.17144019
151	15.4544469	126	15.3450012	42	8.67907264	125	15.7841328	24	6.63370079	98	13.0712312	32	6.32564637	131	9.58150848
26	15.553265	27	19.219047	7	8.45461386	14	10.3326199	2	3.23106978	13	10.1345735	4	4.62153905	11	4.70248028
30	2.34959899	12	1.11833933	10	1.58132088	10	0.96628822	17	3.59575034	13	1.32687419	9	1.36142403	29	1.62314218
101	5.92939128	93	6.49668105	79	9.36404175	62	4.49070596	71	11.2568066	59	4.51392824	53	6.00956474	176	7.38392842
17	5.21971385	12	4.38428604	4	2.47973504	14	5.30346862	6	4.97527559	8	3.20111785	4	2.37211739	18	3.94962945
68	4.3131822	57	4.30213078	40	5.12267019	63	4.93018975	63	10.7918912	45	3.71976332	56	6.86049307	116	5.25814979
4	1.11026384	7	2.31198017	0	0	6	2.05471527	2	1.49921638	2	0.72345263	1	0.53609853	2	0.39671834
3	2.4782675	1	0.98298477	0	0	1	1.019204	0	0	0	0	0	0	0	0
4	1.82609184	6	3.25937055	1	0.92174362	0	0	0	0	1	0.5949446	0	0	1	0.32624863
104	3.17078865	75	2.72091566	41	2.52386038	85	3.19732714	126	10.37463	78	3.09914903	53	3.12096025	124	2.70172856
250	6.50220109	241	7.45859956	169	8.8747189	360	11.5519974	163	11.4492255	340	11.5242642	141	7.08301093	441	8.19681345
35	3.43037027	30	3.49875934	18	3.56199228	33	3.99044279	41	10.8523784	24	3.06547726	19	3.59670624	38	2.66159901
150	4.78342073	138	5.23656224	78	5.02214721	163	6.41311636	149	12.8322174	206	8.56107782	87	5.35852161	172	3.91978135
53	5.25392711	46	5.42607592	26	5.2039011	33	4.03604785	44	11.7795573	40	5.16751882	33	6.3183041	53	3.75465568
57	2.70171785	27	1.52282067	25	2.39250392	43	2.51459348	49	6.27233628	32	1.97664654	26	2.38021888	73	2.47271504
70	11.96405	89	18.1004781	29	10.0075021	78	16.4478439	73	33.695442	54	12.0278455	40	13.2043973	104	12.7028039
36	5.5024089	32	5.81996268	17	5.24622358	29	5.46868051	19	7.84281696	28	5.57727802	22	6.49458571	49	5.35220222
43	8.72466103	37	8.93308964	32	13.1092426	35	8.76157827	26	14.2469393	34	8.99027396	27	10.580892	42	6.08997446
18	3.06138927	8	1.61903374	10	3.43394681	9	1.88852506	21	9.64569361	11	2.4381063	12	3.94190095	14	1.70161051
27	6.00503279	20	5.2929949	13	5.83770957	8	2.19520862	4	2.40259035	11	3.18829286	6	2.57739678	24	3.81459939
11	1.68129161	10	1.81873834	4	1.23440555	12	2.26290228	7	2.88945888	10	1.99188501	2	0.59041688	15	1.63842925
39	4.73123796	20	2.88708813	16	3.91902181	25	3.74183288	24	7.86302296	27	4.2686235	15	3.51463197	33	2.86094954
21	3.10047083	13	2.28387099	15	4.47143712	24	4.37173462	11	4.38600536	15	2.88611423	9	2.56642913	36	3.79836705
53	4.7030038	43	4.54033374	29	5.19571082	43	4.7076277	27	6.47040317	52	6.0133531	17	2.91357897	52	3.29753093
33	4.83105311	31	5.4001948	11	3.25138255	24	4.33484234	15	5.93044454	17	3.24332668	6	1.69651433	37	3.87093313
54	3.43144731	50	3.78071065	29	3.72073797	40	3.13601232	25	4.29033991	41	3.39532486	16	1.96373088	99	4.49577785
77	7.40047747	71	8.11983539	36	6.98584636	78	9.24906458	69	17.9096139	100	12.5251495	71	13.1797076	182	12.5004739
8	1.08002319	6	0.96386055	2	0.54515576	6	0.99937513	6	2.18757254	1	0.17593693	3	0.78224494	2	0.19295639
71	31.5820243	60	31.7579694	30	26.943275	56	30.7329207	9	10.8116566	59	34.201687	6	5.15479355	52	16.5299307
73	4.3972038	68	4.87396614	65	7.90523171	69	5.12787014	31	5.04293704	78	6.12297151	39	4.53729224	126	5.4238835
291	142.203687	359	208.752737	199	196.344373	211	127.213886	83	109.537816	312	198.694738	83	78.3383415	373	130.26051
475	44.1835895	554	61.319275	187	35.1201616	447	51.299024	114	28.6378464	355	43.0337944	159	28.5655718	579	38.4885919
34	5.46136727	22	4.2049904	22	7.13497837	17	3.36903545	6	2.60280621	17	3.55865011	10	3.10242205	50	5.73955926
22	8.2968086	30	13.4626175	13	9.89872493	33	15.3545299	6	6.11093633	21	10.3209955	3	2.18518422	29	7.81578244
26	7.45528406	22	7.50642914	14	8.10524965	28	9.90565213	13	10.0670521	19	7.10000003	10	5.53820795	60	12.2949898
12	1.58307582	18	2.82561401	6	1.59815623	18	2.9297271	12	4.27533188	19	3.26653994	10	2.54799681	27	2.54548362
38	1.58275908	28	1.3877432	13	1.09325654	23	1.18193405	32	3.59955913	22	1.19417452	13	1.04581046	43	1.27992861
3	2.73913777	4	4.34582739	1	1.84348723	0	0	0	0	3	3.5696676	0	0	2	1.30499453
12	5.86406958	6	3.48890368	6	5.91993083	12	7.23491292	1	1.31973273	8	5.09473686	3	2.83150632	2	0.69844778
27	2.42690445	15	1.60435338	11	1.99631519	22	2.43975259	36	8.73895557	17	1.99136897	14	2.43049852	35	2.24824187
11	4.43782785	8	3.84049863	6	4.88738476	8	3.98200634	6	6.53728072	5	2.62882498	2	1.55842596	21	6.05456763
20	6.03404261	9	3.23102819	3	1.82745691	18	6.70015849	9	7.33312359	8	3.14544624	8	4.66172634	7	1.50925454
13	3.4430892	20	6.30310843	10	5.34752022	14	4.57474774	8	5.72219992	9	3.1064283	9	4.60389959	16	3.02838424
21	10.5595746	27	16.155141	6	6.09152303	22	13.648471	6	8.1479151	6	3.9318078	0	0	24	8.62431165
62	6.21715662	58	6.92066732	27	5.46652573	67	8.28913313	49	13.2697982	56	7.31816249	42	8.13444301	92	6.59286252
914	755.045499	991	974.137905	64	106.746689	1532	1561.42053	43	95.9320004	120	129.18797	47	74.9899729	82	48.4090827
153	80.4310453	43	26.8980377	86	91.2805497	33	21.4032841	224	318.015595	97	66.453509	162	164.484776	72	27.0489775
122	8.74562168	117	9.98013874	80	11.5789281	94	8.31367232	83	16.068564	88	8.22105266	56	7.75349113	240	12.2949898
104	22.4121583	115	29.489543	80	34.808703	110	29.2467236	70	40.7395755	128	35.947957	98	40.7901055	236	36.3453134
4	0.59308966	3	0.52929949	3	0.89810917	6	1.09760431	4	1.6017269	3	0.57968961	2	0.57275484	5	0.52980547
101	15.4373139	107	19.4605002	77	23.7623068	147	27.7205529	45	18.5750928	143	28.4839556	71	20.9597993	216	23.5933812
31	2.61695401	15	1.50676497	15	2.55666113	21	2.18719691	45	10.2592362	19	2.09026765	24	3.91312795	30	1.80984642
30	2.47238088	22	2.15742975	14	2.32953731	24	2.44027942	15	3.33851628	17	1.82581573	9	1.43256733	31	1.82575244
25	4.61379588	20	4.3920596	10	3.7261976	24	5.46466827	14	6.9777358	29	6.97477606	7	2.49513943	24	3.16530587
19	2.92986291	13	2.38537637	10	3.11344511	14	2.66351979	39	16.2415108	17	3.41630411	18	5.3609853	24	2.64478891
45	9.23851199	17	4.15296523	16	6.63219076	37	9.37185219	12	6.65332712	28	7.49137343	13	5.15479355	38	5.57518372
83	8.6478884	52	6.44696316	49	10.3080277	49	6.29886438	46	12.943685	61	8.28277228	36	7.24457472	108	8.04158789
39	4.95653501	31	4.6880812	27	6.9282707	28	4.39041724	33	11.3264974	40	6.62502412	29	7.11852443	38	3.45130421
14	4.4158221	7	2.6272502	4	2.54736418	9	3.50235557	12	10.2219299	6	2.4663158	9	5.48282587	22	4.9589792
5	3.27318349	2	1.55793812	0	0	3	2.42301329	0	0	1	0.85312811	0	0	2	0.93565645
18	8.67393626	16	9.1745245	9	8.75656436	5	2.97267834	4	5.20561243	7	4.39597955	3	2.79217984	16	5.50997689
63	4.04035478	57	4.34984387	31	4.01409974	44	3.48149537	27	4.6763912	54	4.51322115	28	3.46828993	76	3.48320166
70	4.30620949	32	2.34243179	19	2.35992515	29	2.20104694	39	6.4793261	21	1.68356664	15	1.78224245	64	2.81360522
316	31.1473166	400	46.9151821	487	96.9192464	556	67.6149201	279	74.2687091	746	95.8266451	418	79.5771255	1300	91.5720591
24	9.46247592	19	8.9138846	10	7.96051305	12	5.83725929	4	4.25913744	16	8.22105266	11	8.37653952	11	3.099362
27	4.0907647	14	2.52399582	6	1.83543707	41	7.66405805	10	4.09174776	26	5.13367044	8	2.34104161	21	2.27376776
5	4.13044584	4	3.93193907	0	0	5	5.09602001	0	0	0	0	1	1.59553134	0	0
3	2.21462202	1	0.87841192	0	0	1	0.91077805	1	1.9936388	0	0	1	1.42579396	1	0.52755098
250	33.7507247	247	39.678926	68	18.5352958	200	33.3125044	57	20.7819391	146	25.686791	53	13.8196605	246	23.7336359
22	4.3617508	15	3.53874516	13	5.2039011	36	8.80592259	9	4.81890979	26	6.71777446	14	5.3609853	41	5.80908992
47	4.97164639	55	6.92285004	24	5.12579377	45	5.87285233	8	2.28539082	39	5.37626767	17	3.47319932	53	4.00649234
26	4.10040623	27	5.06683967	14	4.45788731	25	4.86438274	10	4.25913744	22	4.52157896	6	1.82760862	31	3.49382626
190	8.52806152	181	9.66707659	118	10.6936569	154	8.52808731	108	13.0914755	166	9.70998846	98	8.49573996	318	10.2002289
0	0	0	0	0	0	0	0	0	0	1	1.1898892	0	0	0	0
21	4.1874175	32	7.59270993	13	5.23380858	27	6.6423985	9	4.84660467	23	5.97679978	21	8.08769333	35	4.98747908
39	2.81902928	26	2.23629035	7	1.02159918	17	1.51606595	14	2.73294652	17	1.60139255	3	0.41882698	19	0.98146463
42	5.7370917	39	6.33909075	35	9.65290559	30	5.05589387	32	11.8048534	22	3.91632824	31	8.17866851	79	7.71179836

gsyne_3097	Synechococcus_assembled_mapped	fatty acid/phospholipid synthesis prote	plsX			GO:0003824,GO:0008610	TIGR00182	2698912	2700178	1	176	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Phospholipids		Glycerolipid and Glycerophospho
gsyne_3098	Synechococcus_assembled_mapped	3-oxoacyl-[acyl-carrier-protein] synthase III, chloropl		2.3.1.180		GO:0033818,GO:0004315,GO	UniRef100_C	2700233	2701226	1	92,703	fig|1129.58.peg.3075				
gsyne_3099	Synechococcus_assembled_mapped	acyl transferase domain protein					PF00698.16	2701334	2702177	1	703	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Fatty acids		Fatty Acid Biosynthesis FASII
gsyne_31	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF03928.9	25363	25792	-1	156	fig|1129.58.peg.30				
gsyne_310	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11237.3	261835	262357	1	156	fig|1129.58.peg.309				
gsyne_3100	Synechococcus_assembled_mapped	acyltransferase family protein					PF01553.16	2702266	2702953	1	703	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Phospholipids		Glycerolipid and Glycerophospho
gsyne_3101	Synechococcus_assembled_mapped	tRNA threonylcarbamoyl adenosine mo	yeaZ				TIGR03725	2703543	2704185	-1	145	fig|1129.58.(	Protein Metabolism	Protein biosynthesis		Ribosome biogenesis bacterial
gsyne_3102	Synechococcus_assembled_mapped	hypothetical chloroplast Ycf34 family protein					PF10718.4	2704181	2704433	-1	185					
gsyne_3103	Synechococcus_assembled_mapped	poly A polymerase head domain protein					PF01743.15	2704431	2705715	1	166	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	tRNA nucleotidyltransferase	
gsyne_3104	Synechococcus_assembled_mapped	RNA recognition motif family protein					PF14259.1	2705919	2706348	1	185	fig|1129.58.peg.3081				
gsyne_3105	Synechococcus_assembled_mapped	squalene/phytoene synthase family protein					PF00494.14	2707288	2708206	-1	703	fig|1129.58.peg.3083				
gsyne_3106	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein					PF00561.15	2706356	2707292	1	703	fig|1129.58.(	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental	
gsyne_3107	Synechococcus_assembled_mapped	phytoene desaturase	pds	1.14.99.-		GO:0016117,GO:0016166	TIGR02731	2708216	2709605	-1	76	fig|1129.58.(	Protein Metabolism	Protein processing and modific	Protein deglycation	
gsyne_3108	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhM	1.6.5.-		GO:0006810,GO:0048038,GO	UniRef100_P	2709733	2710081	1	141,703	fig|1129.58.peg.3085				
gsyne_3109	Synechococcus_assembled_mapped	bacterial regulatory helix-turn-helix , lysR family protein					PF00126.22	2710712	2711708	-1	261	fig|1129.58.(	Carbohydrates	CO2 fixation	CO2 uptake, carboxysome	
gsyne_311	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF14233.1	262382	262979	1	156	fig|1129.58.peg.310				
gsyne_3110	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11371.3	2710077	2710722	1	156	fig|1129.58.peg.3086				
gsyne_3111	Synechococcus_assembled_mapped	nnrU family protein					PF07298.6	2711849	2712551	1	185	fig|1129.58.peg.3088				
gsyne_3112	Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, 1.6.-.-				GO:0050136,GO:0055114	TIGR01974	2712597	2714610	1	112	fig|1129.58.peg.3089				
gsyne_3113	Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, chain M family protein					TIGR01972	2714929	2716561	1	112	fig|1129.58.peg.3091				
gsyne_3114	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_B	2716650	2717010	1	156	fig|1129.58.peg.3092				
gsyne_3115	Synechococcus_assembled_mapped	scpA/B family protein					PF02616.9	2717074	2717956	1	93,170	fig|1129.58.peg.3093				
gsyne_3116	Synechococcus_assembled_mapped	methylenetetrahydrofolate reductase family protein					PF02219.12	2719167	2720052	-1	703	fig|1129.58.(	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis	
gsyne_3117	Synechococcus_assembled_mapped	bacterial transferase hexapeptide family protein					PF00132.19	2718002	2719184	1	703	fig|1129.58.peg.3094				
gsyne_3118	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2720366	2720537	-1	856					
gsyne_3119	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein					PF00196.14	2720145	2720385	1	261	fig|1129.58.peg.3096				
gsyne_312	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	263016	263265	1	156	fig|1129.58.peg.311				
gsyne_3120	Synechococcus_assembled_mapped	CYTH domain protein					PF01928.16	2720565	2721084	-1	264	fig|1129.58.peg.3098				
gsyne_3121	Synechococcus_assembled_mapped	ATP-NAD kinase family protein					PF01513.16	2721092	2722004	-1	163	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynth	
gsyne_3122	Synechococcus_assembled_mapped	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L family protein					PF00420.19	2722031	2722361	-1	703	fig|1129.58.peg.3100				
gsyne_3123	Synechococcus_assembled_mapped	NADH-ubiquinone/plastoquinone oxidoreductase chain 6 family protein					PF00499.15	2722360	2722960	-1	703	fig|1129.58.peg.3101				
gsyne_3124	Synechococcus_assembled_mapped	NADH-plastoquinone oxidoreductase, I ndhI		1.6.5.3		GO:0009507,GO:0019684,GO	TIGR00403	2722959	2723562	-1	112	fig|1129.58.peg.3102				
gsyne_3125	Synechococcus_assembled_mapped	NADH dehydrogenase family protein					PF00146.16	2723626	2724745	-1	703	fig|1129.58.peg.3103				
gsyne_3126	Synechococcus_assembled_mapped	2-methylcitrate synthase/citrate synthase II family protein					TIGR01800	2724818	2725961	-1	703	fig|1129.58.(	Carbohydrates	Central carbohydrate metaboli	TCA Cycle	
gsyne_3127	Synechococcus_assembled_mapped	phosphohistidine phosphatase SixA	sixA	3.1.3.-		GO:0000160,GO:0008969	TIGR00249	2726053	2726611	-1	263	fig|1129.58.peg.3105				
gsyne_3128	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11832.3	2726614	2728213	-1	156	fig|1129.58.peg.3106				
gsyne_3129	Synechococcus_assembled_mapped	rhodanese-like domain protein					PF00581.15	2728290	2728635	1	157	fig|1129.58.peg.3107				
gsyne_313	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	263381	263663	1	856	fig|1129.58.peg.312				
gsyne_3130	Synechococcus_assembled_mapped	hrcA C terminal domain protein					PF01628.16	2728697	2729690	1	157	fig|1129.58.(	Stress Response	Heat shock	Heat shock dnaK gene cluster ex	
gsyne_3131	Synechococcus_assembled_mapped	tryptophan synthase, beta subunit	trpB	4.2.1.20		GO:0000162,GO:0004834	TIGR00263	2729696	2730950	-1	70	fig|1129.58.(	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn	
gsyne_3132	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2730966	2731188	-1	856	fig|1129.58.peg.3110				
gsyne_3133	Synechococcus_assembled_mapped	translation initiation factor SUI1 family protein					PF01253.17	2731247	2731571	1	169	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	Translation initiation factors bacte	
gsyne_3134	Synechococcus_assembled_mapped	PDZ domain family protein					PF00595.19	2731578	2732712	1	157	fig|1129.58.peg.3112				
gsyne_3135	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF01594.11	2733346	2734423	-1	156	fig|1129.58.peg.3114				
gsyne_3136	Synechococcus_assembled_mapped	adenylylsulfate kinase	cysC	2.7.1.25		GO:0004020,GO:0006790	TIGR00455	2732718	2733366	1	106	fig|1129.58.(	Amino Acids and Derivatives	Lysine, threonine, methionine,	Cysteine Biosynthesis	
gsyne_3137	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	2734435	2735029	-1	88	fig|1129.58.peg.3115				
gsyne_3138	Synechococcus_assembled_mapped	N5-carboxyaminoimidazole ribonucleot	purE	5.4.99.18		GO:0006189,GO:0004638,GO	UniRef100_C	2735102	2735609	-1	92,703	fig|1129.58.(	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis	
gsyne_3139	Synechococcus_assembled_mapped	putative n-acetylglucosamine-6-phosphate deacetylase				GO:0016787,GO:0008448	UniRef100_A	2735677	2736811	1	703	fig|1129.58.(	Cell Wall and Capsule	Capsular and extracellular poly	Sialic Acid Metabolism	
gsyne_314	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	264453	264567	-1	88	fig|1129.58.peg.314				
gsyne_3140	Synechococcus_assembled_mapped	magnesium protoporphyrin O-methyltr	bchM	2.1.1.11		GO:0015995,GO:0046406	TIGR02021	2736854	2737580	1	191	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_3141	Synechococcus_assembled_mapped	putative lipoprotein				GO:0008150,GO:0003674,GO	lipoP	2737648	2738230	-1	88	fig|1129.58.peg.3119				
gsyne_3142	Synechococcus_assembled_mapped	RNA pseudouridylate synthase family protein					PF00849.17	2738268	2739318	-1	168	fig|1129.58.peg.3120				
gsyne_3143	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein					PF00196.14	2739310	2740057	-1	261	fig|1129.58.peg.3121				
gsyne_3144	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2740066	2740672	-1	156	fig|1129.58.peg.3122				
gsyne_3145	Synechococcus_assembled_mapped	aminotransferase class-V family protein					PF00266.14	2740655	2741804	1	703	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_3146	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2742659	2743997	-1	156	fig|1129.58.peg.3125				
gsyne_3147	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	2741839	2742673	1	88	fig|1129.58.peg.3124				
gsyne_3148	Synechococcus_assembled_mapped	16S rRNA (cytosine(1402)-N(4))-methyl	rsmH	2.1.1.199		GO:0000154,GO:0016434	TIGR00006	2743993	2744923	-1	89	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	16S rRNA modification within P s	
gsyne_3149	Synechococcus_assembled_mapped	NAD(P)H-quinone oxidoreductase subu	ndhH	1.6.5.-		GO:0006810,GO:0016651,GO	UniRef100_P	2744982	2746167	1	141,703	fig|1129.58.peg.3127				
gsyne_315	Synechococcus_assembled_mapped	polyphosphate kinase 2	ppk2	2.7.4.1		GO:0005575,GO:0006793,GO	TIGR03707	263689	264463	1	703	fig|1129.58.peg.313				
gsyne_3150	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF10825.3	2746274	2746589	1	156	fig|1129.58.peg.3128				
gsyne_3151	Synechococcus_assembled_mapped	1,4-dihydroxy-2-naphthoyl-CoA hydrolase		3.1.2.28		GO:0016790	UniRef100_C	2746585	2747035	1	703	fig|1129.58.peg.3129				
gsyne_3152	Synechococcus_assembled_mapped	TM2 domain protein					PF05154.11	2747200	2747482	-1	157	fig|1129.58.peg.3130				
gsyne_3153	Synechococcus_assembled_mapped	AMP-binding enzyme family protein					PF00501.23	2747531	2748779	-1	185	fig|1129.58.peg.3131				
gsyne_3154	Synechococcus_assembled_mapped	o-succinylbenzoate synthase	menC	4.2.1.113		GO:0009234	TIGR01927	2748760	2749738	-1	81	fig|1129.58.(	Miscellaneous	Miscellaneous - no subcategor	Muconate lactonizing enzyme far	
gsyne_3155	Synechococcus_assembled_mapped	1,4-dihydroxy-2-naphthoate phytyltran	menA	2.5.1.-		GO:0004659,GO:0042372	TIGR02235	2749734	2750598	1	141,703	fig|1129.58.peg.3133				
gsyne_3156	Synechococcus_assembled_mapped	isochorismate synthase family protein		5.4.4.2		GO:0005737,GO:0008909,GO	TIGR00543	2750720	2752154	1	81	fig|1129.58.(	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn	
gsyne_3157	Synechococcus_assembled_mapped	ion transport family protein					PF00520.26	2752150	2753002	1	145	fig|1129.58.(	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis	
gsyne_3158	Synechococcus_assembled_mapped	glutathione synthase	gshB	6.3.2.3		GO:0004363,GO:0006750	TIGR01380	2753009	2754005	-1	86	fig|1129.58.(	Stress Response	Heat shock	Heat shock dnaK gene cluster ex	
gsyne_3159	Synechococcus_assembled_mapped	glutaredoxin family protein					PF00462.19	2754001	2754187	-1	112	fig|1129.58.(	Stress Response	Oxidative stress	Glutathione: Redox cycle	
gsyne_316	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	264600	264798	1	156	fig|1129.58.peg.315				
gsyne_3160	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2754315	2755110	1	856	fig|1129.58.peg.3138				
gsyne_3161	Synechococcus_assembled_mapped	fusaric acid resistance family protein					PF04632.7	2755106	2756132	1	94	fig|1129.58.peg.3139				
gsyne_3162	Synechococcus_assembled_mapped	peptide chain release factor 2	prfB			GO:0003747,GO:0006415	TIGR00020	2756218	2757289	1	169	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	Translation termination factors ba	
gsyne_3163	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11688.3	2757257	2757488	1	156	fig|1129.58.peg.3141				
gsyne_3164	Synechococcus_assembled_mapped	putative rRNA maturation factor YbeY				GO:0008150,GO:0046872	TIGR00043	2757491	2758061	1	156	fig|1129.58.peg.3142				
gsyne_3165	Synechococcus_assembled_mapped	prokaryotic diacylglycerol kinase family protein					PF01219.14	2758163	2758619	1	703	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Phospholipids		Glycerolipid and Glycerophospho
gsyne_3166	Synechococcus_assembled_mapped	glutamine amidotransferase of anthranilate synthase/aminodeox				GO:0016884	TIGR00566	2758642	2759239	1	703	fig|1129.58.(	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn	
gsyne_3167	Synechococcus_assembled_mapped	beta-lactamase superfamily domain protein					PF13483.1	2759335	2760040	1	157	fig|1129.58.peg.3145				
gsyne_3168	Synechococcus_assembled_mapped	aminotransferase class I and II family protein					PF00155.16	2760077	2761130	-1	703	fig|1129.58.(	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis	
gsyne_3169	Synechococcus_assembled_mapped	arginine--tRNA ligase	argS	6.1.1.19		GO:0004814,GO:0005737,GO	TIGR00456	2761203	2762997	-1	137	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Arg	
gsyne_3170	Synechococcus_assembled_mapped	adenylate and Guanylate cyclase catalytic domain protein					PF00211.15	2763041	2765111	-1	157	fig|1129.58.peg.3148				
gsyne_3171	Synechococcus_assembled_mapped	ABC transporter, phosphonate, periplasmic substrate-binding family protein					PF12974.2	2765110	2766049	-1	141	fig|1129.58.peg.3149				
gsyne_3172	Synechococcus_assembled_mapped	HAMP domain protein					PF00672.20	2766045	2766978	-1	129	fig|1129.58.peg.3150				
gsyne_3173	Synechococcus_assembled_mapped	nicotinate-nucleotide diphosphorylase	nadC	2.4.2.19		GO:0004514,GO:0019363	TIGR00078	2767077	2767932	-1	163	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynth	
gsyne_3174	Synechococcus_assembled_mapped	tRNA modification GTPase TrmE	trmE	3.6.-.-		GO:0003924,GO:0006400	TIGR00450	2767984	2769334	-1	168	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria	
gsyne_3175	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2769380	2769677	-1	156	fig|1129.58.peg.3153				
gsyne_3176	Synechococcus_assembled_mapped	methyltransferase domain protein					PF08242.7	2769673	2770486	-1	703	fig|1129.58.peg.3154				
gsyne_3177	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein					PF00027.24	2770500	2771649	-1	157	fig|1129.58.peg.3155				
gsyne_3178	Synechococcus_assembled_mapped	voltage gated chloride channel family protein					PF00654.15	2771645	2772917	-1	143	fig|1129.58.peg.3156				
gsyne_3179	Synechococcus_assembled_mapped	relA/SpoT family protein				GO:0003824,GO:0015968,GO	TIGR00691	2772913	2775244	-1	149	fig|1129.58.(	Regulation and Cell signaling	Regulation and Cell signaling -	Stringent Response, (p)ppGpp m	
gsyne_318	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	265287	265665	-1	856	fig|1129.58.peg.316				
gsyne_3180	Synechococcus_assembled_mapped	pseudouridine synthase, RluA family protein		5.4.99.-		GO:0001522,GO:0009451,GO	TIGR00005	2776966	2778181	-1	168	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	RNA pseudouridine syntheses	
gsyne_3181	Synechococcus_assembled_mapped	nickel import ATP-binding protein NikE	nikE	3.6.3.24		GO:0005524,GO:0009898,GO	TIGR02769	2775359	2776991	1	145	fig|1129.58.peg.3158				
gsyne_3182	Synechococcus_assembled_mapped	ribosome biogenesis GTP-binding prote	ylqF			GO:0003924,GO:0005525,GO	TIGR03596	2778177	2779143	-1	185	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	Universal GTPases	
gsyne_3183	Synechococcus_assembled_mapped	universal stress family protein					PF00582.21	2779139	2779517	-1	149	fig|1129.58.peg.3161				
gsyne_3184	Synechococcus_assembled_mapped	phosphoglycerate kinase	pgk	2.7.2.3		GO:0005524,GO:0006096,GO	UniRef100_C	2779641	2780847	1	92,141,703	fig|1129.58.(	Carbohydrates	CO2 fixation	Calvin-Benson cycle	
gsyne_3185	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2780927	2781311	-1	856	fig|1129.58.peg.3163				
gsyne_3186	Synechococcus_assembled_mapped	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein					PF02518.21	2781358	2782612	-1	703	fig|1129.58.peg.3164				
gsyne_3187	Synechococcus_assembled_mapped	transcriptional regulatory , C terminal family protein					PF00486.23	2782622	2783363	-1	261	fig|1129.58.peg.3165				
gsyne_3188	Synechococcus_assembled_mapped	EF hand family protein					PF13202.1	2783491	2783965	1	185	fig|1129.58.peg.3166				
gsyne_3189	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	2784832	2785573	-1	156	fig|1129.58.peg.3168				
gsyne_319	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	265143	265308	1	856					
gsyne_3190	Synechococcus_assembled_mapped	NAD binding domain of 6-phosphogluconate dehydrogenase family protein					PF03446.10	2783961	2784843	1	157	fig|1129.58.(	Carbohydrates	Organic acids	Glycerate metabolism	
gsyne_3191	Synechococcus_assembled_mapped	aminotransferase class I and II family protein					PF00155.16	2786664	2787804	-1	703	fig|1129.58.(	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis	
gsyne_3192	Synechococcus_assembled_mapped	glycosyltransferase family 28 C-terminal domain protein					PF04101.11	2785627	2786704	1	703	fig|1129.58.peg.3169				
gsyne_3193	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	2787775	2787892	-1	856					
gsyne_3194	Synechococcus_assembled_mapped	pentapeptide repeats family protein					PF13599.1	2787898	2788717	1	185	fig|1129.58.peg.3171				
gsyne_3195	Synechococcus_assembled_mapped	bacterial type II and III secretion system family protein					PF00263.16	2788721	2789366	-1	97	fig|1129.58.(	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus	
gsyne_32	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein					TIGR03798	25799	26057	-1	157	fig|1129.58.peg.31				
gsyne_320	Synechococcus_assembled_mapped	ribonucleoside-triphosphate reductase,	nrdJ	1.17.4.2		GO:0016960	TIGR02505	266768	268742	-1	123	fig|1129.58.(	Nucleosides and Nucleotides	Nucleosides and Nucleotides -	Ribonucleotide reduction	
gsyne_321	Synechococcus_assembled_mapped	mechanosensitive ion channel family protein					PF00924.13	269205	271458	1	141	fig|1129.58.(	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis	
gsyne_322	Synechococcus_assembled_mapped	methyltransferase domain protein					PF08242.7	271441	272107	1	703	fig|1129.58.peg.320				
gsyne_323	Synechococcus_assembled_mapped	peptide chain release factor 3	prfC			GO:0003747,GO:0005525,GO	TIGR00503	272119	273766	1	169	fig|1129.58.(	Protein Metabolism	Protein biosynthesis	Translation termination factors ba	
gsyne_324	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	273921	274104	1	856	fig|1129.58.peg.322				
gsyne_325	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF11833.3	274168	274873	1	156	fig|1129.58.peg.323				
gsyne_326	Synechococcus_assembled_mapped	hsp33 family protein					PF01430.14	274875	275790	-1	95	fig|1129.58.(	Virulence, Disease and Defense	Adhesion	Streptococcus pyogenes recomb	
gsyne_327	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	275844	276501	-1	141	fig|1129.58.peg.325				
gsyne_328	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF12049.3	276572	277034	1	156	fig|1129.58.peg.326				
gsyne_329	Synechococcus_assembled_mapped	RNA methyltransferase, RsmE family protein		2.1.1.-		GO:0016436,GO:0031167	TIGR00046	277036	277804	1	156	fig|1129.58.(	RNA Metabolism	RNA processing and modificat	RNA methylation	
gsyne_33	Synechococcus_assembled_mapped	SMP-30/Gluconolaconase/LRE-like region family protein					PF08450.7	26070	26991	-1	185	fig|1129.58.peg.32				
gsyne_330	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	277810	278203	-1	856	fig|1129.58.peg.328				
gsyne_331	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	PF01940.11	278380	279109	1	156	fig|1129.58.peg.329				
gsyne_332	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein					TIGR02937	279112	279904	-1	135	fig|1129.58.peg.330				
gsyne_333	Synechococcus_assembled_mapped	GDSL-like Lipase/Acylhydrolase family protein					PF00657.17	280019	280697	-1	177	fig|1129.58.peg.331				
gsyne_334	Synechococcus_assembled_mapped	putative membrane protein				GO:0008150,GO:0003674,GO	TMHMM	280693	282235	-1	88	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter alkylphosphonat	
gsyne_335	Synechococcus_assembled_mapped	ABC transporter family protein					PF00005.22	282231	282981	-1	141	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter alkylphosphonat	
gsyne_336	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	283150	283381	-1	856	fig|1129.58.peg.334				
gsyne_337	Synechococcus_assembled_mapped	phosphate/phosphite/phosphonate AB	phnD			GO:0030288,GO:0031362,GO	TIGR01098	283441	284401	-1	143	fig|1129.58.(	Membrane Transport	ABC transporters	ABC transporter alkylphosphonat	
gsyne_338	Synechococcus_assembled_mapped	aspartate aminotransferase	aspC	2.6.1.1		GO:0004069,GO:0030170,GO	UniRef100_C	284476	285724	-1	141,703	fig|1129.58.(	Amino Acids and Derivatives	Glutamine, glutamate, aspartat	Glutamine, Glutamate, Aspartate	
gsyne_339	Synechococcus_assembled_mapped	glyoxalase-like domain protein					PF12681.2	285802	286216	1	157	fig|1129.58.peg.337				
gsyne_34	Synechococcus_assembled_mapped	cupin domain protein					PF07883.6	26987	27449	-1	157	fig|1129.58.peg.33				
gsyne_340	Synechococcus_assembled_mapped	uracil-DNA glycosylase, 4 family protein		3.2.2.-		GO:0004844,GO:0006281	TIGR00758	286226	286871	1	132	fig|1129.58.(	DNA Metabolism	DNA repair	Uracil-DNA glycosylase	
gsyne_341	Synechococcus_assembled_mapped	4-hydroxy-3-methylbut-2-en-1-yl dipho	ispG	1.17.7.1		GO:0005737,GO:0019288,GO	TIGR00612	286914	288141	1	76	fig|1129.58.(	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis	
gsyne_342	Synechococcus_assembled_mapped	C-terminal processing peptidase family protein		3.4.21.-		GO:0006508,GO:0019132	TIGR00225	288220	289564	1	138,140	fig|1129.58.peg.340				
gsyne_343	Synechococcus_assembled_mapped	hypothetical protein				GO:0008150,GO:0003674,GO	default	289598	289790	-1	856	fig|1129.58.peg.341				
gsyne_344	Synechococcus_assembled_mapped	transcription-repair coupling factor	mfd	3.6.1.-		GO:0003690,GO:0005515,GO	TIGR00580	289871	293429	-1	132	fig|1129.58.(	RNA Metabolism	Transcription	Transcription factors bacterial	
gsyne_345	Synechococcus_assembled_mapped	DNA polymerase I,gase family protein					PF13298.1	294188	294572	-1	132	fig|1129.58.peg.344				
gsyne_346	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	293524	294214	1	156	fig|1129.58.peg.343				
gsyne_347	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	294580	295378	-1	156	fig|1129.58.peg.345				
gsyne_348	Synechococcus_assembled_mapped	integral membrane , YkoY family protein				GO:0003674,GO:0008150,GO	TIGR03716	295455	296193	1	88	fig|1129.58.peg.346				
gsyne_349	Synechococcus_assembled_mapped	conserved hypothetical protein				GO:0008150,GO:0003674,GO	UniRef100_A	296204	296549	1	156	fig|1129.58.peg.347				
gsyne_35	Synechococcus_assembled_mapped	rutC family protein PH0854					UniRef100_C	27460	27811	-1	185	fig|1129.58.peg.34				



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0.92119061	-1.0432873	0.9347461	-1.0500996	0.47236188	-1.277824	0.58009603	-1.2168598
0.49025197	1.32909793	0.88278812	-1.0776396	0.37262866	1.52782229	0.26778173	1.64644184
0.00180944	2.76277741	0.64802853	-1.1631807	0.51488613	1.25828034	0.24150118	1.46360737
0.29315548	1.4108696	1	-1.0210869	0.66135244	1.1802065	0.62417115	1.2050934
1	1.00129568	1	-1.099791	0.3798158	-1.6118309	0.57642366	-1.4655792
0.49871346	-1.2666522	1	-1.0154782	0.65992021	1.18891218	0.65992021	1.20731437
0.1326947	-1.9842339	0.51063994	-1.390394	0.1326947	-2.0512864	0.40562272	-1.4753274
0.74243739	-1.0981544	0.63542032	1.17492487	0.37999833	-1.2835712	0.15649359	-1.5080997
0.90967277	-1.0420396	0.55509484	-1.2421089	0.73995799	-1.1289324	0.79778033	1.10025085
0.79840499	-1.2051601	0.5029087	1.40917756	0.38979469	1.50659077	0.92521568	1.0691277
0.59381695	1.17709125	0.22519257	1.45432099	0.4058928	1.30588631	0.7244514	-1.1136658
0.46224503	-1.3841118	0.28626747	-1.8593117	0.78974318	-1.1391738	0.50977912	1.63215796
1	1.00991721	0.93552464	1.10763947	0.41946405	1.38443137	0.51723233	1.2498935
0.41324458	1.3317971	0.95172538	1.06293416	0.57092869	1.23952307	0.6551201	1.16613344
0.94243355	-1.0823861	0.10840795	2.15803609	0.43167952	1.47798334	0.49440994	-1.4601221
1	1.1527569	0.71065392	-1.7646978	0.71065392	-2.1369239	1	-1.2109291
0.00994626	-2.4382647	0.49849531	-1.3103876	0.57678309	-1.2158119	0.90428423	1.07778809

47	3.86421805	59	5.77212383	37	6.14204514	74	7.50636503	52	11.5460977	70	7.50024947	28	4.44631482	97	5.69930074
34	3.56391339	42	5.23862577	16	3.38622428	30	3.87974938	13	3.68010063	20	2.73207188	10	2.02454128	41	3.07127111
25	3.08681006	18	2.64461382	6	1.49578324	15	2.28504812	6	2.0007336	13	2.09183369	8	1.90782395	20	1.76476128
26	6.30831728	29	8.37255557	9	4.40889954	34	10.1777854	12	7.86302296	32	10.1182187	16	7.49788153	56	9.70988934
18	3.589215	5	1.18636093	13	5.23380858	9	2.21413283	5	2.69255815	11	2.85846946	6	2.31076952	15	2.13749104
12	1.81811764	5	0.90142708	5	1.52953089	9	1.68235421	4	1.6366991	6	1.18469318	4	1.17052081	14	1.51584517
14	2.2698151	14	2.70091142	8	2.6187856	8	1.60024554	7	3.06498676	10	2.11288737	7	2.19199165	21	2.433144
6	2.4782675	8	3.93193907	7	5.83770957	11	5.60562202	6	6.69293026	6	3.22969926	3	2.39329701	1	0.29517733
29	2.35087992	22	2.12214469	27	4.4192007	20	2.00030692	30	6.56782876	27	2.85239795	21	3.28798748	40	2.31728
37	8.97722074	32	9.23868201	16	7.83804362	83	24.8457703	54	35.3836033	65	20.5526317	21	9.84096951	54	9.36310758
18	2.04092618	12	1.61903374	3	0.68678936	12	1.67868895	11	3.36833745	8	1.18211215	4	0.87597799	15	1.21543608
21	2.33529053	21	2.77882232	6	1.34716375	57	7.82043071	15	4.50485691	50	7.24612014	16	3.43652904	32	2.54306626
34	2.54785169	17	1.51587716	10	1.51301328	17	1.57173144	16	3.23804833	14	1.3672161	14	2.02629034	20	1.07105382
58	17.3478725	30	10.6772483	21	12.6819208	43	15.867952	19	15.3475815	20	7.7958258	13	7.51000095	58	12.397448
81	8.46492575	63	7.83427017	40	8.44006203	67	8.63867489	25	7.05579997	94	12.8020609	28	5.65164113	109	8.14049296
17	2.96395812	16	3.31942595	8	2.8161815	12	2.58130059	8	3.76687532	16	3.63544037	6	2.02047185	29	3.61332655
34	5.48676898	22	4.22454849	27	8.79729257	35	6.96851109	25	10.8954679	32	6.72979195	19	5.92201864	46	5.30495449
8	1.18617932	15	2.64649745	2	0.59873944	15	2.74401078	5	2.00215863	13	2.51198831	7	2.00464194	18	1.90729969
79	4.08489398	73	4.49155186	92	9.60481575	91	5.8053617	50	6.98219252	114	7.68196724	61	6.09202875	162	5.98624911
133	8.48259943	107	8.12046608	76	9.7867484	124	9.7573795	79	13.6073178	119	9.89095398	70	8.62290833	217	9.89061109
28	8.09567384	31	10.6653847	9	5.25393862	21	7.49114942	8	6.24673491	15	5.65197371	11	6.14279565	24	4.9589792
1207	142.441375	753	105.741076	660	157.260748	639	93.0387654	450	143.419934	817	125.650681	311	70.887178	1051	88.6375364
29	3.41076816	19	2.6590571	18	4.27439074	30	4.35321032	32	10.1641788	34	5.21131135	16	3.6345663	33	2.77366633
120	10.567232	82	8.59238462	56	9.95670262	130	14.1239946	43	10.2262539	166	19.0503073	39	6.63319881	163	10.2577869
8	4.86957825	8	5.79443653	3	3.68697447	3	2.25297727	1	1.64387761	3	2.3797784	1	1.17565467	4	1.7399927
54	23.4196279	43	22.1908811	21	18.3887852	39	20.868202	17	19.9114675	36	20.3471053	15	12.5648093	42	13.0173204
10	4.18021025	5	2.48706989	6	5.06403722	16	8.25186855	3	3.38678399	8	4.3581484	2	1.61475461	11	3.28607055
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25	2.85326851	28	3.80259897	16	3.68697447	27	3.80189914	28	8.63035744	29	4.31334835	19	4.18826976	46	3.75185926
17	5.36206969	11	4.12853602	16	10.1894567	23	8.95046424	10	8.51827488	13	5.34368423	3	1.82760862	17	3.83193847
39	6.76567028	37	7.63779164	32	11.2084024	49	10.4876092	22	10.3071126	55	12.4343422	15	5.02592372	61	7.56244328
31	5.35108506	37	7.59979268	22	7.66743944	35	7.45388002	12	5.59409096	29	6.52367114	23	7.66807598	58	7.15474611
67	6.23221157	63	6.97313055	60	11.2685011	69	7.91864129	43	10.8019947	96	11.6373078	47	8.44391116	104	6.91332221
45	4.09792264	41	4.44278155	22	4.04502711	30	3.37059592	25	6.14836113	33	3.91632824	10	1.75885344	63	4.09994343
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17	5.12893622	6	2.1540188	6	3.65491382	10	3.72231027	5	4.07395755	12	4.71816935	8	4.66172634	25	5.39019478
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28	2.9349875	20	2.4945837	12	2.53966821	17	2.19852465	13	3.68010063	10	1.36603594	9	1.82208715	29	2.17236249
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12	5.62633703	2	1.11582055	4	3.78662243	4	2.31386855	3	3.79869015	5	3.05512092	1	0.90557184	10	3.35066162
11	3.53382588	6	2.29363112	3	1.94590319	4	1.58542845	5	4.33801035	3	1.25599416	4	2.48193764	7	1.60707659
18	1.65217834	12	1.31064636	14	2.59453759	10	1.13244889	13	3.22252198	8	0.95694793	19	3.36834394	36	2.36141867
46	4.44569435	79	9.08507927	40	7.80529414	44	5.24648746	45	11.7452537	56	7.05315939	30	5.599915	102	7.04478939
58	9.31645006	56	10.7036119	42	13.6213223	69	13.6743204	35	15.1830362	81	16.9559211	48	14.8916258	178	20.432831
22	3.85508278	13	2.71065497	5	1.7690029	9	1.9457531	22	10.4112249	2	0.45672515	7	2.36912229	4	0.50090699
18	3.6954048	11	2.6872128	7	2.90158346	15	3.79939954	14	7.76221498	16	4.28078482	10	3.96522581	11	1.61386897
32	2.93720593	22	2.40285165	14	2.59453759	35	3.96357112	13	3.22252198	26	3.11008077	8	1.41825008	38	2.49260859
4	3.65218369	2	2.1729137	0	0	1	1.12648864	0	0	0	0	0	0	0	0
34	4.87460881	37	6.3122245	2	0.5789464	29	5.12971271	8	3.0975545	19	3.55000001	15	4.15365596	45	4.61062116
67	11.9825511	75	15.9608351	60	21.6657263	88	19.4174123	69	33.3266527	106	24.7055346	43	14.8532453	126	16.1039015
37	3.6678359	19	2.24120527	10	2.00150043	13	1.58995824	82	21.9528113	20	2.58375941	26	4.97805777	18	1.27516608
79	11.007887	74	12.2695448	49	13.7854347	75	12.8935446	33	12.418208	50	9.07947583	32	8.61202457	160	15.9324633
22	3.77874451	19	3.88327646	16	5.54871405	18	3.81444666	23	10.6689284	8	1.79072434	12	3.98092968	32	3.92790432
27	2.44591414	22	2.37148283	14	2.56066634	12	1.34119796	13	3.1804525	16	1.88891027	9	1.57470195	21	1.35951127
27	2.10041506	33	3.05474639	22	3.45550522	28	2.68740786	19	3.99174764	30	3.04142083	25	3.75629575	67	3.72479379
43	5.36660804	31	4.60376319	51	12.8513606	19	2.92562876	24	8.08929701	38	6.18057556	34	8.1957509	100	8.91902734
39	4.36494857	16	2.1308573	13	2.93768611	24	3.31405689	22	6.64975007	28	4.08400681	20	4.32337524	47	3.75922617
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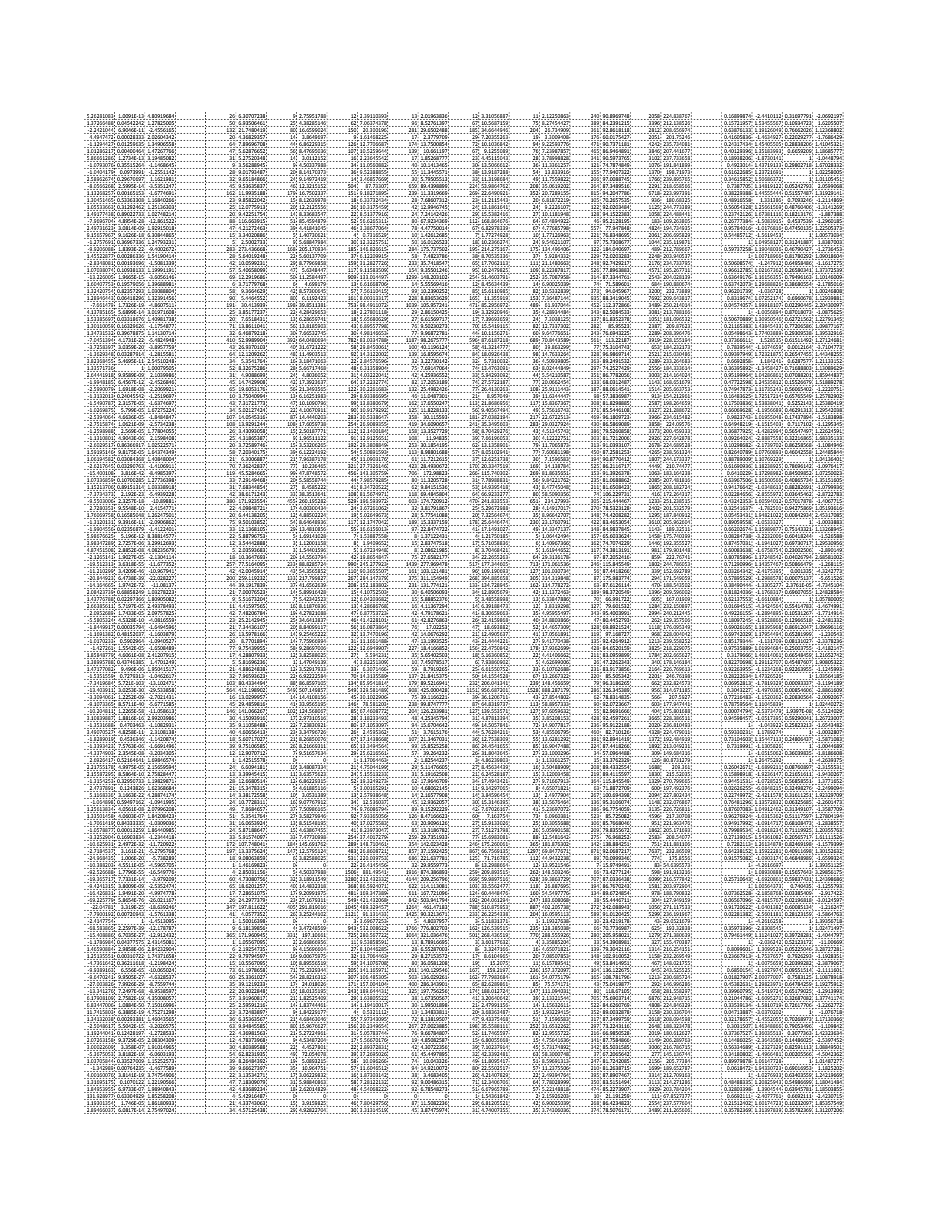
9	2.973921	5	1.96596954	2	1.33433362	3	1.2230448	8	7.13912561	1	0.43062657	1	0.63821254	2	0.47228373
8	1.85043974	6	1.65141441	6	2.8021006	9	2.56839409	7	4.37271444	3	0.90431579	5	2.23374387	13	2.14889099
8	2.95282936	8	3.51364768	3	2.23571856	6	2.73233414	7	6.9777358	5	2.40509519	5	3.5644849	5	1.31887745
28	2.33529053	13	1.29016751	9	1.51555922	9	0.92610364	39	8.78447097	11	1.19560982	5	0.80543649	31	1.84769658
33	3.51214597	23	2.91277081	6	1.28931009	21	2.75747831	13	3.73654389	5	0.69349371	5	1.02779626	20	1.52115926
24	2.89131209	25	3.58379863	12	2.91885479	33	4.90491926	16	5.20561243	12	1.88399124	22	5.11899638	32	2.75498844
92	6.67784214	103	8.89621779	74	10.84495	135	12.0897211	72	14.1139617	124	11.7296191	75	10.5144848	173	8.97388495
33	4.03154784	31	4.50650059	18	4.43994813	22	3.31600176	26	8.57826273	10	1.59210527	11	2.59554746	21	1.83342541
40	4.18021025	21	2.61142339	14	2.95402171	29	3.73912794	19	5.36240798	39	5.31149336	15	3.02766489	40	2.98733687
18	10.0729582	20	13.3178581	7	7.9091549	14	9.66599925	2	3.02261367	2	1.45857386	0	0	3	1.19975303
53	27.8617347	31	19.3916086	7	7.42981218	10	6.48584366	7	9.93798736	9	6.1657895	11	11.1687194	15	5.63520364
17	2.22576478	15	2.33690718	7	1.85044379	9	1.45380797	31	10.9612518	7	1.19437935	3	0.75863	11	1.0292221
35	3.55073414	20	2.41434855	15	3.07247872	19	2.37814267	22	6.02755123	26	3.43745769	16	3.13507912	40	2.89998784
37	3.59591755	33	3.8162938	39	7.65279574	39	4.67634778	38	9.97377843	39	4.93954005	31	5.81899664	101	7.01480251
4	1.80237637	7	3.75321457	1	0.90977292	4	2.22371782	3	3.65068923	1	0.58721805	3	2.61086946	1	0.32201164
16	2.92174695	16	3.47666192	21	7.74264638	19	4.28065681	14	6.90428595	22	5.23551249	7	2.46887481	50	6.52497263
27	6.16305997	20	5.43228424	9	4.14784628	15	4.22433238	11	6.78099513	15	4.4620845	6	2.64522301	15	2.44686474
35	6.10226671	29	6.01645953	26	9.15258988	39	8.38922692	28	13.1840636	44	9.99746103	12	4.04094369	53	6.60366577
22	3.2481123	26	4.56774198	7	2.08667066	31	5.64682388	22	8.77201072	15	2.88611423	9	2.56642913	16	1.68816313
52	5.14011038	30	3.52866327	19	3.79201647	52	6.3417138	22	5.87299863	37	4.7663368	21	4.00928388	64	4.52100668
44	2.55286418	23	1.58789847	21	2.46003815	33	2.36223536	38	5.95424565	34	2.5707974	22	2.46533605	57	2.3633931
71	3.57014188	55	3.29086205	30	3.04576152	66	4.0945413	44	5.97513774	81	5.30794052	19	1.84526668	79	2.83883592
48	5.32075323	34	4.48467172	13	2.90952937	26	3.55581716	26	7.78347161	32	4.62270054	8	1.71277486	52	4.11927985
90	10.0405693	96	12.744034	68	15.3169486	81	11.1489776	61	18.3786574	101	14.6842275	54	11.635579	227	18.0978823
24	2.92174695	27	3.91124465	16	3.93277277	22	3.30436666	19	6.24673491	15	2.3797784	12	2.82157121	37	3.2189865
30	2.31304967	24	2.20188588	10	1.55672255	16	1.52201131	43	8.95365337	24	2.41150878	11	1.63807884	29	1.5978933
25	8.76155178	17	7.08940529	5	3.5380058	14	6.05345408	6	5.67884992	5	2.28362574	3	2.03067625	4	1.00181398
20	2.56057159	16	2.43751204	7	1.80947455	10	1.57957816	14	4.84064329	17	2.83641485	7	1.73094544	27	2.47034019
39	3.53298709	23	2.47927751	12	2.19485686	12	1.34119796	23	5.62695442	9	1.06251203	10	1.74966883	37	2.39532938
31	2.53671721	29	2.82376285	17	2.80870932	9	0.90862998	20	4.41985961	21	2.23946128	10	1.58047916	25	1.46196321
112	5.00118847	85	4.5164165	86	7.7535602	83	4.57264499	72	8.68272034	101	5.87747073	36	3.10481774	157	5.0100369
29	7.98552862	28	9.1745245	13	7.22764042	37	12.5701827	8	5.94927134	19	6.81825399	15	7.97765669	29	5.70676178
52	4.45476233	29	2.95623567	10	1.72969173	38	4.01641874	20	4.62721104	20	2.2328785	12	1.98555011	64	3.91820579
57	3.63539976	55	4.17407135	50	6.43865026	45	3.5409845	37	6.37304756	45	3.74027672	25	3.07961012	76	3.46399282
63	6.78829794	44	5.6414778	30	6.52663182	45	5.98228437	29	8.43891207	49	6.88066364	28	5.82715793	89	6.85324765
46	12.6667006	23	7.53621655	22	12.2313915	42	14.268856	19	14.1295194	43	15.4307854	14	7.44581291	60	11.8070933
89	7.68139629	70	7.18899308	29	5.05353963	93	9.90301203	71	16.5491858	117	13.1598194	29	4.83422182	65	4.00912498
26	7.04757321	14	4.51558628	8	4.37828218	11	3.67868945	13	9.51651021	9	3.17923521	15	7.8530058	30	5.81130375
21	1.74308767	15	1.48153207	8	1.34071799	9	0.92167252	13	2.91414667	11	1.1898892	6	0.96189928	27	1.60158419
16	2.24749765	12	2.00576649	1	0.28361342	4	0.69322378	9	3.41420734	3	0.54917963	5	1.35652462	10	1.00384194
17	3.73308649	13	3.39689673	10	4.43370347	13	3.5220594	6	3.55826672	14	4.00646237	9	3.81715725	37	5.8063997
39	5.47827553	50	8.35736037	31	8.79201604	43	7.45215558	16	6.06970194	39	7.13933521	22	5.96870833	64	6.42458844
5	3.15415864	4	3.00257165	3	3.82104627	1	0.77830124	4	6.8146199	2	1.64421053	1	1.21840575	1	0.45081629
12	1.41615286	9	1.26383756	3	0.71482158	7	1.019204	14	4.46195351	10	1.53795203	2	0.4558661	19	1.60239124
26	2.3739194	11	1.19510253	17	3.1339283	21	2.36562613	27	6.65770431	20	2.3797784	12	2.11617841	30	1.95749179
30	2.89936588	26	2.99002609	15	2.9269853	20	2.38476703	16	4.17609019	13	1.63734057	9	1.6799745	28	1.93386376
0	0	0	0	0	0	0	0	1	2.40259035	0	0	0	0	0	0
47	5.97326013	36	5.44422333	33	8.46788641	15	2.35200924	26	8.92390701	22	3.64376327	20	4.90932719	74	6.72096082
24	3.8730134	14	2.68834904	4	1.3033026	24	4.7784076	30	13.0745614	7	1.47214199	11	3.42853711	11	1.26857607
15	6.05158344	13	6.24081027	5	4.07282063	19	9.45726505	5	5.44773393	6	3.15458998	4	3.11685192	15	4.32469116
189	9.96579911	212	13.3016662	140	14.9047904	247	16.0687269	112	15.9491104	236	16.2172133	70	7.12896981	498	18.765742
76	3.51115396	45	2.47382318	43	4.01099619	39	2.22297757	54	6.73749038	46	2.76954238	40	3.56923122	120	3.96190083
20	3.1257428	18	3.34746164	16	5.0488299	18	3.47080282	7	2.95453678	14	2.85144619	3	0.90557184	16	1.78701953
71	4.48706357	42	3.15844286	35	4.46600732	51	3.97656644	66	11.2646039	45	3.70621227	28	3.41775019	105	4.74219322
10	5.68782705	8	5.41447347	0	0	7	4.91222913	1	1.53608236	5	3.70621227	0	0	2	0.81294741
99	14.6165054	146	25.6496281	79	23.5495688	176	32.0593872	33	13.1580161	149	28.6687347	43	12.2618281	217	22.8957125
38	4.32274856	30	4.06085511	22	5.05296829	41	5.75432555	12	3.68659765	27	4.00270925	16	3.51540019	49	3.98344231
16	2.53484895	13	2.45072915	7	2.23912148	18	3.51834807	11	4.70644411	13	2.68404231	5	1.52996156	19	2.15115536
11	2.4782675	11	2.9489543	15	6.8232969	16	4.44743565	19	11.5605159	16	4.69774438	21	9.13804312	40	6.44023273
41	5.55674042	22	3.54796065	14	3.83099691	16	2.67541051	14	5.12427473	20	3.53248357	12	3.14120232	31	3.00250694
58	6.55489646	67	9.01016005	40	9.1273635	65	9.0632799	26	7.93559158	51	7.51141782	20	4.36562321	87	7.02656662
58	15.3614749	69	21.7457241	45	24.063841	97	31.6964665	30	21.4582497	66	22.7804742	28	14.3232432	111	21.0094157
18	2.57005519	10	1.69898602	5	1.44140977	8	1.40926973	4	1.54240368	9	1.67465888	2	0.5515417	11	1.1224027
17	2.2341957	1	0.15638394	4	1.06140174	4	0.64858437	11	3.90420932	3	0.51381579	6	1.52300719	17	1.59664103
5	0.76760498	9	1.64410727	3	0.92990064	6	1.13645756	7	2.9022441	8	1.60055893	6	1.77908804	8	0.87769543
28	1.89004059	40	3.2128685	29	3.95237924	32	2.66500035	35	6.3804199	48	4.22248619	10	1.30374156	52	2.50843306
17	2.35931066	17	2.8074045	14	3.92294083	16	2.73962036	13	4.87245323	14	2.53208422	4	1.07219706	27	2.67784877
18	8.11069364	28	15.0128583	19	17.2856855	8	4.44743565	11	13.3858605	15	8.80827071	14	12.1840575	40	12.8804655
33	3.57799871	25	3.22541877	48	10.5078772	39	5.21705049	31	9.07728667	44	6.21717108	27	5.65416418	124	9.6080222
42	3.5029358	24	2.38184771	27	4.54667765	28	2.88121132	26	5.85631398	25	2.71729505	20	3.22174597	60	3.57618692
8	2.01134754	3	0.89750783	5	2.5381346	8	2.48154018	5	3.39496463	6	1.9659039	1	0.48559649	9	1.61705844
25	5.63242614	42	11.2596437	11	5.00375106	23	6.39318875	12	7.30137847	19	5.57857145	12	5.22173892	35	5.63520364
18	2.90476005	16	3.0723989	14	4.56155911	10	1.99100317	5	2.17909357	13	2.73397798	0	0	18	2.07585176
63	5.34433236	49	4.94616785	40	6.8511017	54	5.65172293	39	8.93481644	68	7.5175396	16	2.6215087	80	4.84985741
715	55.3737895	668	61.5594211	398	62.2341538	721	68.8918206	220	46.0138955	676	68.2273969	203	30.3649558	1134	62.7620805
23	12.4687834	14	9.03117255	1	1.09457055	15	10.0327894	6	8.78447097	14	9.89095398	7	7.32947208	19	7.36098475
79	2.31109937	42	1.4620448	33	1.94918465	44	1.58810202	51	4.02930203	53	2.02060443	30	1.69508388	92	1.92338148
10	2.71060508	16	5.16067003	6	3.28371163	10	3.34426313	3	2.19611774	5	1.76624178	2	1.04706744	16	3.099362
32	4.82723409	28	5.02604386	16	4.87321843	15	2.7917327	11	4.48135331	23	4.52157896	12	3.49629476	42	4.52776362
32	4.17392421	29	4.50103552	19	5.00375106	29	4.66688149	13	4.57937334	37	6.28941435	15	3.77889001	59	5.49961979
28	3.94910919	13	2.18174668	5	1.4238316	14	2.43614615	24	9.14156328	10	1.83804023	10	2.72407789	20	2.0158452
1	0.30170213	1	0.35900313	1	0.6091523	3	1.11669308	1	0.81479151	1	0.39318078	1	0.58271579	1	0.21560779
139	41.2197313	162	57.164345	28	16.7647044	92	33.6598655	37	29.6319477	41	15.8448494	17	9.73683227	108	22.8875963

gsyne_350	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	296553	297258	1	156	fig|1129.58.peg.348			
gsyne_351	Synechococcus_assembled_mapped	helicase conserved C-terminal domain protein				PF00271.26	297464	298697	1	703	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	ATP-dependent RNA helicases, b
gsyne_352	Synechococcus_assembled_mapped	methionyl-tRNA formyltransferase	fmt	2.1.2.9	GO:0004479,GO:0005737,G	TIGR00460	299494	300532	-1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Translation initiation factors bacte
gsyne_353	Synechococcus_assembled_mapped	dnaJ domain protein				PF00226.26	298715	299498	1	95	fig|1129.58.peg.350			
gsyne_354	Synechococcus_assembled_mapped	modulator of DNA gyrase family protein				PF01523.11	300539	301925	-1	185	fig|1129.58.p	Protein Metabolism	Protein degradation	Putative TldE-TldD proteolytic co
gsyne_355	Synechococcus_assembled_mapped	modulator of DNA gyrase family protein				PF01523.11	301927	303355	-1	185	fig|1129.58.p	Protein Metabolism	Protein degradation	Putative TldE-TldD proteolytic co
gsyne_356	Synechococcus_assembled_mapped	magnesium-protoporphyrin IX monome	acsF	1.14.13.81	GO:0015995,GO:0048529	TIGR02029	303469	304564	-1	191	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis
gsyne_357	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11210.3	304661	305093	-1	156	fig|1129.58.peg.355			
gsyne_358	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	305133	305664	-1	856	fig|1129.58.peg.356			
gsyne_359	Synechococcus_assembled_mapped	polyprenyl P-hydroxybenzoate and phenylacrylic aci		4.1.1.-	GO:0006725,GO:0016831	TIGR00421	305676	306243	-1	703	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Quinone cofactors	Ubiquinone Biosynthesis
gsyne_36	Synechococcus_assembled_mapped	glucose 1-dehydrogenase B	gdhB	1.1.1.47	GO:0030435,GO:0005488,G	UniRef100_P	28030	28837	1	92,141,703	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_360	Synechococcus_assembled_mapped	RNB domain protein				PF00773.14	306310	308620	-1	157	fig|1129.58.p	RNA Metabolism	RNA processing and modificat	RNA processing and degradation
gsyne_361	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01169.14	308625	309024	-1	156	fig|1129.58.peg.359			
gsyne_362	Synechococcus_assembled_mapped	sulfite exporter TauE/SafE family protein				PF01925.14	309058	309412	-1	141	fig|1129.58.peg.360			
gsyne_363	Synechococcus_assembled_mapped	flagellin N-methylase family protein				PF03692.10	309438	309801	-1	91	fig|1129.58.peg.361			
gsyne_364	Synechococcus_assembled_mapped	photosystem II complex subunit Ycf12 family protein				PF05969.6	309888	310017	1	164	fig|1129.58.peg.362			
gsyne_365	Synechococcus_assembled_mapped	single-stranded-DNA-specific exonuclea	recJ	3.1.-.-	GO:0006310,GO:0008297	TIGR00644	310087	311995	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_366	Synechococcus_assembled_mapped	HAD hydrolase, IA, variant 3 family protein			GO:0008152,GO:0016787	TIGR01509	312096	312864	1	703	fig|1129.58.peg.364			
gsyne_367	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	312863	313205	1	156	fig|1129.58.peg.365			
gsyne_368	Synechococcus_assembled_mapped	ribosomal protein L32	rpmF		GO:0000315,GO:0003735,G	TIGR01031	314013	314190	-1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial
gsyne_369	Synechococcus_assembled_mapped	argK family protein				PF03308.11	313201	314050	1	185	fig|1129.58.p	Carbohydrates	CO2 fixation	Photorespiration (oxidative C2 cy
gsyne_37	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	28844	29558	1	88	fig|1129.58.peg.36			
gsyne_370	Synechococcus_assembled_mapped	ATP-dependent zinc metalloprotease F	ftsH2	3.4.24.-	GO:0004222,GO:0005524,G	UniRef100_C	314278	316081	1	##########	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster
gsyne_371	Synechococcus_assembled_mapped	cupin domain protein				PF07883.6	316090	317050	-1	157	fig|1129.58.p	Metabolism of Aromatic Compound	Metabolism of Aromatic Comp	Gentisate degradation
gsyne_372	Synechococcus_assembled_mapped	moaD family protein			GO:0003824,GO:0006777	TIGR01687	317108	317384	-1	82	fig|1129.58.peg.370			
gsyne_373	Synechococcus_assembled_mapped	threonine synthase	thrC	4.2.3.1	GO:0004795,GO:0009088	TIGR00260	317424	318705	-1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Threonine and Homoserine Biosy
gsyne_374	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03699.8	318899	321725	1	156	fig|1129.58.peg.372			
gsyne_375	Synechococcus_assembled_mapped	fructose-bisphosphate aldolase, class II	fba	4.1.2.13	GO:0004332,GO:0006096	TIGR01521	321786	322860	-1	703	fig|1129.58.p	Carbohydrates	CO2 fixation	Calvin-Benson cycle
gsyne_376	Synechococcus_assembled_mapped	oxidoreductase , NAD-binding Rossmann fold family protein				PF01408.17	322911	324021	-1	703	fig|1129.58.peg.374			
gsyne_377	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	324038	324485	-1	156	fig|1129.58.peg.375			
gsyne_378	Synechococcus_assembled_mapped	acetyl-CoA carboxylase, carboxyl transf	accD	6.4.1.2	GO:0003989,GO:0006633,G	TIGR00515	324481	325357	-1	176	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Fatty acids	Fatty Acid Biosynthesis FASII
gsyne_379	Synechococcus_assembled_mapped	type IV leader peptidase family protein				PF01478.13	325392	326238	-1	91,97,140	fig|1129.58.p	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus
gsyne_38	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	30850	32173	-1	157	fig|1129.58.p	Respiration	Electron donating reactions	Respiratory dehydrogenases 1
gsyne_380	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	326252	326525	-1	156	fig|1129.58.peg.378			
gsyne_381	Synechococcus_assembled_mapped	phosphoribulokinase, chromosomal	cfxP	2.7.1.19	GO:0005524,GO:0019253,G	UniRef100_P	326661	327564	-1	119,141,703	fig|1129.58.p	Carbohydrates	CO2 fixation	Calvin-Benson cycle
gsyne_382	Synechococcus_assembled_mapped	3-isopropylmalate dehydrogenase	leuB	1.1.1.85	GO:0003862,GO:0009098	TIGR00169	327644	328730	-1	74	fig|1129.58.p	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios
gsyne_383	Synechococcus_assembled_mapped	UDP-3-O-[3-hydroxymyristoyl] glucosar	lpxD	2.3.1.-	GO:0009245,GO:0016410	TIGR01853	328755	329823	-1	90	fig|1129.58.peg.381			
gsyne_384	Synechococcus_assembled_mapped	glutamate 5-kinase	proB	2.7.2.11	GO:0004349,GO:0006561	TIGR01027	330017	331097	-1	73	fig|1129.58.p	Amino Acids and Derivatives	Proline and 4-hydroxyproline	Proline Synthesis
gsyne_385	Synechococcus_assembled_mapped	mitochondrial PGP phosphatase family protein				PF09419.5	331127	331649	-1	703	fig|1129.58.peg.384			
gsyne_386	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12527.3	331666	332233	-1	156	fig|1129.58.peg.385			
gsyne_387	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03652.10	332258	332714	-1	156	fig|1129.58.peg.386			
gsyne_388	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	332734	333739	-1	156	fig|1129.58.peg.387			
gsyne_389	Synechococcus_assembled_mapped	F420-0:Gamma-glutamyl ligase family protein				PF01996.11	333821	334979	-1	185	fig|1129.58.peg.388			
gsyne_39	Synechococcus_assembled_mapped	voltage gated chloride channel family protein				PF00654.15	29554	30856	1	143	fig|1129.58.peg.37			
gsyne_390	Synechococcus_assembled_mapped	AAA domain protein				PF13604.1	335165	336491	1	157	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism
gsyne_391	Synechococcus_assembled_mapped	glutamine synthetase, type III	glnT	6.3.1.2		TIGR03105	336492	337788	-1	703	fig|1129.58.p	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation
gsyne_392	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	337841	338831	-1	703	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis
gsyne_393	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	338827	339745	-1	121	fig|1129.58.peg.392			
gsyne_394	Synechococcus_assembled_mapped	fumarate hydratase, class II	fumC	4.2.1.2	GO:0004333,GO:0006099	TIGR00979	339825	341202	-1	120	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	TCA Cycle
gsyne_395	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	341222	341792	-1	92	fig|1129.58.peg.394			
gsyne_396	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12452.3	341853	343479	-1	156	fig|1129.58.peg.395			
gsyne_397	Synechococcus_assembled_mapped	ferric uptake regulator family protein				PF01475.14	343520	343967	-1	261	fig|1129.58.p	Stress Response	Oxidative stress	Oxidative stress
gsyne_398	Synechococcus_assembled_mapped	1-(5-phosphoribosyl)-5-[(5-phosphoribo	hisA	5.3.1.16	GO:0000105,GO:0003949	TIGR00007	343983	344757	-1	161	fig|1129.58.p	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis
gsyne_399	Synechococcus_assembled_mapped	coenzyme Q (ubiquinone) biosynthesis Coq4 family protein				PF05019.8	344975	345665	-1	185	fig|1129.58.peg.398			
gsyne_4	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	1844	2030	1	156	fig|1129.58.peg.5			
gsyne_40	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	32218	32596	-1	856	fig|1129.58.peg.39			
gsyne_400	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	345738	346656	1	##########	fig|1129.58.peg.399			
gsyne_401	Synechococcus_assembled_mapped	CDP-alcohol phosphatidyltransferase family protein				PF01066.16	346662	347193	-1	703	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophosphc
gsyne_402	Synechococcus_assembled_mapped	putative proline-rich region				UniRef100_C	347688	349038	-1	185	fig|1129.58.peg.402			
gsyne_403	Synechococcus_assembled_mapped	CBS domain protein				PF00571.23	347227	347692	1	157	fig|1129.58.p	Nucleosides and Nucleotides	Purines	Purine conversions
gsyne_404	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	349174	349813	-1	703	fig|1129.58.peg.403			
gsyne_405	Synechococcus_assembled_mapped	glutathione S-transferase, N-terminal domain protein				PF13417.1	349812	350391	-1	703	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Non-redox reactions
gsyne_406	Synechococcus_assembled_mapped	AIG2-like family protein				PF06094.7	350413	350833	-1	185	fig|1129.58.peg.405			
gsyne_407	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11302.3	350807	351104	-1	156	fig|1129.58.peg.406			
gsyne_408	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_E	351240	351807	1	156	fig|1129.58.peg.407			
gsyne_409	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	352100	352271	-1	156	fig|1129.58.peg.409			
gsyne_41	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	32656	32788	-1	856	fig|1129.58.peg.40			
gsyne_410	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07862.6	351915	352107	1	156	fig|1129.58.peg.408			
gsyne_411	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	352330	352843	1	88	fig|1129.58.peg.410			
gsyne_412	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	352895	353174	1	156	fig|1129.58.peg.411			
gsyne_413	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	353251	353677	1	156	fig|1129.58.peg.412			
gsyne_414	Synechococcus_assembled_mapped	putative hydrolase NIT3			GO:0006807,GO:0005739,G	UniRef100_P	353682	354642	1	160,703	fig|1129.58.peg.413			
gsyne_415	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	354937	355093	-1	856	fig|1129.58.peg.414			
gsyne_416	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	355431	355920	-1	856	fig|1129.58.peg.416			
gsyne_417	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	355108	355435	1	856	fig|1129.58.peg.415			
gsyne_418	Synechococcus_assembled_mapped	MAPEG family protein				PF01124.13	355997	356387	1	185	fig|1129.58.p	Stress Response	Oxidative stress	Glutathione: Non-redox reactions
gsyne_419	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	356558	357908	-1	119,703	fig|1129.58.peg.418			
gsyne_42	Synechococcus_assembled_mapped	esterase/lipase/thioesterase family active site			GO:0006886,GO:0016788,G	UniRef100_C	32948	33626	1	92,703	fig|1129.58.peg.41			
gsyne_420	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	357955	358102	-1	88	fig|1129.58.peg.419			
gsyne_421	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF06041.6	358159	358894	-1	156	fig|1129.58.peg.420			
gsyne_422	Synechococcus_assembled_mapped	superoxide dismutase [Mn]	sodA	1.15.1.1	GO:0006801,GO:0004784,G	UniRef100_P	359214	359901	1	92,141,703	fig|1129.58.p	Stress Response	Oxidative stress	Protection from Reactive Oxygen
gsyne_423	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	359897	360116	1	88	fig|1129.58.peg.423			
gsyne_424	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	360121	360355	-1	156	fig|1129.58.peg.424			
gsyne_425	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	360444	360654	-1	856	fig|1129.58.peg.425			
gsyne_426	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	360715	360976	1	156	fig|1129.58.peg.426			
gsyne_427	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	360988	361165	-1	856	fig|1129.58.peg.427			
gsyne_428	Synechococcus_assembled_mapped	cytochrome P450 family protein				PF00067.17	361208	362444	1	96,102	fig|1129.58.peg.428			
gsyne_429	Synechococcus_assembled_mapped	L,D-transpeptidase catalytic domain protein				PF03734.9	362476	363133	1	138	fig|1129.58.peg.429			
gsyne_43	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	33639	35124	-1	141	fig|1129.58.p	Iron acquisition and metabolism	Iron acquisition and metabolis	Iron acquisition in Streptococcus
gsyne_430	Synechococcus_assembled_mapped	membrane-bound lysozyme-inhibitor of c-type lysozyme family protein				PF09864.4	363155	363704	-1	88	fig|1129.58.peg.430			
gsyne_431	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	363736	364420	-1	156	fig|1129.58.peg.431			
gsyne_432	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	364700	364859	-1	185	fig|1129.58.peg.433			
gsyne_433	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	364940	365060	-1	856	fig|1129.58.peg.434			
gsyne_434	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF00565.12	365083	365704	-1	157	fig|1129.58.peg.435			
gsyne_435	Synechococcus_assembled_mapped	HD domain protein				PF13328.1	365700	366354	-1	157	fig|1129.58.peg.436			
gsyne_436	Synechococcus_assembled_mapped	large conductance mechanosensitive cl	mscL		GO:0006810,GO:0022833	TIGR00220	366525	366903	1	149	fig|1129.58.peg.437			
gsyne_437	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	366877	367111	1	856	fig|1129.58.peg.438			
gsyne_438	Synechococcus_assembled_mapped	penicillin binding transpeptidase domain protein				PF00905.17	367132	367840	1	89	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Beta-lactamase
gsyne_439	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF00565.12	368796	369177	-1	157	fig|1129.58.peg.441			
gsyne_44	Synechococcus_assembled_mapped	iron deficiency-induced protein A	idiA		GO:0055072,GO:0046872,G	UniRef100_C	35336	36401	1	141	fig|1129.58.p	Iron acquisition and metabolism	Iron acquisition and metabolis	Iron acquisition in Streptococcus
gsyne_440	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02696.9	369200	370829	-1	156	fig|1129.58.p	Protein Metabolism	Selenoproteins	Selenoprotein O
gsyne_441	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	370966	371296	-1	156	fig|1129.58.peg.443			
gsyne_442	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	371330	372029	-1	121	fig|1129.58.peg.444			
gsyne_443	Synechococcus_assembled_mapped	orange carotenoid-binding protein			GO:0006810,GO:0031404,G	UniRef100_P	372025	372979	-1	92,141	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio
gsyne_444	Synechococcus_assembled_mapped	RNA recognition motif family protein				PF14259.1	373352	373625	1	185	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism I: anaplerot
gsyne_445	Synechococcus_assembled_mapped	glycogen/starch/alpha-glucan phospho	glgP	2.4.1.1	GO:0004645,GO:0005977	TIGR02093	374219	376670	-1	105	fig|1129.58.p	Carbohydrates	Polysaccharides	Glycogen metabolism
gsyne_446	Synechococcus_assembled_mapped	putative ATLS1-like light-inducible protein				UniRef100_C	373884	374223	1	185	fig|1129.58.peg.448			
gsyne_447	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	376654	376771	1	856	fig|1129.58.peg.450			
gsyne_448	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	377047	377287	-1	856	fig|1129.58.peg.451			
gsyne_449	Synechococcus_assembled_mapped	glutamine synthetase, catalytic domain protein				PF00120.19	377468	379637	1	73	fig|1129.58.p	Amino Acids and Derivatives	Glutamine, glutamate, asparta	Glutamine, Glutamate, Aspartate
gsyne_45	Synechococcus_assembled_mapped	bacterial regulatory s, crp family protein				PF00325.15	36601	37198	1	261	fig|1129.58.peg.44			
gsyne_450	Synechococcus_assembled_mapped	tellurite resistance TerB family protein				PF05099.8	379669	380068	1	94	fig|1129.58.peg.453			
gsyne_451	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	380076	380259	-1	856	fig|1129.58.peg.454			
gsyne_452	Synechococcus_assembled_mapped	ferredoxin-1	petF		GO:0006810,GO:0009055,G	UniRef100_P	380346	380631	-1	92,141	fig|1129.58.peg.455			
gsyne_453	Synechococcus_assembled_mapped	putative NAD-dependent malic enzyme 2			GO:0016619,GO:0046872,G	UniRef100_P	380697	382425	-1	92,141,703	fig|1129.58.peg.456			
gsyne_454	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	380611	380725	1	856				
gsyne_455	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	382550	382799	1	156	fig|1129.58.peg.457			
gsyne_456	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	382866	383229	-1	165	fig|1129.58.peg.458			
gsyne_457	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	383302	383464	1	156	fig|1129.58.peg.459			
gsyne_458	Synechococcus_assembled_mapped	nucleoside 2-deoxyribosyltransferase family protein				PF05014.10	383468	383936	-1	703	fig|1129.58.peg.460			
gsyne_459	Synechococcus_assembled_mapped	phosphoribosyl transferase domain protein				PF00156.22	383935	384319	-1	703	fig|1129.58.peg.461			
gsyne_46	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	37201	37444	-1	856	fig|1129.58.peg.45			
gsyne_460	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	384364	384568	-1	856	fig|1129.58.peg.462			
gsyne_461	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03733.8	384780	385185	-1	156	fig|1129.58.peg.464			
gsyne_462	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	385205	385358	-1	856	fig|1129.58.peg.465			
gsyne_463	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	385450	385630	-1	156	fig|1129.58.peg.466			
gsyne_464	Synechococcus_assembled_mapped	DEXH box helicase, DNA ligase-associated		3.6.4.-		TIGR04121	385710	388197	-1	185	fig|1129.58.peg.467			
gsyne_465	Synechococcus_assembled_mapped	DNA ligase, ATP-dependent, PP_1105 family		6.5.1.1		TIGR04120	388193	389840	-1	185	fig|1129.58.p	DNA Metabolism	DNA repair	DNA Repair Base Excision
gsyne_466	Synechococcus_assembled_mapped	putative exonuclease, DNA ligase-associated				TIGR04122	389839	390895	-1	185	fig|1129.58.peg.469			
gsyne_467	Synechococcus_assembled_mapped	quinolinate synthetase complex, A sub	nadA	2.5.1.72	GO:0008987,GO:0019363,G	TIGR00550	392095	393064	-1	163	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	NAD and NADP	NAD and NADP cofactor biosynth
gsyne_468	Synechococcus_assembled_mapped	putative fructose-bisphosphate aldolase 2, chloroplastic			GO:0016020,GO:0010287,G	UniRef100_C	391016	392099	1	92,703	fig|1129.58.p	Carbohydrates	CO2 fixation	Calvin-Benson cycle
gsyne_469	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	393111	393972	1	703	fig|1129.58.peg.472			
gsyne_47	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	37482	37911	-1	149	fig|1129.58.peg.46			
gsyne_470	Synechococcus_assembled_mapped	glycosyl transferase 1 family protein				PF13528.1	393983	395051	1	703	fig|1129.58.peg.473			
gsyne_471	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	395327	395474	1	856				
gsyne_472	Synechococcus_assembled_mapped	repair family protein				PF04536.9	396183	396990	-1	185	fig|1129.58.peg.476			
gsyne_473	Synechococcus_assembled_mapped	putative endolysin				UniRef100_B	395493	396183	1	185	fig|1129.58.peg.475			
gsyne_474	Synechococcus_assembled_mapped	S-adenosyl-L-methionine-dependent methyltransferase family protein				PF02636.12	397038	398238	1	703	fig|1129.58.peg.477			
gsyne_475	Synechococcus_assembled_mapped	3-dehydroquinate synthase	aroB	4.2.3.4	GO:0003856,GO:0009423	TIGR01357	398270	399389	-1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis
gsyne_476	Synechococcus_assembled_mapped	ATP-dependent DNA helicase RecQ	recQ	3.6.4.12	GO:0004003,GO:0006310	TIGR01389	399414	401253	-1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa
gsyne_477	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	401259	401385	1	856				
gsyne_478	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	401378	402206	1	141	fig|1129.58.peg.480			
gsyne_479	Synechococcus_assembled_mapped	phosphoribosylaminoimidazole carbox	purK	4.1.1.21	GO:0004638,GO:0009152,G	TIGR01161	402268	403540	1	125	fig|1129.58.p	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis



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1	-1.0271712	0.55302428	1.75709935	0.62137553	1.61714853	1	-1.0865417
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1	-1.5828804	0.74088114	1.47781985	0.62701614	-2.0436997	0.31507977	-3.02022
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1	-4.2639375	1	-5.3928274	1	-5.3928274	1	1
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26	3.83867817	9	1.58114146	4	1.19238323	6	1.09293365	9	3.58854984	1	0.19240762	7	1.99611155	17	1.79367333
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9	2.16848406	9	2.58033502	8	3.89180638	11	3.26994618	8	5.20561243	13	4.08198101	4	1.86145323	20	3.44373556
28	5.48859243	20	4.66501246	15	5.9366538	29	7.01350551	9	4.76445883	26	6.64186741	3	1.13580197	37	5.18311385
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20	5.73483389	14	4.77681854	15	8.68419606	27	9.55187884	1	0.77438863	12	4.48421054	3	1.66146239	22	4.50816291
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6	2.26276598	7	3.14127741	7	5.33008265	5	2.32644392	2	2.03697878	2	0.98295195	7	5.09876319	12	3.23411687
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25	2.62846553	9	1.12596437	4	0.84912139	4	0.51886749	26	7.38250489	8	1.09614036	6	1.21840575	14	1.05190468
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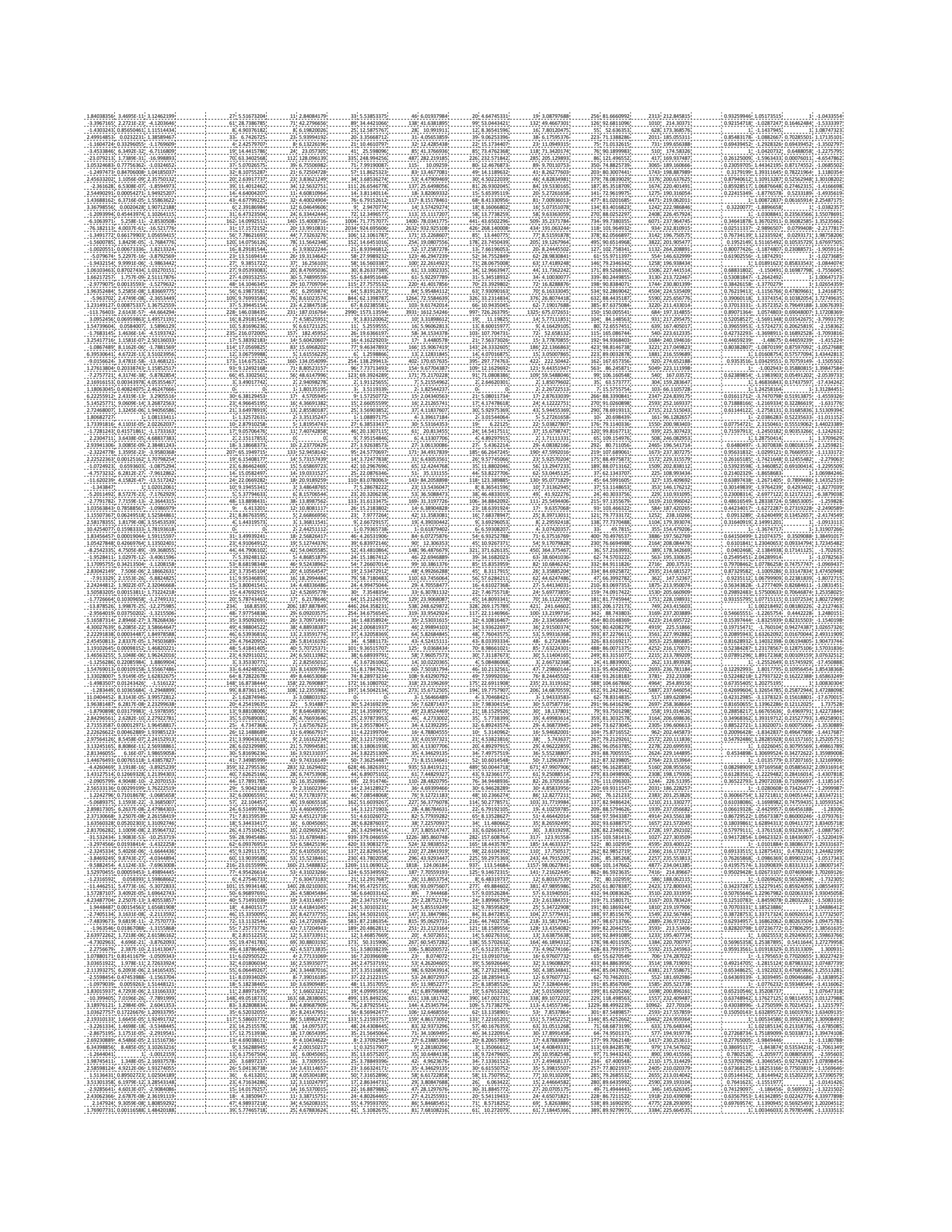
12	2.1572484	3	0.64174135	3	1.0888992	6	1.33077414	9	4.36947779	3	0.70283611	4	1.38885629	9	1.15623867
5	1.23913375	4	1.17958172	0	0	4	1.2230448	1	0.66929303	1	0.32296993	2	0.9573188	8	1.4168512
18	6.30831728	21	8.75750066	13	9.19881508	21	9.08018112	48	45.4307993	17	7.76432751	24	16.24541	23	5.76043038
257	47.1788702	254	55.4840291	179	66.3460326	243	55.0370162	72	35.6956281	228	54.546032	104	36.874502	514	67.4316219
42	25.5652858	49	35.4909237	3	3.68697447	28	21.0277879	4	6.57551043	11	8.72585414	4	4.70261868	10	4.34998175
201	158.496472	133	124.794384	16	25.4736418	206	200.412569	9	19.1661185	34	34.9394738	7	10.6610503	35	19.7232127
44	23.8533247	38	24.5131826	15	16.4185582	31	20.7344314	3	4.39223548	9	6.35847042	7	7.32947208	14	5.4238835
21	4.26088097	15	3.62152283	14	5.73529362	6	1.50198485	20	10.9591841	8	2.11535858	8	3.13507912	24	3.4799854
9	3.35765275	7	3.10750023	0	0	8	3.68228543	9	9.067841	1	0.48619129	6	4.32337524	4	1.06644714
11	2.68769856	18	5.23335552	1	0.49332757	4	1.20581882	9	5.93879727	4	1.27368422	1	0.47191772	5	0.87305972
42	4.55381654	22	2.83836852	13	2.84588342	23	3.07672208	7	2.04970989	18	2.54338817	7	1.46589442	29	2.24703745
23	15.3461949	31	24.6124263	2	2.6943275	21	17.2872679	6	10.8116566	11	9.56487858	5	6.44349194	3	1.43047477
21	4.47000396	20	5.06568837	16	6.87632048	19	4.98972266	13	7.47308778	18	4.99315469	18	7.40013308	30	4.56347779
26	8.27604927	16	6.06023637	11	7.06951985	26	10.210741	6	5.15785451	18	7.46682765	8	4.91833513	17	3.86709387
20	5.33780693	14	4.44611572	8	4.31092399	14	4.60993811	3	2.16233132	7	2.43469637	8	4.12383484	7	1.33510979
77	5.93682748	63	5.77995043	39	6.07121796	66	6.27829666	24	4.99738793	45	4.52157896	23	3.42507394	129	7.10787019
17	2.60985693	12	2.19214302	12	3.71960256	19	3.59878228	11	4.56066929	13	2.60090825	6	1.77908804	24	2.6330863
5	3.54038215	1	0.84255837	4	5.71857264	1	0.87360343	6	11.4735947	1	0.92277122	1	1.36759829	2	1.01203657
21	2.973921	12	2.02214009	9	2.57335769	12	2.09664823	12	4.58943789	7	1.2918797	5	1.36759829	12	1.21444389
32	4.84831372	23	4.14656457	23	7.03584211	36	6.72941682	9	3.68257298	32	6.31836362	22	6.43786444	41	4.43926086
103	48.9542704	88	49.7686534	15	14.3943524	71	41.6337854	14	17.9700593	29	17.962437	17	15.6056079	41	13.9259005
565	251.321743	561	296.937014	105	94.3014623	523	287.023527	75	90.0971381	213	123.473887	91	78.1810356	248	78.835054
16	7.93045601	15	8.84686291	4	4.00300085	17	10.3958808	2	2.6771721	9	5.81345867	6	5.74391282	8	2.8337024
45	17.946075	41	19.4563192	41	33.0132541	22	10.8246494	19	20.463442	44	22.8677557	10	7.70256508	54	15.3899355
146	85.8572674	102	71.3746906	27	32.0579305	44	31.9235423	15	23.8222942	15	11.4955397	10	11.3580197	33	13.8683317
30	2.5263892	17	1.70352215	13	2.21039489	19	1.97408931	26	5.9131714	11	1.20721769	6	0.97590752	18	1.08327216
35	5.54498208	23	4.33590541	25	7.99686243	11	2.1501016	9	3.850727	15	3.09697189	9	2.7539308	53	6.00059127
40	2.80369657	25	2.0851192	23	3.25496534	32	2.76729329	22	4.16448994	21	1.91824562	12	1.624541	42	2.10380936
18	3.41269623	21	4.73766429	14	5.35920879	19	4.44439778	7	3.58419216	10	2.47080818	4	1.46475008	12	1.62589482
39	5.93479849	27	4.88905582	18	5.5304617	24	4.50595454	18	7.39744924	27	5.35450141	19	5.58435968	62	6.74247172
12	7.85564039	7	5.45278343	2	2.64349113	12	9.69205316	3	5.30383153	4	3.41251243	0	0	6	2.80696936
1	0.86739363	0	0	0	0	1	1.0701642	0	0	0	0	0	0	0	0
24	4.02269508	11	2.19390803	5	1.69208973	10	2.06795015	5	2.26330975	5	1.09216883	6	1.94238598	18	2.15607791
13	2.06901232	13	2.46197102	3	0.96402543	7	1.37452283	5	2.14910605	4	0.82964752	3	0.92218784	18	2.04728499
26	7.15943945	9	2.9489543	9	5.00375106	14	4.75628535	23	17.1041551	5	1.79427737	2	1.06368756	26	5.11640711
21	9.34116212	5	2.64649745	0	0	3	1.64640647	5	6.00647588	2	1.15937922	1	0.85913226	0	0
13	1.91120629	10	1.74937967	2	0.59366538	5	0.90691882	23	9.13187942	3	0.57477699	3	0.85185148	6	0.63037871
24	6.55667623	18	5.85146838	13	7.17072987	22	7.41531101	3	2.21341001	10	3.5602984	8	4.22124826	9	1.75711861
49	4.78899016	37	4.30298121	25	4.9332757	41	4.94385716	15	3.95919818	29	3.69368422	11	2.07643797	44	3.07317021
51	3.25871638	28	2.12889519	15	1.93515234	43	3.38983873	31	5.34941387	36	2.99773191	7	0.86387885	70	3.19639543
31	9.77789178	13	4.87917894	17	10.8262978	9	3.50235557	15	12.7774123	6	2.4663158	6	3.65521725	17	3.83193847
24	3.57381065	15	2.65785581	4	1.20261828	24	4.40926024	13	5.22795411	19	3.68712448	7	2.01324555	14	1.48982208
33	3.60050184	36	4.67381437	13	2.86378205	75	10.0958887	25	7.36643268	55	7.82034098	14	2.95022776	59	4.60031089
172	65.5787708	196	88.9223144	23	17.7055807	397	186.749533	12	12.3561789	251	124.716079	25	18.409977	50	13.6235692
197	8.11765056	155	7.60003662	112	9.31814925	187	9.5069219	111	12.3525102	211	11.3307976	110	8.75457813	363	10.689486
18	5.52675585	6	2.19214302	5	3.0996688	11	4.16701106	2	1.6584252	8	3.20111785	7	4.15120543	5	1.09711929
1	0.88963449	0	0	0	0	0	0	1	2.40259035	0	0	0	0	0	0
4	1.73478725	5	2.58033502	1	0.87565644	7	3.74557471	16	18.7402047	2	1.13039474	5	4.18826976	3	0.9298086
60	2.87931494	33	1.88439404	18	1.74404601	20	1.18413743	54	6.9984167	14	0.87554779	16	1.48298348	42	1.4403674
65	11.332781	42	8.71349312	32	11.264726	45	9.67987721	31	14.5966419	32	7.27088075	72	24.2456621	226	28.1590276
17	4.43479448	18	5.58749236	3	1.58013191	9	2.89668506	5	3.52259487	3	1.01990503	7	3.52696401	28	5.21997811
26	14.7883503	23	15.5666112	7	8.03881318	7	4.91222913	5	7.68041177	6	4.44745472	16	17.577001	18	7.31652669
347	120.394235	446	184.132707	155	108.581398	458	196.054082	126	118.06329	363	164.133316	147	98.5081048	704	174.556068
41	2.46966241	27	1.93525126	8	0.9729516	11	0.81748654	16	2.60280621	12	0.94199562	19	2.21047571	29	1.24835414
1	0.91304592	0	0	0	0	0	0	1	2.46581641	0	0	0	0	0	0
9	3.76218922	4	1.98965592	2	1.68801241	1	0.51574179	7	7.90249597	1	0.54476855	3	2.42213191	2	0.59746737
365	104.660719	347	118.39686	240	138.947137	332	117.452732	68	52.6584265	321	119.952632	110	60.9202875	675	138.318635
1	0.6425138	2	1.52908742	0	0	1	0.79271422	0	0	0	0	0	0	1	0.45916474
6	1.33445173	9	2.38184771	5	2.24527291	10	2.74401078	24	14.4155421	7	2.02891364	4	1.71826452	5	0.79470821
22	5.96333118	16	5.16067003	5	2.73642636	11	3.67868945	8	5.85631398	14	4.94547699	2	1.04706744	28	5.4238835
15	6.42513797	10	5.09695805	2	1.72969173	18	9.51257069	3	3.47040828	4	2.2328785	7	5.79118782	6	1.83665896
73	37.2469028	71	43.1067732	7	7.2112883	98	61.6918188	17	23.4252559	31	20.6130806	13	12.8111781	30	10.9389247
60	15.4203311	59	18.0432315	72	37.3613413	101	32.0256547	38	26.375103	53	17.7513841	39	19.3591136	104	19.1012532
35	23.8108054	17	13.7617868	25	34.3394681	21	17.6262339	20	36.7454995	21	18.6182663	10	13.1396698	31	15.0714074
22	12.7217732	15	10.3213401	8	9.34033532	9	6.42098522	10	15.6168373	9	6.78236845	1	1.11687194	19	7.85171707
57	2.38559405	24	1.19523359	16	1.35203889	19	0.98109143	40	4.52115916	31	1.69081964	15	1.21252683	38	1.13655736
25	1.57995196	14	1.05281429	6	0.76560126	12	0.93566269	11	1.87743399	10	0.82360273	4	0.48825003	33	1.49040359
23	2.26705152	9	1.0555916	0	0	8	0.97287655	11	2.92815699	8	1.02763158	5	0.95187949	20	1.40880091
36	3.86701802	22	2.81200596	14	3.03633191	14	1.85539305	13	3.77124863	35	4.89954377	23	4.77177484	69	5.29674249
63	6.05493611	83	9.49220194	87	16.882462	57	6.75893181	45	11.680183	44	5.51106577	64	11.8802998	180	12.363106
22	2.65960415	23	3.30858288	21	5.12579377	23	3.43049152	16	5.22375045	29	4.56884286	19	4.43635543	51	4.40606166
12	2.91153105	11	3.17579694	3	1.46963318	4	1.19738652	4	2.62100765	2	0.63238867	3	1.40585279	10	1.73390881
30	2.92379874	22	2.55134249	11	2.164544	20	2.40486338	15	3.94807684	24	3.04825548	13	2.44707896	25	1.74121461
54	38.2361272	49	41.2853602	5	7.1482158	53	46.3009818	5	9.56132894	11	10.1504834	1	1.36759829	3	1.51805486
39	5.03023813	21	3.22302069	15	3.90627406	32	5.09223115	21	7.3149498	19	3.19368031	22	5.48056118	44	4.05567072
39	5.88319155	37	6.64155795	27	8.22355609	90	16.7503962	15	6.11093633	51	10.0261099	6	1.74814738	37	3.98874414
22	1.90826598	17	1.75462781	13	2.27670673	14	1.49822988	11	2.57677815	23	2.5999079	4	0.67012316	30	1.8596172
47	4.37184991	32	3.54190758	28	5.25863382	41	4.70527961	25	6.28022947	39	4.72765629	23	4.13212674	60	3.98845512
42	2.9438814	19	1.5846906	30	4.24560696	28	2.42138163	22	4.16448994	26	2.37497077	17	2.30143308	47	2.35426285
4	3.30435667	0	0	1	1.66791702	0	0	0	0	1	1.07656642	0	0	3	1.771064
21	2.63989364	15	2.24376958	19	4.82245573	22	3.41211775	24	8.1479151	20	3.2765065	13	3.15637721	18	1.61705844
34	2.78220597	29	2.82376285	20	3.30436391	42	4.24027326	23	5.08283855	34	3.62579445	16	2.52876665	42	2.45609819

gsyne_48	Synechococcus_assembled_mapped	sulfite exporter TauE/SafE family protein				PF01925.14	37873	38710	-1	141	fig|1129.58.peg.47					
gsyne_480	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	403732	404095	-1	856	fig|1129.58.peg.482					
gsyne_481	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09876.4	404995	405274	-1	156	fig|1129.58.peg.484					
gsyne_482	Synechococcus_assembled_mapped	sulfotransferase domain protein				PF00685.22	404169	405006	-1	703	fig|1129.58.peg.483					
gsyne_483	Synechococcus_assembled_mapped	ATP-dependent Clp protease adaptor ClpS family protein				PF02617.12	405561	405843	-1	138	fig|1129.58.peg.486					
gsyne_484	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	405340	405565	1	856	fig|1129.58.peg.485					
gsyne_485	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	406023	406212	1	856	fig|1129.58.peg.488					
gsyne_486	Synechococcus_assembled_mapped	radical SAM domain , CofH subfamily protein				TIGR00423	406208	407456	1	156	fig|1129.58.peg.489	Cofactors, Vitamins, Prosthetic Gr	Coenzyme F420	Coenzyme F420 synthesis		
gsyne_487	Synechococcus_assembled_mapped	photosystem II biogenesis protein Psp2 psb29			GO:0003674,GO:0010207,G	TIGR03060	408734	409409	-1	164	fig|1129.58.peg.491					
gsyne_488	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	407446	408742	1	156	fig|1129.58.peg.490					
gsyne_489	Synechococcus_assembled_mapped	ATP-dependent Clp endopeptidase, prc clpP	3.4.21.92		GO:0004176,GO:0004252,G	TIGR00493	409508	410099	1	138	fig|1129.58.peg.487	Regulation and Cell signaling	Regulation and Cell signaling - cAMP signaling in bacteria			
gsyne_49	Synechococcus_assembled_mapped	inner membrane protein ygaP ygaP			GO:0016021,GO:0005886	UniRef100_P	38709	39225	-1		fig|1129.58.peg.1	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria		
gsyne_490	Synechococcus_assembled_mapped	amidase family protein				PF01425.16	410253	411825	-1	703	fig|1129.58.peg.493					
gsyne_491	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	411937	412366	-1	88	fig|1129.58.peg.494					
gsyne_492	Synechococcus_assembled_mapped	coenzyme Q (ubiquinone) biosynthesis Coq4 family protein				PF05019.8	412400	413219	-1	185	fig|1129.58.peg.495					
gsyne_493	Synechococcus_assembled_mapped	ATP-dependent zinc metalloprotease FtsH FtsH2	3.4.24.-		GO:0004222,GO:0005524,G	UniRef100_C	413270	415235	-1	##########	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster		
gsyne_494	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08865.6	415321	415630	-1	156	fig|1129.58.peg.497					
gsyne_495	Synechococcus_assembled_mapped	ftsX-like permease family protein				PF02687.16	415749	416979	-1	141	fig|1129.58.peg.498					
gsyne_496	Synechococcus_assembled_mapped	pyruvate kinase pyk	2.7.1.40		GO:0004743,GO:0005737,G	TIGR01064	417023	418481	-1	116	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism I: anaplerot		
gsyne_497	Synechococcus_assembled_mapped	mazG nucleotide pyrophosphohydrolase domain protein				PF03819.12	418541	418871	1	703	fig|1129.58.peg.500					
gsyne_498	Synechococcus_assembled_mapped	YGGT family protein				PF02325.12	419394	419685	-1	185	fig|1129.58.peg.502					
gsyne_499	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	418909	419401	1	156	fig|1129.58.peg.501					
gsyne_5	Synechococcus_assembled_mapped	phosphate-starvation-inducible E family protein				PF06146.7	2041	2551	1	149	fig|1129.58.peg.6					
gsyne_50	Synechococcus_assembled_mapped	ETHE1, mitochondrial domain protein ETHE1	3.-.-.-		GO:0005759,GO:0046872,G	UniRef100_C	39265	40393	-1	141,703	fig|1129.58.peg.49					
gsyne_500	Synechococcus_assembled_mapped	segregation and condensation protein ScpB			GO:0005515,GO:0007059,G	TIGR00281	419753	420335	-1	93,170	fig|1129.58.peg.503					
gsyne_501	Synechococcus_assembled_mapped	threonine ammonia-lyase, biosynthetic ilvA	4.3.1.19		GO:0004794,GO:0009097	TIGR01124	420359	421904	-1	74	fig|1129.58.j	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios		
gsyne_502	Synechococcus_assembled_mapped	1-deoxy-D-xylulose-5-phosphate synth dxs	2.2.1.7		GO:0005737,GO:0008615,G	TIGR00204	422061	423969	1	76,84,162	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis		
gsyne_503	Synechococcus_assembled_mapped	FAD binding domain protein				PF01494.14	423985	425158	1	157	fig|1129.58.peg.506					
gsyne_504	Synechococcus_assembled_mapped	photosystem I reaction center subunit I psaK			GO:0003674,GO:0009538,G	TIGR03049	425176	425443	-1	164	fig|1129.58.j	Photosynthesis	Electron transport and photopt	Photosystem I		
gsyne_505	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12159.3	425514	425844	-1	156	fig|1129.58.peg.508					
gsyne_506	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10693.4	425840	426134	-1	156	fig|1129.58.peg.509					
gsyne_507	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	426156	426342	-1	856	fig|1129.58.peg.510					
gsyne_508	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	426422	426962	-1	156	fig|1129.58.peg.511					
gsyne_509	Synechococcus_assembled_mapped	phosphotransferase enzyme family protein				PF01636.18	426939	428082	-1	703	fig|1129.58.peg.512					
gsyne_51	Synechococcus_assembled_mapped	tellurite resistance TehB family protein				PF03848.9	40403	41072	-1	94	fig|1129.58.peg.50					
gsyne_510	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11334.3	428163	428421	-1	156						
gsyne_511	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	428531	430274	-1	856	fig|1129.58.peg.515					
gsyne_512	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	430255	430504	-1	856	fig|1129.58.peg.516					
gsyne_513	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	430615	430762	-1	856	fig|1129.58.peg.517					
gsyne_514	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	430927	431047	-1	856						
gsyne_515	Synechococcus_assembled_mapped	ABC-2 transporter family protein				PF06182.6	431549	432353	-1	141	fig|1129.58.peg.518					
gsyne_516	Synechococcus_assembled_mapped	ABC-2 transporter family protein				PF06182.6	432349	433141	-1	141	fig|1129.58.peg.519					
gsyne_517	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	433142	434126	-1	141	fig|1129.58.peg.520					
gsyne_518	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	434122	434251	-1	856	fig|1129.58.peg.521					
gsyne_519	Synechococcus_assembled_mapped	orotate phosphoribosyltransferase pyrE	2.4.2.10		GO:0004588,GO:0009220	TIGR00336	434494	435982	-1	126	fig|1129.58.j	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis		
gsyne_52	Synechococcus_assembled_mapped	bacterial regulatory , arsR family protein				PF01022.15	41136	41457	1	261	fig|1129.58.peg.51					
gsyne_520	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	436154	436313	1	856	fig|1129.58.peg.523					
gsyne_521	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	436349	437315	-1	856	fig|1129.58.peg.524					
gsyne_522	Synechococcus_assembled_mapped	rhomboid family protein				PF01694.17	437494	438037	-1	140	fig|1129.58.peg.525					
gsyne_523	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	438062	438590	-1	156	fig|1129.58.peg.526					
gsyne_524	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03479.10	438624	439197	-1	156						
gsyne_525	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	439203	439362	-1	856						
gsyne_526	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	439335	439521	1	856	fig|1129.58.peg.528					
gsyne_527	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	439627	439813	-1	856	fig|1129.58.peg.529					
gsyne_528	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	439495	439654	1	856						
gsyne_529	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	439996	440587	1	156	fig|1129.58.peg.530					
gsyne_53	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	41475	41715	-1	156	fig|1129.58.peg.52					
gsyne_530	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	440684	441089	1	856	fig|1129.58.peg.531					
gsyne_531	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	441070	441544	1	856	fig|1129.58.peg.532					
gsyne_532	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	441540	441717	1	156	fig|1129.58.peg.533					
gsyne_533	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	441742	443257	1	703	fig|1129.58.j	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental		
gsyne_534	Synechococcus_assembled_mapped	sensory box protein			GO:0004871,GO:0007165	TIGR00229	443413	444214	1	264	fig|1129.58.peg.535					
gsyne_535	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	444319	444487	1	856	fig|1129.58.peg.536					
gsyne_536	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	444548	444770	1	156	fig|1129.58.peg.537					
gsyne_537	Synechococcus_assembled_mapped	polysaccharide pyruvyl transferase CsaI csaB	2.-.-.-		GO:0042545,GO:0046919	TIGR03609	444815	445859	1	105	fig|1129.58.peg.538					
gsyne_538	Synechococcus_assembled_mapped	zinc-binding alcohol dehydrogenase family protein			GO:0004024,GO:0006113,G	TIGR02817	445862	446915	1	114	fig|1129.58.peg.539					
gsyne_539	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	446940	447129	1	856	fig|1129.58.peg.540					
gsyne_54	Synechococcus_assembled_mapped	pyridoxamine 5'-phosphate oxidase pdxH	1.4.3.5		GO:0004733,GO:0008615,G	TIGR00558	41963	42638	-1	84	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthe		
gsyne_540	Synechococcus_assembled_mapped	ahpC/TSA family protein				PF00578.16	447690	448263	-1	96,149	fig|1129.58.j	Stress Response	Oxidative stress	Rubrerythrin		
gsyne_541	Synechococcus_assembled_mapped	peptidase_C39 like family protein				PF13529.1	447134	447725	1	138	fig|1129.58.peg.541					
gsyne_542	Synechococcus_assembled_mapped	ribosomal protein L28 rpmB			GO:0000311,GO:0003735,G	TIGR00009	448287	448524	-1	158	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial		
gsyne_543	Synechococcus_assembled_mapped	mechanosensitive ion channel family protein				PF00924.13	448584	449613	-1	141	fig|1129.58.peg.544					
gsyne_544	Synechococcus_assembled_mapped	glycerol kinase glpK	2.7.1.30		GO:0006072,GO:0005524,G	UniRef100_C	449699	451214	1	92,141,703	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho		
gsyne_545	Synechococcus_assembled_mapped	alpha amylase, catalytic domain protein				PF00128.19	452645	454325	-1	105	fig|1129.58.peg.547					
gsyne_546	Synechococcus_assembled_mapped	glucosylglycerol 3-phosphatase stpA	3.1.3.69		GO:0006970	TIGR02399	454452	455655	-1	703						
gsyne_547	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	457249	458290	-1	141	fig|1129.58.peg.549					
gsyne_548	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	455754	457269	1	156	fig|1129.58.peg.548					
gsyne_549	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	458286	459084	-1	141	fig|1129.58.j	Carbohydrates	Di- and oligosaccharides	Maltose and Maltodextrin Utilizati		
gsyne_55	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	42894	43047	1	856	fig|1129.58.peg.54					
gsyne_550	Synechococcus_assembled_mapped	binding--dependent transport system inner membrane component family protein				PF00528.17	459083	459959	-1	141	fig|1129.58.j	Carbohydrates	Di- and oligosaccharides	Maltose and Maltodextrin Utilizati		
gsyne_551	Synechococcus_assembled_mapped	bacterial extracellular solute-binding family protein				PF13416.1	459958	461212	-1	185	fig|1129.58.j	Carbohydrates	Di- and oligosaccharides	Maltose and Maltodextrin Utilizati		
gsyne_552	Synechococcus_assembled_mapped	glucosylglycerol-phosphate synthase ggpS	2.4.1.213		GO:0006970,GO:0033828	TIGR02398	461211	462711	-1	703	fig|1129.58.j	Carbohydrates	Di- and oligosaccharides	Trehalose Biosynthesis		
gsyne_553	Synechococcus_assembled_mapped	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein				PF02518.21	462881	464789	-1	703	fig|1129.58.j	Protein Metabolism	Protein folding	Protein chaperones		
gsyne_554	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	464980	465190	-1	156	fig|1129.58.peg.555					
gsyne_555	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12204.3	465182	465986	-1	156	fig|1129.58.peg.556					
gsyne_556	Synechococcus_assembled_mapped	4Fe-4S binding domain protein				PF00037.22	466000	466225	-1	157	fig|1129.58.j	Respiration	Respiration - no subcategory	Soluble cytochromes and functio		
gsyne_557	Synechococcus_assembled_mapped	tRNA synthetase class II core domain family protein				PF00587.20	466251	467430	-1	703	fig|1129.58.j	Amino Acids and Derivatives	Histidine Metabolism	Histidine Biosynthesis		
gsyne_558	Synechococcus_assembled_mapped	inositol monophosphatase family protein				PF00459.20	467460	468363	-1	703	fig|1129.58.peg.559					
gsyne_559	Synechococcus_assembled_mapped	2Fe-2S iron-sulfur cluster binding domain protein				PF00111.22	468359	468725	-1	112	fig|1129.58.j	Respiration	Respiration - no subcategory	Soluble cytochromes and functio		
gsyne_56	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	43120	44020	1	703	fig|1129.58.peg.55					
gsyne_561	Synechococcus_assembled_mapped	phosphate ABC transporter, ATP-bindin pstB	3.6.3.27		GO:0005524,GO:0006817,G	TIGR00972	469022	469817	-1	143	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism		
gsyne_562	Synechococcus_assembled_mapped	phosphate ABC transporter, permease pstA			GO:0005887,GO:0006817,G	TIGR00974	469854	470736	-1	143	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism		
gsyne_563	Synechococcus_assembled_mapped	phosphate ABC transporter, permease pstC			GO:0005887,GO:0006817,G	TIGR02138	470742	471696	-1	143	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism		
gsyne_564	Synechococcus_assembled_mapped	chaperone protein DnaK dnaK			GO:0005524,GO:0006457,G	TIGR02350	471787	474112	1	95	fig|1129.58.j	Protein Metabolism	Protein folding	Protein chaperones		
gsyne_565	Synechococcus_assembled_mapped	dnaJ C terminal domain protein				PF01556.13	474159	475056	1	95	fig|1129.58.j	Protein Metabolism	Protein folding	Protein chaperones		
gsyne_566	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11360.3	475104	475527	1	156	fig|1129.58.j	Cell Wall and Capsule	Cell Wall and Capsule - no sut	UDP-N-acetylmuramate from Fru		
gsyne_567	Synechococcus_assembled_mapped	methylthioadenosine phosphorylase mtnP	2.4.2.28		GO:0006168,GO:0017061,G	TIGR01694	476420	477260	-1	102,127	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Salvage		
gsyne_568	Synechococcus_assembled_mapped	N-acetylmuramic acid 6-phosphate eth murQ			GO:0006040,GO:0009254,G	TIGR00274	475523	476435	1	89	fig|1129.58.peg.567					
gsyne_569	Synechococcus_assembled_mapped	peptidyl-prolyl cis-trans isomerase B ppiB	5.2.1.8		GO:0006457,GO:0003755,G	UniRef100_P	477400	477841	1	92,703	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	Queuosine-Archaeosine Biosynth		
gsyne_57	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11845.3	44030	44660	-1	156	fig|1129.58.peg.56					
gsyne_570	Synechococcus_assembled_mapped	GTP cyclohydrolase II ribA	3.5.4.25		GO:0003935,GO:0009231	TIGR00505	477856	479410	-1	85	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Riboflavin, FMN, FAD	Riboflavin, FMN and FAD metabc		
gsyne_571	Synechococcus_assembled_mapped	phosphoribosylglycinamide formyltrans purN	2.1.2.2		GO:0004644,GO:0009152	TIGR00639	480609	481185	-1	125	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	5-FCL-like protein		
gsyne_572	Synechococcus_assembled_mapped	N-acetyl-gamma-glutamyl-phosphate r argC	1.2.1.38		GO:0003942,GO:0006592	TIGR01850	479554	480619	1	73	fig|1129.58.j	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis -- gjo		
gsyne_573	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF06868.6	481338	481686	1	156	fig|1129.58.peg.573					
gsyne_574	Synechococcus_assembled_mapped	M61 glycyl aminopeptidase family protein				PF05299.7	481694	483434	1	138	fig|1129.58.peg.574					
gsyne_575	Synechococcus_assembled_mapped	N-acetylmuramoyl-L-alanine amidase family protein				PF01510.20	483434	484277	1	90	fig|1129.58.j	Virulence, Disease and Defense	Resistance to antibiotics and t	Beta-lactamase		
gsyne_576	Synechococcus_assembled_mapped	putative dnaB-like helicase			GO:0004386	UniRef100_A	484289	485027	-1	703	fig|1129.58.peg.576					
gsyne_577	Synechococcus_assembled_mapped	phosphoglucose isomerase family protein				PF00342.14	485281	486886	1	117	fig|1129.58.peg.577					
gsyne_578	Synechococcus_assembled_mapped	leucine--tRNA ligase leuS	6.1.1.4		GO:0004823,GO:0005737,G	TIGR00396	486898	489556	-1	137	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Leu		
gsyne_579	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	489617	489857	-1	156	fig|1129.58.peg.579					
gsyne_58	Synechococcus_assembled_mapped	photosystem II q(b) protein psbA	1.10.3.9		GO:0009055,GO:0009538,G	TIGR01151	44766	45846	-1	112,164	fig|1129.58.j	Photosynthesis	Electron transport and photopt	Photosystem II		
gsyne_580	Synechococcus_assembled_mapped	diaminopimelate epimerase dapF	5.1.1.7		GO:0008837,GO:0009089	TIGR00652	489862	491089	1	71	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Lysine Biosynthesis DAP Pathwa		
gsyne_581	Synechococcus_assembled_mapped	aminotransferase class-V family protein				PF00266.14	491093	492290	1	703	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	tRNA modification Bacteria		
gsyne_582	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09353.5	492314	492950	1	156	fig|1129.58.peg.582					
gsyne_583	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14221.1	493001	493514	1	156	fig|1129.58.peg.583					
gsyne_584	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	494807	495746	-1	156	fig|1129.58.peg.585					
gsyne_585	Synechococcus_assembled_mapped	D-alanyl-D-alanine carboxypeptidase/D dacB	3.4.16.4		GO:0008717,GO:0009002,G	TIGR00666	493515	494811	1	89	fig|1129.58.j	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Murein Hydrolases		
gsyne_586	Synechococcus_assembled_mapped	pantetheine-phosphate adenylyltransf coaD	2.7.7.3		GO:0004595,GO:0015937	TIGR01510	495755	496241	-1	83	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Coenzyme A	Coenzyme A Biosynthesis		
gsyne_587	Synechococcus_assembled_mapped	flavin reductase like domain protein				PF01613.13	496349	496832	1	703	fig|1129.58.peg.587					
gsyne_588	Synechococcus_assembled_mapped	excinuclease ABC subunit C uvrC	3.1.25.-		GO:0006289,GO:0009380,G	TIGR00194	496842	498843	1	132	fig|1129.58.j	DNA Metabolism	DNA repair	DNA repair, UvrABC system		
gsyne_589	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	498839	499151	1	156	fig|1129.58.peg.589					
gsyne_59	Synechococcus_assembled_mapped	oxygen-independent coproporphyrinog hemN	1.3.99.22		GO:0006779,GO:0051989	TIGR00538	46408	47770	-1	79	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi		
gsyne_590	Synechococcus_assembled_mapped	FAD binding domain of DNA photolyase family protein				PF03441.9	499147	500698	1	132	fig|1129.58.peg.590					
gsyne_591	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10929.3	500746	500980	1	156	fig|1129.58.peg.591					
gsyne_592	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03653.8	500976	501570	1	156	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi		
gsyne_593	Synechococcus_assembled_mapped	PHP domain protein				PF02811.14	501574	502225	1	703	fig|1129.58.peg.593					
gsyne_594	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	502251	502767	1	156	fig|1129.58.peg.594					
gsyne_595	Synechococcus_assembled_mapped	cobaltochelatase, CobN subunit cobN	6.6.1.2		GO:0009236,GO:0051116	TIGR02257	502784	506492	-1	79	fig|1129.58.peg.595					
gsyne_596	Synechococcus_assembled_mapped	branched-chain amino acid aminotrans ilvE	2.6.1.42		GO:0004084,GO:0009082	TIGR01122	506584	507502	1	74	fig|1129.58.j	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios		
gsyne_597	Synechococcus_assembled_mapped	methionine synthase metH	2.1.1.13		GO:0008705,GO:0009086	TIGR02082	507558	511140	1	71	fig|1129.58.j	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis		
gsyne_598	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF13319.1	511185	511461	1	156	fig|1129.58.peg.598					
gsyne_599	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	511516	511744	-1	156	fig|1129.58.peg.599					
gsyne_6	Synechococcus_assembled_mapped	acetyltransferase family protein				PF00583.19	3012	3486	-1	703	fig|1129.58.peg.7					
gsyne_60	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11320.3	45991	46423	1	156	fig|1129.58.j	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism		
gsyne_600	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09996.4	511886	512246	1	156	fig|1129.58.peg.600					
gsyne_601	Synechococcus_assembled_mapped	NAD-dependent glycerol-3-phosphate dehydrogenase family protein				PF07479.9	512253	513180	1	184	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho		
gsyne_602	Synechococcus_assembled_mapped	phenazine biosynthesis , PhzF family protein				TIGR00654	513179	514061	1	185	fig|1129.58.peg.602					
gsyne_603	Synechococcus_assembled_mapped	spoIID/LytB domain protein			GO:0003674,GO:0005575,G	TIGR02669	514057	515017	1	157	fig|1129.58.peg.603					
gsyne_604	Synechococcus_assembled_mapped	ATP adenylyltransferase family protein				PF09830.4	515016	515850	1	703	fig|1129.58.peg.604					
gsyne_605	Synechococcus_assembled_mapped	putative sigma factor SigF				UniRef100_A	516577	516760	-1	185						
gsyne_606	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein				TIGR02937	515919	516621	1	135	fig|1129.58.j	Stress Response	Stress Response - no subcate	SigmaB stress responce regulati		
gsyne_607	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11850.3	516965	518576	1	156	fig|1129.58.peg.606					
gsyne_608	Synechococcus_assembled_mapped	dnaJ domain protein				PF00226.26	518601	519756	1	95	fig|1129.58.peg.607					



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0.75448263	-1.1026537	0.2044885	-1.5140892	0.62419002	-1.1784793	0.47431646	1.28478224
0.22415349	-2.019402	0.74722477	1.25716769	1	-1.0754899	0.74722477	-1.3520712
0.91047268	1.05739587	0.06704085	2.23536069	0.91047268	1.04824639	0.09156959	-2.1324764
0.3220077	-1.7810272	0.39602847	1.82007406	1	1.06099772	0.39602847	-1.7154363
0.20503426	1.58921058	0.21285397	1.59868156	0.18449004	1.6382919	0.96786001	1.02477688
0.15177331	1.6066653	0.98517392	-1.0108496	0.62092071	1.17529706	0.60143762	1.18804854
0.06388998	2.00147057	0.69931533	1.3480365	7.8225E-05	5.98369782	0.00047526	4.43882479
0.63918745	1.1616559	0.06929565	1.76932009	0.89039821	1.0340912	0.10196879	-1.7109904
0.16468132	1.55699623	0.76379646	1.10936367	0.94603578	1.02999449	0.8262837	-1.0770579
0.31018916	-1.9852921	0.41571202	-1.6050041	0.52920145	-1.6718521	1	-1.0416498
0.49777483	-1.2875123	0.73498945	1.15579664	0.92702704	-1.0842856	0.60348755	-1.2532137
1	-1.0433079	0.81336953	-1.1049203	0.95406736	-1.0630434	0.90450649	1.03939341
0.50561993	-1.3365447	0.37410623	-1.5259611	0.85805112	-1.1617168	0.53669009	1.31353972
1	1.0324884	0.53081847	1.27243104	0.53081847	1.30532259	1	1.02584937
0.8300271	1.0868479	0.35475808	1.41357917	0.2546436	1.49661989	0.87294435	1.05874501
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1	-1.0209565	0.22256103	1.50213899	0.40743925	1.32937622	0.74531845	-1.1299578
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0.39655953	-1.7827477	0.82763266	-1.3726308	1	-1.1337552	0.82763266	1.21069408
0.25374416	-1.5471267	0.57280689	-1.247823	0.74387239	-1.1293794	0.82262236	1.10487495
0.24799384	-1.8355455	1	1.05054043	0.78684259	-1.2346026	0.78684259	-1.2969999
0.67752847	-1.1451925	0.94461311	1.03253423	0.88544592	-1.0535157	0.81266779	-1.087791
0.84490953	1.19910837	0.65009492	1.41171708	0.84490953	1.1801231	0.86645896	-1.1962456
0.78651406	-1.1067705	0.64093949	-1.1900089	0.71721092	-1.1447278	0.92595478	1.03955622
0.64701174	1.19054411	0.36972371	1.40259156	0.64701174	1.19404789	0.67238657	-1.1746527
0.13014899	-1.7303647	0.16087023	-1.7139436	0.32099302	-1.4439075	0.71558307	1.18701758
0.17437597	-17.434242	0.10591735	-25.599891	0.10591735	-25.599891	1	1
1	1.07356076	1	1.05654587	1	-1.1574395	1	-1.2228879
0.23797484	-1.7878159	0.07351125	2.57366297	0.18437136	2.09589804	0.71009919	-1.2279524
0.2192216	-1.6144912	0.59360777	-1.3408919	0.43836392	-1.3266883	0.90178404	1.01070606
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0.90353266	-1.114816	1	1.10740807	1	1.11679253	1	1.00847426
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1	-1.2216874	0.42751141	-2.3462232	0.42751141	-2.6265203	1	-1.1194674
1	-1.6726988	1	1.80379459	1	-1.2232054	1	-2.2064112
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1	-1.0169493	0.30954345	1.40071983	0.6101841	-1.2512611	0.09334794	-1.7526662
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1	-1.0253195	0.56274106	-1.1823546	0.76297649	-1.1051535	0.81619341	1.06985548
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27	3.35765275	11	1.62773822	13	3.26409568	15	2.30142839	12	4.03015156	12	1.94476515	8	1.92150011	20	1.7774119
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14	2.82407227	11	2.64034281	2	0.81456413	8	1.99100317	7	3.81341375	4	1.05152999	4	1.55842596	6	0.86493823
43	2.84716992	32	2.52124337	12	1.60425607	48	3.92121235	78	13.9478623	23	1.98466252	20	2.55772199	44	2.08201417
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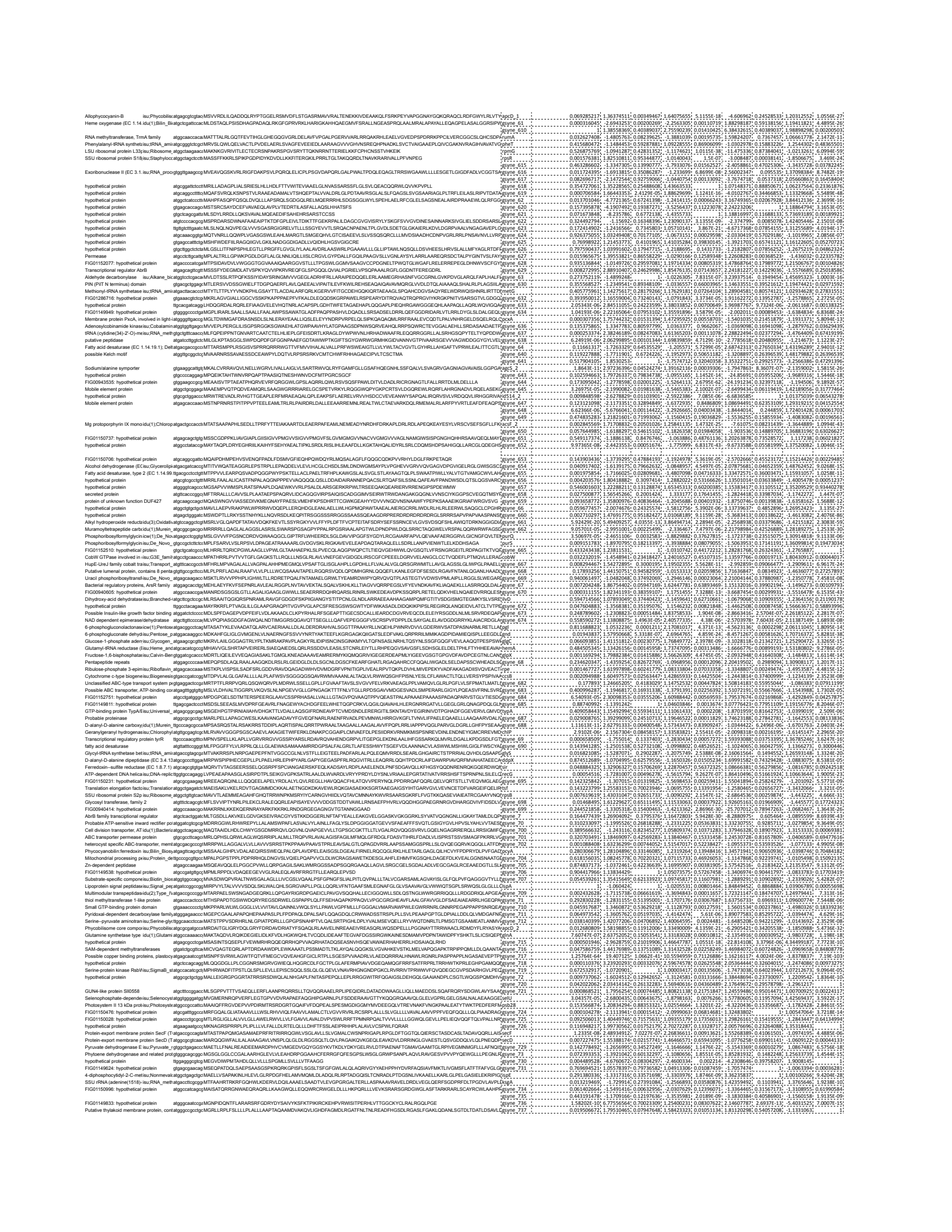
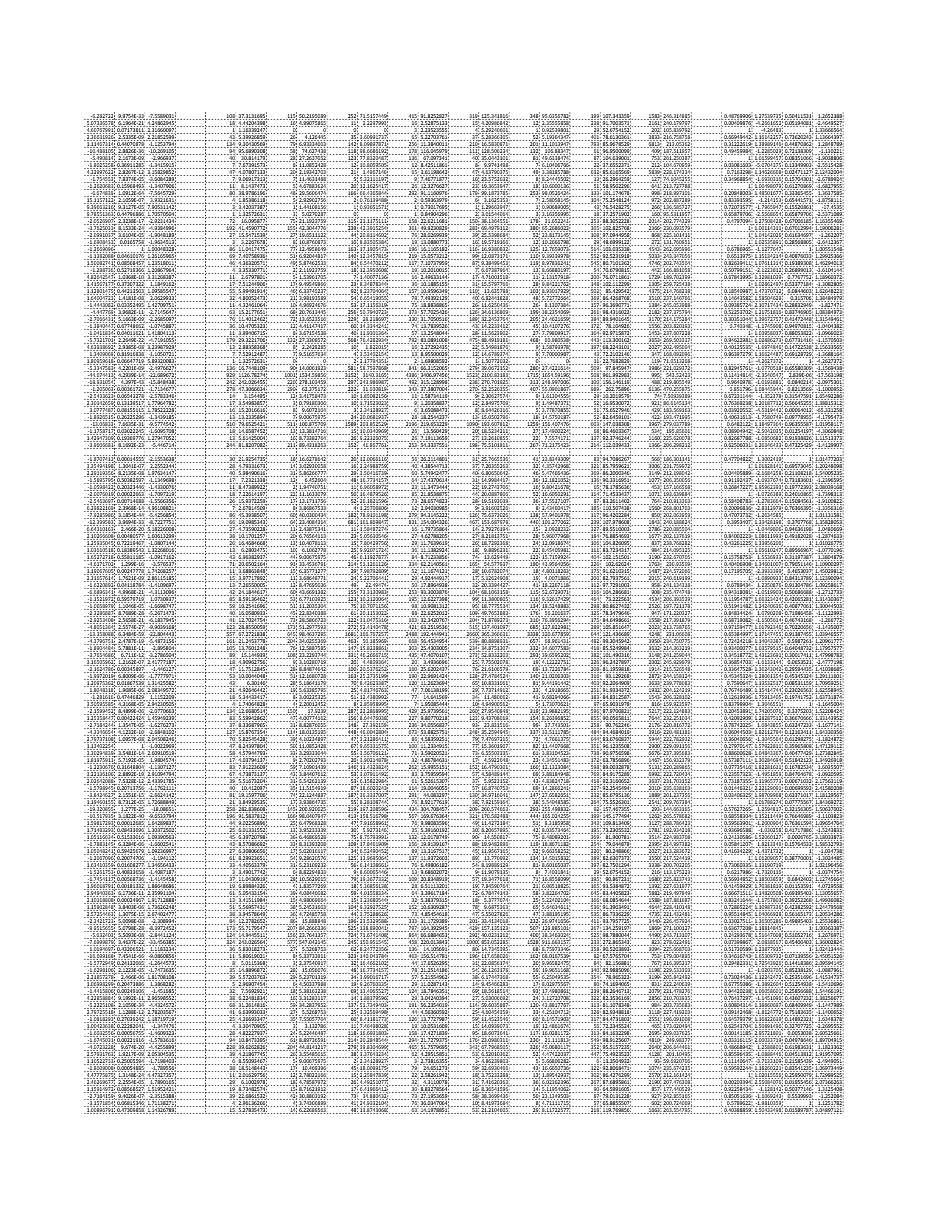
56	4.73893103	47	4.73271203	24	4.10063502	65	6.78640714	66	15.0835794	71	7.83005138	33	5.39367423	61	3.68899672
121	8.63824105	79	6.71099477	90	12.9726879	125	11.0099198	84	16.1952387	148	13.7694174	63	8.68678173	211	10.7648623
16	5.04665382	6	2.25192874	6	3.82104627	7	2.72405434	1	0.85182749	7	2.87736843	3	1.82760862	6	1.35244887
23	8.22682614	26	11.066179	10	7.22190875	21	9.26740135	14	13.5238591	19	8.85670106	9	6.21763759	24	6.13481963
27	5.71210437	39	9.81786006	20	8.54298962	30	7.83046978	13	7.42752017	31	8.54688707	17	6.94639863	36	5.44278205
27	5.51050068	21	5.09995627	7	2.88451532	25	6.29508355	6	3.30709495	13	3.45767803	8	3.15352076	23	3.35460358
27	2.49144978	31	3.40384619	10	1.8630988	25	2.84618139	22	5.4825067	17	2.04433092	11	1.9604667	44	2.90153038
48	8.58451424	29	6.17152292	20	7.22190875	19	4.19239585	21	10.1428943	33	7.69134566	18	6.21763759	54	6.90167208
56	3.77274121	46	3.68762441	30	4.08072902	35	2.90918424	46	8.36941182	37	3.24851304	13	1.69157303	31	1.4925083
109	5.94628335	79	5.12821299	78	8.59134616	100	6.73059247	71	10.4603344	160	11.3750414	67	7.05947356	140	5.45799598
38	3.37196499	27	2.85090723	13	2.32911175	22	2.40855371	21	5.0325358	28	3.23795936	14	2.39941797	41	2.59997631
228	88.8834817	237	109.939667	139	109.40786	225	108.218852	70	73.6974343	352	178.830988	125	94.1184216	294	81.9067351
16	5.04665382	7	2.6272502	2	1.27368209	9	3.50235557	1	0.85182749	3	1.2331579	4	2.4368115	3	0.67622444
10	3.54038215	9	3.79151268	2	1.42964316	7	3.05761201	2	1.91226579	4	1.84554243	3	2.05139743	6	1.51805486
235	131.508066	157	104.545186	98	110.728169	97	66.9715663	42	63.474887	124	90.4315793	29	31.3444705	236	94.3805719
17	3.27682036	15	3.44044669	9	3.50262574	6	1.4268856	4	2.08224497	12	3.01438598	4	1.48916258	11	1.51524364
114	10.381404	85	9.21064467	48	8.82551368	87	9.77472815	46	11.3129845	86	10.2061887	35	6.15598705	119	7.7443376
12	1.86703561	6	1.11081687	3	0.94241051	11	2.11153475	14	5.88257548	1	0.20276139	5	1.5025183	13	1.44544237
174	70.1983679	164	78.7302219	96	78.1981561	163	81.1333791	44	47.9400586	178	93.5861693	48	37.402223	254	73.231437
93	5.5537079	75	5.32943549	56	6.75204963	61	4.49432127	95	15.3211657	52	4.04685209	49	5.65164113	114	4.86509147
66	27.5893876	60	29.8448387	36	30.3842233	38	19.5981878	27	30.4810559	12	6.5372226	17	13.7254142	45	13.4430159
3	2.12422929	2	1.68511674	0	0	6	5.24162059	0	0	0	0	0	0	0	0
0	0	1	1.03213401	0	0	1	1.0701642	0	0	1	1.13039474	0	0	1	0.6198724
30	3.88385206	17	2.61884748	3	0.78416994	6	0.958356	15	5.24446028	5	0.84357817	5	1.25022978	18	1.66532884
23	3.02273536	16	2.50214305	10	2.65350435	13	2.10789919	8	2.83942496	8	1.37017544	2	0.50766906	21	1.97232127
21	2.22137392	13	1.63631001	5	1.0678737	15	1.95761745	18	5.14212935	16	2.20564828	11	2.24736426	18	1.36069551
1	0.80687779	2	1.92024931	0	0	1	0.99550158	0	0	0	0	0	0	0	0
10	1.75231036	5	1.0425596	14	4.95320812	10	2.16194789	5	2.36618747	10	2.28362574	6	2.03067625	16	2.00362796
17	5.51240809	11	4.24428937	8	5.23757121	8	3.20049107	7	6.12997351	10	4.22577473	5	3.13141665	17	3.939376
2	1.3092734	0	0	0	0	2	1.61534219	0	0	2	1.70625621	0	0	0	0
18	1.9395137	10	1.28215405	4	0.87021758	12	1.59527583	24	6.98392723	14	1.9659039	7	1.45678948	18	1.38605009
207	39.6796642	135	30.7929483	117	45.2825649	107	25.3055403	57	29.5080572	165	41.2188138	50	18.5116896	186	25.4798379
19	3.74556338	14	3.28406275	1	0.39802565	14	3.40506792	3	1.59717654	7	1.79835527	3	1.14225539	8	1.12704073
23	4.17802165	15	3.24230578	10	3.66767094	10	2.24118158	9	4.41523148	12	2.8407826	6	2.10509894	16	2.07705935
14	9.16491378	14	10.9055669	4	5.28698225	7	5.65369768	7	12.3756069	14	11.9437935	4	5.0575333	9	4.21045404
24	13.430611	18	11.9860723	7	7.9091549	18	12.4277133	19	28.7148298	12	8.75144316	6	6.48506286	4	1.59967071
10	5.59608791	4	2.66357163	2	2.25975854	3	2.07128555	3	4.5339205	2	1.45857386	0	0	0	0
5	3.27318349	6	4.67381437	0	0	3	2.42301329	1	1.76794384	0	0	0	0	0	0
48	8.45378559	39	8.17324391	46	16.35744	28	6.08418227	26	12.3666326	19	4.36091372	38	12.9262336	137	17.243151
9	3.90327132	12	6.19280404	2	1.75131287	8	4.28065681	5	5.85631398	1	0.56519737	0	0	1	0.3099362
21	5.39711589	5	1.52908742	2	1.03781504	5	1.58542845	3	2.08224497	4	1.3397271	3	1.48916258	9	1.65299307
4	0.87837329	3	0.78389925	5	2.21685174	6	1.62556588	4	2.37217781	0	0	3	1.27238575	1	0.15692972
0	0	2	1.39950374	1	1.18733076	0	0	0	0	2	1.53273863	0	0	1	0.42025248
31	2.12983781	21	1.71681696	12	1.66461422	36	3.05155733	24	4.45311796	24	2.14886921	19	2.52125546	41	2.01305096
23	2.98877204	19	2.93790953	11	2.88605867	28	4.48907831	20	7.01880327	30	5.0804258	9	2.25884212	27	2.50734903
44	27.2609425	42	30.9640202	10	12.5093777	20	15.28806	17	28.4449536	17	13.7262219	23	27.5229156	27	11.954682
7	3.28202994	6	3.34746164	4	3.78662243	17	9.83394133	5	6.33115025	3	1.83307255	4	3.62228736	4	1.34026465
53	5.28412209	48	5.69453245	33	6.64291089	46	5.65833946	18	4.84660467	48	6.23666064	24	4.62153905	59	4.20373237
23	2.27351036	20	2.35244218	10	1.99579814	19	2.31716466	23	6.13995312	19	2.44757836	12	2.29101936	15	1.05961094
11	6.05798723	16	10.4851709	7	7.78361276	15	10.19204	1	1.48731784	10	7.17710947	2	2.12737512	7	2.75498844
15	2.31304967	14	2.56886686	5	1.55672255	12	2.28301697	5	2.08224497	14	2.81342691	8	2.38266013	13	1.43259399
15	2.72479673	13	2.80999834	6	2.20060256	29	6.49942657	7	3.43406893	18	4.26117389	5	1.75424912	19	2.46650798
20	3.52241066	17	3.56269606	15	5.33394783	13	2.82479891	25	11.8909929	19	4.36091372	21	7.14344487	48	6.04139598
234	102.769675	206	107.655496	47	41.6768126	328	177.728536	25	29.6522227	127	72.6886745	40	33.9302867	158	49.589792
48	4.85538123	30	3.61096445	18	3.67622527	28	3.49441372	31	8.46860564	34	4.48203163	24	4.68890842	57	4.12043461
35	2.4046556	26	2.1255829	7	0.97102496	18	1.52577867	24	4.45311796	9	0.80582595	10	1.32697656	35	1.71845814
49	3.03587769	39	2.87523045	15	1.87640665	21	1.6052463	42	7.02757677	13	1.04965226	14	1.67530791	38	1.6825108
46	3.98006053	14	1.44138415	29	5.06614197	39	4.16323231	57	13.3190981	35	3.94651531	11	1.83824309	59	3.64812684
30	2.99963214	29	3.45036152	11	2.22068491	42	5.18119845	21	5.67066714	61	7.94859703	19	3.66926227	47	3.35838649
48	3.29781339	41	3.35188073	36	4.99384264	42	3.56015022	50	9.27732907	42	3.76052112	26	3.45013905	74	3.63331149
23	3.00000803	24	3.72499491	14	3.68697447	57	9.17283603	30	10.5677846	75	12.7488129	19	4.78659401	53	4.94033642
3	2.04092618	2	1.61903374	0	0	3	2.51803342	0	0	0	0	0	0	0	0
33	3.92109447	34	4.80719948	22	5.2779292	74	10.8482399	17	5.45519658	77	11.9233418	9	2.0654481	45	3.82113123
64	5.31226718	51	5.03720903	28	4.69251296	87	8.90950102	29	6.50078872	113	12.2234073	19	3.04601437	93	5.51656777
148	10.2699405	164	13.5415982	44	6.16462131	276	23.6292256	52	9.74490646	186	16.8202738	53	7.10330552	209	10.3642665
99	5.40075276	112	7.2703779	57	6.27829143	165	11.1054776	69	10.1656771	157	11.1617594	67	7.05947356	247	9.62946433
2	0.991307	3	1.76937258	1	1.00075021	0	0	0	0	0	0	0	0	0	0
20	2.5892347	22	3.38909674	12	3.13667977	24	3.83342401	26	9.09039782	23	3.88045956	18	4.50082721	30	2.77554806
13	6.01392914	9	4.95424323	7	6.53823472	21	11.9858391	11	13.7428168	10	6.02877195	9	8.04147794	17	5.62017643
35	3.08995185	26	2.73134699	24	4.27801618	38	4.13905748	15	3.57637495	51	5.86769789	15	2.55772199	62	3.91166298
25	2.8817064	7	0.96012466	13	3.0255239	11	1.56435963	5	1.55649541	11	1.65240427	0	0	16	1.31800112
26	7.39417517	11	3.72245051	3	1.72260283	12	4.21048211	8	6.14432942	9	3.33559104	5	2.7464064	12	2.43884223
21	2.42870215	9	1.23856081	10	2.33508383	18	2.56839409	8	2.49869396	18	2.71294738	6	1.34024632	18	1.48769376
28	3.66596551	21	3.27167006	13	3.43653847	24	3.87682126	32	11.3148406	14	2.3887587	10	2.52876665	19	1.77774726
30	3.54038215	17	2.38724872	13	3.09756018	33	4.80481887	16	5.09937544	28	4.30626568	10	2.27933048	29	2.44575505
41	4.47335078	43	5.58261161	29	6.38843689	30	4.03835548	23	6.77711806	57	8.10471701	24	5.0575333	74	5.76988146
359	19.6463288	300	19.5356594	279	30.8275263	730	49.2883198	200	29.5586825	846	60.335265	233	24.6275547	966	37.778974
40	4.64157124	28	3.86618758	14	3.28005086	27	3.86547605	7	2.19366945	27	4.08303117	12	2.68945751	42	3.48289509
44	10.827041	32	9.36972715	29	14.4079641	42	12.7508926	17	11.2972865	30	9.62038078	24	11.4063517	62	10.9027202
29	3.59348788	9	1.32702944	8	2.00150043	19	2.90473141	13	4.35040467	5	0.80742482	11	2.63262671	41	3.6306812
32	3.65218369	41	5.56809135	28	6.45220532	44	6.19568749	45	13.8702173	46	6.84186291	17	3.74739926	59	4.81216732
57	13.4534522	43	12.07667	25	11.913693	37	10.7744423	27	17.2103921	50	15.3795203	20	9.11732193	54	9.10832914
24	3.965228	15	2.9489543	2	0.66716681	10	2.03840801	11	4.90814886	9	1.93781956	10	3.19106268	16	1.88913493
71	4.7555944	34	2.7098499	34	4.59804152	44	3.63607915	31	5.60759022	33	2.88054258	20	2.58734812	67	3.20706184
18	3.2527261	16	3.44044669	18	6.56742327	22	4.90491926	18	8.78447097	25	5.88747261	14	4.88631472	26	3.35764217
26	2.54109682	10	1.16296789	6	1.18398617	13	1.56756447	13	3.43130509	8	1.01894737	13	2.45397214	20	1.39689555
59	17.6469738	54	19.219047	27	16.3053267	63	23.2483948	12	9.69320934	42	16.3712342	21	12.13154	93	19.8786666
62	3.7088555	54	3.8438094	35	4.22730693	48	3.54261253	48	7.75456747	53	4.13178767	34	3.92830819	95	4.06123297
45	5.5562581	27	3.96692074	25	6.23243015	33	5.02710587	28	9.33675681	32	5.14912907	20	4.76955987	54	4.76485546
60	8.46237684	55	9.23046672	27	7.68869066	51	8.87453242	29	11.0460556	47	8.63878908	24	6.53778695	87	8.76892663
216	14.0080017	171	13.1958815	162	21.2121634	195	15.602394	93	16.2882153	205	17.3256764	98	12.2751533	454	21.0409024
77	3.0153187	57	2.65605591	33	2.60917945	70	3.38200877	77	8.14331695	73	3.72545445	34	2.57157873	100	2.79852099
6	2.60218088	7	3.61246902	5	4.37828218	4	2.14032841	3	3.51378839	2	1.13039474	0	0	9	2.7894258
211	20.3355617	342	39.2210922	149	28.9939575	553	65.7556449	73	19.0004854	406	50.9933628	103	19.1729682	270	18.596172
50	4.24153362	28	2.82638163	25	4.28193856	45	4.70976911	50	11.4548929	49	5.41705059	21	3.44073017	61	3.69801627
40	3.47827018	19	1.96596954	5	0.87785106	19	2.03840801	8	1.87871727	19	2.15313284	7	1.17565467	20	1.24285193
18	2.94586514	13	2.53164945	13	4.29567308	13	2.62493106	6	2.65191576	17	3.62579445	10	3.16095831	20	2.33914113
46	9.33335831	20	4.8286971	18	7.37394893	48	12.0158788	19	10.4112249	34	8.99027396	14	5.48638846	56	8.11996594
72	7.98112985	66	8.70553922	61	13.6524071	49	6.70134773	43	12.8726646	61	8.8120229	41	8.77797113	150	11.882538
55	4.41728235	43	4.10942243	29	4.70259938	48	4.75628535	33	7.15771708	62	6.48930314	41	6.35996519	90	5.16560333
8	1.71337013	13	3.31302274	5	2.16211466	11	2.90661882	12	6.94081657	11	3.07020794	2	0.82731255	15	2.2958237
55	11.8525837	71	18.2065874	25	10.8777197	105	27.917327	25	14.5498484	97	27.2418112	18	7.4920602	82	12.6284564
49	2.54886283	43	2.66157495	26	2.73068274	43	2.75964382	32	4.49540143	51	3.45727927	20	2.0093648	56	2.0817304
11	3.66974226	4	1.58789847	4	2.6943275	5	2.05800808	2	1.80194276	12	5.2172065	3	1.93304758	12	2.86094954
32	2.44551507	18	1.6368645	8	1.23440555	21	1.9800395	17	3.50862864	19	1.89229076	15	2.21406331	51	2.78532973
55	3.69103671	25	1.99639073	16	2.16796951	33	2.73233414	32	5.79967651	34	2.97357224	13	1.68502923	54	2.58979571
11	4.89298968	8	4.23439592	2	1.79621833	9	4.9392194	1	1.20129518	3	1.73906883	1	0.85913226	6	1.90729969
18	3.15415864	10	2.0851192	12	4.24560696	5	1.08097394	3	1.41971248	11	2.51198831	3	1.01533812	10	1.25226748
11	1.75877049	5	0.95127558	5	1.61411325	11	2.1699182	3	1.29540586	9	1.87530925	2	0.61762503	7	0.79983536
148	29.8544783	165	39.6051421	127	51.724822	132	32.8515523	107	58.2907531	105	27.6026623	94	36.62301	328	47.2832901
83	2.32989226	87	2.90600837	37	2.0970413	62	2.14725504	64	4.85183294	64	2.34127066	27	1.46386128	101	2.02612014
35	3.96846757	36	4.85710121	46	10.5307702	33	4.6163946	29	8.88016237	53	7.83149298	20	4.37988995	107	8.67011069
117	3.39983431	86	2.97365241	56	3.28554509	93	3.33417993	77	6.04269583	103	3.90052457	41	2.30109294	143	2.96957297
23	8.67393626	18	8.07757048	14	10.6601653	16	7.44462054	5	5.09244694	12	5.89771169	13	9.46913164	32	8.62431165
17	7.76089034	18	9.77811164	24	22.1218468	18	10.1383977	24	29.5897969	6	3.5696676	17	14.989597	26	8.48246442
13	2.8547132	9	2.35169774	3	1.33011104	5	1.35463823	8	4.74435563	5	1.43087942	1	0.42412858	6	0.94157833
9	2.16848406	4	1.14681556	2	0.9729516	3	0.8918035	3	1.95210466	2	0.62799708	0	0	3	0.51656033
13	3.75870571	10	3.44044669	5	2.91885479	9	3.21049261	2	1.56168373	4	1.50719299	5	2.79217984	9	1.8596172
20	2.24567929	17	2.27136286	7	1.58695018	14	1.93945616	9	2.72915603	19	2.78025891	4	0.86747335	21	1.68509002
26	3.06833119	14	1.96596954	14	3.33583404	20	2.91201144	7	2.23097675	17	2.61451845	8	1.82346439	21	1.771064
36	3.90327132	21	2.70935177	29	6.34850916	46	6.15344417	22	6.44194538	40	5.65197371	19	3.97885627	39	3.02187795
23	2.87051128	12	1.78210188	8	2.01589971	14	2.15572645	7	2.35937829	17	2.76499433	3	0.72315449	18	1.60542492
16	9.10052329	16	10.828947	7	8.03881318	13	9.12271124	5	7.68041177	12	8.89490944	3	3.29568768	15	6.09710557
18	2.66890346	11	1.9407648	9	2.6943275	22	4.02454914	63	25.2271987	9	1.73906883	16	4.58203871	8	0.84768875
47	3.03668532	36	2.76773365	29	3.78309671	39	3.1088569	32	5.58367366	35	2.9470254	31	3.86849498	57	2.63186047
39	3.51463391	26	2.78810225	22	4.00300085	24	2.66846139	20	4.86758564	18	2.11398497	17	2.95898539	48	3.09131171

gsyne_609	Synechococcus_assembled_mapped	allophycocyanin subunit alpha-B	apcD		GO:0006810,GO:0022900,G	UniRef100_P	520935	521430	-1	92	fig|1129.58.j	Photosynthesis	Light-harvesting complexes	Phycobilisome		
gsyne_61	Synechococcus_assembled_mapped	heme oxygenase family protein				PF01126.15	47814	48507	-1	185	fig|1129.58.j	Iron acquisition and metabolism	Iron acquisition and metabolism	Heme, hemin uptake and utilizati		
gsyne_610	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	521426	521573	-1	856						
gsyne_611	Synechococcus_assembled_mapped	23S rRNA (uracil-5-)-methyltransferase	rumA	2.1.1.-	GO:0000154,GO:0008649	TIGR00479	521540	522902	1	168	fig|1129.58.peg.611					
gsyne_612	Synechococcus_assembled_mapped	phenylalanine--tRNA ligase, beta subun	pheT	6.1.1.20	GO:0004826,GO:0006432,G	TIGR00472	522904	525367	-1	137	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Phe		
gsyne_613	Synechococcus_assembled_mapped	ribosomal protein L33	rpmG		GO:0000315,GO:0003735,G	TIGR01023	525511	525679	1	158	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Ribosome LSU bacterial		
gsyne_614	Synechococcus_assembled_mapped	ribosomal protein S18	rpsR		GO:0000314,GO:0003735,G	TIGR00165	525747	525969	1	158	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial		
gsyne_615	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11848.3	528001	528157	-1	156						
gsyne_616	Synechococcus_assembled_mapped	RNB domain protein				PF00773.14	526042	528013	1	157	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	RNA processing and degradation		
gsyne_617	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	528153	528285	-1	856						
gsyne_618	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	528248	528479	-1	856	fig|1129.58.peg.616					
gsyne_619	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03683.8	528491	528842	-1	156	fig|1129.58.peg.617					
gsyne_62	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	48604	48973	1	156	fig|1129.58.peg.61					
gsyne_620	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	528901	529051	-1	856	fig|1129.58.peg.618					
gsyne_621	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	529047	529176	-1	856	fig|1129.58.peg.619					
gsyne_622	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	529219	529984	-1	703	fig|1129.58.peg.620					
gsyne_623	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	530070	530862	1	703	fig|1129.58.peg.621					
gsyne_624	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	530935	531232	1	856	fig|1129.58.peg.622					
gsyne_625	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	531300	531459	-1	856	fig|1129.58.peg.623					
gsyne_626	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein				PF00999.16	531523	532855	-1	145	fig|1129.58.peg.624					
gsyne_627	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	532957	534550	-1	88	fig|1129.58.peg.625					
gsyne_628	Synechococcus_assembled_mapped	FAD dependent oxidoreductase family protein				PF12831.2	534604	536407	-1	703	fig|1129.58.peg.626					
gsyne_629	Synechococcus_assembled_mapped	transcriptional regulator, AbrB family domain protein			GO:0003700,GO:0006355	TIGR01439	536528	536732	1	261	fig|1129.58.peg.627					
gsyne_63	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11266.3	48980	49682	-1	156	fig|1129.58.j	Secondary Metabolism	Hydrocarbons	Alkane biosynthesis in bacteria		
gsyne_630	Synechococcus_assembled_mapped	PIN domain protein				PF01850.16	536728	537115	1	157	fig|1129.58.peg.628					
gsyne_631	Synechococcus_assembled_mapped	methionine--tRNA ligase	metG	6.1.1.10	GO:0004825,GO:0005737,G	TIGR00398	537182	538751	1	137	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Met		
gsyne_632	Synechococcus_assembled_mapped	lipopolysaccharide-assembly, LptC-related family protein				PF06835.8	538791	539931	1	90	fig|1129.58.peg.630					
gsyne_633	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	540640	541075	1	156	fig|1129.58.peg.631					
gsyne_634	Synechococcus_assembled_mapped	repair family protein				PF04536.9	541084	541792	1	185	fig|1129.58.peg.633					
gsyne_635	Synechococcus_assembled_mapped	proton extrusion protein PcxA	pcxA		GO:0016021,GO:0015992,G	UniRef100_P	541799	542939	1		fig|1129.58.peg.634					
gsyne_636	Synechococcus_assembled_mapped	cobinamide kinase / cobinamide phosphate guanyltransferase family protein				PF02283.11	542928	543516	1	79	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Cobalamin synthesis		
gsyne_637	Synechococcus_assembled_mapped	spoU rRNA Methylase family protein				PF00588.14	543527	543998	1	168	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	RNA methylation		
gsyne_638	Synechococcus_assembled_mapped	lysM domain protein				PF01476.15	544159	545203	1	90	fig|1129.58.peg.638					
gsyne_64	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	50371	51142	-1	121	fig|1129.58.peg.64					
gsyne_640	Synechococcus_assembled_mapped	putative kelch motif				UniRef100_C	545529	545688	1	185	fig|1129.58.peg.639					
gsyne_641	Synechococcus_assembled_mapped	putative Kelch motif domain protein				UniRef100_A	545648	545777	1	157						
gsyne_642	Synechococcus_assembled_mapped	amino acid carrier family protein	agcS		GO:0005416,GO:0006865,G	TIGR00835	546032	547421	1	141	fig|1129.58.peg.640					
gsyne_643	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	547718	547859	1	856	fig|1129.58.peg.641					
gsyne_644	Synechococcus_assembled_mapped	PAP_fibrillin family protein				PF04755.7	547870	548041	1	185	fig|1129.58.peg.642					
gsyne_645	Synechococcus_assembled_mapped	integrase core domain protein				PF00665.21	548096	549101	1	157	fig|1129.58.peg.643					
gsyne_646	Synechococcus_assembled_mapped	ID514 domain protein	id514		GO:0015074,GO:0003677	UniRef100_C	549070	549583	1	92,141	fig|1129.58.peg.644					
gsyne_647	Synechococcus_assembled_mapped	istB-like ATP binding family protein				PF01695.12	549624	550443	1	154	fig|1129.58.peg.645					
gsyne_648	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	550429	550609	1	856						
gsyne_649	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	550598	550766	1	856						
gsyne_65	Synechococcus_assembled_mapped	magnesium-protoporphyrin IX monom	acsF	1.14.13.81	GO:0015995,GO:0048529	TIGR02029	51228	52233	-1	191	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Chlorophyll Biosynthesis		
gsyne_650	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	551083	551293	1	856						
gsyne_651	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF12518.3	551326	551722	1	156	fig|1129.58.peg.648					
gsyne_652	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	551817	552327	-1	856	fig|1129.58.peg.649					
gsyne_6523	Synechococcus_assembled_umapped	GDP-L-fucose synthase 1	GER1	1.1.1.271	GO:0016853,GO:0050577,G	UniRef100_C	47555	48521	1	141,703						
gsyne_653	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF10929.3	552546	552780	-1	156	fig|1129.58.peg.650					
gsyne_654	Synechococcus_assembled_mapped	zinc-binding dehydrogenase family protein				PF00107.21	553214	554213	1	703	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Phospholipids	Glycerolipid and Glycerophospho		
gsyne_655	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	554310	555453	1	121	fig|1129.58.peg.652					
gsyne_656	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	555474	555876	-1	856	fig|1129.58.peg.653					
gsyne_657	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	555835	556057	-1	856	fig|1129.58.peg.654					
gsyne_658	Synechococcus_assembled_mapped	putative secreted protein				UniRef100_D	556192	556618	1	185	fig|1129.58.peg.655					
gsyne_659	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF04248.7	556650	556929	1	156	fig|1129.58.peg.656					
gsyne_66	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	52232	52679	-1	856	fig|1129.58.peg.66					
gsyne_660	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	556934	557258	-1	856	fig|1129.58.peg.657					
gsyne_661	Synechococcus_assembled_mapped	ahpC/TSA family protein				PF00578.16	557411	558002	1	96,149	fig|1129.58.j	Stress Response	Oxidative stress	Rubrerythrin		
gsyne_662	Synechococcus_assembled_mapped	LD-carboxypeptidase family protein				PF02016.10	558069	559044	-1	138	fig|1129.58.j	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Murein Hydrolases		
gsyne_663	Synechococcus_assembled_mapped	phosphoribosylformylglycinamidine syr	purQ	6.3.5.3	GO:0004642,GO:0009152	TIGR01737	559051	559690	-1	125	fig|1129.58.j	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis		
gsyne_664	Synechococcus_assembled_mapped	phosphoribosylformylglycinamidine syr	purS		GO:0004642,GO:0009152	TIGR00302	559707	559977	-1	125	fig|1129.58.j	Nucleosides and Nucleotides	Purines	De Novo Purine Biosynthesis		
gsyne_665	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	560071	560425	1	156	fig|1129.58.peg.662					
gsyne_666	Synechococcus_assembled_mapped	cobalamin biosynthesis protein CobW	cobW		GO:0009236	TIGR02475	560448	561504	-1	79	fig|1129.58.j	Protein Metabolism	Protein processing and modific	G3E family of P-loop GTPases (r		
gsyne_667	Synechococcus_assembled_mapped	hupE / UreJ family protein				PF04955.7	561505	562093	-1	185	fig|1129.58.j	Membrane Transport	Cation transporters	Transport of Nickel and Cobalt		
gsyne_668	Synechococcus_assembled_mapped	pentapeptide repeats family protein				PF13599.1	562301	562811	-1	185	fig|1129.58.peg.665					
gsyne_669	Synechococcus_assembled_mapped	putative uracil phosphoribosyltransferase			GO:0006223,GO:0016757,G	UniRef100_A	562869	563514	1	92,141,703	fig|1129.58.j	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis		
gsyne_67	Synechococcus_assembled_mapped	bacterial regulatory , arsR family protein				PF01022.15	52810	53116	1	261	fig|1129.58.peg.67					
gsyne_670	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	563558	563855	1	156	fig|1129.58.peg.667					
gsyne_671	Synechococcus_assembled_mapped	dihydroxy-acid dehydratase	ilvD	4.2.1.9	GO:0004160,GO:0009097,G	TIGR00110	563908	565600	1	74	fig|1129.58.j	Amino Acids and Derivatives	Branched-chain amino acids	Branched-Chain Amino Acid Bios		
gsyne_672	Synechococcus_assembled_mapped	bacterial extracellular solute-binding s, 3 family protein				PF00497.15	565719	566703	1	185	fig|1129.58.peg.669					
gsyne_673	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	566839	567265	-1	156	fig|1129.58.peg.670					
gsyne_674	Synechococcus_assembled_mapped	complex I intermediate-associated 30 family protein				PF08547.7	567278	567830	-1	185	fig|1129.58.peg.671					
gsyne_675	Synechococcus_assembled_mapped	6-phosphogluconolactonase	pgl	3.1.1.31	GO:0006098,GO:0017057	UniRef100_P	567838	568567	-1	92,703	fig|1129.58.j	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway		
gsyne_676	Synechococcus_assembled_mapped	6-phosphogluconate dehydrogenase	gnd	1.1.1.44	GO:0004616,GO:0005737,G	TIGR00873	568571	569987	-1	117	fig|1129.58.j	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway		
gsyne_677	Synechococcus_assembled_mapped	glucose-1-phosphate adenylyltransfera	glgC	2.7.7.27	GO:0005978,GO:0008878	TIGR02091	570070	571366	-1	105	fig|1129.58.j	Carbohydrates	Polysaccharides	Glycogen metabolism		
gsyne_678	Synechococcus_assembled_mapped	glutamyl-tRNA reductase	hemA	1.2.1.70	GO:0005737,GO:0006779,G	TIGR01035	571509	572814	-1	79	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Heme and Siroheme Biosynthesi		
gsyne_679	Synechococcus_assembled_mapped	fructose-1,6-bisphosphatase, class II	glpX	3.1.3.11	GO:0006094,GO:0042132	TIGR00330	572915	573920	-1	117	fig|1129.58.j	Carbohydrates	CO2 fixation	Calvin-Benson cycle		
gsyne_68	Synechococcus_assembled_mapped	pentapeptide repeats family protein				PF13599.1	53115	53742	1	185	fig|1129.58.peg.68					
gsyne_680	Synechococcus_assembled_mapped	ribulose-phosphate 3-epimerase	rpe	5.1.3.1	GO:0004750,GO:0006098	TIGR01163	574152	574836	1	117	fig|1129.58.j	Carbohydrates	CO2 fixation	Calvin-Benson cycle		
gsyne_681	Synechococcus_assembled_mapped	cytochrome c-type biogenesis protein	CccsB			TIGR03144	575094	576000	-1	112,140	fig|1129.58.j	Respiration	Respiration - no subcategory	Biogenesis of c-type cytochrome		
gsyne_682	Synechococcus_assembled_mapped	putative permease YjgP/YjgQ family protein				PF03739.9	576069	577236	-1	141	fig|1129.58.peg.679					
gsyne_683	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	577262	577991	-1	141	fig|1129.58.peg.680					
gsyne_684	Synechococcus_assembled_mapped	ostA-like family protein				PF03968.9	577987	578563	-1	185	fig|1129.58.peg.681					
gsyne_685	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF03745.9	578588	578981	-1	156	fig|1129.58.peg.682					
gsyne_686	Synechococcus_assembled_mapped	GTP-binding protein TypA/BipA	typA		GO:0005525,GO:0006412,G	TIGR01394	578991	580800	-1	129,149,169	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Universal GTPases		
gsyne_687	Synechococcus_assembled_mapped	peptidase U32 family protein				PF01136.14	580996	582531	-1	138	fig|1129.58.peg.685					
gsyne_688	Synechococcus_assembled_mapped	D-alanyl-D-alanine carboxypeptidase family protein				PF02557.12	583530	584289	-1	89	fig|1129.58.j	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Murein Hydrolases		
gsyne_689	Synechococcus_assembled_mapped	geranylgeranyl reductase	chlP		GO:0015995,GO:0045550	TIGR02028	584426	585794	1	191	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Chlorophyll Biosynthesis		
gsyne_69	Synechococcus_assembled_mapped	sigma-54 interaction domain protein				PF00158.21	53746	55801	-1	263	fig|1129.58.peg.69					
gsyne_690	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	585900	586875	-1	121	fig|1129.58.peg.688					
gsyne_691	Synechococcus_assembled_mapped	glycine--tRNA ligase, beta subunit	glyS	6.1.1.14	GO:0004820,GO:0006426,G	TIGR00211	587084	589250	-1	137	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Glycyl-tRNA synthetase		
gsyne_692	Synechococcus_assembled_mapped	D-alanyl-D-alanine dipeptidase	ddpX	3.4.13.22	GO:0006508,GO:0008237,G	UniRef100_P	591146	591866	-1	92,189,703	fig|1129.58.peg.692					
gsyne_693	Synechococcus_assembled_mapped	sulfite reductase, ferredoxin dependen	sir	1.8.7.1	GO:0000103,GO:0050311	TIGR02042	589370	591164	1	106	fig|1129.58.peg.691					
gsyne_694	Synechococcus_assembled_mapped	ATP-dependent DNA helicase RecG	recG	3.6.4.12	GO:0004003,GO:0006268,G	TIGR00643	591870	594288	-1	132	fig|1129.58.j	DNA Metabolism	DNA replication	DNA-replication		
gsyne_695	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	594323	595532	-1	156	fig|1129.58.peg.695					
gsyne_696	Synechococcus_assembled_mapped	translation elongation factor Ts	tsf		GO:0003746,GO:0006414	TIGR00116	595531	596188	-1	169	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Translation elongation factors ba		
gsyne_697	Synechococcus_assembled_mapped	ribosomal protein S2	rpsB		GO:0000314,GO:0003735,G	TIGR01011	596322	597045	-1	158	fig|1129.58.j	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial		
gsyne_698	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	597168	598101	-1	90	fig|1129.58.peg.698					
gsyne_699	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	598195	598351	-1	156	fig|1129.58.peg.699					
gsyne_7	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	3616	3982	1	165	fig|1129.58.peg.8					
gsyne_70	Synechococcus_assembled_mapped	putative inward rectifier potassium channel			GO:0016020,GO:0005242	UniRef100_C	56017	56851	1	141	fig|1129.58.peg.70					
gsyne_700	Synechococcus_assembled_mapped	ABC exporter ATP-binding subunit, DevA family protein			GO:0005524,GO:0006810,G	TIGR02982	598398	599109	-1	141	fig|1129.58.peg.700					
gsyne_701	Synechococcus_assembled_mapped	ABC exporter transmembrane subunit, DevC family protein			GO:0006810,GO:0016021,G	TIGR01185	599114	600317	-1	147	fig|1129.58.peg.701					
gsyne_702	Synechococcus_assembled_mapped	ABC exporter membrane fusion , DevB family protein			GO:0006810,GO:0042626,G	TIGR02971	600328	601186	-1	141	fig|1129.58.peg.702					
gsyne_703	Synechococcus_assembled_mapped	phycocyanobilin:ferredoxin oxidoreduc	pcyA	1.3.7.5	GO:0010024,GO:0050620,G	UniRef100_C	601224	601956	-1	92,141,703	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Tetrapyrroles	Bilin Biosynthesis		
gsyne_704	Synechococcus_assembled_mapped	peptidase M16 inactive domain protein				PF05193.16	602033	603290	1	140	fig|1129.58.j	Protein Metabolism	Protein processing and modific	Protein deglycation		
gsyne_705	Synechococcus_assembled_mapped	peptidase M16 inactive domain protein				PF05193.16	603286	604567	1	140	fig|1129.58.peg.705					
gsyne_706	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11347.3	604583	604730	-1	156	fig|1129.58.peg.706					
gsyne_707	Synechococcus_assembled_mapped	bioY family protein				PF02632.9	604887	605460	1	77	fig|1129.58.j	Cofactors, Vitamins, Prosthetic Gro	Biotin	Biotin biosynthesis		
gsyne_708	Synechococcus_assembled_mapped	signal peptidase II	lspA	3.4.23.36	GO:0005887,GO:0006508,G	TIGR00077	605456	605927	1	97	fig|1129.58.j	Protein Metabolism	Protein processing and modific	Signal peptidase		
gsyne_709	Synechococcus_assembled_mapped	FHA domain protein				PF00498.21	605970	608034	1	157	fig|1129.58.j	Membrane Transport	Protein and nucleoprotein secr	Type IV pilus		
gsyne_71	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	56860	57511	1	703	fig|1129.58.peg.71					
gsyne_710	Synechococcus_assembled_mapped	small GTP-binding domain protein			GO:0005525	TIGR00231	608046	609612	1	157	fig|1129.58.peg.710					
gsyne_711	Synechococcus_assembled_mapped	aminotransferase class-V family protein				PF00266.14	609773	611420	-1	703	fig|1129.58.peg.711					
gsyne_712	Synechococcus_assembled_mapped	alanine--glyoxylate aminotransferase			GO:0008483,GO:0030170	UniRef100_C	611728	612898	-1	141,703	fig|1129.58.j	Carbohydrates	CO2 fixation	Photorespiration (oxidative C2 cy		
gsyne_713	Synechococcus_assembled_mapped	phycobiliprotein beta chain	apcD		GO:0006810,GO:0022900,G	UniRef100_P	612968	613499	-1	92	fig|1129.58.j	Photosynthesis	Light-harvesting complexes	Phycobilisome		
gsyne_714	Synechococcus_assembled_mapped	glutamine synthetase, type I	glnA	6.3.1.2	GO:0004356,GO:0006542	TIGR00653	613729	615148	1	73	fig|1129.58.j	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation		
gsyne_715	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	615220	615448	-1	856	fig|1129.58.peg.716					
gsyne_716	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	615626	616682	1	703	fig|1129.58.peg.717					
gsyne_717	Synechococcus_assembled_mapped	putative copper binding proteins, plastocyanin				UniRef100_A	616738	617062	1	185	fig|1129.58.peg.718					
gsyne_718	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	617075	617348	-1	856	fig|1129.58.peg.719					
gsyne_719	Synechococcus_assembled_mapped	histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein				PF02518.21	617665	618067	-1	703	fig|1129.58.j	Stress Response	Stress Response - no subcate	SigmaB stress responce regulati		
gsyne_72	Synechococcus_assembled_mapped	NAD(P)-binding Rossmann-like domain protein				PF13450.1	59077	60274	-1	157	fig|1129.58.peg.73					
gsyne_720	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	617384	617672	1	156						
gsyne_721	Synechococcus_assembled_mapped	GUN4-like family protein				PF05419.7	618132	618855	-1	185	fig|1129.58.peg.721					
gsyne_722	Synechococcus_assembled_mapped	tRNA 2-selenouridine synthase	selU	2.9.1.-	GO:0001887,GO:0006400,G	TIGR03167	618961	620005	1	168	fig|1129.58.j	Protein Metabolism	Selenoproteins	Selenocysteine metabolism		
gsyne_723	Synechococcus_assembled_mapped	photosystem II reaction center protein	psb28		GO:0003674,GO:0009523,G	TIGR03047	620030	620402	1	164	fig|1129.58.j	Photosynthesis	Electron transport and photopl	Photosystem II		
gsyne_724	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01594.11	620412	621468	1	156	fig|1129.58.peg.724					
gsyne_725	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01594.11	621464	622466	1	156	fig|1129.58.peg.725					
gsyne_726	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	622467	622674	-1	856	fig|1129.58.peg.726					
gsyne_727	Synechococcus_assembled_mapped	#NAME?	secF		GO:0015450,GO:0031522,G	TIGR00966	622670	623663	-1	97	fig|1129.58.peg.727					
gsyne_728	Synechococcus_assembled_mapped	#NAME?	secD		GO:0015450,GO:0031522,G	TIGR01129	623662	625144	-1	97	fig|1129.58.peg.728					
gsyne_729	Synechococcus_assembled_mapped	transketolase, pyrimidine binding domain protein				PF02779.19	625219	626203	-1	157	fig|1129.58.j	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-Co		
gsyne_73	Synechococcus_assembled_mapped	flavin containing amine oxidoreductase family protein				PF01593.19	57500	59081	1	109	fig|1129.58.peg.72					
gsyne_730	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	626250	626370	-1	88	fig|1129.58.peg.730					
gsyne_731	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11282.3	626372	626723	-1	156	fig|1129.58.peg.731					
gsyne_732	Synechococcus_assembled_mapped	4-(cytidine 5'-diphospho)-2-C-methyl-D	ispE	2.7.1.148	GO:0016114,GO:0050515	TIGR00154	626742	627675	-1	76	fig|1129.58.j	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Isoprenoid Biosynthesis		
gsyne_733	Synechococcus_assembled_mapped	dimethyladenosine transferase	ksgA	2.1.1.-	GO:0000154,GO:0000179	TIGR00755	627685	628498	-1	168	fig|1129.58.j	RNA Metabolism	RNA processing and modificat	RNA methylation		
gsyne_734	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF02021.12	628837	629209	-1	156	fig|1129.58.peg.735					
gsyne_735	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	628587	628881	1	856						
gsyne_736	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	629254	629485	-1	156	fig|1129.58.peg.736					
gsyne_737	Synechococcus_assembled_mapped	pentapeptide repeats family protein				PF13599.1	629624	630110	1	185	fig|1129.58.peg.737					





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18	2.70356455	18	3.21704106	3	0.90977292	3	0.55592946	4	1.62252855	6	1.1744361	7	2.03067625	17	1.82473261
1	0.70807643	0	0	0	0	0	0	0	0	1	0.92277122	0	0	1	0.50601829
43	3.28616087	27	2.45529675	35	5.40052427	18	1.69717671	25	5.159748	28	2.78863901	20	2.95208441	70	3.82300159
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7	4.67058106	8	6.35159388	1	1.34716375	1	0.82320323	1	1.80194276	3	2.60860325	1	1.28869839	0	0
47	2.4820396	21	1.31962339	21	2.23912148	35	2.28041078	52	7.41621496	40	2.75286391	28	2.85592824	50	1.88697839
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3	2.0817447	2	1.65141441	0	0	2	1.71226273	0	0	0	0	1	1.34024632	0	0
1	0.80687779	3	2.88037397	1	1.62912825	0	0	0	0	1	1.05152999	0	0	0	0
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86	6.72034701	78	7.25283356	33	5.20660584	78	7.52007278	48	10.1298404	65	6.61942866	37	5.58435968	149	8.32080969
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4	2.04092618	2	1.2142753	0	0	2	1.25901671	0	0	1	0.66493808	0	0	0	0
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17	4.57230749	17	5.44070639	6	3.25825651	21	6.96851109	7	5.08455167	11	3.85560997	4	2.07790128	9	1.72987647
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47	7.15219306	29	5.2512081	29	8.9101883	46	8.63641287	21	8.63035744	55	10.9073177	23	6.76001435	108	11.7449507
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43	3.8352623	34	3.60848907	15	2.70125379	53	5.83225735	30	7.22630002	63	7.32286568	22	3.78989963	55	3.50570509
21	2.99839772	19	3.22807343	18	5.18907518	14	2.46622203	21	8.09761933	23	4.27968379	13	3.58502103	16	1.63258575
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4	1.05941206	4	1.26062169	2	1.06950404	6	1.96060617	0	0	5	1.7257935	4	2.04617759	4	0.75709606
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37	5.07408129	32	5.22186375	28	7.7528475	24	4.06070211	12	4.44431733	30	5.36155608	24	6.35689956	54	5.29219124
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47	5.01753851	53	6.73268952	14	3.01764679	122	16.0689271	30	8.64932526	78	10.8517895	15	3.09287613	47	3.58572342
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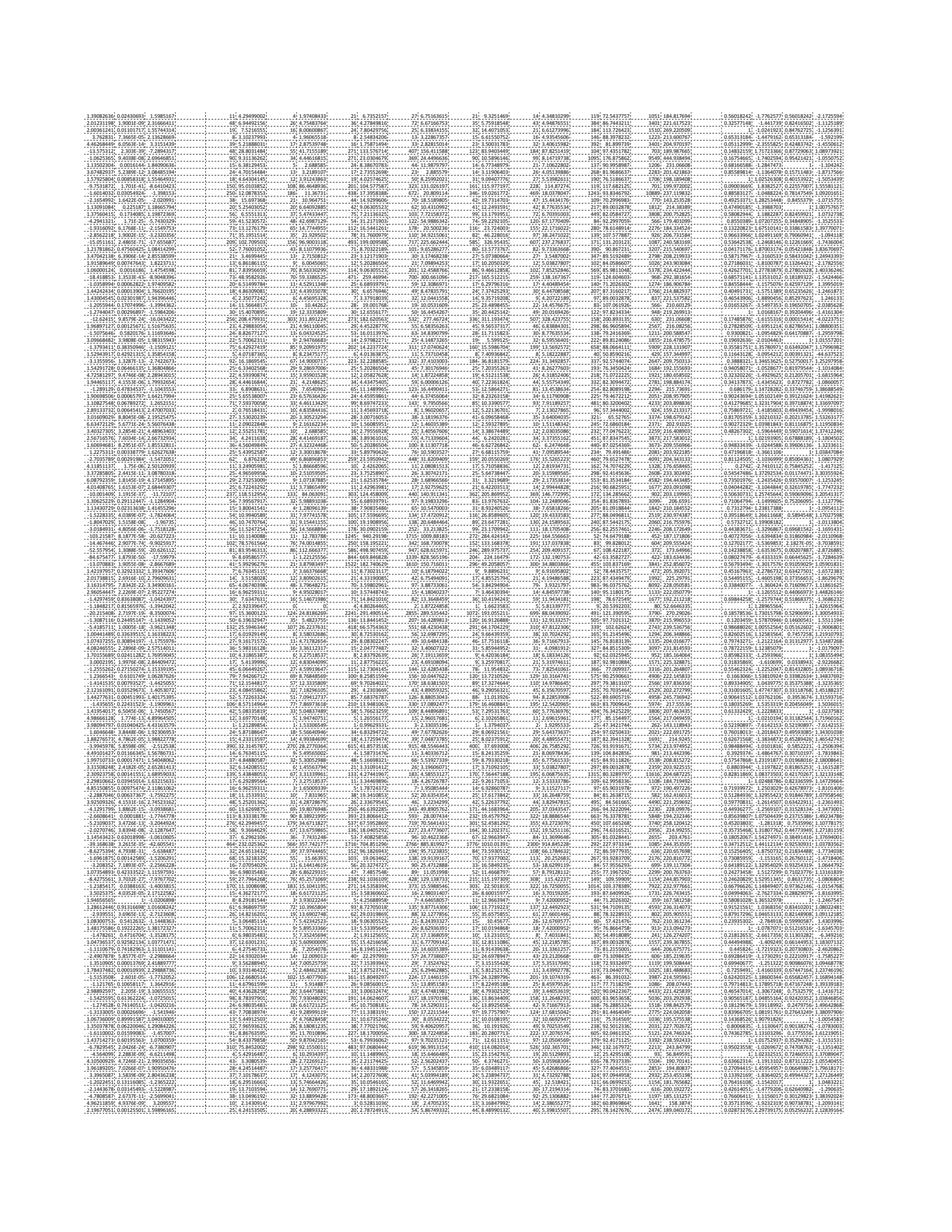
67	2.88413761	45	2.30501391	24	2.08593096	29	1.54018669	39	4.5339205	27	1.51467285	13	1.08084381	43	1.32280463
39	3.35765275	32	3.278242	23	3.99803435	35	3.71769202	52	12.0904547	51	5.72209745	24	3.99080791	63	3.87612518
40	6.33712238	36	6.78663456	57	18.2328463	62	12.1187544	35	14.9750494	99	20.4400145	33	10.0977463	118	13.359807
81	11.6612255	79	13.5333754	81	23.5446212	159	28.2416777	55	21.384051	75	14.0713038	53	14.7371484	223	22.9429951
21	2.3427995	18	2.38950638	8	1.80199395	22	3.02811736	19	5.72449984	31	4.50704013	17	3.66305265	40	3.18905415
259	172.811499	145	115.122639	183	246.530966	153	125.950095	99	178.392334	346	300.858908	114	146.911616	157	74.8615129
196	55.7407051	171	57.8671853	125	71.7751177	181	63.5081052	57	43.7783471	188	69.6767906	69	37.9004083	307	62.3937137
44	5.49141288	26	3.86122074	17	4.28378688	25	3.84951152	22	7.41518892	30	4.87940176	15	3.61577246	51	4.54870394
25	3.65988872	13	2.26459782	4	1.18232093	25	4.51546077	6	2.37217781	11	2.09862315	3	0.84825717	21	2.1970161
45	3.89353747	37	3.80937239	30	5.24083652	64	6.83197097	95	22.1984969	74	8.34406093	43	7.18585934	72	4.4519514
43	5.21649313	35	5.05240423	42	10.2874323	61	9.13007222	32	10.4840306	54	8.537247	12	2.81170558	92	7.97598053
27	3.83928326	17	2.87643903	6	1.72260283	17	2.98242483	18	6.9123706	9	1.66779552	7	1.92248448	14	1.42265797
61	5.05117052	59	5.81345168	29	4.84850342	63	6.43630977	28	6.26164359	35	3.77697527	24	3.83841429	111	6.56857627
33	2.68140418	34	3.2873589	19	3.11709083	38	3.80948381	14	3.07216471	35	3.70621227	11	1.7263126	50	2.90338361
3	2.12422929	6	5.05535023	0	0	4	3.49441372	3	5.73679737	3	2.76831365	1	1.36759829	1	0.50601829
37	6.72116527	31	6.70076528	28	10.2694786	29	6.49942657	24	11.7739506	28	6.62849272	14	4.91189752	51	6.62062668
19	4.19884813	5	1.31482039	5	2.23097181	27	7.3616391	42	25.0665159	16	4.60797856	12	5.12196047	13	2.05308056
61	3.07622158	41	2.46031943	39	3.97100012	43	2.67541051	39	5.31154059	37	2.43166311	33	3.21425354	76	2.73897107
13	2.07854694	16	3.04408186	8	2.58258119	10	1.97265291	17	7.34063319	12	2.50041233	7	2.16168762	14	1.59967071
51	3.38981417	40	3.16362914	28	3.75760616	46	3.77222631	34	6.10313181	43	3.72467233	22	2.82427386	76	3.60998486
38	2.40152698	38	2.85763878	18	2.29680377	42	3.27481942	24	4.09621961	40	3.2944109	11	1.34268757	48	2.16785976
84	7.4729297	94	9.95083042	73	13.1123938	105	11.5248453	56	13.454506	103	11.941606	51	8.76314904	154	9.79080509
173	33.9116604	215	50.1488839	135	53.4298842	207	50.0619187	63	33.3512118	234	59.7768067	66	24.9876433	237	33.1999455
124	9.09571329	169	14.7510061	88	13.033026	271	24.525539	85	16.8384503	187	17.8760099	61	8.64218031	239	12.5284993
324	147.913439	597	324.307369	565	520.785143	892	502.413931	223	274.93853	747	444.423617	184	162.240345	1106	360.830987
36	3.54842847	29	3.4013507	20	3.98025653	40	4.86438274	14	3.72674526	33	4.23898028	11	2.09413488	47	3.31068214
11	3.53382588	8	3.05817483	9	5.83770957	14	5.54899957	22	19.0872456	7	2.93065303	7	4.34339086	26	5.96914163
8	3.05017539	3	1.36105583	5	3.84903928	9	4.23361663	6	6.17808947	10	4.96876809	5	3.6819954	9	2.45224246
35	9.06232146	30	9.2429911	25	13.069499	19	6.06958802	17	11.8874433	24	8.09835038	8	4.0007353	30	5.55109612
39	3.39131342	31	3.20763451	26	4.56482553	30	3.21853896	31	7.28002941	36	4.07962012	14	2.35130934	58	3.6042706
5	1.80707005	6	2.58033502	1	0.7297137	5	2.22950876	1	0.97605233	4	1.88399124	0	0	5	1.29140083
32	4.60690391	18	3.08355388	13	3.77876636	26	4.61813598	14	5.44321299	41	7.69231276	18	5.00506926	30	3.08650158
38	3.78861584	16	1.89817748	12	2.41560396	22	2.70616235	33	8.8854419	12	1.55916516	8	1.54051302	32	2.27999044
68	19.0266989	64	21.308573	56	31.6366196	53	18.2963557	24	18.135682	59	21.5139644	31	16.7530791	165	32.9932084
41	4.04126576	28	3.28406275	13	2.58716674	14	1.70253396	18	4.79152962	23	2.9544408	12	2.28451078	27	1.90188123
25	2.5969869	36	4.44991907	26	5.45318978	25	3.20408444	23	6.4524657	49	6.63345417	17	3.41080651	56	4.15722807
4	2.01134754	3	1.79501566	2	2.03050768	6	3.72231027	1	1.35798585	1	0.6553013	1	0.97119299	3	1.07803896
28	2.9349875	24	2.99350044	49	10.3703119	61	7.88882373	27	7.64328592	71	9.69885518	18	3.6441743	116	8.68944996
94	6.60202436	65	5.43228424	98	13.8970576	127	11.0049274	68	12.8981166	145	13.2718411	62	8.41045264	189	9.48630637
228	24.117774	207	26.0550902	176	37.5891543	212	27.6676599	116	33.1381669	253	34.8768134	97	19.8176667	364	27.516287
39	2.56761681	26	2.03684889	15	1.9939046	29	2.35557965	48	8.53443859	32	2.74555079	19	2.41600381	56	2.63475176
6	5.20436176	5	5.16067003	1	1.75131287	1	1.0701642	0	0	3	3.39118422	0	0	0	0
38	11.2687035	17	5.99872756	20	11.9747889	26	9.51257069	15	12.0129518	25	9.66149351	11	6.30030323	50	10.5961094
11	1.22718069	14	1.85850496	10	2.25249244	8	1.10113359	19	5.72449984	9	1.30849552	3	0.64642106	11	0.87698989
29	3.7128288	18	2.74220105	41	10.598351	43	6.79218609	26	8.98976611	41	6.84076522	21	5.19283631	76	6.95355017
19	5.31628351	15	4.9941968	12	6.77927563	9	3.10692833	15	11.3348013	15	5.46965197	7	3.78295333	37	7.39847703
39	13.8074904	42	17.6937258	30	21.4446474	20	8.73603431	21	20.0787908	23	10.611869	25	17.0949786	139	35.1682709
4	1.80237637	4	2.14469404	0	0	3	1.66778837	4	4.86758564	2	1.1744361	2	1.74057964	1	0.32201164
15	3.21256898	14	3.56787064	15	6.48634397	16	4.2278092	40	23.1360552	15	4.18664719	17	7.03215664	26	3.97942775

gsyne_738	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	630123	630561	1	156	fig|1129.58.peg.738				
gsyne_739	Synechococcus_assembled_mapped	linear amide C-N hydrolases, choloylglycine hydrolase family protein				PF02275.13	630582	631764	-1	703	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Bile hydrolysis	
gsyne_74	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO		60263	60695	-1	156	fig|1129.58.peg.74				
gsyne_740	Synechococcus_assembled_mapped	peptidase S24-like family protein				PF00717.18	631822	632263	1	138	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial UmuCD sys	
gsyne_741	Synechococcus_assembled_mapped	impB/mucB/samB family protein				PF00817.15	632255	633533	1	132	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial UmuCD sys	
gsyne_742	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	633536	633821	-1	156	fig|1129.58.peg.742				
gsyne_743	Synechococcus_assembled_mapped	DNA primase	dnaG	2.7.7.-	GO:0003677,GO:0006269,GO	UniRef100_P	633855	635967	-1	92,141,703	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication	
gsyne_744	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	636860	637262	-1	156	fig|1129.58.peg.745				
gsyne_745	Synechococcus_assembled_mapped	eamA-like transporter family protein				PF00892.15	636013	636886	1	141	fig|1129.58.peg.744				
gsyne_746	Synechococcus_assembled_mapped	holliday junction DNA helicase RuvA	ruvA	3.6.4.12	GO:0006310,GO:0009378,GO	TIGR00084	637338	638001	1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication	
gsyne_747	Synechococcus_assembled_mapped	ribosomal protein S15	rpsO		GO:0000314,GO:0003735,GO	TIGR00952	638061	638331	1	158	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial	
gsyne_748	Synechococcus_assembled_mapped	DNA polymerase III subunit alpha	dnaE-C	2.7.7.7	GO:0003887,GO:0003677,GO	UniRef100_P	638722	642259	-1	##########	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication	
gsyne_749	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11947.3	638334	638748	1	156	fig|1129.58.peg.748				
gsyne_75	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08241.7	60777	61428	1	703	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Asp and As	
gsyne_750	Synechococcus_assembled_mapped	aspartyl/glutamyl-tRNA(Asn/Gln) amidotGatA		6.3.5.-	GO:0006424,GO:0030956,GO	TIGR00132	642361	643822	-1	137	fig|1129.58.peg.750				
gsyne_751	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF08846.5	643854	644097	-1	156	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Conserved gene cluster possibly	
gsyne_752	Synechococcus_assembled_mapped	RNA 2'-O ribose methyltransferase substrate binding family protein				PF08032.7	644149	645100	1	168	fig|1129.58.peg.752				
gsyne_753	Synechococcus_assembled_mapped	ribonuclease III domain protein				PF00636.21	645816	646161	-1	166	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Conserved gene cluster possibly	
gsyne_754	Synechococcus_assembled_mapped	anti-anti-sigma factor family protein			GO:0006355,GO:0045152	TIGR00377	646237	646585	-1	263	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Conserved gene cluster possibly	
gsyne_755	Synechococcus_assembled_mapped	carbamoyl-phosphate synthase, small s carA		6.3.5.5	GO:0004088,GO:0005951,GO	TIGR01368	646712	647858	-1	126	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis	
gsyne_756	Synechococcus_assembled_mapped	anthranilate phosphoribosyltransferase trpD2		2.4.2.18	GO:0000162,GO:0004048	UniRef100_C	647889	648924	-1	92,703	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for synt	
gsyne_757	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11691.3	648961	649285	-1	156	fig|1129.58.peg.757				
gsyne_758	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	649338	651105	1	141	fig|1129.58.peg.758				
gsyne_759	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	651207	651462	1	88	fig|1129.58.peg.759				
gsyne_76	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	61424	61949	1	156	fig|1129.58.peg.76				
gsyne_760	Synechococcus_assembled_mapped	peptide-methionine (S)-S-oxide reducta msrA		1.8.4.11	GO:0000317,GO:0006979,GO	TIGR00401	651501	652257	1	140,149	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Peptide methionine sulfoxide redi	
gsyne_761	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	652264	652555	1	156	fig|1129.58.peg.761				
gsyne_762	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	652562	652769	1	156	fig|1129.58.peg.762				
gsyne_763	Synechococcus_assembled_mapped	rho termination factor, N-terminal domain protein				PF07498.7	652843	653176	1	165	fig|1129.58.peg.763				
gsyne_765	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	653320	653530	-1	156					
gsyne_766	Synechococcus_assembled_mapped	exonuclease family protein				PF00929.19	653676	654591	-1	703	fig|1129.58.peg.765				
gsyne_767	Synechococcus_assembled_mapped	peroxiredoxin Q, chloroplastic	PRX1	1.11.1.15	GO:0004601,GO:0009534,GO	UniRef100_C	654669	655134	1	92,703	fig|1129.58.p	Stress Response	Oxidative stress	Rubrerythrin	
gsyne_768	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF07082.6	655197	655857	1	156	fig|1129.58.peg.767				
gsyne_769	Synechococcus_assembled_mapped	acetate--CoA ligase	acs	6.2.1.1	GO:0003987,GO:0019427	TIGR02188	655857	657852	-1	185	fig|1129.58.p	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism II: acetyl-Co	
gsyne_77	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	62016	62226	1	856					
gsyne_770	Synechococcus_assembled_mapped	solanesyl diphosphate synthase	sds		GO:0010236,GO:0050347	TIGR02749	658630	659602	-1	81	fig|1129.58.p	Fatty Acids, Lipids, and Isoprenoid	Isoprenoids	Polyprenyl Diphosphate Biosynth	
gsyne_771	Synechococcus_assembled_mapped	HAD hydrolase, IA, variant 3 family protein			GO:0008152,GO:0016787	TIGR01509	657962	658637	1	703	fig|1129.58.peg.769				
gsyne_772	Synechococcus_assembled_mapped	glutamate racemase	murI	5.1.1.3	GO:0008881,GO:0009252	TIGR00067	659653	660472	-1	89	fig|1129.58.p	Amino Acids and Derivatives	Glutamine, glutamate, aspartat	Glutamine, Glutamate, Aspartate	
gsyne_773	Synechococcus_assembled_mapped	N-acetylmuramoyl-L-alanine amidase family protein				PF01520.13	660468	661545	-1	89	fig|1129.58.p	Cell Wall and Capsule	Cell Wall and Capsule - no sut	Recycling of Peptidoglycan Amin	
gsyne_774	Synechococcus_assembled_mapped	carbon-nitrogen hydrolase family protein				PF00795.17	661584	662403	-1	703	fig|1129.58.peg.773				
gsyne_775	Synechococcus_assembled_mapped	2-phosphosulpholactate phosphatase family protein				PF04029.9	662451	663207	-1	703	fig|1129.58.peg.774				
gsyne_776	Synechococcus_assembled_mapped	ubiD decarboxylase family protein	ubiD	4.1.1.-	GO:0016831	TIGR00148	663214	664813	1	157	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Quinone cofactors	Ubiquinone Biosynthesis	
gsyne_777	Synechococcus_assembled_mapped	rrf2 family protein				TIGR00738	664809	665256	1	157	fig|1129.58.p	RNA Metabolism	Transcription	Rrf2 family transcriptional regulat	
gsyne_778	Synechococcus_assembled_mapped	3-phosphoshikimate 1-carboxyvinyltrar aroA		2.5.1.19	GO:0003866,GO:0009423	TIGR01356	665294	666602	1	70	fig|1129.58.p	Amino Acids and Derivatives	Aromatic amino acids and deri	Common Pathway For Synthesis	
gsyne_779	Synechococcus_assembled_mapped	methyltransferase domain protein				PF13659.1	666582	667482	1	703	fig|1129.58.peg.778				
gsyne_78	Synechococcus_assembled_mapped	phosphomethylpyrimidine kinase	thiD	2.7.4.7	GO:0008972,GO:0009228	TIGR00097	62188	62992	1	162	fig|1129.58.peg.77				
gsyne_780	Synechococcus_assembled_mapped	UDP-N-acetylmuramoyl-tripeptide--D-a murF		6.3.2.10	GO:0009252,GO:0047480	TIGR01143	668852	670223	-1	89	fig|1129.58.peg.780				
gsyne_781	Synechococcus_assembled_mapped	UDP-N-acetylglucosamine diphosphory glmU		2.7.7.23	GO:0003977,GO:0005737,GO	TIGR01173	667510	668860	1	89,90,100	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Sialic Acid Metabolism	
gsyne_782	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	670227	671013	-1	156	fig|1129.58.p	Stress Response	Stress Response - no subcate	SigmaB stress responce regulatio	
gsyne_783	Synechococcus_assembled_mapped	glycogen/starch synthase, ADP-glucose glgA		2.4.1.21	GO:0004373,GO:0005978,GO	TIGR02095	671022	672564	-1	105	fig|1129.58.p	Carbohydrates	Polysaccharides	Glycogen metabolism	
gsyne_784	Synechococcus_assembled_mapped	L,D-transpeptidase catalytic domain protein				PF03734.9	672605	673184	-1	138	fig|1129.58.peg.783				
gsyne_785	Synechococcus_assembled_mapped	naphthoate synthase	menB	4.1.3.36	GO:0008935,GO:0009234	TIGR01929	673254	674115	-1	81	fig|1129.58.peg.784				
gsyne_786	Synechococcus_assembled_mapped	2-succinyl-5-enolpyruvyl-6-hydroxy-3-c menD		2.2.1.9	GO:0009234,GO:0070204	TIGR00173	674092	675907	-1	81	fig|1129.58.peg.785				
gsyne_787	Synechococcus_assembled_mapped	signal peptidase I	lepB	3.4.21.89	GO:0006465,GO:0009004,GO	TIGR02227	675929	676565	1	97	fig|1129.58.p	Protein Metabolism	Protein processing and modific	Signal peptidase	
gsyne_788	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF05542.6	676594	676936	1	156	fig|1129.58.peg.787				
gsyne_789	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF14234.1	676955	678110	-1	156	fig|1129.58.peg.788				
gsyne_79	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF06267.7	63357	64032	-1	156	fig|1129.58.peg.79				
gsyne_790	Synechococcus_assembled_mapped	manganese transport system membran mntB			GO:0005524,GO:0042626,GO	UniRef100_C	678112	678952	-1	141,703	fig|1129.58.peg.789				
gsyne_791	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	678948	679680	-1	141	fig|1129.58.peg.790				
gsyne_792	Synechococcus_assembled_mapped	periplasmic solute binding family protein				PF01297.12	679697	680528	-1	185	fig|1129.58.peg.791				
gsyne_793	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	680773	680959	-1	156	fig|1129.58.peg.792				
gsyne_794	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	681106	681328	-1	156	fig|1129.58.peg.794				
gsyne_795	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	681406	681571	-1	856					
gsyne_796	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	681750	681927	1	856	fig|1129.58.peg.795				
gsyne_797	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	681931	683101	-1	90	fig|1129.58.peg.796				
gsyne_798	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	683145	683322	-1	856	fig|1129.58.peg.797				
gsyne_799	Synechococcus_assembled_mapped	NAD dependent epimerase/dehydratase family protein				PF01370.16	683412	684093	1	119	fig|1129.58.peg.798				
gsyne_8	Synechococcus_assembled_mapped	AAA domain protein				PF13476.1	4000	6733	-1	157	fig|1129.58.peg.9				
gsyne_80	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	62984	63377	1	156	fig|1129.58.peg.78				
gsyne_800	Synechococcus_assembled_mapped	dienelactone hydrolase family protein				PF01738.13	684199	684871	-1	96,184	fig|1129.58.peg.799				
gsyne_801	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	684120	684237	1	88					
gsyne_802	Synechococcus_assembled_mapped	photosystem II a(b) protein	psbA	1.10.3.9	GO:0009055,GO:0009538,GO	TIGR01151	684939	686016	-1	112,164	fig|1129.58.p	Photosynthesis	Electron transport and photopl	Photosystem II	
gsyne_803	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF05128.7	686160	687540	-1	156	fig|1129.58.peg.801				
gsyne_804	Synechococcus_assembled_mapped	cation diffusion facilitator transporter family protein			GO:0006812,GO:0008324,GO	TIGR01297	687710	688592	-1	145	fig|1129.58.p	Virulence, Disease and Defense	Resistance to antibiotics and t	Cobalt-zinc-cadmium resistance	
gsyne_805	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	688584	689067	1	156	fig|1129.58.peg.803				
gsyne_806	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	689115	689619	1	156	fig|1129.58.peg.804				
gsyne_807	Synechococcus_assembled_mapped	tryptophan--tRNA ligase	trpS	6.1.1.2	GO:0004830,GO:0005737,GO	TIGR00233	689685	690714	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Trp	
gsyne_808	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF10792.4	691566	691962	-1	156	fig|1129.58.peg.807				
gsyne_809	Synechococcus_assembled_mapped	phage lysozyme family protein				PF00959.14	691039	691576	1	152	fig|1129.58.peg.806				
gsyne_81	Synechococcus_assembled_mapped	amidase, hydantoinase/carbamoylase family protein		3.5.-.-		TIGR01879	64028	65297	1	185	fig|1129.58.p	Nucleosides and Nucleotides	Nucleosides and Nucleotides -	Hydantoin metabolism	
gsyne_810	Synechococcus_assembled_mapped	threonine--tRNA ligase	thrS	6.1.1.3	GO:0004829,GO:0005737,GO	TIGR00418	692170	693871	1	137	fig|1129.58.p	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Thr	
gsyne_811	Synechococcus_assembled_mapped	glucokinase	glk	2.7.1.2	GO:0004340,GO:0005975	TIGR00749	693870	694869	1	116	fig|1129.58.peg.809				
gsyne_812	Synechococcus_assembled_mapped	homoserine kinase	thrB	2.7.1.39	GO:0004413,GO:0009088	TIGR00191	694900	695863	1	71	fig|1129.58.p	Amino Acids and Derivatives	Lysine, threonine, methionine,	Methionine Biosynthesis	
gsyne_813	Synechococcus_assembled_mapped	proton-translocating NADH-quinone oxidoreductase, chain M family protein				TIGR01972	696058	697612	1	112	fig|1129.58.peg.811				
gsyne_814	Synechococcus_assembled_mapped	peptidase M3 family protein				PF01432.15	697664	699779	1	138	fig|1129.58.p	Protein Metabolism	Protein degradation	Protein degradation	
gsyne_815	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	699817	701230	1	156	fig|1129.58.peg.813				
gsyne_816	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	702280	702835	-1	88	fig|1129.58.peg.815				
gsyne_817	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	702176	702317	1	856					
gsyne_818	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	702824	703523	-1	88	fig|1129.58.peg.816				
gsyne_819	Synechococcus_assembled_mapped	alpha/beta hydrolase fold family protein				PF00561.15	703576	704182	-1	703	fig|1129.58.p	Miscellaneous	Plant-Prokaryote DOE project	Synechocystis experimental	
gsyne_82	Synechococcus_assembled_mapped	asparagine synthase	asnB	6.3.5.4	GO:0004066,GO:0006529	TIGR01536	65318	67382	-1	71	fig|1129.58.p	Amino Acids and Derivatives	Glutamine, glutamate, aspartat	Glutamine, Glutamate, Aspartate	
gsyne_820	Synechococcus_assembled_mapped	folB domain protein				TIGR00526	704193	704547	-1	157	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Folate biosynthesis cluster	
gsyne_821	Synechococcus_assembled_mapped	glutamate-5-semialdehyde dehydrogen proA		1.2.1.41	GO:0004350,GO:0006561	TIGR00407	704564	705869	-1	73	fig|1129.58.p	Amino Acids and Derivatives	Proline and 4-hydroxyproline	Proline Synthesis	
gsyne_822	Synechococcus_assembled_mapped	ROK family protein				PF00480.15	705920	706811	-1	157	fig|1129.58.p	Cell Wall and Capsule	Capsular and extracellular poly	Sialic Acid Metabolism	
gsyne_823	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF04357.8	706820	711191	1	156	fig|1129.58.peg.821				
gsyne_824	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF10726.4	711329	711791	1	156	fig|1129.58.peg.822				
gsyne_825	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF14229.1	711810	712203	1	156	fig|1129.58.peg.823				
gsyne_826	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	712275	712551	1	156	fig|1129.58.peg.824				
gsyne_827	Synechococcus_assembled_mapped	hydrolase CocE/NonD family protein			GO:0008152,GO:0016787	TIGR00976	712606	714169	1	703	fig|1129.58.peg.825				
gsyne_828	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	714190	714943	1	156	fig|1129.58.peg.826				
gsyne_829	Synechococcus_assembled_mapped	1,4-alpha-glucan branching enzyme	glgB	2.4.1.18	GO:0003844,GO:0005978	TIGR01515	715021	717340	1	105	fig|1129.58.p	Carbohydrates	Polysaccharides	Glycogen metabolism	
gsyne_83	Synechococcus_assembled_mapped	aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain protein				PF00185.19	67385	68501	-1	703	fig|1129.58.p	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis	
gsyne_830	Synechococcus_assembled_mapped	uroporphyrinogen decarboxylase	hemE	4.1.1.37	GO:0004853,GO:0006779	TIGR01464	717366	718425	1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi	
gsyne_831	Synechococcus_assembled_mapped	polysaccharide biosynthesis family protein				PF02719.10	718421	719426	1	90	fig|1129.58.peg.829				
gsyne_832	Synechococcus_assembled_mapped	cytochrome c6	petJ		GO:0006810,GO:0009055,GO	UniRef100_P	719541	719883	1	92,141	fig|1129.58.p	Respiration	Respiration - no subcategory	Soluble cytochromes and functio	
gsyne_833	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	720122	720344	-1	156	fig|1129.58.peg.831				
gsyne_834	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_B	720735	721494	-1	156	fig|1129.58.peg.833				
gsyne_835	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	720367	720754	1	856	fig|1129.58.peg.832				
gsyne_836	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	721585	722467	-1	156	fig|1129.58.peg.834				
gsyne_837	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	722579	722942	1	156	fig|1129.58.peg.835				
gsyne_838	Synechococcus_assembled_mapped	ATP-dependent chaperone protein ClpB clpB			GO:0006457,GO:0042623	TIGR03346	723077	725696	1	95	fig|1129.58.p	Protein Metabolism	Protein folding	Protein chaperones	
gsyne_839	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11139.3	727357	727945	-1	156	fig|1129.58.peg.838				
gsyne_84	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	68705	68870	-1	856	fig|1129.58.peg.83				
gsyne_840	Synechococcus_assembled_mapped	mechanosensitive ion channel family protein				PF00924.13	725893	727390	1	141	fig|1129.58.peg.837				
gsyne_841	Synechococcus_assembled_mapped	pterin 4 alpha carbinolamine dehydratase family protein				PF01329.14	728021	728321	-1	76	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Pterin carbinolamine dehydratase	
gsyne_842	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	728351	728630	-1	156	fig|1129.58.peg.840				
gsyne_843	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF01894.12	728638	728968	-1	156	fig|1129.58.peg.841				
gsyne_844	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	728956	729103	1	856					
gsyne_845	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	729213	729714	1	856	fig|1129.58.peg.842				
gsyne_846	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,GO	default	729744	729984	1	856	fig|1129.58.peg.843				
gsyne_847	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	730122	730374	1	156	fig|1129.58.peg.844				
gsyne_848	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11026.3	730778	731210	-1	156	fig|1129.58.peg.846				
gsyne_849	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF04134.7	730370	730805	-1	156	fig|1129.58.p	Dormancy and Sporulation	Dormancy and Sporulation - no	Persister Cells	
gsyne_85	Synechococcus_assembled_mapped	sodium:solute symporter family protein				PF00474.12	68874	70305	-1	145	fig|1129.58.peg.84				
gsyne_850	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	731292	731694	1	149	fig|1129.58.peg.847				
gsyne_851	Synechococcus_assembled_mapped	carboxypeptidase Taq (M32) metallopeptidase family protein				PF02074.10	731684	733226	1	138	fig|1129.58.p	Protein Metabolism	Protein degradation	Metallocarboxypeptidases (EC 3.	
gsyne_852	Synechococcus_assembled_mapped	voltage gated chloride channel family protein				PF00654.15	733821	735729	-1	143	fig|1129.58.peg.850				
gsyne_853	Synechococcus_assembled_mapped	inorganic pyrophosphatase	ppa	3.6.1.1	GO:0000287,GO:0004427,GO	UniRef100_C	733270	733858	1	92,141,703	fig|1129.58.p	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_854	Synechococcus_assembled_mapped	porphobilinogen deaminase	hemC	2.5.1.61	GO:0004418,GO:0005737,GO	TIGR00212	735796	736750	-1	79	fig|1129.58.p	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi	
gsyne_855	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF08854.5	736858	737266	-1	156	fig|1129.58.peg.852				
gsyne_856	Synechococcus_assembled_mapped	PAP2 superfamily protein				PF01569.16	737258	737945	-1	185	fig|1129.58.peg.853				
gsyne_857	Synechococcus_assembled_mapped	dolichyl-phosphate-mannose-mannosyltransferase family protein				PF13231.1	737944	739699	-1	703	fig|1129.58.p	Cell Wall and Capsule	Gram-Negative cell wall comp	Lipid A-Ara4N pathway (Polymyx	
gsyne_858	Synechococcus_assembled_mapped	glycosyl transferase 2 family protein				PF00535.21	739708	740803	-1	90	fig|1129.58.peg.855				
gsyne_859	Synechococcus_assembled_mapped	RNA polymerase sigma factor RpoD	rpoD		GO:0006352,GO:0016987	TIGR02393	740879	741578	-1	165	fig|1129.58.p	RNA Metabolism	Transcription	Transcription initiation, bacterial s	
gsyne_86	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,GO	TMHMM	70308	70434	-1	88	fig|1129.58.peg.85				
gsyne_860	Synechococcus_assembled_mapped	primosomal protein N'	priA	3.6.1.-	GO:0003688,GO:0004003,GO	TIGR00595	742856	745079	1	132	fig|1129.58.p	DNA Metabolism	DNA replication	DNA-replication	
gsyne_861	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11353.3	745080	746208	-1	156	fig|1129.58.peg.858				
gsyne_862	Synechococcus_assembled_mapped	acetylglutamate kinase	argB	2.7.2.8	GO:0006561,GO:0005515,GO	UniRef100_C	746215	747106	-1	92,141,703	fig|1129.58.p	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis -- gjo	
gsyne_863	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	PF11016.3	747115	747604	-1	156	fig|1129.58.peg.860				
gsyne_864	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_A	747650	747887	1	156	fig|1129.58.peg.861				
gsyne_865	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,GO	UniRef100_C	747891	748389	-1	141	fig|1129.58.p	DNA Metabolism	DNA repair	DNA repair, bacterial RecFOR pa	
gsyne_866	Synechococcus_assembled_mapped	precorrin-6x reductase CbiJ/CobK family protein				PF02571.9	748421	749219	1	79	fig|1129.58.peg.863				
gsyne_867	Synechococcus_assembled_mapped	pfkB carbohydrate kinase family protein				PF00294.19	749507	750515	-1	703	fig|1129.58.peg.865				



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1	1.02818243	0.95547558	1.0334126	0.67349803	1.18236915	0.71414363	1.14414045
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0.23130265	-1.6276631	0.73032374	1.13731732	0.65964515	-1.2240952	0.43650432	-1.3921847
0.23881911	-2.1399932	1	-1.2266649	0.85471802	-1.3052851	1	-1.0640926
0.00379913	-2.4295185	0.00575428	-2.4098208	0.16725057	-1.5807038	0.18356431	1.52452394
0.00170969	-3.3102289	0.11988802	-1.7566012	0.0936315	-2.0241499	0.90014783	-1.1523104
1	-1.1599382	0.27738872	3.72199369	0.12015928	5.5462713	0.8193226	1.49013453
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56	3.98965446	39	3.30621981	34	4.89072999	47	4.13122937	36	6.92656438	31	2.87821248	30	4.12806876	83	4.22582416
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25	3.31066269	13	2.04851024	8	2.13900809	12	1.96060617	10	3.57637495	17	2.93384895	5	1.278861	9	0.85173307
62	4.18508987	49	3.93576391	29	3.95237924	44	3.66437548	46	8.38569472	31	2.72702233	37	4.82384377	45	2.17075938
11	1.9774777	5	1.06956892	2	0.7259328	2	0.44359138	6	2.91298519	1	0.2342787	2	0.69442815	6	0.77082578
25	3.02227744	10	1.43851429	16	3.90536668	17	2.53558069	51	16.6507046	18	2.8358335	18	4.20286304	29	2.50540761
29	1.66310183	9	0.61416238	10	1.15789281	11	0.77830124	14	2.16828815	7	0.5231579	8	0.88611327	32	1.31146557
25	4.09147937	11	2.14216492	4	1.32174556	4	0.8076711	8	3.53588769	5	1.06641013	7	2.21267082	10	1.16957057
237	72.1306278	137	49.6148627	114	70.0525149	234	87.8661135	92	75.61837	228	90.4315793	76	44.6748775	337	73.2971926
54	4.86641619	35	3.75321457	22	4.00300085	34	3.7803203	17	4.1374478	39	4.58030077	16	2.78492743	67	4.31495593
15	2.31304967	5	0.91745245	9	2.8021006	8	1.52201131	6	2.49869396	6	1.20575439	1	0.29783252	13	1.43259399
54	6.69132226	33	4.8657746	35	8.75656436	43	6.57386582	29	9.70474888	40	6.45939852	27	6.46190192	78	6.9071496
46	6.54100111	32	5.41447347	24	6.8904113	45	7.89465396	17	6.52835001	37	6.85649269	24	6.59137536	49	4.97930289
56	7.01430225	65	9.68790042	8	2.02317733	69	10.6630079	25	8.45677109	49	7.99846098	16	3.87074751	50	4.475613
11	6.1556967	11	7.32482198	3	3.38963782	7	4.83299963	6	9.067841	1	0.72928693	2	2.16168762	7	2.79942374
102	47.8238648	78	43.5170013	27	25.5597014	61	35.2864953	10	12.6623005	24	14.6645804	20	18.1114368	40	13.4026465
81	51.09737	86	64.5552906	24	30.5683701	54	42.0282669	11	18.7402047	31	25.4852633	18	21.9313035	19	8.56550953
9	5.29257128	2	1.39950374	1	1.18733076	0	0	3	4.76445883	1	0.76636932	2	2.27160394	6	2.52151485
41	3.6475014	21	2.22305786	19	3.41281483	13	1.4268856	22	5.28569877	21	2.43469637	8	1.37461161	37	2.35233629
7	4.11644433	3	2.09925561	2	2.37466152	1	0.72553505	2	3.17630589	2	1.53273863	1	1.13580197	3	1.26075742
14	2.13982569	12	2.182486	5	1.54300694	8	1.50860152	7	2.88945888	2	0.398377	5	1.47604221	10	1.09228617
65	2.47554712	48	2.17529889	22	1.69171825	39	1.83255341	47	4.83419112	35	1.73715987	15	1.10338611	61	1.660251
16	4.23764825	9	2.8363988	10	5.34752022	5	1.63383848	9	6.43747491	16	5.52253919	14	7.16162158	25	4.73185038
30	4.64675157	16	2.9489543	14	4.37828218	11	2.10210826	12	5.0196977	10	2.01856204	6	1.79497276	14	1.549681
2	1.77926898	0	0	0	0	2	2.19520862	1	2.40259035	1	1.15937922	3	5.15479355	2	1.27153313
204	19.6609222	289	33.1429698	159	30.9398607	541	64.3287593	91	23.6855365	410	51.4957604	119	22.1512934	324	22.3154064
50	3.77127663	38	3.41052976	44	6.70067534	55	5.11817662	29	5.90723845	68	6.68407325	24	3.49629476	70	3.77313635
132	15.5776814	116	16.2894619	70	16.6791702	113	16.4528646	36	11.4735947	54	8.30494096	47	10.7128533	96	8.09629257
17	3.66352587	9	2.30787728	9	3.91597909	12	3.19055166	7	4.07395755	15	4.21265121	5	2.08112783	7	1.07803896
28	5.78262417	12	2.9489543	14	5.83770957	8	2.03840801	18	10.0393954	23	6.19025692	9	3.58994551	22	3.24695067
36	3.64153592	16	1.92584771	16	3.2677558	26	3.24481274	19	5.19043571	14	1.84554243	11	2.14908303	38	2.74695641
10	2.62846553	6	1.87660728	5	2.65350435	4	1.29716873	4	2.83942496	8	2.74035089	2	1.01533812	11	2.06624133
17	3.29512662	13	2.99837812	3	1.1740645	11	2.63057123	2	1.04693881	5	1.26301088	4	1.49748193	9	1.24667075
45	3.69103671	27	2.63523576	15	2.48413173	28	2.8335317	23	5.09485471	30	3.20679359	16	2.53474482	48	2.81360522
79	4.83415142	71	5.16977174	71	8.77200804	95	7.17217632	51	8.4281344	91	7.25685513	39	4.60931275	129	5.64116682
71	7.39759128	58	7.19084353	47	9.88729189	47	6.04176787	24	6.75322693	44	5.97445869	29	5.83590742	79	5.88227263
23	2.48598796	32	4.11567454	27	5.89226761	32	4.26732143	31	9.04900851	22	3.09890147	11	2.29637221	72	5.561472
52	3.48297054	52	4.14447632	34	4.59804152	44	3.63607915	33	5.96937023	64	5.58650683	41	5.30406364	81	3.87719416
107	5.26587903	83	4.86054596	78	7.75049101	137	8.31843948	64	8.50619222	139	8.91488619	51	4.84769947	176	6.18993148
42	3.09388809	36	3.15556894	22	3.27209199	23	2.09034197	31	6.16715867	18	1.72799196	11	1.56504348	47	2.47422529
12	2.25053481	6	1.33898466	4	1.51464897	9	2.08248169	15	7.5973803	4	0.9776387	6	2.17337242	16	2.14442344
1	0.73820734	1	0.87841192	0	0	0	0	0	0	0	0	0	0	0	0
24	3.57381065	18	3.18942697	11	3.30720027	14	2.57206847	26	10.4559082	9	1.74653265	27	7.7653757	49	5.21437727
15	2.57641671	14	2.8613616	7	2.4275624	8	1.69530963	16	7.42186326	12	2.68608651	9	2.98569726	5	0.61373505
390	19.6676462	280	16.8021815	182	18.5313339	301	18.7278736	60	8.1716009	351	23.0679392	50	4.87008112	296	10.6675715
14	4.11644433	10	3.49875934	3	1.78099614	9	3.26490774	5	3.97038236	4	1.53273863	2	1.13580197	8	1.6810099
37	2.95113234	35	3.32181059	30	4.83120792	33	3.24739482	62	13.3550884	39	4.05382942	25	3.85128254	66	3.76198422
33	3.85508278	6	0.83404768	10	2.35867053	14	2.01781803	12	3.78589995	9	1.37017544	6	1.35378417	13	1.08529848
139	3.31002647	68	1.92683905	45	2.16359861	125	3.67249212	71	4.56607596	114	3.53781745	52	2.39165439	126	2.14423946
17	3.83004978	8	2.14469404	9	4.09397814	9	2.50168255	10	6.08448206	9	2.64248121	6	2.61086946	14	2.25408146
16	4.23764825	3	0.94546627	6	3.20851213	11	3.59444465	2	1.43054998	5	1.7257935	3	1.5346332	6	1.13564409
18	6.78829794	11	4.93629307	11	8.37584417	17	7.90990933	6	6.11093633	16	7.86361559	4	2.91357897	32	8.62431165
48	3.19653697	32	2.53576109	22	2.95807165	22	1.80757102	18	3.23727145	26	2.25645016	3	0.38586746	47	2.23677565
60	8.29380359	70	11.5138455	29	8.09371686	48	8.18611661	31	11.5726364	35	6.30499059	30	8.00944018	105	10.3723669
113	5.07195238	90	4.80683366	45	4.07808948	124	6.8667716	92	11.1519976	112	6.55131752	54	4.6813261	101	3.23969534
276	25.7420044	189	20.9756266	91	17.1365023	178	20.4827127	131	32.9968659	225	27.3482599	81	14.5913914	368	24.5282842
58	5.70071731	68	7.95298724	50	9.92245253	72	8.73108472	40	10.6176797	74	9.47866412	27	5.12558792	110	7.72645484
37	3.83206736	36	4.43663573	32	6.69158351	51	6.51682082	19	5.31438642	54	7.28851535	28	5.60102941	42	3.10861383
464	141.217769	594	215.118456	620	380.987362	394	147.945507	339	278.637255	418	165.791229	436	256.292718	1161	252.516441
32	15.0035654	43	23.9901418	11	10.4132117	19	10.9908756	20	25.324601	7	4.27716929	18	16.3002931	29	9.7169187
68	9.32533859	55	8.97507831	42	11.6292712	30	5.07587764	27	9.99971399	29	5.18283755	36	9.53534934	128	12.5444533
16	4.30334822	11	3.52045708	17	9.23172677	6	1.99100317	13	9.44273882	5	1.75254999	8	4.15580256	25	4.8052124
36	4.24845858	28	3.93193907	37	8.81613282	29	4.22241658	28	8.92390701	19	2.92210885	26	5.92625926	72	6.07221943
59	16.91776	83	28.3197099	77	44.5788731	77	27.2405434	50	38.7194313	37	13.8263158	86	47.6285884	274	56.1471199
170	6.75633065	192	9.07994177	118	9.46872481	191	9.36546909	98	10.5185571	152	7.87262317	137	10.5162512	382	10.8495421
15	2.65528661	18	3.79151268	2	0.71482158	7	1.528806	8	3.82453158	4	0.92277122	3	1.02569872	10	1.26504571
8	5.04665382	3	2.25192874	4	5.09472835	7	5.44810867	2	3.40730995	4	3.28842107	0	0	3	1.35244887
61	4.24136362	75	6.20521447	53	7.44044747	45	3.86031175	55	10.3277681	42	3.80573781	32	4.297383	98	4.86953869
26	9.02089371	20	8.25707205	17	11.9089275	17	7.27711658	12	11.2441228	23	10.3996316	10	6.70123162	17	4.21513232
5	1.86536264	7	3.10750023	2	1.5065057	1	0.46028568	5	5.03768944	7	3.40333901	4	2.88225016	7	1.8662825
11	3.4695745	9	3.37789311	1	0.63684104	14	5.44810867	5	4.25913744	3	1.2331579	2	1.21840575	5	1.12704073
6	4.24845858	5	4.21279186	0	0	3	2.62081029	1	1.91226579	0	0	1	1.36759829	1	0.50601829
37	7.68708124	16	3.95548362	10	4.19476137	17	4.35755484	24	13.4660154	16	4.3320517	16	6.42034167	47	6.97820426
6	2.60218088	8	4.12853602	2	1.75131287	4	2.14032841	0	0	4	2.26078948	2	1.67530791	2	0.6198724
22	9.08698084	14	6.88089337	6	5.00375106	17	8.66323402	5	5.57744188	9	4.84454889	3	2.39329701	17	5.01801467
9	2.16848406	14	4.01385447	4	1.94590319	10	2.97267834	10	6.50701553	7	2.19798977	3	1.39608992	14	2.41061489
10	2.39281	5	1.42363311	1	0.48312079	7	2.06652398	8	5.16971165	4	1.24733213	3	1.38646171	10	1.70999283
106	7.71016556	106	9.1745245	64	9.39907956	126	11.3073954	44	8.64328101	140	13.2708817	52	7.30532587	179	9.30458361
11	2.84815817	11	3.38909674	8	4.18223969	11	3.51397201	10	6.99261371	11	3.71174393	5	2.50045956	22	4.07080382
40	2.70005798	26	2.08836453	16	2.18062303	20	1.66562522	21	3.82825194	17	1.49546386	11	1.43411572	46	2.21899848
98	5.34619971	75	4.86855663	44	4.8464004	92	6.19214507	36	5.30383153	93	6.61174283	38	4.00388053	125	4.87321069
24	4.24845858	19	4.00215227	25	8.93526975	23	5.02321973	19	9.0832625	25	5.76732011	20	6.83799145	53	6.70474229
43	4.69156301	42	5.45278343	23	5.06669133	46	6.19214507	25	7.36643268	59	8.38909305	19	4.00388053	50	3.89856855
13	3.31650504	9	2.73211943	6	3.09055213	27	8.49836279	6	4.13386869	9	2.99222137	4	1.97095048	19	3.46399282
32	4.84831372	28	5.04799165	14	4.2826865	26	4.86013437	20	8.18349552	17	3.35663067	19	5.55997383	27	2.92341569
91	5.39711589	98	6.91618001	58	6.94537754	102	7.46370931	84	13.454506	129	9.97066131	85	9.73683227	121	5.12851695
54	5.13306913	51	5.76863938	27	5.18196685	53	6.21574825	16	4.10744213	41	5.07903391	19	3.48831235	59	4.00794209
310	46.1617209	321	56.8781143	148	44.4968764	324	59.5250132	76	30.563424	352	68.3088324	112	32.2119288	606	64.4880128
4	3.30435667	6	5.89790861	1	1.66791702	7	7.13442802	2	4.46195351	8	8.61253136	3	4.78659401	5	2.95177333
43	2.01338332	28	1.5600406	12	1.13445368	33	1.90636538	27	3.41420734	22	1.3424391	17	1.53739457	36	1.20461033
28	2.58372569	19	2.08622831	22	4.09881736	27	3.0738759	23	5.73171155	35	4.20891659	9	1.60401821	50	3.29719362
37	4.32236554	18	2.50214305	10	2.35867053	11	1.58542845	20	6.30983324	27	4.11052633	16	3.61009111	27	2.25408146
18	3.83143197	13	3.29269744	3	1.28931009	18	4.72710568	10	5.74852906	12	3.32876979	11	4.52230355	17	2.58597075
19	8.34454627	14	7.31639295	7	6.20718486	9	4.87669763	5	5.93044454	13	7.44057298	6	5.089543	3	0.94157833
38	7.94239947	32	7.95862366	20	8.44006203	38	9.79909391	23	12.982672	45	12.2572924	17	6.86270708	40	5.97467374
10	1.30435132	11	1.70728933	3	0.79006596	5	0.80463474	5	1.76129744	7	1.1898892	0	0	18	1.67785011
25	2.58152865	20	2.45746192	23	4.79526143	56	7.13442802	14	3.90420932	57	7.67053574	7	1.39608992	51	3.763511

gsyne_868	Synechococcus_assembled_mapped	cutA1 divalent ion tolerance family protein					PF03091.10	749226	749547	1	96	fig|1129.58.peg.864			
gsyne_869	Synechococcus_assembled_mapped	adenylosuccinate synthase	purA	6.3.4.4	GO:0004019,GO:0009152	TIGR00184	750523	751837	-1	125	fig|1129.58.1	Nucleosides and Nucleotides	Purines	Purine conversions	
gsyne_87	Synechococcus_assembled_mapped	nif11-like leader peptide domain protein				TIGR03798	70503	70719	-1	157	fig|1129.58.peg.86				
gsyne_870	Synechococcus_assembled_mapped	photosystem II protein Psb27	psb27		GO:0003674,GO:0009523,G	TIGR03044	751990	752398	-1	164	fig|1129.58.1	Photosynthesis	Electron transport and photopl	Photosystem II	
gsyne_871	Synechococcus_assembled_mapped	proline--tRNA ligase	proS	6.1.1.15	GO:0004827,GO:0005737,G	TIGR00409	752433	754263	-1	137	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	tRNA aminoacylation, Pro	
gsyne_872	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	754266	754389	1	856	fig|1129.58.peg.869				
gsyne_873	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	754453	754897	1	156	fig|1129.58.peg.870				
gsyne_874	Synechococcus_assembled_mapped	ubiE/COQ5 methyltransferase family protein				PF01209.13	755736	756393	-1	703	fig|1129.58.peg.872				
gsyne_875	Synechococcus_assembled_mapped	inorganic pyrophosphatase	ppa	3.6.1.1	GO:0000287,GO:0004427,G	UniRef100_P	755228	755744	1	92,141,703	fig|1129.58.1	Phosphorus Metabolism	Phosphorus Metabolism - no s	Phosphate metabolism	
gsyne_876	Synechococcus_assembled_mapped	2Fe-2S iron-sulfur cluster binding domain protein				TIGR03811.22	756523	756883	1	112	fig|1129.58.peg.86		Respiration - no subcategory	Soluble cytochromes and functio	
gsyne_877	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	757216	758665	-1	156	fig|1129.58.peg.875				
gsyne_878	Synechococcus_assembled_mapped	transcriptional regulator, Spx/MgsR family protein				TIGR01617	756879	757251	1	156	fig|1129.58.1	Respiration	Electron accepting reactions	Anaerobic respiratory reductases	
gsyne_879	Synechococcus_assembled_mapped	amidohydrolase family protein				PF13594.1	759454	760753	-1	703	fig|1129.58.1	Nucleosides and Nucleotides	Pyrimidines	De Novo Pyrimidine Synthesis	
gsyne_88	Synechococcus_assembled_mapped	ahpC/TSA antioxidant enzyme family protein				PF13911.1	70747	71425	-1	185	fig|1129.58.peg.87				
gsyne_880	Synechococcus_assembled_mapped	signal peptidase I	lepB	3.4.21.89	GO:0006465,GO:0009004,G	TIGR02227	758835	759495	1	97	fig|1129.58.1	Protein Metabolism	Protein processing and modific	Signal peptidase	
gsyne_881	Synechococcus_assembled_mapped	alpha-ribazole phosphatase	cobC	3.1.3.73	GO:0009236,GO:0019175	TIGR03162	760749	762069	-1	79	fig|1129.58.peg.878				
gsyne_882	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	762065	762185	-1	856	fig|1129.58.peg.879				
gsyne_883	Synechococcus_assembled_mapped	CAAX protease self-immunity family protein				PF02517.11	762259	763606	1	157	fig|1129.58.peg.880				
gsyne_884	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	763706	764153	1	156	fig|1129.58.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton	
gsyne_885	Synechococcus_assembled_mapped	penicillin binding transpeptidase domain protein				PF00905.17	764152	765955	1	89	fig|1129.58.1	Cell Division and Cell Cycle	Cell Division and Cell Cycle - r	Bacterial Cytoskeleton	
gsyne_886	Synechococcus_assembled_mapped	transaldolase	tal	2.2.1.2	GO:0004801,GO:0006098	TIGR00874	766044	767217	1	117	fig|1129.58.1	Carbohydrates	Central carbohydrate metaboli	Pentose phosphate pathway	
gsyne_887	Synechococcus_assembled_mapped	geranylgeranyl reductase family protein		1.3.1.-	GO:0015995,GO:0030494,G	TIGR02032	767635	768787	-1	191	fig|1129.58.peg.885				
gsyne_888	Synechococcus_assembled_mapped	cyclic nucleotide-binding domain protein				PF00027.24	767258	767639	1	157	fig|1129.58.1	Regulation and Cell signaling	Regulation and Cell signaling -	cAMP signaling in bacteria	
gsyne_889	Synechococcus_assembled_mapped	ribosome-recycling factor	frr		GO:0005737,GO:0006412,G	TIGR00496	768783	769323	-1	169	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Translation termination factors ba	
gsyne_89	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	71474	71615	1	856	fig|1129.58.peg.88				
gsyne_890	Synechococcus_assembled_mapped	UMP kinase	pyrH	2.7.4.22	GO:0015949,GO:0033862	TIGR02075	769360	770074	-1	124	fig|1129.58.peg.887				
gsyne_891	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	770225	770375	1	856	fig|1129.58.peg.888				
gsyne_892	Synechococcus_assembled_mapped	cob(I)yrinic acid a,c-diamide adenosyltr	cobO	2.5.1.17	GO:0008817,GO:0009236	TIGR00708	770387	771068	-1	79	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Cobalamin synthesis	
gsyne_893	Synechococcus_assembled_mapped	phage integrase family protein				PF00589.17	771121	772174	-1	132,152	fig|1129.58.peg.890				
gsyne_894	Synechococcus_assembled_mapped	ferrochelatase	hemH	4.99.1.1	GO:0004325,GO:0006779	TIGR00109	772447	773623	1	79	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Heme and Siroheme Biosynthesi	
gsyne_895	Synechococcus_assembled_mapped	peptidase M22 family protein				PF01551.17	773654	774134	1	138	fig|1129.58.peg.892				
gsyne_896	Synechococcus_assembled_mapped	acetolactate synthase, large subunit, bi	ilvB	2.2.1.6	GO:0003984,GO:0005948,G	TIGR00118	774274	776416	1	74	fig|1129.58.1	Carbohydrates	Fermentation	Acetolactate synthase subunits	
gsyne_897	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	776421	776637	1	88	fig|1129.58.peg.894				
gsyne_898	Synechococcus_assembled_mapped	tic22-like family protein				PF04278.7	776655	777411	-1	185	fig|1129.58.peg.895				
gsyne_899	Synechococcus_assembled_mapped	periplasmic binding family protein				PF13458.1	777484	778678	1	185	fig|1129.58.peg.896				
gsyne_9	Synechococcus_assembled_mapped	calcineurin-like phosphoesterase family protein				PF00149.23	6723	7923	-1	703	fig|1129.58.peg.10				
gsyne_90	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF07386.6	71611	72004	1	156	fig|1129.58.peg.89				
gsyne_900	Synechococcus_assembled_mapped	phosphoenolpyruvate synthase	ppsA	2.7.9.2	GO:0006094,GO:0008986,G	TIGR01418	778670	781073	1	116	fig|1129.58.1	Carbohydrates	Central carbohydrate metaboli	Pyruvate metabolism I: anaplerot	
gsyne_901	Synechococcus_assembled_mapped	respiratory-chain NADH dehydrogenase 24 Kd subunit				PF01257.14	781111	781570	1	703	fig|1129.58.peg.898				
gsyne_902	Synechococcus_assembled_mapped	respiratory-chain NADH dehydrogenase 51 Kd subunit				PF01512.12	781566	783132	1	703	fig|1129.58.peg.899				
gsyne_903	Synechococcus_assembled_mapped	4Fe-4S binding domain protein				PF00037.22	783128	783845	1	157	fig|1129.58.peg.900				
gsyne_904	Synechococcus_assembled_mapped	NADH ubiquinone oxidoreductase, 20 Kd subunit				PF01058.17	783841	784405	1	703	fig|1129.58.peg.901				
gsyne_905	Synechococcus_assembled_mapped	NAD-reducing hydrogenase hoxS subun	hoxH	1.12.1.2	GO:0008901,GO:0016151,G	UniRef100_P	784424	785900	1	141,703	fig|1129.58.peg.902				
gsyne_906	Synechococcus_assembled_mapped	hydrogenase maturation protease family protein				TIGR00072	785902	786382	1	138	fig|1129.58.peg.903				
gsyne_907	Synechococcus_assembled_mapped	hydrogenase nickel insertion protein Hy	hypA		GO:0006464,GO:0008901	TIGR00100	786365	786716	1	140	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_908	Synechococcus_assembled_mapped	hydrogenase accessory protein HypB	hypB		GO:0000166,GO:0006464,G	TIGR00073	786752	787412	1	140	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_909	Synechococcus_assembled_mapped	carbamoyltransferase HypF	hypF		GO:0003998,GO:0006464	TIGR00143	787395	789750	1	140	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_91	Synechococcus_assembled_mapped	acetolactate synthase, catabolic	alsS	2.2.1.6	GO:0003984,GO:0006113,G	TIGR02418	72083	73727	1	114	fig|1129.58.1	Carbohydrates	Fermentation	Acetoin, butanediol metabolism	
gsyne_910	Synechococcus_assembled_mapped	hupF/HypC family protein				PF01455.13	789727	789919	1	185	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_911	Synechococcus_assembled_mapped	ferredoxin (flavodoxin) oxidoreductase	nifJ	1.2.7.1		TIGR02176	789915	793458	1	112	fig|1129.58.1	Carbohydrates	Central carbohydrate metaboli	Pyruvate:ferredoxin oxidoreducta	
gsyne_912	Synechococcus_assembled_mapped	SOR/SNZ family protein				PF01680.12	793454	794453	1	185	fig|1129.58.peg.909				
gsyne_913	Synechococcus_assembled_mapped	hydrogenase expression/formation pro	hypD		GO:0006464,GO:0016530	TIGR00075	794449	795520	1	140	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_914	Synechococcus_assembled_mapped	hydrogenase expression/formation pro	hypE			TIGR02124	795550	796543	1	703	fig|1129.58.1	Respiration	Electron donating reactions	NiFe hydrogenase maturation	
gsyne_915	Synechococcus_assembled_mapped	hicA domain protein				UniRef100_D	796615	797353	1	157	fig|1129.58.peg.912				
gsyne_916	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	797487	797718	1	856	fig|1129.58.peg.913				
gsyne_917	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	797789	797918	-1	856	fig|1129.58.peg.914				
gsyne_918	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	798458	798656	1	856	fig|1129.58.peg.915				
gsyne_919	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	798723	798939	1	856	fig|1129.58.peg.916				
gsyne_92	Synechococcus_assembled_mapped	alpha-acetolactate decarboxylase	budA	4.1.1.5	GO:0006113,GO:0045151,G	TIGR01252	73740	74595	1	114	fig|1129.58.1	Carbohydrates	Fermentation	Acetoin, butanediol metabolism	
gsyne_920	Synechococcus_assembled_mapped	ABC transporter family protein				PF00005.22	799039	801265	1	141	fig|1129.58.peg.917				
gsyne_921	Synechococcus_assembled_mapped	hlyD secretion family protein				PF00529.15	801267	802491	1	97	fig|1129.58.peg.918				
gsyne_922	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	802588	803278	1	856	fig|1129.58.peg.919				
gsyne_923	Synechococcus_assembled_mapped	ZIP Zinc transporter family protein				PF02535.17	803354	804107	-1	145	fig|1129.58.peg.920				
gsyne_924	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	804103	804541	-1	88	fig|1129.58.peg.921				
gsyne_925	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	804750	805041	1	856	fig|1129.58.peg.922				
gsyne_926	Synechococcus_assembled_mapped	lysR substrate binding domain protein				PF03466.15	805052	805829	-1	157	fig|1129.58.peg.923				
gsyne_927	Synechococcus_assembled_mapped	bacterial regulatory s, luxR family protein				PF00196.14	806149	806749	-1	261	fig|1129.58.peg.924				
gsyne_928	Synechococcus_assembled_mapped	HAD ATPase, P-type, IC family protein		3.6.3.-		TIGR01494	807184	809785	-1	185	fig|1129.58.peg.925				
gsyne_929	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	809811	810000	-1	856	fig|1129.58.peg.926				
gsyne_93	Synechococcus_assembled_mapped	PPOX class putative FMN-dependent enzyme, alr4033		1.-.-.-	GO:0003824,GO:0008150,G	TIGR04026	74604	75141	-1	185	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Pyridoxine	Pyridoxin (Vitamin B6) Biosynthe	
gsyne_930	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	809999	810230	-1	856	fig|1129.58.peg.927				
gsyne_931	Synechococcus_assembled_mapped	chlorophyll A-B binding family protein				PF00504.16	810318	810504	-1	185	fig|1129.58.peg.928				
gsyne_932	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	810533	810719	-1	856	fig|1129.58.peg.929				
gsyne_933	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	810757	810940	-1	856	fig|1129.58.peg.930				
gsyne_934	Synechococcus_assembled_mapped	phosphatidylethanolamine-binding family protein				PF01161.15	811099	811702	-1	185	fig|1129.58.peg.931				
gsyne_935	Synechococcus_assembled_mapped	putative membrane protein			GO:0008150,GO:0003674,G	TMHMM	811751	811868	1	88	fig|1129.58.peg.932				
gsyne_936	Synechococcus_assembled_mapped	bacterial capsule synthesis PGA_cap family protein				PF09587.5	811849	813019	1	185	fig|1129.58.peg.933				
gsyne_937	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF11964.3	813046	813772	1	156	fig|1129.58.peg.934				
gsyne_938	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	813833	814142	1	856	fig|1129.58.peg.935				
gsyne_939	Synechococcus_assembled_mapped	hsp20/alpha crystallin family protein				PF00011.16	814223	814658	1	185	fig|1129.58.peg.936				
gsyne_94	Synechococcus_assembled_mapped	thiamine pyrophosphate enzyme, C-terminal TPP binding domain protein				PF02775.16	75171	76833	-1	157	fig|1129.58.1	Carbohydrates	Central carbohydrate metal	Pyruvate metabolism II: acetyl	
gsyne_940	Synechococcus_assembled_mapped	diguanylate cyclase domain protein			GO:0009966,GO:0009975	TIGR00254	814724	815768	-1	264,710	fig|1129.58.peg.937				
gsyne_941	Synechococcus_assembled_mapped	abrB-like transcriptional regulator family protein				PF14250.1	815751	816144	-1	165	fig|1129.58.peg.938				
gsyne_942	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	816169	816376	-1	856	fig|1129.58.peg.939				
gsyne_943	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	816365	816536	-1	856					
gsyne_944	Synechococcus_assembled_mapped	dienelactone hydrolase			GO:0016787	UniRef100_C	816581	817256	1	703	fig|1129.58.peg.940				
gsyne_945	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	817291	817414	1	856	fig|1129.58.peg.941				
gsyne_946	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	817410	817674	1	856	fig|1129.58.peg.942				
gsyne_947	Synechococcus_assembled_mapped	RNA polymerase sigma factor, sigma-70 family protein				TIGR02937	817739	818579	-1	135	fig|1129.58.1	RNA Metabolism	Transcription	Transcription initiation, bacterial s	
gsyne_948	Synechococcus_assembled_mapped	methyltransferase domain protein				PF08242.7	818631	819831	-1	703	fig|1129.58.peg.944				
gsyne_949	Synechococcus_assembled_mapped	HAD ATPase, P-type, IC family protein		3.6.3.-		TIGR01494	819992	822683	1	185	fig|1129.58.peg.945				
gsyne_95	Synechococcus_assembled_mapped	amidohydrolase family protein				PF01979.15	77051	78833	1	703	fig|1129.58.peg.94				
gsyne_950	Synechococcus_assembled_mapped	phosphoribosyl transferase domain protein				PF00156.22	822657	823359	1	703	fig|1129.58.peg.946				
gsyne_951	Synechococcus_assembled_mapped	tspO/MBR family protein				PF03073.10	823561	824008	-1	185	fig|1129.58.peg.947				
gsyne_952	Synechococcus_assembled_mapped	photosystem II q(b) protein	psbA	1.10.3.9	GO:0009055,GO:0009538,G	TIGR01151	824248	825304	1	112,164	fig|1129.58.1	Photosynthesis	Electron transport and photopl	Photosystem II	
gsyne_953	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	825473	825593	-1	856					
gsyne_954	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	825622	825772	1	856	fig|1129.58.peg.949				
gsyne_955	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	825787	825916	-1	856	fig|1129.58.peg.950				
gsyne_956	Synechococcus_assembled_mapped	chromate transporter, chromate ion tra	chr		GO:0015109,GO:0015703	TIGR00937	825955	827272	-1	143	fig|1129.58.1	Virulence, Disease and Defense	Resistance to antibiotics and t	Resistance to chromium compou	
gsyne_957	Synechococcus_assembled_mapped	fatty acid desaturase family protein				PF00487.19	827307	828294	-1	121	fig|1129.58.peg.952				
gsyne_958	Synechococcus_assembled_mapped	beta-lactamase superfamily domain protein				PF13483.1	828303	829038	-1	157	fig|1129.58.peg.953				
gsyne_959	Synechococcus_assembled_mapped	glucose inhibited division A family protein				PF01134.17	829119	830802	-1	168	fig|1129.58.peg.954				
gsyne_96	Synechococcus_assembled_mapped	amidohydrolase family protein				PF07969.6	78878	80573	1	703	fig|1129.58.peg.95				
gsyne_960	Synechococcus_assembled_mapped	FAD binding domain of DNA photolyase family protein				PF03441.9	831231	832959	1	132	fig|1129.58.1	DNA Metabolism	DNA repair	DNA repair, bacterial photolyase	
gsyne_961	Synechococcus_assembled_mapped	multi-copper polyphenol oxidoreductase laccase family protein				PF02578.10	833093	833912	-1	703	fig|1129.58.peg.956				
gsyne_962	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF06485.6	833923	834841	-1	156	fig|1129.58.peg.957				
gsyne_963	Synechococcus_assembled_mapped	S1 RNA binding domain protein				PF00575.18	834837	836112	-1	157	fig|1129.58.1	Protein Metabolism	Protein biosynthesis	Ribosome SSU bacterial	
gsyne_964	Synechococcus_assembled_mapped	creatinine amidohydrolase family protein				PF02633.9	836286	837114	-1	109	fig|1129.58.1	Amino Acids and Derivatives	Amino Acids and Derivatives -	Creatine and Creatinine Degrada	
gsyne_965	Synechococcus_assembled_mapped	long-chain fatty aldehyde decarbonylase		4.1.99.5	GO:0043447	TIGR04059	837211	837925	1	185	fig|1129.58.peg.960				
gsyne_966	Synechococcus_assembled_mapped	long-chain fatty acyl-ACP reductase		1.1.1.-	GO:0043447	TIGR04058	838004	839072	1	703	fig|1129.58.1	Amino Acids and Derivatives	Arginine; urea cycle, polyamin	Arginine Biosynthesis -- ggo	
gsyne_967	Synechococcus_assembled_mapped	acetyl-CoA carboxylase, carboxyl transf	accA	6.4.1.2	GO:0003989,GO:0006633,G	TIGR00513	839128	840118	1	176	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Plerin synthesis related cluster	
gsyne_968	Synechococcus_assembled_mapped	short chain dehydrogenase family protein				PF00106.20	840283	840901	1	703	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Plerin synthesis related cluster	
gsyne_969	Synechococcus_assembled_mapped	GTP cyclohydrolase I family protein				PF01227.17	840922	841645	1	78	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Folate and pterines	Plerin synthesis related cluster	
gsyne_97	Synechococcus_assembled_mapped	cobalamin synthesis cobW C-terminal domain protein				PF07683.9	80569	81466	1	157	fig|1129.58.1	Regulation and Cell signaling	Regulation and Cell signaling -	Zinc regulated enzymes	
gsyne_970	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	841724	842246	-1	156	fig|1129.58.peg.965				
gsyne_971	Synechococcus_assembled_mapped	N-[5'phosphoribosyl]anthranilate (PRA) isomerase family protein				PF00697.17	842255	842948	-1	70	fig|1129.58.peg.966	Amino Acids and Derivatives	Aromatic amino acids and deri	Chorismate: Intermediate for syn	
gsyne_972	Synechococcus_assembled_mapped	peptidase M50 family protein				PF02163.17	843004	844231	1	140	fig|1129.58.peg.967				
gsyne_973	Synechococcus_assembled_mapped	biotin/lipoate A/B ligase family protein				PF03099.14	844250	844973	-1	140	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Lipoic acid	Lipoic acid metabolism	
gsyne_974	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF08847.6	845766	846225	-1	156	fig|1129.58.peg.970				
gsyne_975	Synechococcus_assembled_mapped	sulfite exporter TauE/SafE family protein				PF01925.14	845015	845774	1	141	fig|1129.58.peg.969				
gsyne_976	Synechococcus_assembled_mapped	photosystem I reaction center subunit I	psaM		GO:0003674,GO:0009538,G	TIGR03053	846353	846485	1	164	fig|1129.58.peg.971				
gsyne_977	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_C	846545	847049	1	156	fig|1129.58.peg.972				
gsyne_978	Synechococcus_assembled_mapped	light-dependent protochlorophyllide reductase		1.3.1.33	GO:0015995,GO:0016630	TIGR01289	847076	848072	1	191	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_979	Synechococcus_assembled_mapped	light-independent protochlorophyllide	bchL	1.18.-.-	GO:0015995,GO:0016491	TIGR01281	848346	849231	-1	191	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_98	Synechococcus_assembled_mapped	sugar (and other) transporter family protein				PF00083.19	81462	82995	1	141	fig|1129.58.peg.97				
gsyne_980	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_B	848086	848350	1	156	fig|1129.58.peg.974				
gsyne_981	Synechococcus_assembled_mapped	amidohydrolase family protein				PF07969.6	849416	851270	-1	703	fig|1129.58.peg.976				
gsyne_982	Synechococcus_assembled_mapped	light-independent protochlorophyllide	bchB	1.18.-.-	GO:0015995,GO:0016491	TIGR01278	851368	852967	-1	191	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_983	Synechococcus_assembled_mapped	light-independent protochlorophyllide	bchN	1.18.-.-	GO:0015995,GO:0016491	TIGR01279	852970	854248	-1	191	fig|1129.58.1	Cofactors, Vitamins, Prosthetic Gr	Tetrapyrroles	Chlorophyll Biosynthesis	
gsyne_984	Synechococcus_assembled_mapped	NAD binding domain of 6-phosphogluconate dehydrogenase family protein				PF03446.10	854362	855067	-1	157	fig|1129.58.1	Potassium metabolism	Potassium metabolism - no su	Potassium homeostasis	
gsyne_985	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	854263	854398	1	856					
gsyne_986	Synechococcus_assembled_mapped	cation transport family protein				PF02386.11	855092	856439	-1	141	fig|1129.58.peg.980				
gsyne_987	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF09835.4	857553	857994	-1	156	fig|1129.58.peg.982				
gsyne_988	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF01595.15	856549	857563	1	156	fig|1129.58.peg.981				
gsyne_989	Synechococcus_assembled_mapped	citrate transporter family protein				PF03600.11	858113	859919	-1	144	fig|1129.58.peg.983				
gsyne_99	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	UniRef100_A	83947	84382	-1	156	fig|1129.58.peg.99				
gsyne_990	Synechococcus_assembled_mapped	rrf2 family protein				TIGR00738	860106	860535	1	157	fig|1129.58.1	Miscellaneous	Plant-Prokaryote DOE project	Iron-sulfur cluster assembly	
gsyne_991	Synechococcus_assembled_mapped	hypothetical protein			GO:0008150,GO:0003674,G	default	863375	863699	-1	856					
gsyne_992	Synechococcus_assembled_mapped	HAD ATPase, P-type, IC family protein		3.6.3.-		TIGR01494	860652	863415	1	185	fig|1129.58.peg.985				
gsyne_993	Synechococcus_assembled_mapped	ammonium transporter family protein	amt		GO:0008519,GO:0015696	TIGR00836	863786	865250	-1	145	fig|1129.58.1	Nitrogen Metabolism	Nitrogen Metabolism - no subc	Ammonia assimilation	
gsyne_994	Synechococcus_assembled_mapped	conserved hypothetical protein			GO:0008150,GO:0003674,G	PF14105.1	865617	865833	1	156	fig|1129.58.peg.987				
gsyne_995	Synechococcus_assembled_mapped	sodium/calcium exchanger family protein				PF01699.19	866130	867216	-1	145	fig|1129.58.peg.988				
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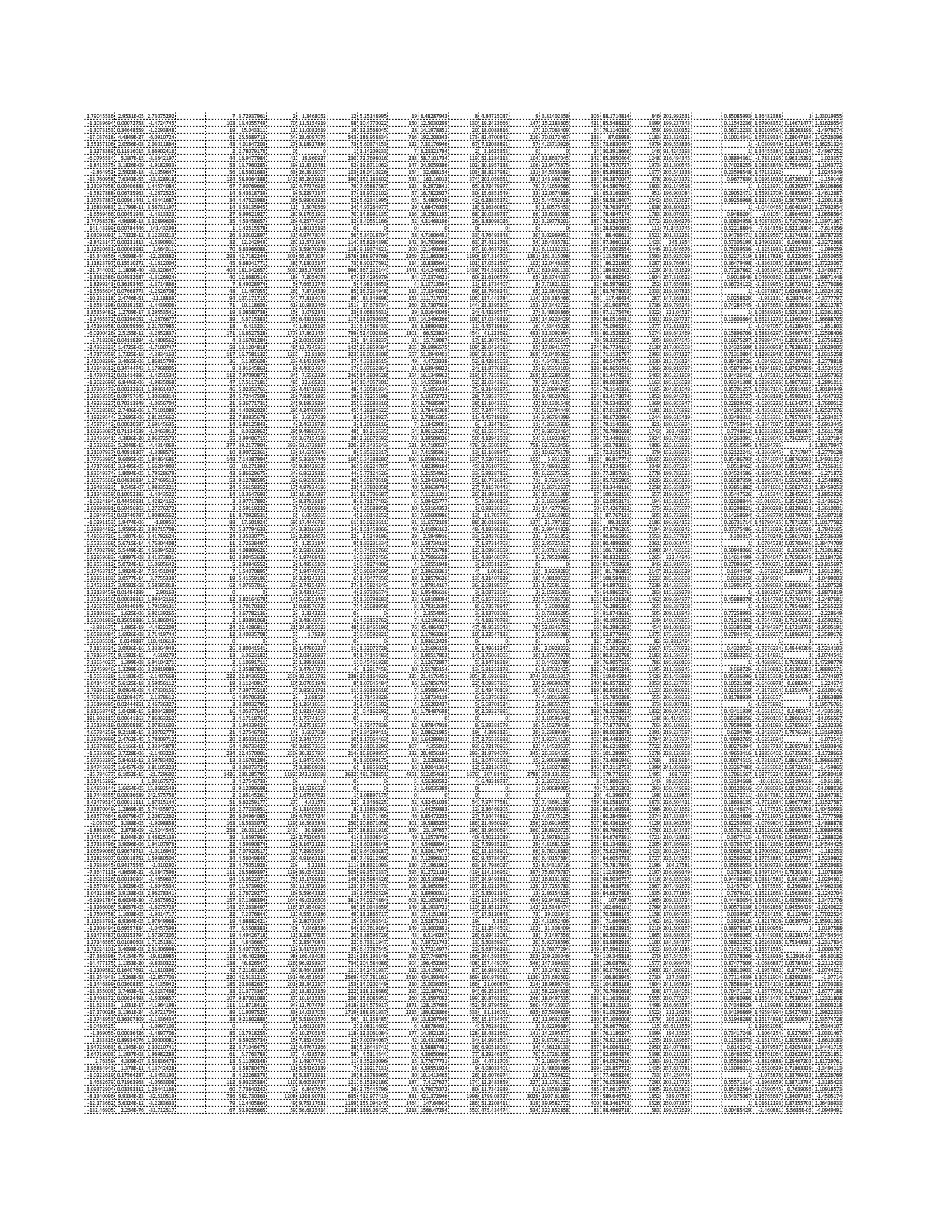

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53	8.39668715	40	7.54070507	33	10.5558584	39	7.62308747	19	8.12931255	40	8.25859172	19	5.81385392	64	7.24599701
56	11.2962891	67	16.082088	44	17.9204108	95	23.6431626	21	11.4402413	73	19.1904224	18	7.01291681	66	9.51432056
124	35.8522699	150	51.6067003	80	46.7016766	128	45.6603393	51	39.8229351	122	45.9693861	41	22.8958747	216	44.6308128
67	4.81286732	33	2.8207389	27	3.91597909	46	4.07681601	58	11.2518828	51	4.77433804	23	3.19106268	46	2.36141867
14	3.91726154	10	3.32946454	12	6.77927563	15	5.17821389	6	4.5339205	5	1.82321732	6	3.24253143	11	2.19954723
34	2.72437721	37	3.52784834	25	4.04460248	33	3.26239434	13	2.81319471	29	3.02830924	16	2.47620568	54	3.09220412
14	2.14929394	11	2.00946444	5	1.5498344	13	2.46232472	13	5.38988189	8	1.60055893	10	2.96514673	20	2.19423858
27	4.25811416	29	5.44216112	8	2.54736418	36	7.00471115	13	5.53687867	24	4.9326316	15	4.56902156	33	3.7192344
35	2.75988881	26	2.43958947	26	4.13946679	36	3.50235557	25	5.3239218	21	2.15802632	12	1.82760862	45	2.53584164
1	0.86739363	1	1.03213401	0	0	0	0	0	0	0	0	0	0	0	0
26	2.00910773	31	2.8504369	19	2.96436032	24	2.28810164	26	5.42589447	28	2.8196929	16	2.38796672	34	1.87756451
32	7.45143518	26	7.20415682	31	14.5746843	17	4.88397086	7	4.40206151	10	3.03461676	8	3.59797671	42	6.98916532
70	4.04110175	31	2.12952773	25	2.91399812	39	2.77779727	27	4.20953018	34	2.55796481	29	3.23353938	60	2.47536399
293	25.9996248	318	33.5773518	241	43.1781486	270	29.5595227	183	43.8549548	255	29.4885585	155	26.5649847	622	39.443543
45	4.06590762	39	4.1930444	18	3.28371163	28	3.12131226	22	5.36828781	41	4.82772754	11	1.91962364	42	2.71194175
404	110.370717	511	166.116686	211	116.386462	425	143.250326	148	109.194894	355	126.390593	139	73.3441886	594	115.969829
40	7.71016556	18	4.12853602	23	8.95115468	18	4.28065681	27	14.0551536	26	6.53116962	25	9.30726614	88	12.1219492
7	5.16745139	5	4.3920596	0	0	4	3.64311218	2	3.9872776	1	0.96203808	1	1.42579396	0	0
48	6.99746118	26	4.5101654	21	6.18110425	30	5.3957859	28	11.0236498	29	5.50948697	20	5.63128708	78	8.12605835
94	65.2280007	54	44.5881891	19	26.6199557	37	31.6768604	8	14.9921638	15	13.5647369	3	4.02073897	10	4.9589792
71	6.15849474	69	7.12172464	34	5.95446376	60	6.42098522	39	9.13584981	65	7.34756582	23	3.85320818	116	7.19051984
19	1.87811725	17	1.99957585	9	1.79621833	19	2.31716466	22	5.87299863	8	1.03055931	7	1.33642796	29	2.04858115
39	3.45187259	36	3.79151268	47	8.39915357	38	4.1496163	46	10.9955283	36	4.15247048	23	3.93184508	59	3.73188486
18	3.90327132	4	1.03213401	5	2.18914109	10	2.67541051	2	1.1712628	6	1.69559211	0	0	6	0.9298086
171	8.30948516	180	10.408074	182	17.8565234	215	12.889933	103	13.5170945	205	12.9821245	91	8.5407854	312	10.8347445
4	1.92754139	2	1.14681556	1	0.9729516	13	7.72896369	2	2.60280621	10	6.27997078	3	2.79217984	4	1.37749422
58	7.98552862	49	8.02770894	43	11.9534053	66	11.211244	26	9.66756593	58	10.4068087	32	8.50950047	111	10.9215613
117	10.1995029	132	13.692632	88	15.4889983	116	12.4762862	54	12.7132042	121	13.7465089	64	10.7758498	168	10.4661873
36	3.12261705	24	2.47712161	16	2.8021006	24	2.56839409	17	3.98229351	14	1.58255264	8	1.34024632	41	2.54147684
9	2.38367714	9	2.8363988	11	5.88227224	8	2.61414157	3	2.14582497	8	2.7612696	4	2.04617759	13	2.4605622
112	4.85134013	90	4.63880452	53	4.63518513	84	4.48907831	68	7.95464371	93	5.24977333	60	5.01964915	91	2.8168983
47	10.65817	48	12.9522699	38	17.3986638	29	8.11366324	24	14.6981998	26	7.68372896	18	7.88380191	54	8.75113977
46	3.05747945	33	2.60999404	26	3.48920572	35	2.87017219	60	10.7702326	35	3.03171003	29	3.72290646	59	2.80248825
24	3.48409155	26	4.49129442	13	3.81038784	7	1.25374886	15	5.88081738	7	1.32431183	6	1.68231756	32	3.31981871
21	3.87558854	25	5.4900745	8	2.98095808	13	2.96002865	8	3.9872776	10	2.40509519	4	1.42579396	20	2.63775489
38	2.67975267	29	2.43348668	13	1.85098108	21	1.82710962	61	11.6174033	16	1.47043218	16	2.17926232	50	2.5198065
22	4.77066494	8	2.06426801	2	0.87565644	2	0.5350821	12	7.02757677	2	0.56519737	5	2.09413488	28	4.3391068
14	4.15162761	4	1.41146531	2	1.19747889	8	2.92694483	0	0	2	0.77291948	1	0.57275484	1	0.21192219
31	4.88894589	32	6.00514331	23	7.32367201	27	5.25353336	11	4.68505118	17	3.49394738	6	1.82760862	45	5.07168327
55	2.43091207	41	2.15630544	15	1.33858309	21	1.14514386	30	3.58093084	26	1.49759303	18	1.53658814	54	1.70563616
377	23.8691531	413	31.1146967	368	47.0425647	418	32.6517253	142	24.2801923	452	37.2947754	240	29.3484597	920	41.6264677
10	5.42121016	13	8.3860888	4	4.37828218	9	6.01967364	3	4.39223548	10	7.06496713	7	7.32947208	6	2.3245215
148	4.34798498	92	3.21613306	72	4.27077144	83	3.00842096	81	6.42657317	84	3.21602568	36	2.04271243	179	3.75807484
60	6.25148559	47	5.82706286	20	4.20735825	20	2.57096505	20	5.62768911	22	2.98722935	11	2.21362005	34	2.531611
43	4.17903932	34	3.93193907	11	2.15848085	18	2.15831436	19	4.98688921	22	2.78640721	7	1.31396698	31	2.1530582
55	5.76515401	33	4.11606311	25	5.29097544	26	3.36244946	21	5.94477794	26	3.55169345	8	1.61963302	59	4.41963403
24	3.38495074	18	3.02088002	14	3.98672849	13	2.26213571	23	8.76066481	12	2.20564828	13	3.54130126	28	2.82218329
14	6.30831728	13	6.97025563	2	1.81954584	11	6.11522402	3	3.65068923	7	4.11052633	1	0.87028982	19	6.11822109
3	2.42063337	7	6.7208726	0	0	0	0	2	4.35818715	0	0	0	0	0	0
3	1.57707932	7	4.37875033	1	1.06140174	5	3.24292183	3	4.25913744	2	1.37017544	0	0	1	0.37568024
11	5.30073882	6	3.44044669	0	0	5	2.97267834	1	1.30140311	0	0	0	0	0	0
89	10.8348116	70	10.1402639	71	17.4516791	89	13.3676651	42	13.8085719	81	12.8508034	53	12.4619395	144	12.5279475
70	3.27318349	37	2.05870395	14	1.32174556	21	1.21150665	28	3.53588769	8	0.48750178	10	0.90313095	48	1.60398249
24	2.04092618	13	1.31546491	6	1.03018404	10	1.04918059	18	4.13386869	12	1.32987617	7	1.14972111	15	0.91157706
11	1.65936172	4	0.71800627	3	0.91372846	9	1.67503962	22	8.96270661	9	1.76931351	6	1.74814738	2	0.21560779
18	2.48814108	9	1.48035156	6	1.67456211	6	1.02326458	23	8.58614958	4	0.72057035	1	0.26698134	10	0.98784446
10	2.37642089	5	1.4138822	2	0.95962349	1	0.29319567	7	4.49251483	5	1.54848595	1	0.45898847	9	1.52845249
5	1.78844047	2	0.85124454	0	0	1	0.44130483	0	0	0	0	0	0	0	0
7	0.93772284	7	1.11582055	0	0	4	0.6611053	13	4.70314018	4	0.69831335	5	1.29367406	7	0.67013232
19	3.29609578	9	1.85784121	2	0.70052515	4	0.85613136	11	5.1535563	6	1.35647369	6	2.01036949	9	1.11577032
62	2.48112594	35	1.66665237	19	1.53517622	13	0.64185166	39	4.21492494	13	0.67797609	14	1.08209046	58	1.65871277
0	0	3	1.96596954	0	0	2	1.35893867	1	1.48731784	0	0	0	0	0	0
12	2.32597173	14	3.22902259	3	1.1740645	11	2.63057123	3	1.57040822	12	3.03122612	5	1.87185241	20	2.77037944
5	2.25297046	1	0.53617351	0	0	4	2.22371782	3	3.65068923	2	1.1744361	1	0.87028982	4	1.28804655
5	2.79804395	2	1.33178581	2	2.25975854	0	0	1	1.51130683	1	0.72928693	2	2.16168762	0	0
2	1.11921758	3	1.99767872	1	1.12987927	1	0.69042852	1	1.51130683	1	0.72928693	0	0	0	0
24	13.6507849	21	14.2129929	4	4.59360753	25	17.5436755	2	3.07216471	15	11.1186368	4	4.39425024	10	4.06473705
12	2.07138776	6	1.23239881	2	0.69703995	5	1.06484	3	1.39852274	2	0.44990836	4	1.33357843	8	0.98686153
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	2.31304967	9	0.95273908	9	1.6165965	4	0.43904172	7	1.68181325	8	0.92750338	1	0.17182645	20	1.27153313
13	1.86382101	7	1.19420464	5	1.44736601	4	0.70754658	8	3.0975545	4	0.74736842	1	0.2769104	7	0.71720774
2	0.67370379	2	0.80165748	0	0	2	0.8311955	3	2.72915603	1	0.43898825	0	0	2	0.48145429
6	1.435686	7	1.99308636	2	0.96624158	4	1.18087085	15	9.69320934	0	0	4	1.84861562	5	0.85499641
222	13.9033491	267	19.897457	192	24.2781279	149	11.5129579	91	15.3913234	163	13.3035627	69	8.34629931	545	24.3920908
19	1.89430792	10	1.18636093	2	0.40260066	6	0.73804428	16	4.30809304	6	0.77958258	6	1.15538476	11	0.78374671
17	4.50250126	7	2.20608795	0	0	4	1.30707078	3	2.14582497	3	1.0354761	2	1.0230888	4	0.75709606
6	3.01702131	2	1.19667711	3	3.04576152	5	3.10192523	2	2.7159717	3	1.9659039	0	0	0	0
3	1.82609184	1	0.72430457	0	0	3	2.25297727	3	4.93163282	0	0	0	0	0	0
16	2.46725298	6	1.10094294	5	1.55672255	4	0.76100566	3	1.24934698	0	0	1	0.29783252	4	0.44079815
3	2.53871305	1	1.00696001	0	0	1	1.04406264	0	0	0	0	0	0	1	0.60475356
3	1.18280949	4	1.87660728	0	0	4	1.9457531	2	2.12956872	0	0	2	1.52300719	4	1.12704073
21	2.60218088	14	2.06426801	6	1.50112532	15	2.29320901	15	5.0196977	11	1.77633459	3	0.7179891	18	1.5939576
20	1.73478725	13	1.34177421	8	1.4010503	6	0.64209852	12	2.81103071	8	0.90431579	11	1.8428387	15	0.9298086
64	2.47550466	48	2.20925005	43	3.35814731	41	1.95659899	46	4.8051807	62	3.12528312	34	2.5400432	72	1.99022577
234	13.6680208	259	18.0015291	241	28.4219799	190	13.6923366	97	15.3013456	207	15.7570176	114	12.8609496	590	24.627927
13	1.92754139	6	1.05859898	2	0.59873944	6	1.09760431	7	2.80302208	7	1.35260909	3	0.85913226	11	1.16557203
8	1.86285879	7	1.93958068	2	0.94030221	2	0.57458481	3	1.88659779	4	1.2138467	5	2.24873544	4	0.66563479
140	13.7603521	180	21.0520251	111	22.0278446	325	39.4111463	322	85.4723219	315	40.3483675	449	85.2366288	769	54.0149434
3	2.60218088	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	5.55131921	8	6.60565764	0	0	0	0	0	0	0	0	0	0	0	0
2	1.61375558	1	0.96012466	0	0	0	0	0	0	0	0	0	0	0	0
51	4.03071298	29	2.72727892	16	2.55316683	15	1.462639	35	7.47046886	15	1.54495864	14	2.13706703	46	2.59809844
16	1.68733107	6	0.7529245	3	0.63877673	11	1.43122264	11	3.13286097	9	1.2369061	8	1.62947881	7	0.52755098
26	3.68199743	18	3.03321014	7	2.00150043	11	1.92192755	6	2.29471895	11	2.03009668	5	1.36759829	29	2.93490606
163	10.0809384	142	10.4501268	58	7.24250599	163	12.437559	42	7.0150499	106	8.54344688	43	5.13641639	128	5.65730247
258	15.8433668	259	18.9255014	199	24.6733636	268	20.3047084	90	14.9258268	301	24.0884118	93	11.0303459	616	27.0330194
39	2.34919107	24	1.72022334	15	1.82428424	15	1.11475438	18	2.92815699	14	1.09899489	12	1.39608992	53	2.28147481
22	2.79599411	15	2.26842639	15	3.84903928	20	3.13601232	13	4.46195351	13	2.15313284	8	1.96373088	25	2.27059487
38	4.30862193	33	4.45234277	19	4.34966596	50	6.99453728	11	3.36833745	32	4.72844859	10	2.18994497	39	3.1601338
34	2.7756596	31	3.01140275	17	2.8021006	41	4.12957481	26	5.73229792	43	4.57477401	22	3.46887284	51	2.97538752
23	2.89131209	20	2.99169277	21	5.33008265	22	3.41211775	10	3.39496463	27	4.42328377	11	2.67078072	22	1.97640475
111	16.181629	135	23.4181665	94	27.6678	154	27.6983676	56	22.0472997	145	27.5474349	78	21.9620196	281	29.2746461
94	9.16123605	76	8.81372859	30	5.90330182	110	13.2267486	49	12.897051	63	8.00167064	38	7.15300004	110	7.66134427
67	7.04428763	53	6.63067907	52	11.0385781	88	11.4150848	33	9.37010237	93	12.7426316	48	9.74724599	152	11.4206794
10	1.68425947	18	3.60745866	10	3.40060752	14	2.90918424	5	2.27429669	4	0.8779765	5	1.62651253	15	1.80545359
157	22.6026223	181	31.0068473	78	22.6725982	293	52.0428401	88	34.2144817	251	47.0919635	74	20.5763958	328	33.7457506
143	16.5936172	123	16.9836097	71	16.6345437	138	19.7568776	41	12.8486354	153	23.1371766	38	8.51661544	199	16.5022886
22	4.38681834	13	3.08453841	25	10.0650165	26	6.39638374	15	8.07767445	28	7.27610408	8	3.08102603	36	5.12997848
19	2.85376258	9	1.60852053	4	1.21303056	7	1.29716873	33	13.3858605	12	2.34887219	13	3.77125589	13	1.39538376
47	3.98704161	42	4.23957245	31	5.30960382	42	4.3957845	24	5.49834858	39	4.31153006	23	3.76841876	77	4.66798776
19	2.73534919	11	1.88439404	6	1.74404601	9	1.59858553	9	3.49920835	13	2.439026	9	2.50253463	26	2.67496803
13	2.94800448	5	1.34919478	8	3.66287659	8	2.23825193	3	1.83727497	7	2.06869626	2	0.87597799	10	1.62058144
24	3.29129597	13	2.12138215	12	3.32264893	19	3.21472251	11	4.07395755	14	2.50205951	10	2.64870815	43	4.21415229
113	89.1049816	98	91.9537569	2	3.18420522	71	69.0742349	1	2.12956872	1	1.02763158	2	3.04601437	3	1.69056109
138	28.5000763	241	59.2248323	50	20.8489628	254	64.7194542	35	19.5210466	94	25.2993109	41	16.3541962	178	26.2707827
42	4.38922076	40	4.97413979	18	3.79802792	33	4.25486972	27	7.62026397	24	3.2686113	30	6.05532978	59	4.40632188
220	25.8747929	197	27.5702236	170	40.3692459	142	20.6051955	96	30.4925365	177	27.1294738	86	19.5357939	312	26.2237544
185	12.5610819	214	17.2897595	110	15.0797977	229	19.183374	82	15.0361721	236	20.8824391	55	7.21267591	303	14.7022573
33	13.0109044	23	10.7904919	11	8.75656436	25	12.1609569	8	8.51827488	15	7.70723687	6	4.56902156	20	5.63520364
107	6.0071921	98	6.54686942	88	9.97511539	73	5.05643928	79	11.9779626	73	5.3410237	37	4.01206424	177	7.1014508
111	7.22556792	99	7.66838774	74	9.7258651	48	3.85500051	65	11.4269541	83	7.04110796	72	9.05232039	225	10.4668886
89	7.24864157	90	8.72225921	119	19.5686603	51	5.12472999	84	18.4762582	68	7.21754389	79	12.4271666	191	11.1169604
38	5.61037579	19	3.3379653	23	6.85620358	27	4.91820144	54	21.5312991	38	7.31148939	21	5.98833464	68	7.17469331
0	0	1	0.91745245	1	1.55672255	0	0	1	2.08224497	1	1.00479533	1	1.48916258	1	0.55099769
85	6.56823681	68	6.25257126	45	7.02085338	80	7.62700546	36	7.51277695	68	6.8478256	32	4.77593345	77	4.25213139
17	4.0124331	16	4.49364465	1	0.47654772	11	3.20321258	4	2.54968772	10	3.07590406	2	0.91173219	3	0.50601829
22	2.25830293	22	2.6872128	12	2.48707153	12	1.51975982	23	6.37610516	16	2.14039241	9	1.78435162	34	2.49416114
61	3.51568181	39	2.67463297	46	5.35284997	68	4.83529341	64	9.96157062	74	5.5580871	53	5.89975541	84	3.45975293
13	3.110653	3	0.85417987	2	0.96624158	4	1.18087085	10	6.46213956	9	2.80649729	1	0.46215391	3	0.51299785
9	2.18364829	12	3.46450575	1	0.48987773	5	1.49673315	8	5.24201531	2	0.63238867	4	1.87447038	13	2.25408146
8	2.57005519	8	3.05817483	4	2.59453759	7	2.77449979	9	7.80841864	9	3.76798247	1	0.62048441	21	4.82122978
112	4.2192437	113	5.06541336	44	3.34669995	100	4.64783584	51	5.18865603	66	3.24021945	29	2.11005122	105	2.82677967
60	4.70982964	44	4.10985487	24	3.80375646	49	4.74552452	26	5.51182492	55	5.62639916	26	3.94190095	88	4.93654038
736	354.667616	1268	727.081067	471	458.260201	1642	976.227567	312	406.037769	719	451.529899	444	413.242617	1635	563.050763
79	7.57172336	53	6.04454169	26	5.0313961	77	9.10526449	33	8.54180602	65	8.11885726	29	5.36838997	106	7.26038391
67	30.9948656	60	33.0282882	14	13.0764694	24	13.6981018	10	12.4934698	11	6.63164915	33	29.4854191	54	17.8523251

gsyne_997	Synechococcus_assembled_mapped	conserved hypothetical protein	GO:0008150,GO:0003674,G(	PF04087.9	867235	868366	-1	156 fig|1129.58.peg.989
gsyne_998	Synechococcus_assembled_mapped	conserved hypothetical protein	GO:0008150,GO:0003674,G(	UniRef100_B	868414	869269	-1	156 fig|1129.58.peg.990
gsyne_999	Synechococcus_assembled_mapped	sodium/hydrogen exchanger family protein		PF00999.16	869281	870616	-1	145 fig|1129.58.peg.991

hypothetical protein	atggccgaacccMAEPTSLASLEAGFEREARLDEPFVVLTVAAGLIATLGLLADSAAVVIGAMLIAPWILPLRSASFAIIDGRLNLAGRALLTLAVGVTITIALSAGLGWLA	gsyne_997	0.033427729	1.39711347	0.16484817	1.24543471	0.7304255	-1.0613432	0.42177213	-1.1217878	0.00143836
hypothetical protein	atgcctctccgtaMPSPYATARIALATRHGKERALALPFRWGLGAELALCPADTDQLGTFSGEIPRLADAFSTCKAARLGIEASGLQLGLASEASFGPHPAMPMLAVGT	gsyne_998	0.267613382	-1.4065184	0.59551462	-1.2126375	1.6734E-07	3.00751073	0.63369216	1.15988362	9.5026E-26
Na+/H+ antiporter	atgcttccccctttgMLPPLALIAEISPHQLEVAETLLQVGRFLVIFLAARIAEVMVRLQLPTILGELVAGVLIGVSGLHLIVPPDTQAQISDALLSLLGSLAEIRPEEVAEIYNE	gsyne_999	0.054317348	-1.3630088	0.90637538	-1.0149109	0.90839876	1.02987199	0.0491942	1.34298367	0.01038569

Gene	Nitrogen	Phosphate	Zinc	Viral 30min	Viral 5hr	Viral 12hr
YefM protein (antitoxin to YoeB)	-1.6	-1.4	-1.3	-1.2	-1.1	-1.2
RelE/StbE replicon stabilization toxin	2.2	1.5	2.1	-1.0	-2.0	-1.6
Death on curing protein, Doc toxin	1.8	1.2	2.2	-1.8	1.3	-1.3
VapC toxin protein	1.4	-1.2	1.7	-1.0	1.4	-1.1
RelB/StbD replicon stabilization protein (antitoxin to RelE/StbE)	-1.0	-1.0	-2.8	1.0	-1.0	-2.1
RelE/StbE replicon stabilization toxin	2.3	3.1	10.6	2.5	-1.3	1.7
Death on curing protein, Doc toxin	-1.5	-1.3	1.1	-1.4	-1.4	-1.3
Prevent host death protein, Phd antitoxin	40.4	24.4	191.0	1.0	1.0	1.0

-1.4828169	0.02988919	-1.3218337		58	8.7701894	34	6.49824576	93	11.5511884	185	17.9154821	86	14.7892566	119	14.3129862	339	80.0321341	2843	193.610629		0.4349732	1.24171955	0.65472971	1.15698159
4.23011921	2.7287E-21	3.6470204		14	2.80030609	9	2.27539194	15	2.46451502	20	2.56202437	17	3.86717036	17	2.7047598	263	82.1328586	2311	208.184682		0.19923997	-2.1664609	0.91635801	1.09894756
1.40372459	0.76258957	1.04522834		53	6.78950618	56	9.06747948	67	7.05017443	106	8.69648947	78	11.3638066	117	11.9220378	410	82.0030292	3982	229.739108		0.18013844	-1.5192508	0.14731188	-1.5913801

0.04306582	1.77833302	0.80701492	-1.0732405	0.22605998	1.43215352	0.14681343	1.53704521
0.62219669	-1.1987491	0.16417487	2.38082695	0.42567742	1.80726799	0.54720613	-1.3173624
0.03487772	-2.0859865	0.91127342	-1.0474769	0.46814851	-1.3730364	0.57726501	-1.3108035

58	5.33780693	36	3.94236862	36	6.68936482	47	5.33662786	30	7.45631488	44	5.27717439	33	5.86579956	115	7.56342981
14	1.70435239	9	1.30374822	1	0.2457983	7	1.05138939	8	2.63020417	9	1.42786704	1	0.23513093	18	1.56599343
53	4.13230222	57	5.28823715	17	2.67616349	38	3.65539233	13	2.73733328	37	3.75951509	15	2.25884212	28	1.56012829