PREDICTED LIGHT-REGULATED MECHANISMS IN FRESHWATER *MICROBACTERIACEAE*

by

Priscilla Hempel

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MICROBACTERIACEAE

by

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ABSTRACT

Light is an environmental cue and the most abundant source of energy on Earth. Many organisms in surface environments use and rely on light for energy, orientation with respect to time of day, location, and regulation of physiological processes. This includes microbes, which are the most abundant organisms on Earth. Microbes can sense and use light in a wide variety of ways. One way that microbes use light, is as a source of information and multiple light-sensing proteins that regulate physiological processes have been identified. However, the conversion of light to information and the subsequent cellular response(s) has only been characterized in a few species. Moreover, little is known about how bacteria use light as information that then enhances growth. While the use of light as a source of energy in photoautotrophs and photoheterotrophs has been highly characterized, the biological pathways involved in light-enhanced growth of bacteria lacking identifiable photosystems and functional rhodopsins had not been characterized. Sequence analyses, including genomic and transcriptomic, provide a comprehensive approach to the prediction of which metabolic processes are regulated by light. Insight into the bacterial use of light as a source of information to enhance growth expands our knowledge of bacterial sensing and provides insight into bacterial metabolism for future experiments.

Identifying genes and biological functions present in bacterial species with light-enhanced growth, yet lacking identifiable photosystems and functional rhodopsins, is crucial for identifying potential light-capturing systems and predicting which proteins may be involved in the cellular response to light. Chapter 2 presents

the genome sequences and annotations of three Actinobacteria species within the *Microbacteriaceae* family: *Aurantimicrobium photophilum* strain MWH-Mo1, *Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3 as well as the genome comparison of these three species and *Rhodoluna lacicola* strain MWH-Ta8. Previously, light-enhanced growth was observed in the two *Aurantimicrobium* species and *R. lacicola*, while *Microbacterium* sp. strain 10M-3C3 does not have light enhanced growth.

Chapter 3 presents a pangenome analysis of 27 *Microbacteriaceae,* including *R. lacicola*, *A. photophilum*, *Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3. This was done to identify trends in the genetic differences between *Microbacteriaceae* isolated from different environments. Multiple predicted genes were found to be enriched in marine *Microbacteriaceae* and a few predicted genes were found to be enriched in terrestrial (freshwater and soil) *Microbacteriaceae*. These results contribute to our understanding of how *Microbacteriaceae* are specialized for their environment. Additionally, from the pangenome enrichment analysis, I was able to identify genes that are good candidates for further analysis to understand the light-enhanced growth phenotype in freshwater *Microbacteriaceae*.

Lastly, the transcriptomes of two *Microbacteriaceae* with light-enhanced growth, *R. lacicola* and *A. photophilum*, are analyzed in Chapter 4. This work shows that although *R. lacicola* and *A. photophilum* have the same light-enhanced growth phenotype, which genes are light-regulated and their light-regulated expression patterns differed greatly. These results indicate that different mechanism(s) may be responsible for the increased growth rates in the light. Additionally, it suggests that *R.*

lacicola and *A. photophilum* may have different signal transduction pathways and/or regulatory proteins that respond to light and darkness. The phylogenetic profiling and expression analyses within this work identified predicted regulatory proteins that are good candidates for future experiments testing the effects of light on physiological and biochemical properties of freshwater Actinobacteria, and identifying the cellular activities that correspond to light-induced transcriptional changes in these organisms.

Chapter 1

INTRODUCTION

1.1 General Overview of Problem and Significance

Light is Earth's most vital energy resource. Sunlight provides warmth, fuels photosynthesis, and allows organisms to find their way in the daytime. Light sensing is a common function in many living organisms, even bacteria (Gomelsky and Hoff, 2011). In fact, Earth's most abundant organisms, bacteria, (Morris et al., 2002) have evolved multiple ways to sense light (van der Horst and Hellingwerf, 2004; Montgomery, 2007; Purcell and Crosson, 2008), which is Earth's most abundant energy resource (Energy On a Sphere, n.d.). Initially, only phototrophic bacteria that use sunlight as a source of energy were thought to be sensitive to light. However, the discovery of light sensors in non-phototrophic heterotrophic bacteria has changed this view (Davis et al., 1999; Gomelsky and Klug, 2002; Losi et al., 2002; Crosson et al., 2003; Memmi et al., 2008). Still, light's role in heterotrophic nutrient cycling within surface environments is not widely characterized.

Actinobacteria are a highly abundant phylum in surface freshwater environments, where they are regularly exposed to light. Actinobacteria are of great interest in studying surface environments, because they play an important role in heterotrophic carbon cycling, some are known to sense light, and have streamlined genomes. Additionally, their abundance relative to photosynthetic microbes may be useful in assessing freshwater health (Ghai et al., 2014). Together, this makes Actinobacteria top candidates for studying light's role in mediating heterotrophic

biological processes. To understand how anthropogenic environmental changes affect non-phototrophic heterotrophic bacteria and freshwater health, we must first identify how bacterial biological processes are regulated by their ecosystem's natural resources, especially light.

Light's effect on heterotrophic growth has not been widely studied, although light is known to affect multiple biological processes in non-phototrophic heterotrophic bacteria (Burchard and Dworkin, 1966; Bhaya, 2004; Sancar, 2008; Ziegelhoffer and Donohue, 2009). Next generation sequencing has allowed for identification of genes predicted to encode photosensory proteins in many species previously thought to be non-photo-sensitive (van der Horst et al., 2007). Here we investigate how light regulates non-phototrophic heterotrophic bacterial transcription. Using whole genome and transcriptome sequencing data, our goal is to identify putative light-regulated genes and biological processes by characterizing their response to light/dark cycling over time. Further understanding of how freshwater non-phototrophic heterotrophic bacteria use and respond to light, can help define their roles in freshwater nutrient cycling and maintaining healthy ecosystems.

1.2 Bacteria Sense and Respond to Light

Bacteria have evolved many different ways to sense and respond to light. Light-sensitive compounds are found in photosynthetic, photoheterotrophic, and non-phototrophic heterotrophs (Eelderink-Chen et al., 2021). While photosynthetic microbes capture light energy to convert it to chemical energy, heterotrophic microbes consume organic carbon from their environment as a source of energy. Heterotrophic bacteria that sense light can be categorized as phototrophic or non-phototrophic. Photoheterotrophs generate chemical energy using light via bacteriochlorophyll-

(Kolber et al., 2000) or rhodopsin-based (Béjà et al., 2000) photosystems. The (bacterio)chlorophyll-based photosystems absorb light energy and transfer this energy as electrons to the electron transport chain and/or cellular electron carriers such as ferredoxin (Singh et al., 2020). Rhodopsins are proteins that have a covalently bound chromophore, retinal, attached. When retinal absorbs a photon, this induces a conformational change in the rhodopsin protein which results in ion transport or signal transduction (Spudich et al., 2000). Non-phototrophic bacteria can contain multiple different light-sensing proteins that control gene expression (van der Horst et al., 2007; Elías-Arnanz et al., 2011). These include phytochromes (Auldridge and Forest, 2011), vitamin B_{12}-dependent regulators (Padmanabhan et al., 2017), heliorhodopsin (Pushkarev et al., 2018), phototropins (Losi, 2004), xanthopsins (Kort et al., 1996), BLUF (blue-light sensing using FAD) domain containing proteins (Park and Tame, 2017), photolyases, and cryptochromes (Selby and Sancar, 2006). These light-sensing proteins can regulate motility (Bhaya, 2004), pigment production (Burchard and Dworkin, 1966), and stress responses (Ziegelhoffer and Donohue, 2009). In both photosynthetic and heterotrophic bacteria, light can enable the formation of reactive oxygen species that cause photo-oxidative cell damage (Ziegelhoffer and Donohue, 2009). Conversely, light can initiate DNA repair of UV damage (Sancar, 2008). These many light-sensing proteins and responses demonstrate that light affects multiple biological processes in a diverse distribution of bacteria. An increase in bacterial genomic data has revealed that many species likely contain light-sensing proteins and thus many more species may sense light than previously thought. Transcriptomic and genomic data continues to reveal uncharacterized light responses and light-sensing capabilities in a highly diverse and global distribution of nonphototrophic bacteria.

This influx of information can provide insight into biogeochemical processes and the ecological niches of these bacteria.

1.3 *Microbacteriaceae* in Freshwater

Freshwater is a finite natural resource that is crucial for the survival of many organisms. Freshwater ecosystems, include lakes, ponds, rivers, reservoirs, glaciers, groundwater, and wetlands. Most of the freshwater on Earth's surface and groundwater is unsuitable for human consumption without treatment. Additionally, freshwater is prone to nutrient pollution resulting from human activity (Gleick, 1993). Anthropogenic fluxes of nutrients into freshwater, such as nitrogen and phosphorus, can cause harmful algal blooms (Paerl et al., 2011, 2016; Schindler et al., 2016). These harmful algal blooms generate a large excess of organic material which reduces light penetration and ultimately leads to depleted dissolved oxygen levels, in a process called eutrophication(Glibert, 2017). This imbalance in nutrient cycling further reduces freshwater availability.

Microbes play a key role in biogeochemical cycling in illuminated freshwater (Lindeman, 1942; Cotner and Biddanda, 2002; Pernthaler, 2005; Linz et al., 2018). In these environments, heterotrophic bacteria have an important role in the carbon cycle, in that they consume organic carbon, store carbon as biomass, and release CO_2 into the atmosphere (Berggren et al., 2010; Benner, 2011; Pernthaler, 2013). Phytoplankton and inflow of organic matter from terrestrial sources are likely sources of carbohydrates for freshwater heterotrophic bacteria (Pérez and Sommaruga, 2006; Eckert et al., 2012). Actinobacteria are a highly abundant phylum of heterotrophs in freshwater (Glöckner et al., 2000; Zwart et al., 2002; Warnecke et al., 2005; Allgaier and Grossart, 2006; Buck et al., 2009; Newton et al., 2011) and have the capacity for

efficient uptake of nutrients such as phosphorus, nitrogen, and carbon, priming them for success in healthy or oligotrophic conditions. Metagenomic analyses have shown that Actinobacteria have an inverse proportion in abundance to primary producing bacteria in relatively healthy freshwater (Ghai et al., 2014). Together, this suggests that heterotrophic Actinobacteria have a critical role in freshwater nutrient cycling and may contribute to maintaining oligotrophic freshwater.

In surface freshwater, microbes are regularly exposed to sunlight. Light-sensing proteins that regulate gene expression are common in many types of microbes, including heterotrophs (Eelderink-Chen et al., 2021). Metatranscriptomic analyses of freshwater bacterial communities show that heterotrophic bacteria have differential gene expression of complex regulatory networks, including those of energy uptake, in response to light (Vila-Costa et al., 2013; Linz et al., 2018). Many Actinobacteria species in the *Microbacteriaceae* family are highly abundant in surface freshwater and potentially photoheterotrophs, since many encode actinorhodopsins and/or heliorhodopsins which can harvest light energy for ion pumping (Ghai et al., 2014; Dwulit-Smith et al., 2018; Pushkarev et al., 2018). Currently, *Microbacteriaceae* are known to specifically mediate fluxes of vitamins, amino acids, reduced sulfur, and organic carbon (Garcia et al., 2018; Linz et al., 2018). Additionally, *Microbacteriaceae* in wetlands have higher abundances at sites with higher soil organic carbon levels (Yang et al., 2020). As highly abundant photoheterotrophs, *Microbacteriaceae* species likely have a strong metabolic link to organic carbon availability and light availability in freshwater ecosystems. This points to light being an important input in heterotrophic carbon consumption dynamics.

1.4 Light-Enhanced Growth of Three *Microbacteriaceae* Species

Prior work identified three *Microbacteriaceae* species that grow faster in light than in dark: *Rhodoluna lacicola*, *Aurantimicrobium* sp. strain MWH-Uga1, and *Aurantimicrobium photophilum* (previously called *Aurantimicrobium* sp. strain MWH-Mo1). *Rhodoluna lacicola* strain MWH-Ta8 was originally isolated from the hypertrophic Meiland Bay, Lake Taihu, China (Sharma et al., 2009; Hahn et al., 2014), *Aurantimicrobium* sp. strain MWH-Uga1 was originally isolated from a freshwater pond in Uganda (Sharma et al., 2009), and *Aurantimicrobium photophilum* strain MW-Mo1 was originally isolated from Lake Mondsee, Austria (Boucher et al., 2006). Grown in 0.3% nutrient broth, soytone, and yeast extract (NSY) medium in constant white light (40 mol photons m^{-2} s^{-1}) vs. constant darkness at 28°C, all three species grow faster and reach higher cell densities in the light (**Figure 1.1**) (Maresca et al., 2019). A fourth *Microbacteriaceae*, *Microbacterium* sp. strain 10M-3C3 originally isolated from the oligotrophic freshwater Lake Matano, Indonesia (Hempel et al., 2019) does not grow faster in light compared to in dark, demonstrating that light-enhanced growth is not a phenotype of all *Microbacteriaceae*.

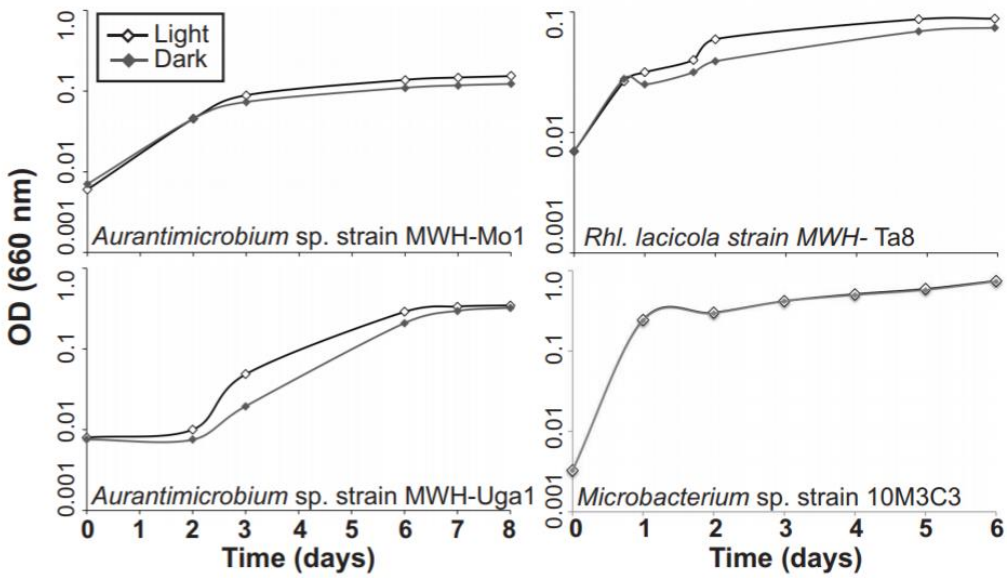

Figure 1.1 Light enhances growth of some *Actinobacteria*. Freshwater *Microbacteriaceae s*trains were grown in constant white light and constant dark. For each strain, growth at $OD_{660\ nm}$ was measured with four replicates, whose averages are plotted. In all cases, error bars are plotted but are smaller than the symbols. *Aurantimicrobium photophilum* strain MW-Mo1, *Aurantimicrobium* sp. strain MWH-Uga1, and *Rhodoluna lacicola* strain MWH-Ta8 all grow slightly faster in the light than in the dark. *Microbacterium* sp. strain 10M-3C3, which branches separately from the others within the *Microbacteriaceae*, grows at identical rates in light and darkness. Figure reproduced from (Maresca et al., 2019) with permission from the Journal of Bacteriology.

Multiple possible explanations were explored via laboratory experiments, however the light-sensing mechanism and the regulatory response to light in these species remained unclear. Scanning electron microscopy (SEM) images confirmed that cell size and shape are similar in light vs. dark conditions. Additionally, light-enhanced growth was measured regardless of the liquid medium's age, thus confirming that light degrading the organic carbon and making it more bioavailable is not the cause of the observed phenotype. Polymerase chain reaction (PCR) indicated *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium* sp. strain MWH-Uga1

encode actinorhodopsins (Sharma et al., 2009), which could enhance their growth rate in the light, however, the actinorhodopsin in *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium* sp. strain MWH-Uga1 are nonfunctional in the absence of exogenous retinal (Keffer et al., 2015), the necessary cofactor for rhodopsin function. Since NSY medium does not include retinal, actinorhodopsin cannot be responsible for *R.lacicola* strain MWH-Ta8 and *Aurantimicrobium* sp. strain MWH-Uga1's light-enhanced growth. Although rhodopsin may contribute to enhanced growth in the light in some actinobacterial species and under some conditions, it is not responsible for the observed growth rate phenotype in these species.

To determine what the light sensor might be, attention was turned to the carotenoids that each of the three species produce. Carotenoids were ruled out as the cause of the light-enhanced growth due to a white mutant of *Rhodoluna lacicola*. This white mutant, *Rhodoluna lacicola* strain TaW, has a frameshift mutation in the *crtB* gene which encodes phytoene synthase, the first step in carotenoid biosynthesis (Maresca et al., 2019). Strain TaW still grows faster in light than in dark, however wild-type *Rhodoluna lacicola* strain MWH-Ta8 grows faster than strain TaW under all conditions. Therefore, the carotenoids likely contribute to fitness under both dark and light conditions but are not related to the light-enhanced growth phenotype.

Next, to identify the specific wavelengths of light that stimulate growth in these *Microbacteriaceae*, *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium photophilum* strain MW-Mo1 were grown in constant illumination by light-emitting diodes (LEDs) emitting light at 375 nm, 425 nm, 525 nm, 650 nm, or in constant dark. Neither red (650 nm) nor green (525 nm) light enhanced growth in either strain (**Figure 1.2**) (Maresca et al., 2019). However, both strains grew significantly faster

when illuminated with near-UV light (375 nm). Blue light (425 nm) may also have enhanced growth, though to a smaller degree (**Figure 1.2**). In both *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium photophilum* strain MW-Mo1, growth in near-UV light was 15% faster than growth in the dark. If a rhodopsin-based photosystem were responsible, green light should have stimulated growth since the absorption maximum for the actinorhodopsin from *Rhodoluna lacicola* strain MWH-Ta8 is 527 nm (Keffer et al., 2015). Thus, the light-enhanced growth phenotype is not mediated by rhodopsin-based photosystems but rather by a pigment or protein that absorbs blue or near-UV light.

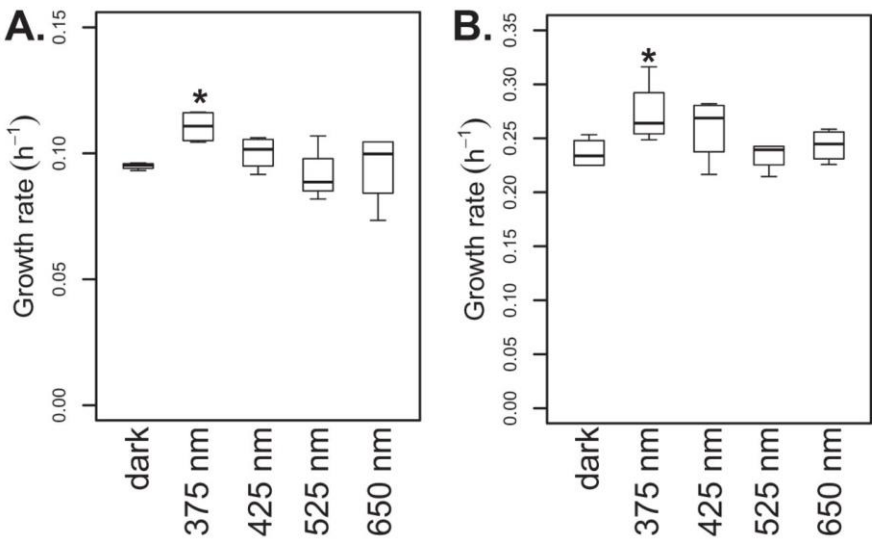

Figure 1.2 Near-UV light enhances growth of some Actinobacteria. *Rhodoluna lacicola* strain MWH-Ta8 (A) and *Aurantimicrobium photophilum* strain MWH-Mo1 (B) were grown in constant darkness or with LEDs of the wavelength specified. Growth was monitored by measuring the OD660, and growth rates were calculated from two time points within the exponential-growth phase (in both cases, within the first 24 h of growth). Boxes indicate the range of growth rates between the 25th and 75th quartiles, and the bold line indicates the median growth rate. Asterisks indicate that the mean of the growth rate in light of this wavelength is significantly different from the mean growth rate in the dark, with a P value of <0.05, as calculated by a one-sided *t* test. All light intensities were ~3 μmol photons m^{-2} s^{-1}. Figure reproduced from (Maresca et al., 2019) with permission from the Journal of Bacteriology.

Increased growth in near-UV light combined with the lack of functional photosystem suggested that light regulates metabolic processes in these *Microbacteriaceae* species, however which metabolic processes are light-responsive and their transcriptional regulatory response to light was uncharacterized. *Aurantimicrobium photophilum* strain MW-Mo1, *Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3 did not have annotated genomes, thereby making it difficult to identify genes that encode photosensory proteins or pigments. Additionally, shared predicted metabolic processes that could be related to the light-enhanced growth phenotype remained unclear. Therefore, to explore this possibility we took a bioinformatics approach to analyze the genetics of these species. DNA and RNA sequencing generates large amounts of data that provide comprehensive insight into an organism's biological functions and when they are up or down regulated. In using bioinformatics techniques, our goal here is to identify potential light sensors, identify genes that could be related to the observed phenotype, and characterize *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium photophilum* strain MWH-Mo1's transcriptional responses to light/dark cycling. Understanding the transcriptional response to light in these *Microbacteriaceae* may contribute to our understanding of light's effect on carbon cycling in freshwater. Characterizing light's effect on the dynamics of heterotrophic carbon consumption can provide context for changes in freshwater ecosystems that occur after an anthropogenic increase of carbon (Cole et al., 2007; Holmes et al., 2008).

1.5 Next Generation Sequencing

Genome sequencing is a crucial step to understanding genetic diversity. While the genome sequence and annotation of *Rhodoluna lacicola* strain MWH-Ta8 was

previously published, it does not encode a previously identified pathway that explains the observed near-UV light enhanced growth. This suggested that *Rhodoluna lacicola* strain MWH-Ta8 absorbs light energy and may use it for information via a currently unknown pathway. By sequencing and annotating the genomes of two other *Microbacteriaceae* with a similar light-enhanced growth phenotype, and another *Microbacteriaceae* species that does not grow faster in light vs. dark, our goal is to compare these genomes and identify homologous genes. In doing so, we will be able to explore questions about the light-enhanced growth phenotype, including which currently known light sensor(s) could be involved, which predicted genes, and which predicted biological processes are shared by phenotypically similar *Microbacteriaceae* species. Sequencing these *Microbacteriaceae* genomes can improve our understanding of how *Actinobacteria* relate light to growth thus affecting environmental nutrient cycling as well as help identify how widespread those abilities are among other species.

Profiling the transcriptional activity of thousands of genes generates a comprehensive picture of which cellular functions may be associated with environmental conditions. High-throughput transcriptome sequencing captures a global snapshot of RNA transcripts and is useful for identifying differentially expressed genes between conditions and over time. Transcriptomic analyses have identified light-regulated genes and mechanisms in a wide variety of microbes. For example, transcriptomic analyses of the radioresistant bacterium *Deinococcus gobiensis*, showed that genes that encode regulatory proteins, DNA photolyase, and a DNA helicase were upregulated upon exposure to UV irradiation (Yuan et al., 2012). Metatranscriptomic analyses of freshwater bacterial communities has shown that

freshwater microbes' gene expression of photosynthesis, sugar transport and carbon fixation follows a diel cycle (Linz et al., 2020). In doing high-throughput transcriptome studies of two *Microbacteriaceae* isolates with light-enhanced growth, we can explore questions about how *Actinobacteria* use light in previously uncharacterized ways, including which metabolic processes light regulates transcription of, when transcription of certain processes and genes is upregulated/downregulated, and which genes are likely co-regulated in response to light.

1.6 Dissertation Work

Based on previous studies, I hypothesize that certain heterotrophic freshwater *Microbacteriaceae* convert light to information used to change transcription regulation, which results in increased growth. My studies had three goals in analyzing -omics data to better understand the effect that light has on heterotrophic bacterial species from freshwater environments. The first aim was to do genomic comparisons of four *Microbacteriacea* to identify genes of interest that may be related to the light-enhanced growth phenotype. The second aim was to identify co-occurrence of genes of interest in *Microbacteriacea* isolated from various environments. The third aim was to investigate the transcriptomic response to light/dark cycling for *Rhodoluna lacicola* and *Aurantimicrobium photophilum*. Each of these goals were in effort to predict which genes and pathways are related to light-enhanced growth phenotype and that are likely regulated by light/dark-cycling to characterize how some *Actinobacteria* species respond to changing light regimes. Because *Actinobacteria* are ubiquitous in surface

freshwater environments, understanding how light affects their carbon metabolism will contribute to our broader understanding of carbon cycling in freshwater environments.

Chapter 2

MICROBACTERIACEAE WITH LIGHT-ENHANCED GROWTH HAVE SIMILAR GENOMES

Some of the work in this chapter is published in the *Journal of Bacteriology* and *Microbiology Resource Announcements*.

Light Modulates the Physiology of Nonphototrophic *Actinobacteria*

Maresca JA, Keffer JL, Hempel PP, Polson SW, Shevchenko O, Bhavsar J, Powell D, Miller KJ, Singh A, Hahn MW. 2019. J Bacteriology 201:e00740-18. https://doi.org/10.1128/JB.00740-18.

Complete Genome Sequence of *Microbacterium* sp. Strain 10M-3C3, Isolated from an Extremely Phosphorus-Poor Lake

Hempel P, Keffer JL, Shevchenko O, Henny C, Polson SW, Maresca JA. 2019. *Microbiology Resource Announcements* 8(4):e01649-18. https://doi-org.udel.idm.oclc.org/10.1128/MRA.01649-18

2.1 Abstract

To predict which genes could be related to the light-enhanced growth phenotype observed in *Rhodoluna lacicola* strain MWH-Ta8, *Aurantimicrobium photophilum* strain MWH-Mo1, and *Aurantimicrobium* sp. strain MWH-Uga1, the genomes of the two *Aurantimicrobium* strains and a *Microbacterium* strain that does not have the light-enhanced growth phenotype, all originally isolated from surface freshwater, were sequenced, annotated, and compared to the genome of *R. lacicola*. The two *Aurantimicrobium* strains and *R. lacicola* share 48%-62% of their genes. 71

of those shared genes are not shared with *Microbacterium* sp. strain 10M-3C3, which does not grow faster in constant light vs. constant dark. Some of the 71 genes encode proteins related to transcriptional regulation, transmembrane transport, carbohydrate metabolism, DNA uptake, and biofilm dispersal. I also identified genes that are unique to *Rhodoluna lacicola* strain MWH-Ta8, *Aurantimicrobium photophilum*, and *Aurantimicrobium* sp. strain MWH-Uga1 in comparison to each other. These unique genes include 10 that encode transcription factors in *R. lacicola* and 10 that encode transcription factors in *A. photophilum*. This work determined which genes and Gene Ontology terms are shared among and unique to *Microbacteriaceae* species with the light-enhanced growth phenotype, which could be related to the enhanced growth previously observed. Here I explore the possibilities of a shared vs. different light-mediated signal cascade in two closely related freshwater Actinobacteria, *R. lacicola* and *A. photophilum*. This work resulted in publishing three genomes which can be used to understand genetic diversity of *Microbacteriaceae*.

2.2 Introduction

Genes that encode light sensing proteins are widespread in aquatic and soil surface bacterial communities, as shown in metagenomic studies (Béjà et al., 2000; Rusch et al., 2007; Fuhrman et al., 2008; Singh et al., 2009; Finkel et al., 2013). Light-sensing proteins have a wide range of functions that includes light-drive ion pumps, light-gated ion channels, photoactivated enzymes, photosensory receptors, and light-activated transcriptional regulators (Kandori, 2015). To better understand light sensing mechanisms' subsequent effects in microbes, freshwater Actinobacteria containing light sensors have been the focus of study (Sharma et al., 2008; Ghai et al., 2014; Chazan et al., 2022). Freshwater Actinobacteria are good candidates for investigation

into light activated and/or regulated mechanisms of metabolism and growth, because Actinobacteria can be cultured in laboratory conditions, encode light sensing proteins, and are a highly abundant component of freshwater microbial communities (Glöckner et al., 2000; Zwart et al., 2002; Hahn et al., 2003, 2004; Warnecke et al., 2005; Allgaier and Grossart, 2006; Buck et al., 2009; Sharma et al., 2009; Newton et al., 2011; Keffer et al., 2015; Neuenschwander et al., 2015). It is estimated that in some environments up to 95% of freshwater microbes may contain genes encoding rhodopsins (Finkel et al., 2013), which are a family of light-sensing proteins. Freshwater Actinobacteria are also known to have small genomes (Ghai et al., 2014). The genome reduction observed in freshwater Actinobacteria may have led to auxotrophy of various compounds including amino acids, vitamins, and reduced sulfur resulting in dependencies on neighboring organisms for these and other compounds (Neuenschwander et al., 2015). Additionally, freshwater Actinobacteria have low GC content, less than 55%, compared to the typical high GC content of Actinobacteria which is generally much greater than 55% (Ventura et al., 2007; Ghai et al., 2012; Doroghazi and Metcalf, 2013; Neuenschwander et al., 2018). The ubiquity and high abundance of Actinobacteria in freshwater environments is thought to be due to their small cell size and small genomes, which encode fewer metabolic functions than average (Mondav et al., 2020). Therefore, freshwater Actinobacteria genomes are likely to encode unique mechanisms that allow them to efficiently compete with other surface freshwater bacteria for resources.

Previous work showed that *R. lacicola* and *A. photophilum* lack functional actinorhodopsins, yet still grow faster in light (Keffer et al., 2015). Additionally, light-enhanced growth was specifically observed in blue light compared to other

wavelengths of light and dark (Maresca et al., 2019). Blue light sensors are found in organisms across all kingdoms of life (Losi and Gärtner, 2012), however blue light-enhanced growth has not been characterized in any other freshwater Actinobacteria. Blue light sensors in Actinobacteria species with light-enhanced growth have not been exhaustively studied, though we do predict that cryptochrome proteins could be the blue-light sensors related to blue light-enhanced growth (Maresca et al., 2019). Additionally, which genes and proteins may be involved in the relationship of blue light reception to enhanced growth is not understood. I hypothesize that closely related Actinobacterial species with light-enhanced growth share a blue light sensor and mechanism(s) that relay blue light sensing to increased growth. Therefore, I annotated the genomes of *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1, both of which have light-enhanced growth, as well as the genome of *Microbacterium* sp. strain 10M-3C3 which does not have light enhanced growth. I then compared the genomes of three strains with light-enhanced growth, *R. lacicola, A. photophilum, Aurantimicrobium* sp. strain MWH-Uga1, and one strain without light-enhanced growth, *Microbacterium* sp. strain 10M-3C3.

A. photophilum and *Aurantimicrobium* sp. strain MWH-Uga1 were originally isolated from surface waters of Lake Mondsee in Austria and a freshwater pond in Uganda, respectively (Hahn et al., 2003, 2004). *Microbacterium* sp. strain 10M-3C3 was originally isolated from the extremely-phosphorus limited Lake Matano in Indonesia. Based on 16S rRNA sequences, *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 belong to the Luna2 subgroup of Actinobacteria and fall within the *Aurantimicrobium* genus (**Figure 2.1**). Because of their high similarity to *Aurantimicrobium minutum* (Nakai et al., 2016), these two strains are classified as

Aurantimicrobium species. Originally isolated as *Actinobacterium* sp. strains MWH-Mo1 and strain MWH-Uga1, *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 were given a genus designation, and strain MWH-Mo1 a species designation, in part due to this genome sequencing (Maresca et al., 2019; Hahn et al., 2021). Due to its 16S similarity to other *Microbacterium* species as compared to other *Microbacteriaceae*, isolate 10M-3C3 falls within the *Microbacterium* genus (**Figure 2.1**) (Hempel et al., 2019). All three species sequenced in this work belong to the *Microbacteriaceae* family.

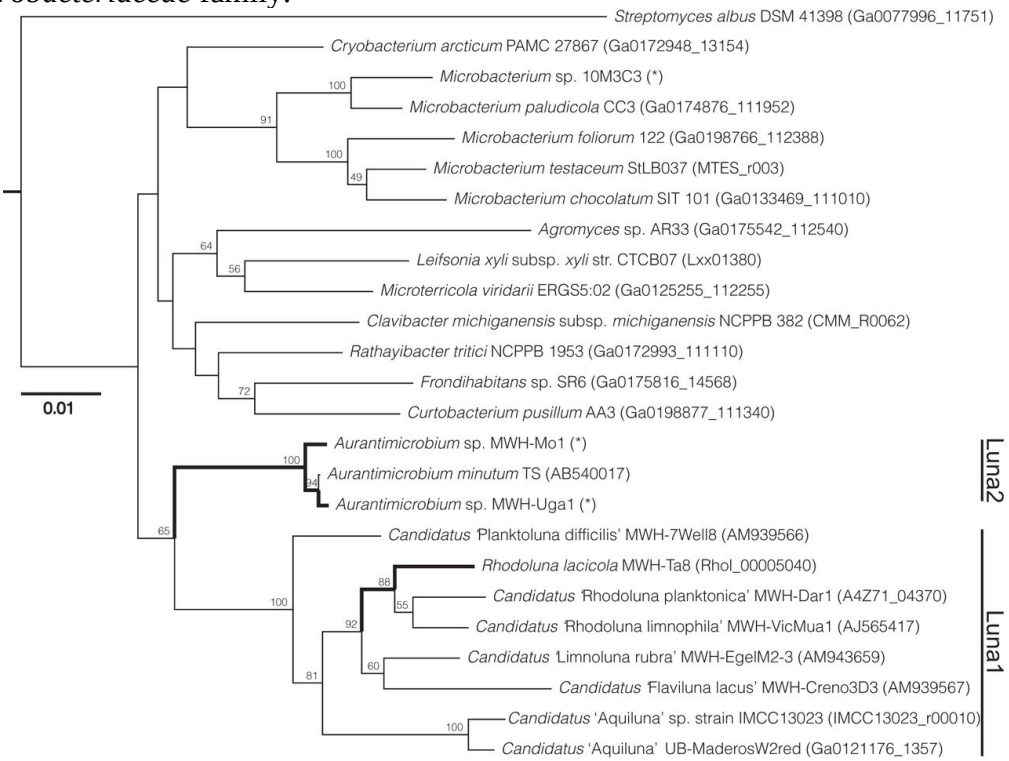

Figure 2.1 Phylogenetic Tree of 16S rRNA Gene Sequences. 16S rRNA gene sequences of the organisms described here (denoted with bold lines and asterisks) were compared with those of other sequenced actinobacterial genomes in a phylogenetic tree. All organisms in this tree except the outgroup, *Streptomyces albus*, belong to the family *Microbacteriaceae*. *R. lacicola* is a member of the Luna1 subgroup of *Actinobacteria*. The two *Aurantimicrobium* strains, closely related to *Aurantimicrobium minutum*, belong to the acIII subgroup; the phylogeny of freshwater *Actinobacteria* is described in reference (Newton et al., 2011). Figure reproduced from (Maresca et al., 2019) with permission from the Journal of Bacteriology.

Freshwater Actinobacteria have historically been difficult to isolate and grow in pure culture, making it difficult to study their biological mechanisms and understand how they respond to changes in their environment. Contributing complete genome sequences that belong to the *Microbacteriaceae* family is critical for understanding their current diversity and future systematics. Previous work showed that three species, *R. lacicola*, *A. photophilum,* and *Aurantimicrobium* sp. strain MWH-Uga1 grow faster in light than in dark, despite lacking functional actinorhodopsins. Here, I investigate the genomes of Actinobacteria with and without light-enhanced growth. Using whole genome sequencing and genome comparison analyses, I identify genes that are good candidates for further study because they may be related to the light-enhanced growth phenotype. I also explore the possibilities of shared vs. unique mechanisms that relay blue-light sensing to increased growth.

Because I hypothesize that closely related freshwater Actinobacteria species with blue light-enhanced growth share mechanism(s) that relay blue-light sensing to increase growth, I identified which genes are shared by the three Actinobacteria species with light-enhanced growth. I then combined this with previous transcriptome analyses from constant light vs. constant dark growth conditions to identify shared genes with significant differential expression. I also identified genes shared by and unique to these three species in comparison to *Microbacterium* sp. strain 10M-3C3, which does not have light-enhanced growth as well as genes that are unique to each of the three Actinobacteria species with blue-light enhanced growth in comparison to each other. Furthermore, I identified which predicted transcription factors and signal transduction proteins are in these categories of genes. Additionally, I annotated GO-slim terms to the predicted proteins of, *R. lacicola* and *A. photophilum* and show their

distribution in the shared and unique gene categories. These analyses identify genes and gene ontology functional characteristics that could be related to the light-enhanced growth phenotype and are good candidates for future expression analyses.

2.3 Materials and Methods

2.3.1 DNA Extraction, Library Preparation, and Sequencing

Cultures (500 ml) of *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 were grown in 0.3% NSY medium (Hahn et al., 2004) with shaking at room temperature (25°C) for 14 days. Cells were harvested by centrifugation, and DNA was extracted using the PowerSoil DNA isolation kit (catalog no. 12888-50; MoBio, Carlsbad, CA) following the manufacturer's instructions. DNA was stored at -20°C until processing. For *Microbacterium* sp. strain 10M-3C3, water was collected from Lake Matano at position 2°28′00″S and 121°17′00″E at a 10-m depth on 5 October 2013 and filtered through a 0.2-µm filter. The filtrate was inoculated into inorganic basal medium and acclimatized to increasing concentrations of nutrient broth-soytone-yeast (NSY) extract medium. Following acclimation, liquid cultures were transferred to 0.3% NSY agar plates, and single colonies were restreaked to isolation. Genomic DNA was extracted from cells grown in liquid NSY medium using the above methods for the *Aurantimicrobium* species. DNA extraction was done by Dr. Jessica L Keffer, University of Delaware.

The single-molecule real-time (SMRT) libraries for PacBio sequencing were prepared using the standard PacBio protocol for 20-kb libraries (Pacific Biosciences, 2016). DNA fragments larger than 10 kb were selected by BluePippin (Sage Science). The average fragment size of the library was 25 kb, as measured by a fragment

analyzer (Advanced Analytical Technologies, Inc.). Sequencing was performed in a single SMRT cell in a Pacific Biosciences RSII single-molecule sequencer using P6-C4 chemistry with a 6-h movie. Library preparation and sequencing was done by Dr. Olga Shevchenko, University of Delaware DNA Sequencing & Genotyping Center, Delaware Biotechnology Institute.

2.3.2 Genome Assembly

For both *Aurantimicrobium* genomes, the reads were initially assembled using Hierarchical Genome Assembly Process 3 (HGAP3) software from PacBio, with a seed read fragment length of 10 kb. The initial assembly of the *A. photophilum* genome resulted in two contigs, one linear (32,252 bp, 37X coverage) and one circular (1,787,627 bp, 500X coverage). The initial assembly of the *Aurantimicrobium* sp. strain MWH-Uga1 genome resulted in a single circular contig (1,639,476 bp, 850X coverage). For *Microbacterium* sp. strain 10M-3C3, reads were assembled using HGAP3 with 23-kb seed read fragment lengths. Reads of inserts were filtered by quality 0.8 and read length 1 kb using the PreAssembler filter version 1 protocol. Initial genome assemblies were done by Dr. Olga Shevchenko, University of Delaware DNA Sequencing & Genotyping Center, Delaware Biotechnology Institute.

To confirm that the small linear contig from the *A. photophilum* initial assembly was a segment of the genome, the two contigs were aligned using Gepard (version 1.40) (Krumsiek et al., 2007). The initial assembly of the *Aurantimicrobium* sp. strain MWH-Uga1 genome resulted in a single circular contig (1,639,476 bp, 850X coverage). To confirm circularity, the contig was aligned with itself using Gepard (version 1.40). The initial assembly of *Microbacterium* sp. strain 10M-3C3 resulted in

a single circular contig 3,387,846 bp long with 407X coverage. Again, to confirm circularity, the contig was aligned with itself using Gepard (version 1.40).

2.3.3 Genome Annotation

For both the *Aurantimicrobium* genomes and the *Microbacterium* genome, RAST (version 2.0) (Aziz et al., 2008; Overbeek et al., 2014) and PROKKA (version 1.11) (Seemann, 2014) were used to identify open reading frames (ORFs) and annotate the genome with default settings. Default PROKKA parameters were used; for RAST, the classic RAST defaults were used (annotation scheme, classic RAST; gene caller, RAST; FIGfam version, Release70; automatically fix errors, yes; backfill gaps, yes). These annotations were compared using BEACON, which compares start and stop sites and annotations generated by different annotation systems. Fifty comparisons between the PROKKA and RAST annotations were made by iterating the offset value from 1 to 50. Using these comparisons as a guide, entries that were not matched by BEACON were manually matched. This comparison led to a consensus annotation which contained elements from the RAST and PROKKA annotations. Because PROKKA did not annotate rRNAs, the three rRNA genes identified by RAST were manually added to the PROKKA annotations in both genomes. A custom biopython script was then used to number the predicted start sites, stop sites, and locus tag numbers of the annotation features for both genomes such that *dnaA* is the first feature. Scripts are available at (https://github.com/MarescaLab/contig_to_linear_genome)

2.3.4 Sequence Comparison

A fasta file containing the amino acid sequences of all predicted proteins in the genomes of *R. lacicola*, *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 was uploaded to the EFI-Enzyme Similarity Tool website (https://efi.igb.illinois.edu/efi-est/index.php). This tool calculates the similarities between all sequences and generates a sequence similarity network, which can be used to identify clusters of homologous proteins. In the sequence similarity network, nodes represent proteins and edges represent a sequence alignment score that falls above the lower limit (here set to 35). The sequence similarity network was visualized in Cytoscape using the yFiles organic layout. Nodes and edges in the network were counted and sorted to identify the number of ORFs shared by all three genomes, shared by two genomes, or unique to one genome.

2.3.5 Gene Ontology Assignment

Gene Ontology (GO) slim terms were assigned to protein sequences of *R. lacicola* and *A. photophilum* to analyze predicted functions according to the GO database, which is the key functional classification of the National Center for Biotechnology Information (NCBI) (Gene Ontology Consortium, 2004). For *R. lacicola* and *A. photophilum*, protein sequences from the originally published genome annotation and NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) annotation were assigned GO-slim terms with the Blast2GO (version 5.2.5) suite of tools (Götz et al., 2008), using BLASTP against the non-redundant protein database with an e-value cutoff $<1_e^{-3}$. The GO-slim function was applied to generate general GO-slim terms to obtain an overview of the predicted biological processes, cellular location, and molecular functions of proteins in each organism.

2.3.6 Data Availability

The *A. photophilum* and *Aurantimicrobium* sp. MWH-Uga1 genomes have been deposited in the DDBJ/ENA/GenBank database under the accession numbers CP023994.1 and CP030929.1, respectively. NCBI's PGAP annotation of *A. photophilum* is in the NCBI RefSeq database under the accession numbers NZ_CP023994. For *R. lacicola*, the originally published genome annotation is available in the DDBJ/ENA/GenBank database under accession number CP007490 (Hahn et al., 2014). NCBI's PGAP annotation of *R. lacicola* is in the NCBI RefSeq database under the accession number NZ_CP007490. The complete assembled, annotated genome sequence of *Microbacterium* sp. strain MWH-10M-3C3 has been deposited in the DDBJ/ENA/GenBank database under the accession no. CP034245.

2.4 Results

2.4.1 Genome Sequences of *Aurantimicrobium photophilum* strain MWH-Mo1, *Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3

The three *Microbacteriaceae* genomes were sequenced at the University of Delaware Sequencing Center using a PacBio RSII system. All three have circular genomes, as determined by the Gepard analysis during genome annotation. The complete *A. photophilum* chromosome is 1.75 Mb in length, which contains 1,792 open reading frames (ORFs) and 1 rRNA operon. The GC content is 54.6%. The genome of *Aurantimicrobium* sp. strain MWH-Uga1 is smaller, at 1.6 Mb, but with 1,618 ORFs has a higher coding density. Its GC content is similar to that of *A. photophilum* (52.4%). The GC content of both *Aurantimicrobium* species is similar to other freshwater Actinobacteria (Table 2.1). The *Microbacterium* sp. strain 10M-3C3 chromosome is 3.38 Mb in length and contains 3404 ORFs and 1 rRNA operon. The

GC content is 71.6%, which is at the higher end of known microbial GC contents that range from ~15 – 75% (Brocchieri, 2014).

Species/ strain	*R. lacicola* strain MWH-Ta8	*A. photophilum* strain MWH-Mo1	*Aurantimicrobium* sp. strain MWH-Uga1	*Microbacterium* sp. strain 10M-3C3
Closed Genome Length (Mbp)	1.43	1.75	1.61	3.38
% GC Content	51.5	54.6	52.4	71.6
No. of 16S-23S-5S rRNA operons	1	1	1	1
No. of tRNAs	39	42	41	53
No. of open reading frames	1338	1745	1618	3404
Coding Density	92.68	93.76	94.95	92.43
Genbank Accession Number	GCA_000699505.1	GCA_003194085.1	GCA_003325955.1	GCA_003931875.1
Sequenced in This Work	No	Yes	Yes	Yes

Table 2.1 Genome characteristics of *A. photophilum, Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3 (sequenced in this work) as well as *R. lacicola*. The two *Aurantimicrobium* strains have genome lengths less than 1.8 Mbp, have moderate GC content, and high coding density, similar to *R. lacicola. Microbacterium* 10M-3C3 has a genome length of 3.38 Mbp, which is larger than the three species with light-enhanced growth. It also has high coding density, similar to *R. lacicola*, and high GC content.

2.4.2 Genome Comparison

The *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 and *R. lacicola* share a light-enhanced growth phenotype, but PCR analysis previously demonstrated that only *R. lacicola* and *Aurantimicrobium* sp. strain MWH-Uga1 encode actinorhodopsins (Sharma et al., 2009). Therefore, the *A. photophilum*, *Aurantimicrobium* sp. strain MWH-Uga1, and the *Microbacterium* genomes were sequenced to identify genes, especially potential light-capturing systems, shared by the three species with the cryptic light-enhanced growth phenotype and not in the *Microbacterium* genome.

The *A. photophilum* and *Aurantimicrobium* sp. strain MWH-UGA1 genomes share 1,301 genes with each other and 842 genes with *Rhodoluna lacicola* strain MWH-Ta8 (**Figure 2.2**), as assessed by Enzyme Function Initiative-Enzyme Similarity Tool (EFI-EST) analysis. The majority of these shared genes encode housekeeping or central metabolic functions (**Table A.2**). *R. lacicola* has 458 unique genes that do not have best reciprocal blast hits in either *A. photophilum* or *Aurantimicrobium* sp. strain MWH-Uga1. *A. photophilum* has 420 unique genes that do not have best reciprocal blast hits in either *R. lacicola* or *Aurantimicrobium* sp. strain MWH-Uga1. *Aurantimicrobium* sp. strain MWH-Uga1 has 288 unique genes that do not have best reciprocal blast hits in either *R. lacicola* or *A. photophilum* (**Figure 2.2**).

No complete pathway for any type of motility was identified in the *R. lacicola*, nor in either *Aurantimicrobium* genome. The genome sequences suggest that both are heterotrophic aerobes with the ability to utilize amino acids and other small organic molecules. There are no identifiable genes involved in dissimilatory sulfate reduction pathways, suggesting that, like other freshwater *Actinobacteria*, these organisms

require exogenous reduced sulfur. The genome of *A. photophilum* also lacks a pathway for asparagine biosynthesis, suggesting that it is auxotrophic for at least one amino acid, like other freshwater Actinobacteria.

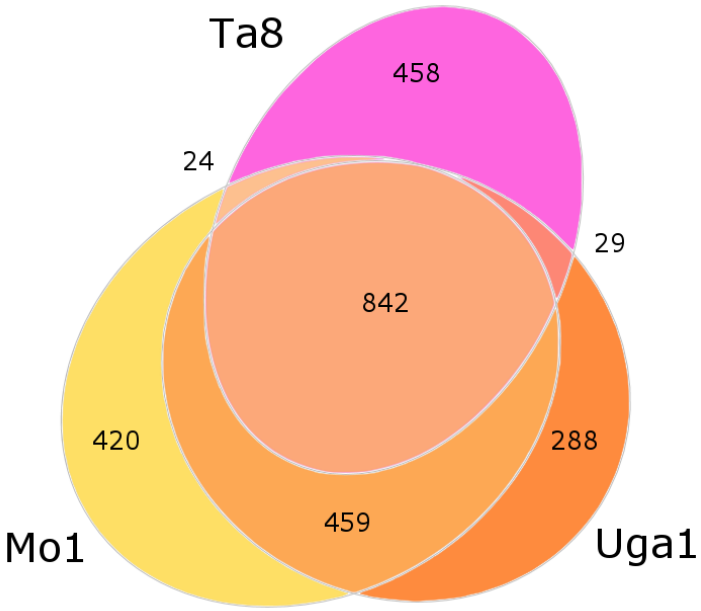

Figure 2.2 Whole Genome Comparisons. The predicted open reading frames in the genomes of *R. lacicola*, *A. photophilum*, and *Aurantimicrobium* sp. strain MWH-Uga1 were compared using EFI-EST, and the overlaps are depicted in a Euler plot using the program eulerAPE (http://www.eulerdiagrams.org/eulerAPE/). The two Aurantimicrobium spp. are very closely related (their 16S rRNA genes are 99.5% identical), and their genomes share a total of 1312 genes. Figure reproduced from (Maresca et al., 2019) with permission from the Journal of Bacteriology.

GO-slim terms were assigned to the predicted protein sequences of *R. lacicola* and *A. photophilum* to summarize their predicted functions. 1347 proteins in *R. lacicola* and 1738 proteins in *A. photophilum* passed the BLAST analysis which finds sequences similar to the query in the NCBI non-redundant protein database. 1186

proteins in *R. lacicola* and 1512 proteins in *A. photophilum* were mapped, which retrieves GO-slim terms associated to the hits obtained by the BLAST analysis. Finally, 1157 proteins in *R. lacicola* and 1467 proteins in *A. photophilum* were assigned GO-slim terms, which selects a subset of the most specific GO-term annotations for a query sequence (**Table 2.2**).

Term Assignment Step	***R. lacicola***	***A. photophilum***
BLASTED	1347	1738
MAPPED	1186	1512
SELECTION	1157	1467
Total number of proteins	1353	1746

Table 2.2 Number of predicted protein sequences that passed each step in GO-slim term assignment.

GO-slim term assignments in each of the three broad categories, biological process, molecular function, and cellular component indicate that *A. photophilum* and *R. lacicola* have highly similar distributions of protein encoding genes. Biological process GO-slim terms with the largest proportions in both species includes metabolic processes of cellular nitrogen compounds, small molecules, cellular amino acids, DNA, carbohydrates, and cofactors processes as well as translation. Differences between the two species include the proportion of predicted proteins annotated with the transposition term, which is greater in *A. photophilum* than in *R. lacicola* (**Figure 2.3**).

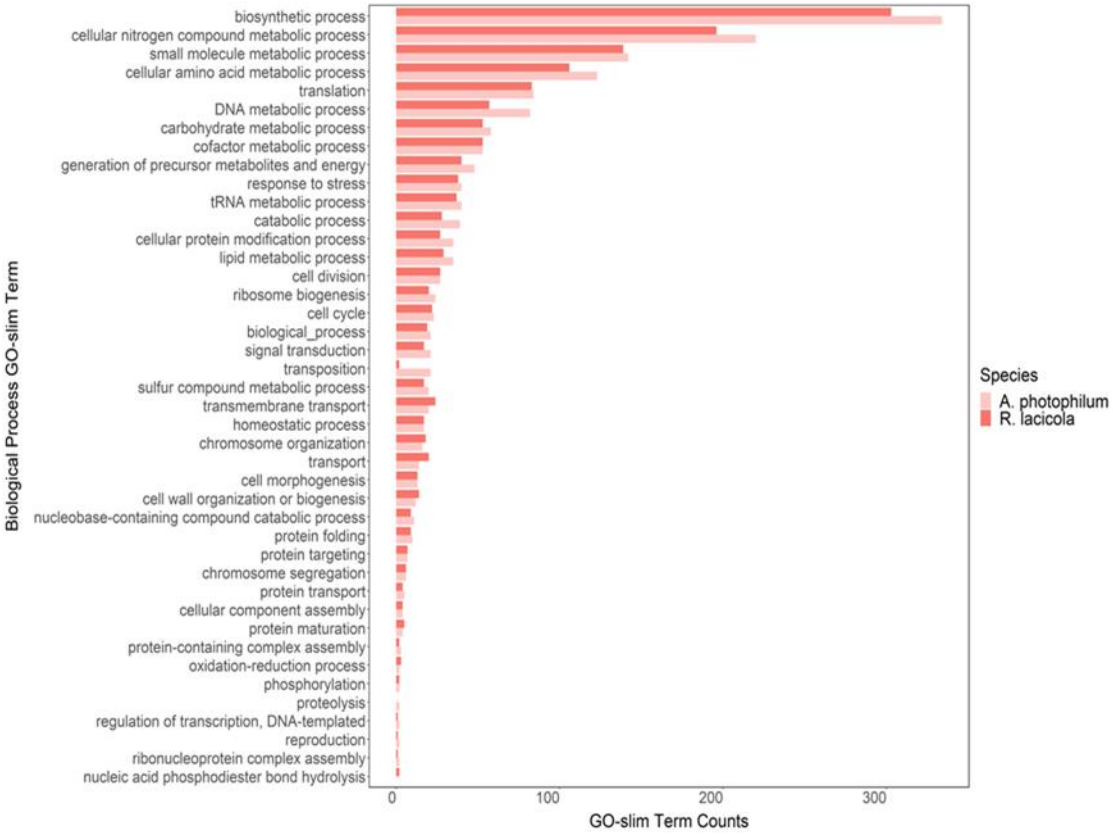

Figure 2.3 Biological Process GO-slim Term Counts. Number of predicted proteins annotated with a biological process GO-slim term in *A. photophilum* (light red) and *R. lacicola* (dark red). GO-slim terms with counts greater than one are plotted. *A. photophilum* generally has greater counts for each GO-slim term, likely due to its larger genome size. The distribution of biological process GO-slim terms is similar between the two species, although transposition has a noticeably greater proportion in *A. photophilum*.

The largest proportions of molecular functions in both species includes higher order GO-slim terms including ion binding, oxidoreductase activity, DNA binding, and transmembrane transport activity. The largest proportions of specific enzymatic activity in both species include lyase, ligase, kinase, isomerase, methyltransferase, and ATPase functions. Differences between the two species indicate that two *R. lacicola* predicted proteins, *Rhola_00001270* and *Rhola_00005270*, are assigned the molecular

function GO-slim term endonuclease activity, while no *A. photophilum* genes were assigned this molecular function GO-slim term (**Figure 2.4**). *Rhola_00001270* is annotated as type II toxin-antitoxin system RelE/ParE family toxin and *Rhola_00005270* is annotated as HNH endonuclease in the *R. lacicola* RefSeq annotation.

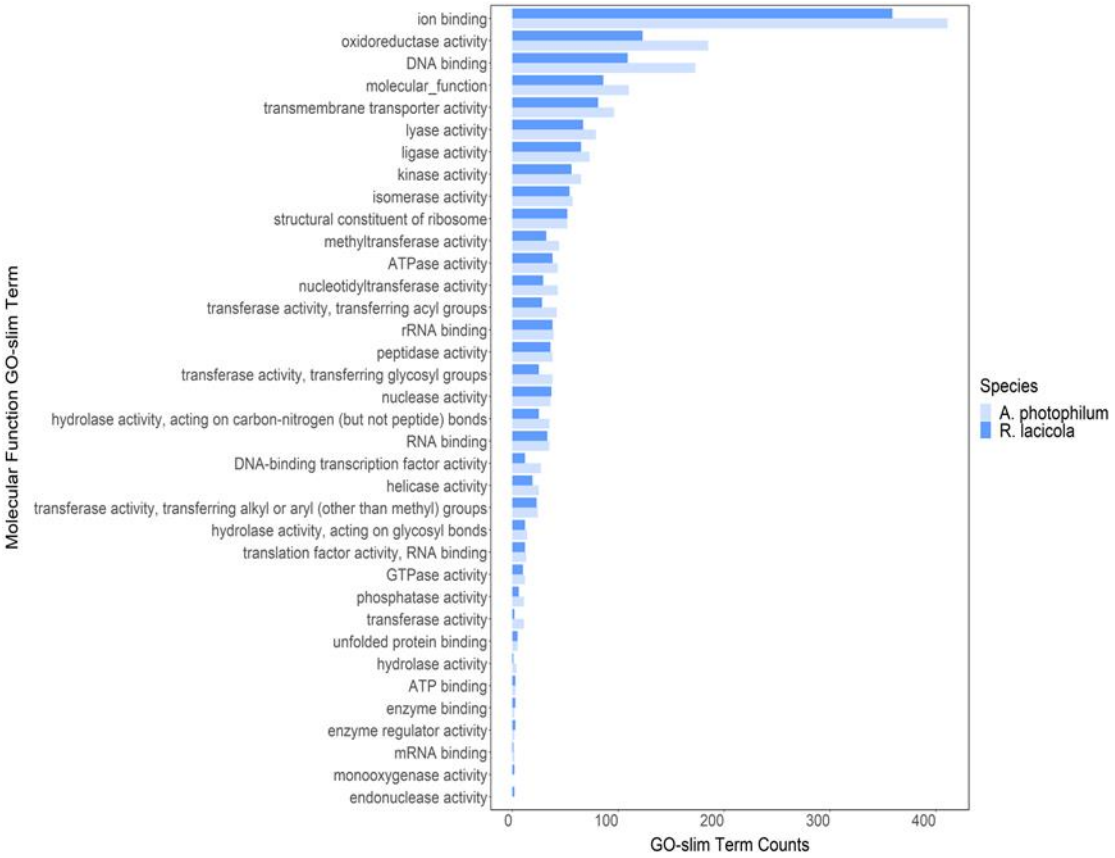

Figure 2.4 Molecular Function GO-slim Term Counts. Number of predicted proteins annotated with a molecular function GO-slim term in *A. photophilum* (light blue) and *R. lacicola* (dark blue). GO-slim terms with more than one count are plotted. The distribution of molecular GO-slim terms is similar between the two species, though *A. photophilum* generally has greater counts for each GO-slim term, again likely due to its larger genome size.

The distribution of cellular compartment GO-slim terms is similar between *R. lacicola* and *A. photophilum*. The largest proportions of cellular component GO-slim

terms in both species includes the higher order term cellular compartment as well as cytoplasm, plasma membrane, protein-containing complex, and ribosome. Differences in cellular component GO-slim term distribution indicates that *A. photophilum* encodes two predicted proteins, *AURMO_00873* and *AURMO_00874*, annotated as WYL domain-containing proteins in the RefSeq annotation, that are assigned the cellular component GO-slim term proteasome complex (**Figure 2.5**).

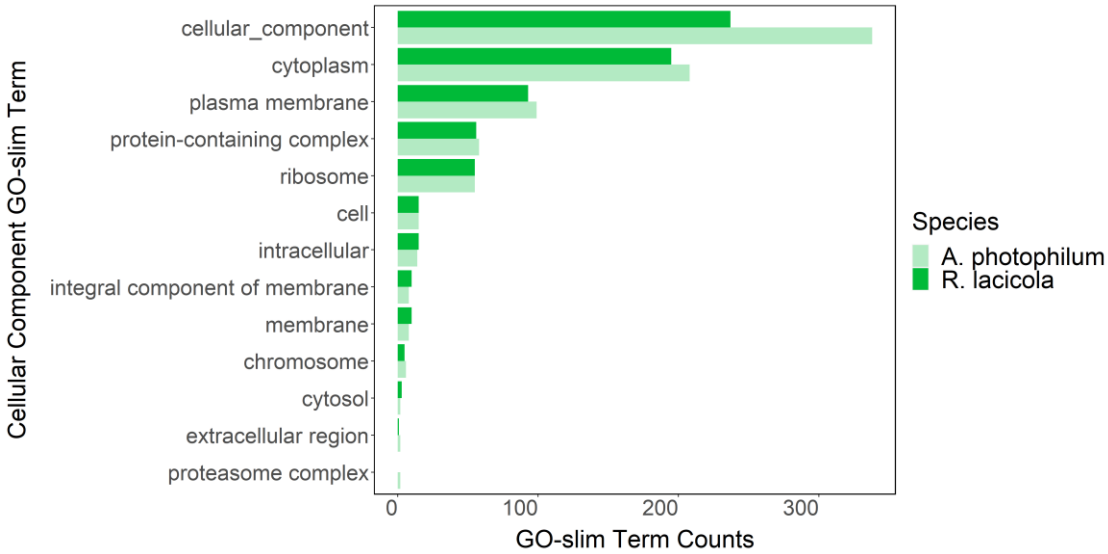

Figure 2.5 Cellular Component GO-slim Term Counts. Number of predicted proteins annotated with a cellular component GO-slim term in *A. photophilum* (light green) and *R. lacicola* (dark green). GO-slim terms with more than one count are plotted.

2.4.2.1 Genes Shared by Actinobacteria Species with Light-Enhanced Growth

Of the 842 genes shared by the *Aurantimicrobium* species and *R. lacicola*, 71 genes are not shared with *Microbacterium* sp. strain 10M-3C3 (**Table A.5**). This set of genes does not include genes that encode for the cryptochrome/photolyase family (CPF) of proteins, shared by the *Aurantimicrobium* species and *R. lacicola*, because *Microbacterium* sp. strain 10M-3C3 also has two genes that encode predicted CPF

proteins. Additionally, this set of genes does not include genes that encode for rhodopsins because all three genomes do no encode the same type of rhodopsin. Only *R. lacicola* and *Aurantimicrobium sp.* strain MWH-Uga1 encode actinorhodopsins and only the *Aurantimicrobium* species encode heliorhodopsins. The actinorhodopsins and heliorhodopsin gene sequences are dissimilar, such that they are not best reciprocal BLAST hits.

GO-slim terms analyses of the *R. lacicola* 71 shared genes set predict that proteins encoded by these genes are generally related to transmembrane transport, metabolism, cell signaling, and cell wall biosynthesis. Biological Process GO-slim terms assigned to the *R. lacicola* 71 predicted proteins of the shared genes set indicate that these predicted proteins include those related to several metabolic processes, protein processing, transmembrane transport, cell morphogenesis, and response to stress. Cellular compartment GO-slim terms assigned to the *R. lacicola* 71 predicted proteins of the shared genes set indicate that these predicted proteins are found in the cytoplasm, plasma membrane, and protein-containing complex(es) (**Figure 2.6**). Molecular function GO-slim terms represented in this set of predicted proteins includes transmembrane transport, kinase activity, peptidase activity, nuclease activity, helicase activity, DNA binding, and DNA-binding transcription factor activity (**Figure 2.6**).

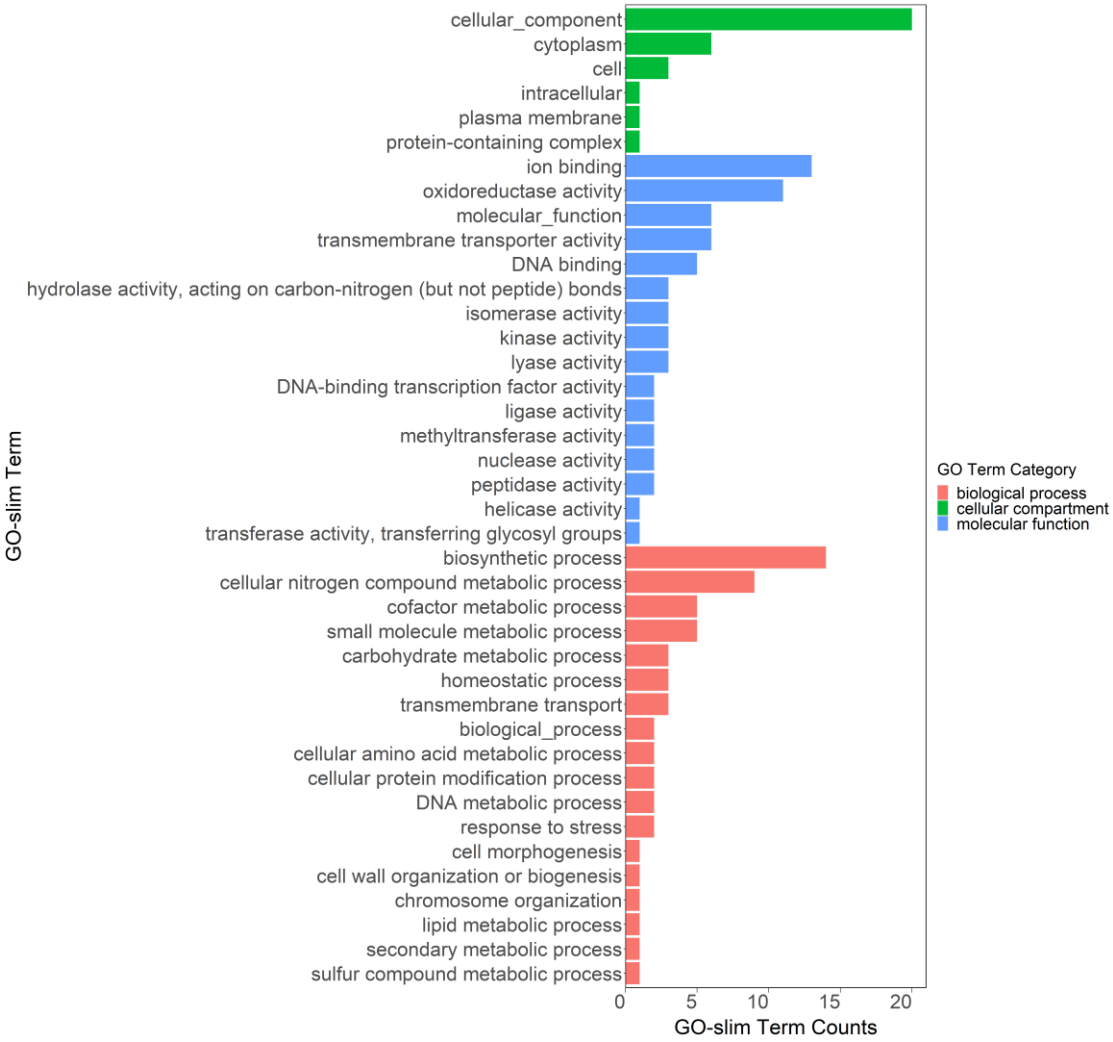

Figure 2.6 GO-slim Term Counts of the predicted proteins encoded by the 71 genes shared by three species with light-enhanced growth and not shared by *Microbacterium* sp. strain 10M-3C3. Number of *R. lacicola* predicted proteins annotated with biological process, molecular function, and cellular compartment GO-slim terms in the set of 71 genes shared by *A. photophilum*, *Aurantimicrobium* sp. strain MWH-Uga1, *R. lacicola* and not shared with *Microbacterium* sp. strain 10M-3C3. GO-slim terms with counts greater than or equal to one are plotted. Biological process GO-slim terms are colored in red, molecular function GO-slim terms are colored in blue, and cellular compartment GO-slim terms are colored in green.

Specifically, the 71 shared gene set encodes 4 predicted transcriptional regulators, *Rhola_00000310*: transcriptional regulator IclR family, *Rhola_00002220*:

MarR family transcriptional regulator, *Rhola_00004340*: Lrp/AsnC family transcriptional regulator for *asnA*, *asnC* and *gidA*, and *Rhola_00013990*: DNA-binding transcriptional regulator MocR family contains an aminotransferase domain. These 4 transcriptional regulators are generally related to or predicted to control expression of genes encoding proteins related to metabolism (Deng et al., 2011; Milano et al., 2016; Grove, 2017; Suvorova and Gelfand, 2021). Additionally, MarR family transcriptional regulator proteins are known to be ligand-responsive transcription factors well suited to control expression of virulence genes and antibiotic efflux pumps (Ellison and Miller, 2006; Wilkinson and Grove, 2006). Other predicted nucleotide-binding proteins in the 71 shared gene set include *Rhola_0000340*: metallo-beta-lactamase family protein, *Rhola_00013550*: 3-methyladenine DNA glycosylase AlkD, *Rhola_00006590*: bifuctional RNase H/acid phosphatase, *Rhola_00007150*: Holliday junction branch migration protein RuvA, *Rhola_00006080*: competence protein ComEA, and *Rhola_00005640*: single-stranded DNA-binding protein.

The 71 shared gene set also includes 11 genes encoding predicted proteins related to transmembrane transport, specifically transport of sugar, sulfate, and cations. The *R. lacicola* predicted proteins of these 11 genes and their locus tags are: *Rhola_00012910*: PTS system, fructose-specific IIA component, *Rhola_00002410*: Predicted $Fe^{2+/}Mn^{2+}$ transporter, VIT1/CCC1 family, *Rhola_00005720*: monovalent cation H^+ antiporter-2, CPA2 family, *Rhola_00003100*: Predicted arabinose efflux permease, MFS family, *Rhola_00005700*: small conductance mechanosensitive channel, *Rhola_00009420*: Sugar phosphate permease, *Rhola_00002740*: Glycerol uptake facilitator (Major Intrinsic Protein Family), *Rhola_00012550*: cation diffusion

facilitator family transporter, *Rhola_00004690*: sulfate permease, SulP family, *Rhola_00002610*: DMT family transporter, and *Rhola_00003560*: Permease of the drug/metabolite transporter (DMT) superfamily.

Additionally, 4 genes encoding predicted proteins related to protein processing are in the 71 shared gene set. The *R. lacicola* predicted proteins of these 4 genes and their locus tags are: *Rhola_00007220*: peptidyl-prolyl cis-trans isomerase B (cyclophilin B), *Rhola_00005630*: peptide-methionine (S)-S-oxide reductase, *Rhola_00001450*: dolichol-phosphate mannosyltransferase, and *Rhola_00004630*: Predicted Zn-dependent peptidase. 6 genes encoding predicted protein related to amino acid biosynthesis/metabolism are also in the 71 shared gene set. The *R. lacicola* predicted proteins of these 6 genes and their locus tags are *Rhola_00008090*: methionine synthase (B12-dependent), *Rhola_00011170*: adenosylhomocysteinase, *Rhola_00000270*: formiminoglutamase, *Rhola_00006310*: Phosphoglycerate dehydrogenase, *Rhola_00005580*: agmatine deiminase, and *Rhola_00007340*: 3-dehydroquinate dehydratase.

2.4.2.2 Genes Unique to *Actinobacteria* species with Light-Enhanced Growth

The best reciprocal blast hit analysis with an alignment score of ≥ 35 cutoff identified 458 *R. lacicola* genes as unique from both of the Aurantimicrobium species and 420 *A. photophilum* genes unique from *R. lacicola* and *Aurantimicrobium* sp. strain MWH-Uga1. GO-slim term assignment resulted in 354 of the 458 *R. lacicola* unique predicted proteins and 302 of the 420 *A. photophilum* unique predicted proteins being assigned GO terms. Of the 458 *R. lacicola* unique predicted proteins, 195 were originally annotated as hypothetical proteins and of the 420 *A. photophilum* unique predicted proteins, 204 were originally annotated as hypothetical proteins. As a result

of the alignment score ≥ 35 cutoff used in the sequence comparison methods, 12 *R. lacicola* genes and 8 *A. photophilum* genes encoding predicted ribosomal proteins were included in their respective unique gene sets. However, the predicted ribosomal protein encoding genes do have best reciprocal blast hits below the alignment score cutoff in the other two species. The inclusion of these 12 genes in the *R. lacicola* unique gene set and 8 genes in the *A.photophilum* unique gene set that encode predicted ribosomal proteins explains the presence of the GO-terms ribosome, structural constituent of ribosome, mRNA binding, rRNA binding, RNA binding, and translation in the *R. lacicola* and *A. photophilum* unique predicted protein set of GO-terms.

The *R. laciciola* and *A. photophilum* predicted proteins of their unique gene sets do have some similarities among their GO-slim terms. Molecular function GO-slim terms DNA binding, ion binding, oxido-reductase activity, and transmembrane transporter activity have a large proportion in both the *R. laciciola* and *A. photophilum* predicted proteins of unique gene sets (**Figure 2.7**). Additionally, biological process GO-slim terms that have large proportions in both *R. laciciola* and *A. photophilum* predicted proteins of unique gene sets includes biosynthetic process, cellular nitrogen compound metabolic process and translation (**Figure 2.8**). Cellular compartment GO-slim terms and their counts among the predicted proteins of the unique gene sets of *R. lacicola* and *A. photophilum* are quite similar, with GO-slim terms cellular component, plasma membrane, and protein-containing complex, having the largest proportions in both (**Figure 2.9**).

While the *R. laciciola* and *A. photophilum* predicted proteins of their unique gene sets have some similarities among their GO-slim terms, there are many

differences between their molecular function and biological process categories. *A. photophilum* has a greater number of predicted proteins from the unique gene set assigned the molecular function GO-slim terms transferase activity transferring acyl groups, ATPase activity, and DNA-binding transcription factor activity than *R. lacicola's* unique set of predicted proteins (**Figure 2.7**). *R. lacicola* has a higher number of predicted proteins from the unique gene set assigned the molecular function GO-slim terms isomerase activity, kinase activity, and lyase activity (**Figure 2.7**) Molecular function GO-slim terms assigned to the *A. photophilum* predicted proteins of the unique gene set that are not assigned in the *R. lacicola* set are dioxygenase activity, hydrolase activity, hydrolase activity acting on acid anhydrides, and peptidoglycan binding (**Figure 2.7**). The molecular function GO-slim terms assigned to the *R. lacicola* predicted proteins of the unique gene set that are not assigned to the *A. photophilum* set are ligase activity, endonuclease activity, monooxygenase activity, enzyme binding, enzyme regulator activity, hydrolase activity acting on ester bonds, N-acetyltransferase activity, transferase activity transferring alkyl or aryl (other than methyl) groups, 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase activity, 5-amino-6-(5-phosphoribosylamino)uracil reductase activity, and carbohydrate transmembrane transporter activity (**Figure 2.7**). The 458 *R. lacicola* genes unique from both of the Aurantimicrobium species includes multiple genes encoding predicted transcriptional regulators including *Rhola_00000060* 'Transciptional regulator', *Rhola_00002820* 'Lrp/AsnC family transcriptional rgulator', *Rhola_00011050* 'WhiB family transcriptional regulator', and *Rhola_00002790* 'PadR transcriptional regulator' (**Table A.3**).

A. photophilum has 420 genes that are unique from *R. lacicola* and *Aurantimicrobium* sp. strain MWH-Uga1 and 224 of those genes had significant differential expression in light vs. dark. This group includes multiple genes encoding predicted transcriptional regulators. Among the transcriptional regulators are *AURMO_00914* 'transcriptional repressor frmR', *AURMO_01196* 'anaerobic benzoate catabolism transcriptional regulator', and *AURMO_01752* 'transcriptional repressor dicA'. Also included in the 224 unique genes with differential expression is *AURMO_01075* 'Transposase', *AURMO_01487* 'Bacteriocin (Lactococcin 972)', and *AURMO_00464* 'Mitochondrial ribosomal death-associated protein 3' (**Table A.4**). *A. photophilum* has a higher number of predicted proteins from the unique gene set assigned the biological process GO-slim term DNA metabolic processes than *R. lacicola's* unique gene set predicted proteins (**Figure 2.8**). *R. lacicola* has a higher number of predicted proteins from the unique gene set assigned the biological process GO-slim terms small molecule metabolic processes (**Figure 2.8**). Biological process GO-slim terms assigned to the *A. photophilum* predicted proteins of the unique gene set that are not assigned in the *R. lacicola* set are transposition, cell wall organization or biogenesis, regulation of transcription, DNA-templated, methylation, proteolysis, regulation of apoptotic process, ribonucleotide complex assembly, and ribosome biogenesis (**Figure 2.8**). The biological process GO-slim terms assigned to the *R. lacicola* predicted proteins of the unique gene set that are not assigned to the *A. photophilum* set are cofactor metabolic process, cell cycle, cell division, lipid metabolic process, nucleid acid phosphodiester bond hydrolysis, phosphorylation, tRNA metabolic process, carbohydrate transmembrane transport, cellular component

assembly, chromosome organization, protein folding, reproduction, riboflavin biosynthetic process, and terpenoid biosynthetic process (**Figure 2.8**).

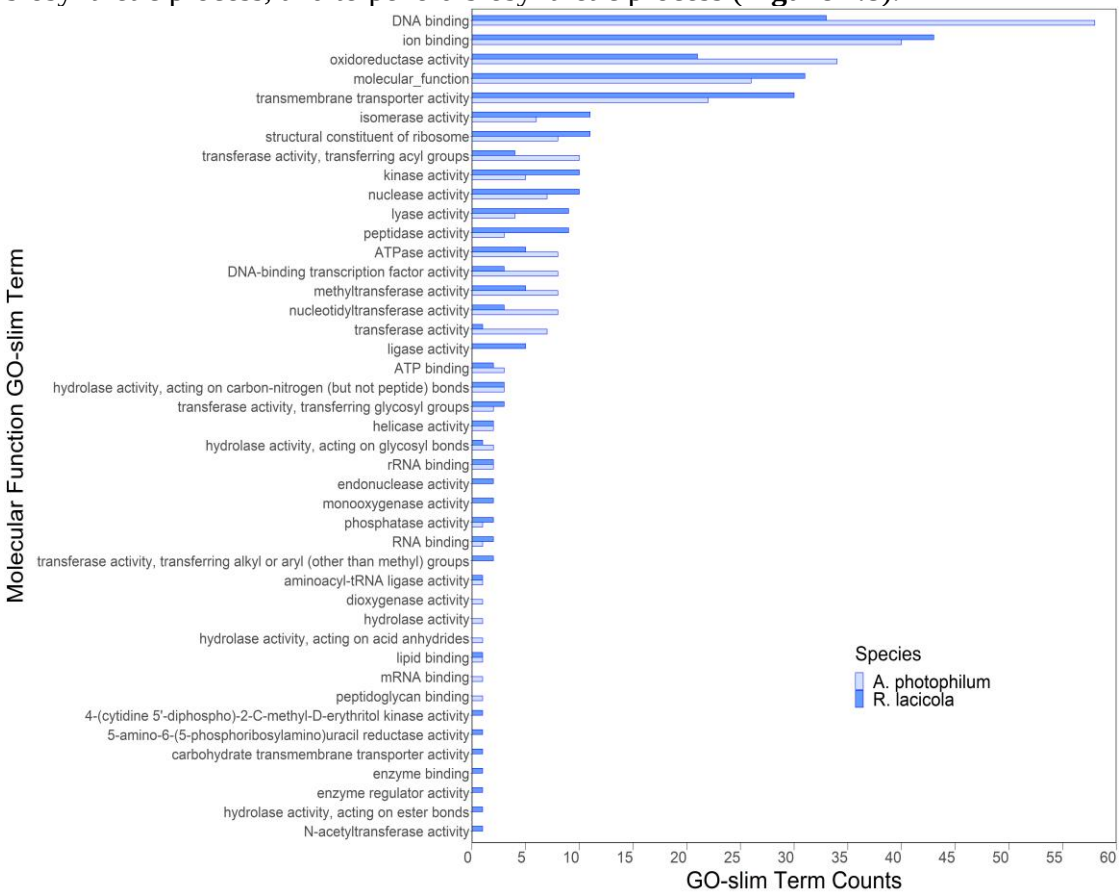

Figure 2.7 Molecular Function GO-slim term counts of the predicted proteins encoded by the *R. lacicola* unique genes set and the *A. photophilum* unique genes set. Number of predicted proteins annotated with molecular function GO-slim terms in the 458 *R. lacicola* genes not shared with *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 (dark blue). Number of predicted proteins annotated with molecular function GO-slim terms in the 420 *A. photophilum* genes not shared with *Aurantimicrobium* sp. strain MWH-Uga1 and *R. lacicola* (light blue). Molecular function GO-slim terms with counts greater than or equal to one in either species' unique gene set are plotted.

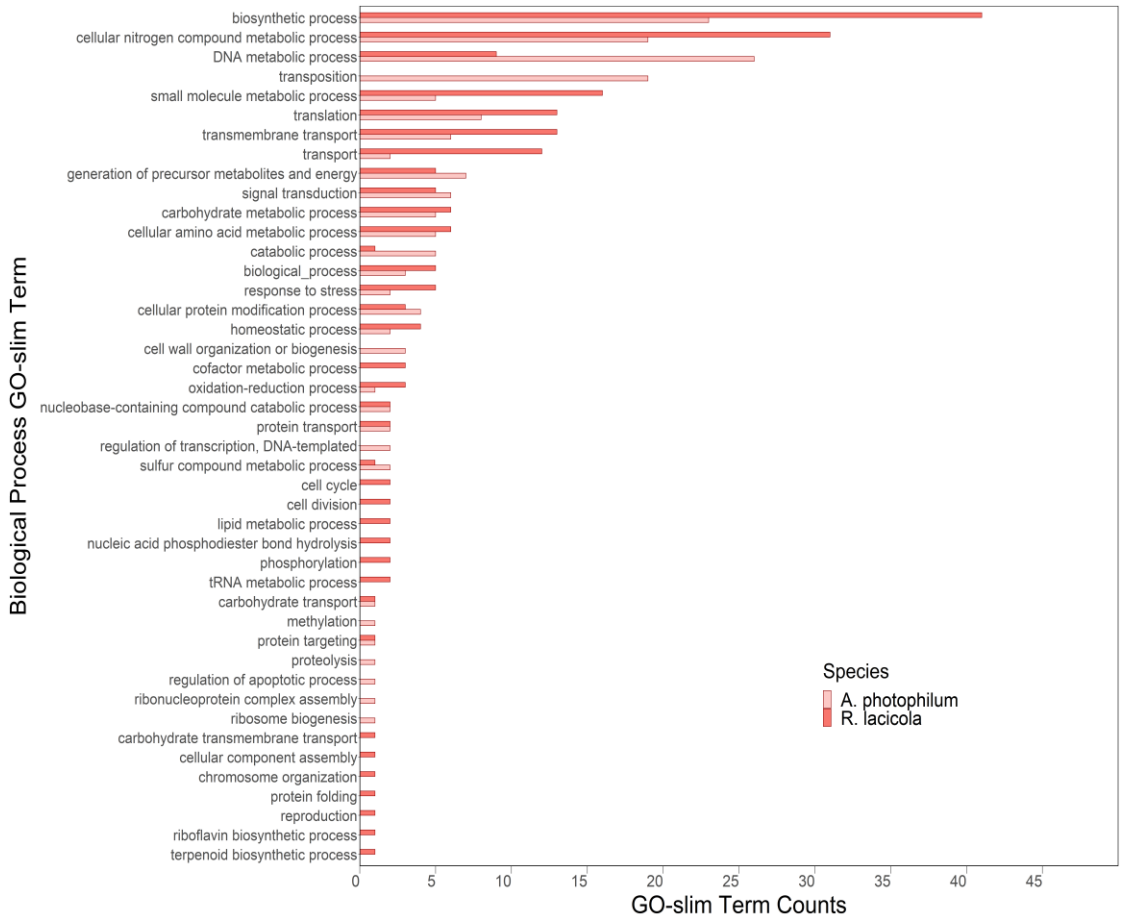

Figure 2.8 Biological Process GO-slim term counts of the predicted proteins encoded by the *R. lacicola* unique genes set and the *A. photophilum* unique genes set. Number of predicted proteins annotated with biological process GO-slim terms in the 458 *R. lacicola* genes not shared with *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 (dark red). Number of predicted proteins annotated with biological process GO-slim terms in the 420 *A. photophilum* genes not shared with *Aurantimicrobium* sp. strain MWH-Uga1 and *R. lacicola* (light red). Biological process GO-slim terms with counts greater than or equal to one in either species' unique gene set are plotted.

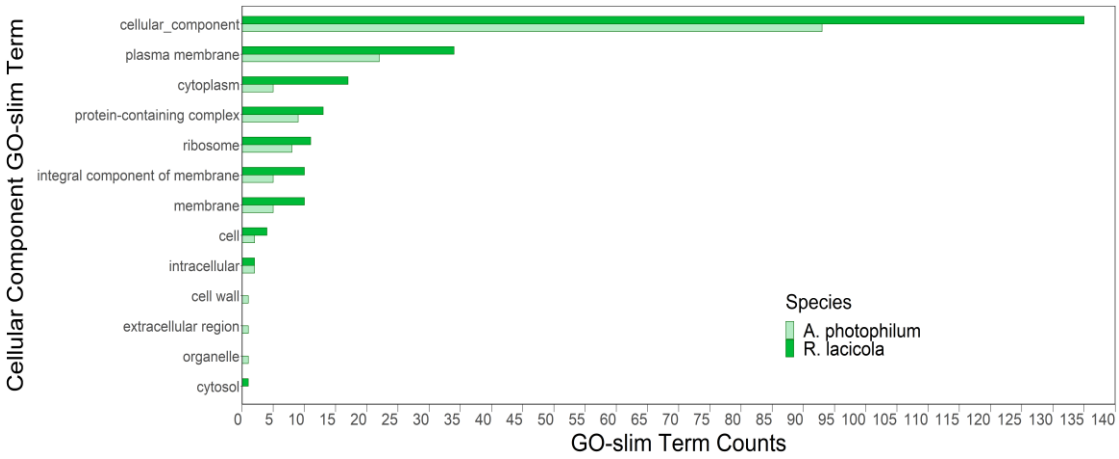

Figure 2.9 Cellular Component GO-slim term counts of the predicted proteins encoded by the *R. lacicola* unique genes set and the *A. photophilum* unique genes set. Number of predicted proteins annotated with cellular component GO-slim terms in the 458 *R. lacicola* genes not shared with *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1 (dark green). Number of predicted proteins annotated with cellular component GO-slim terms in the 420 *A. photophilum* genes not shared with *Aurantimicrobium* sp. strain MWH-Uga1 and *R. lacicola* (light green). Cellular component GO-slim terms with counts greater than or equal to one in either species' unique gene set are plotted.

2.5 Discussion

R. lacicola and two *Aurantimicrobium* genomes that were isolated from surface freshwater, share a light-enhanced growth phenotype, belong to the *Microbacteriaceae* family, and have broadly similar genomes. We found that *Aurantimicrobium* species have characteristic genomes of freshwater Actinobacteria, which are small and streamlined (Hahn et al., 2014, 2021). *Microbacterium* sp. strain 10M-3C3, which is a more distantly related to *R. lacicola* than the *Aurantimicrobium* species and does not have the light-enhanced growth phenotype, has high coding density and a larger genome than *R. lacicola* and the two *Aurantimicrobium* species sequenced here. Together, these four species make good candidates to study freshwater *Actinobacteria* light-mediated growth because they can be grown in pure

culture for future experiments and additionally, their genomes are now sequenced and annotated.

Previous transcriptome analyses indicate that in constant white light vs. constant dark conditions, *R. lacicola* and *A. photophilum* upregulate carbohydrate metabolism in the light and upregulate functions related to protein production in the dark (Maresca et al., 2019). Because no known mechanisms can explain the blue light-enhanced growth in *R. lacicola* and the two *Aurantimicrobium* species sequenced here, this presented multiple uncharacterized possibilities of how a likely signal transduction cascade is initiated, transduced, and ultimately controls growth. Through genome comparisons, my goals are to identify genes that may be related to blue-light enhanced growth that are good candidates for further study and hypothesize which steps in the likely signal transduction cascade they may be involved in.

R. lacicola, *A. photophilum*, *Aurantimicrobium* sp. strain MWH-Uga1, and *Microbacterium* sp. strain 10M-3C3 all encode predicted cryptochrome proteins, a type of photoreceptor. The mechanism of bacterial cryptochrome signal transduction is not well characterized, however it is likely that blue light causes a redox reaction in cryptochromes that initiates a conformational change and binding to an effector molecule (Partch et al., 2005). This starts a light-dependent signal cascade that likely leads to a transcription factor binding to DNA and controlling the transcriptional rate of certain genes. In *Rhodobacter sphaeroides*, cryptochromes have been shown to affect the expression of photosynthesis genes under semi-aerobic conditions (Shimada et al., 1992; Hendrischk et al., 2009). *R. lacicola* and the two *Aurantimicrobium* species do not have photosynthesis genes, so it is likely their predicted cryptochromes affect the expression of genes related to other biological pathways. Both *R. lacicola*

and *A. photophilum* has differential expression in light vs. dark conditions of genes related to sugar transport and protein processing (Maresca et al., 2019). Therefore, genes whose expression are most likely to be light regulated are genes related to carbohydrate metabolism and protein processing.

While there are numerous possible similarities and differences between *R. lacicola* and *A. photophilum* in the predicted signal transduction cascade, there are some most likely steps. The most likely steps include a blue light-sensing molecule which may undergo a conformational change and bind to another molecule, starting a signal cascade, leading to regulation of transcription factor(s) binding to DNA, thus controlling the rate of transcription of certain genes related to growth. Since similar biological functions respond to light vs. dark conditions in *R. lacicola* and *A. photophilum* and these two species are closely related within the *Microbacteriaceae* family, I think that homologous genes, related to increased growth, carbohydrate metabolism, and protein processing, are transcriptionally regulated by light (**Figure 2.10 A & C**). Therefore, I hypothesize that closely related freshwater Actinobacteria species with blue light-enhanced growth share mechanism(s) that relay blue-light sensing to increase growth. It is possible that upon sensing light, CryB binds different molecules in *R. lacicola* and *A. photophilum* resulting is different signal cascades that may affect the expression of homologous or non-homologous genes (**Figure 2.10 C & D**). However, this is unlikely given the similarity of the *R. lacicola* and *A. photophilum* CryB protein sequences and functional domains (Maresca et al., 2019). Therefore, I think the most likely scenario is that the signal cascade, transcription factors, and genes with light-mediated transcription are homologous between *R. lacicola* and *A. photophilum* (**Figure 2.10 A**).

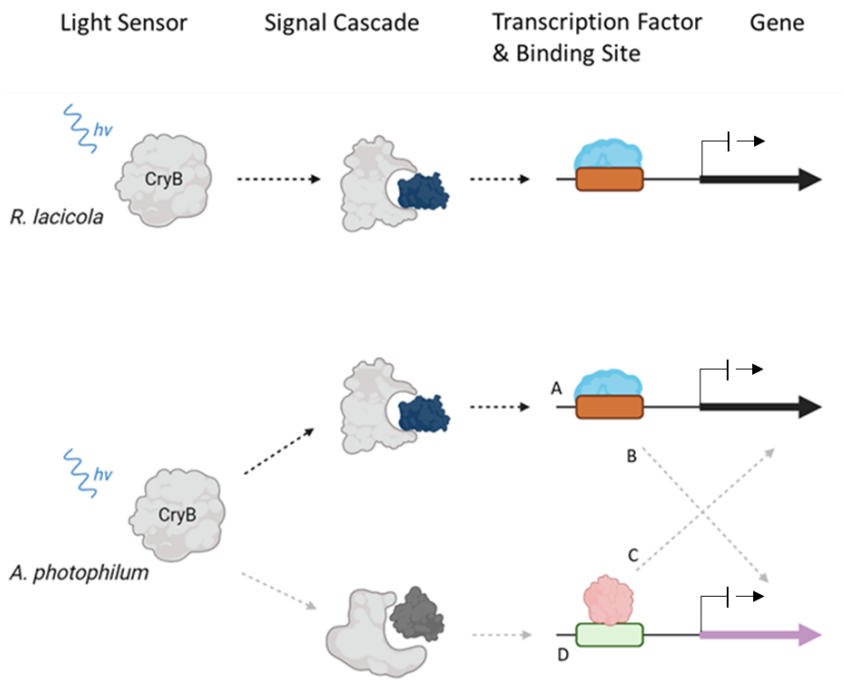

Figure 2.10 Putative signal transduction cascade steps in *R. lacicola* vs. *A. photophilum* blue-light mediated growth. Blue light sensing may induce a conformational change in CryB protein, the likely blue-light sensor, that subsequently induces binding to other molecule(s), initiates a signal transduction cascade that causes a transcription factor to bind to DNA, which then controls the transcription rate of certain genes. *R. lacicola* and *A. photophilum* blue light mediated signal cascades may be similar (A) or different (B, C, & D) based on downstream effector molecules, transcription factors, and transcribed genes. The signal transduction cascade may involve homologous (A & B) or non-homologous (C & D) transcription factors that ultimately control the transcription of homologous (A & C) or non-homologous (B & D) genes.

The genome comparisons show that *R. laciciola* and the two *Aurantimicrobium* species share a large percentage of their genome and have similar distributions of predicted protein functions, indicating they may have similar mechanisms to obtain and use energy. If *R. laciciola* and the two *Aurantimicrobium* species share a light-regulated mechanism to obtain and use energy, they may also share a light-regulated signal transduction cascade. Previous transcriptome analyses showed similar

transcriptional effects of constant light vs. dark on genes related to carbohydrate metabolism and protein processing in both *R. lacicola* and *A. photophilum* (Maresca et al., 2019). These previous analyses combined with the genome comparisons establish that some genes related to carbohydrate metabolism and protein processing with significant differential expression are shared between *R. lacicola* and *A. photophilum*. Specifically, twenty-two genes shared by *R. lacicola* and *A. photophilum* have significant differential expression in constant light vs. constant dark and a similar response (either upregulated in light or upregulated in the dark) in both species (**Table A.1**). This group includes genes that encode predicted proteins involved in the TCA cycle, ATP synthesis, propionyl-CoA metabolism, ribosomal proteins, RNA metabolism and processing, and amino acid metabolism as well as a predicted two-component OmpR family response regulator and sensor kinase.

Typical two-component signal transduction in bacteria consists of a sensor kinase that senses a signal via a conformational change, which leads to phosphoryl transfer to a response regulator, thus affecting the binding affinity of the DNA binding domain on the response regulator (Gross and Beier, 2012). Two-component regulatory systems are widely distributed in Actinobacteria and it is estimated that greater than 50% are known to respond to environmental changes (Huang et al., 2015). Specifically, OmpR two-component regulatory systems have been characterized to respond to environmental nutrient limitation/excess and regulate phosphate, nitrogen, and carbon metabolism in actinobacterial species (Martín and Liras, 2020). It may be that the shared predicted two-component OmpR family response regulator and predicted sensor kinase (*Rhola_00010430* and *Rhola_00010440*) are part of the

predicted light-medicated signal cascade in *R. lacicola* and *A. photophilum* and are good candidates for future study.

Interestingly, all of the twenty-two genes with differential expression in light vs. dark that are shared by *R. lacicola* and *A. photophilum* are also shared with *Microbacterium* sp. strain 10M-3C3, which does not have the light-enhanced growth phenotype. Though this is a comparison to only one genome without the light-enhanced growth phenotype, the presence of all twenty-two genes in *Microbacterium* sp. strain 10M-3C3 may indicate that the putative signal transduction in *R. lacicola* and *A. photophilum* is more complex than our model and/or that it does not always result in increased growth rate. Each protein in the putative signal transduction cascade may be autoregulated, regulated by another molecule/process, or be constitutively expressed. Thus, genes without significant differential expression in light vs. dark may still be related to the light-enhanced growth phenotype. This could mean that while *Microbacterium* sp. strain 10M-3C3 shares a putative light-sensor and genes related to growth that are transcriptionally light-regulated in some species, it may have an incomplete or different light-mediated signal transduction pathway compared to *R. lacicola* and the two *Aurantimicrobium* species. Therefore, genes shared by *R. lacicola*, the two *Aurantimicrobium* species, and not in the *Microbacterium* sp. strain 10M-3C3 genome are good candidates for further study to determine if they transcriptionally respond to light and what role they may have in a blue-light mediated signal transduction cascade.

Because we hypothesize that *R. lacicola* and the two *Aurantimicrobium* species share a similar blue-light mediated signal transduction cascade, genes that are shared by *R. lacicola* and the two *Aurantimicrobium* species are of interest since they

are more likely to be involved in the relay of light to information than genes that are not shared by all three species with the light-enhanced growth phenotype. Furthermore, genes that are shared by all three species and not found in *Microbacterium* sp. strain 10M-3C3 are of particular interest, since *Microbacterium* sp. strain 10M-3C3 does not have light-enhanced growth. Among those 71 shared genes that are not found in the *Microbacterium* sp. strain 10M-3C3 genome, I identified genes encoding predicted proteins related to metabolism, protein processing, and nucleotide binding including four transcription factors.

2.5.1 Shared Genes Related to Transcription Regulation

Four transcription factors, *Rhola_00000310*: transcriptional regulator IclR family, *Rhola_00002220*: MarR family transcriptional regulator, *Rhola_00013990*: DNA-binding transcriptional regulator MocR family contains an aminotransferase domain, and *Rhola_00004340*: Lrp/AsnC family transcriptional regulator for *asnA, asnC* and *gidA* are among the 71 shared gene set. Interestingly, all four of the genes in *Aurantimicrobium photophilum* and only *Rhola_00004340* had differential expression in response to constant light vs. constant dark (**Table A.5**). The differences in differential expression among species shows that the proposed model for the light-mediated signal cascade may be more complex and/or may differ between *R. lacicola* and *A. photophilum*. Given each of the four transcription factors is light-regulated in at least one species, here I consider which biological processes are most likely to be affected.

The IclR-family of transcription factors is a large group that includes repressors, activators, and dual regulatory role proteins (Suvorova and Gelfand, 2021). This large group of proteins is named after its best characterized member, the *E. coli* IclR protein

that controls the glyoxylate shunt though, members of the IclR family have also been characterized to control genes related to multidrug resistance, aromatic molecule degradation, quorum sensing, plant pathogenicity, and sporulation (Gui et al., 1996; Molina-Henares et al., 2006). The *A. photophilum* homolog to *Rhola_00000310*: transcriptional regulator IclR family is *AURMO_00523*: pca regulon regulatory protein. PcaR transcription factor is a member of the IclR family of proteins and is characterized in *Pseudomonas putida* to activate *pca* genes (pcaBDC, pcaIJ, pcaK, and pcaF) which are part of the protocatechuate (PCA) degradation pathway (Molina-Henares et al., 2006). *AURMO_00523* has higher expression in dark vs light, which suggests that *A. photophilum* increases PCA degradation in the dark (Maresca et al., 2019). PCA is an intermediate in aromatic compound degradation which can generate acetyl-CoA and succinate that are used for energy production (Ornston and Stanier, 1964). Therefore, *A. photophilum* may be exposed to more aromatic compounds within its natural environment in dark vs light and/or use aromatic compounds a source of energy in the dark more so than in light.

The MocR family of transcriptional factors is another group of regulators that are generally involved in controlling expression of proteins related to multiple metabolic pathways or in transmembrane transport of substrates, particularly related to pyridoxal phosphate (PLP) chemistry (Milano et al., 2016; Tramonti et al., 2018). In *Actinobacteria,* MocR transcription factors have been predicted to regulate expression of *YczE* uncharacterized membrane proteins. Very little is known about YczE uncharacterized membrane proteins, however a few studies in *Bacillus* species suggest it is related to transmembrane transport and/or positive regulation of antibiotic synthesis via an unknown posttranscriptional event (Yao et al., 2003; Koumoutsi et al.,

2007) Additionally, genome comparisons in *Mycobacteria* show that YczE proteins co-occur with genes involved in metabolism and membrane transport of compounds containing sulfur (Milano et al., 2018). Both *AURMO_01605*: Membrane protein YczE and the *R. lacicola* homolog, *Rhola_00008300*: Putative membrane protein, have higher expression in light vs dark (Maresca et al., 2019). Interestingly, *Rhola_00013990*: 'DNA-binding transcriptional regulator MocR family contains an aminotransferase domain' does not have differential expression in light vs dark while the *A. photophilum* homolog, *AURMO_00011*: 2-aminoadipate transaminase, has higher expression in light vs dark (Maresca et al., 2019). If it is true that MocR family transcriptional factors regulate expression of YczE proteins, then the comparative analyses here suggest that this regulation is specific among even closely related species. In *A. photophilum*, it may be that *AURMO_00011* is part of the proposed light-mediated signal cascade that affects transmembrane transport which ultimately increases energy resulting in faster growth in light vs dark.

Lrp/AsnC family of transcriptional regulators are widely distributed in prokaryotes and regulate expression of genes encoding proteins related to cellular metabolism (Thaw et al., 2006). They are also known as feast/famine regulatory proteins and are known to regulate metabolic pathways in response to environmental cues, in particular exogenous amino acids (Deng et al., 2011). Both *Rhola_00004340*: Lrp/AsnC family transcriptional regulator and the *A. photophilum* homolog *AURMO_01192*: Regulatory protein AsnC have higher expression in light vs dark indicating this regulatory protein is light-responsive (Maresca et al., 2019). It may be that this Lrp/AsnC family transcriptional regulator is part of the proposed light-mediated signal cascade. Furthermore, light in *R. lacicola* and *A. photophilum's*

surface freshwater environments may be linked to the detection of exogenous nutrient availability via Lrp/AsnC family transcriptional regulators.

The MarR family of transcription factors was named after the multiple antibiotic resistance regulator in *E. coli*, however they are ubiquitously found in bacteria (Deochand and Grove, 2017). MarR family transcription factors are known to be environmental sensors that can function as activators or repressors. They have been characterized to control virulence gene expression as well as genes related to metabolism (Ellison and Miller, 2006; Wilkinson and Grove, 2006; Grove, 2017). *Rhola_00002220*: MarR family transcriptional regulator does not have significant differential expression in light vs dark while *AURMO_01565*: MarR family protein has higher expression in light vs dark (Maresca et al., 2019). This suggests that *A. photophilum* may have light-regulated genes related to virulence, specifically, mediating DNA interactions. It is not completely surprising that this gene's expression differs between species, given it is thought that MarR family proteins likely provide species-specific regulation due to their species-specific diversity at the amino acid level (Ellison and Miller, 2006).

Each of these four transcriptional regulators are predicted to be generally related to transmembrane transport and/or metabolism which are two biological functions that are significantly represented among differentially expressed genes in previous transcriptome analyses (Maresca et al., 2019). The results of the previous transcriptome analyses suggest that these transcriptional regulators and the biological processes they regulate could be transcriptionally regulated by light. However, from those results alone, their regulatory targets' responses over time to light and dark cannot be determined. Therefore, these transcription factors are good candidates for

further study to understand how they transcriptionally respond to light. Identifying which genes, if any, share a similar response will give insight into which genes are co-regulated and which biological pathways may be responsible for the light-enhanced growth phenotype.

Transcription factor binding is one likely step in the proposed signal cascade, and the next likely step is the transcriptional activation or repression of genes. Genes that are shared by *R. lacicola* and the two *Aurantimicrobium* species, not found in *Microbacterium* sp. strain 10M-3C3, and have differential expression in light vs. dark are of particular interest since they are most likely to be part of the light-regulated signal cascade. Among those 71 shared genes that are not found in the *Microbacterium* sp. strain 10M-3C3 genome, the genes encoding predicted proteins related to metabolism, and protein processing that have similar transcriptional responses are good candidates for the homologous genes with light-regulated expression in the proposed shared signal cascade (**Figure 2.10 A & C**).

2.5.2 Shared Genes Related to Amino Acid Metabolism

Among the 71 shared genes encoding predicted proteins related to amino acid metabolism is the gene encoding *Rhola_00008090* methionine synthase (B-12 dependent). Methionine synthase is found in all domains of life and is necessary for methionine and methyl group metabolism (Deobald et al., 2020). In both *R. lacicola* and *A. photophilum*, the shared predicted gene that encodes methionine synthase had higher expression in constant light vs. constant dark, suggesting that methionine biosynthesis and the S-adenosylmethionine (SAM) cycle may be positively light regulated (Maresca et al., 2019). Since methionine synthase is found in all domains of life, it may be the shared predicted genes encoding methionine synthase in *R. lacicola*

and *A. photophilum* are regulated by a shared signal transduction pathway that is unique to species with the light enhanced growth phenotype.

2.5.3 Shared Genes Related to Protein Processing

I also identified four genes encoding predicted proteins related to protein processing among the 71 shared genes. Those genes encode *Rhola_00001450* dolichol-phosphate mannosyltransferase, *Rhola_00004630* Predicted Zn-dependent peptidase, *Rhola_00005630* peptide-methionine (S)-S-oxide reductase, and *Rhola_00007220* peptidyl-prolyl cis-trans isomerase (cyclophilin B). Interestingly, of the four genes encoding proteins related to protein processing described here, none had differential expression in light vs. dark in both *R. lacicola* and *A. photophilum* (Maresca et al., 2019). This shows that although *R. lacicola* and *A. photophilum* share genes not in *Microbacterium* sp. strain 10M-3C3, the transcriptional response of their shared genes differs in light vs dark. Meaning, the biological pathways that are light regulated may differ between *R. lacicola* and *A. photophilum*. Even though light regulated biological pathways may differ between *R. lacicola* and *A. photophilum*, it could be that the different light regulated pathways ultimately contribute to the same general function, such as protein processing, in both *R. lacicola* and *A. photophilum*.

In previous transcriptome analyses, *Rhola_00004630* Predicted Zn-dependent peptidase had higher expression in constant dark vs. constant light (Maresca et al., 2019). Proteases are ubiquitous in heterotrophic bacteria and are necessary for regulated protein degradation which plays a role in many biological functions (T. Supuran and Mastrolorenzo, 2011). Our results indicate that *R. lacicola* positively regulates predicted Zn-dependent peptidase in dark compared to in light and this regulation is not the same in *A. photophilum*.

In *A. photophilum*, *AURMO_00791*, a putative peptidyl-prolyl *cis-trans* isomerase has higher expression in constant light vs. constant dark (Maresca et al., 2019). Peptidyl-prolyl *cis/trans* isomerases (PPIases) assist in protein folding by catalyzing isomerization of peptidyl-prolyl bonds (Göthel and Marahiel, 1999). More recent studies show PPIases may also be involved in processes such as signal transduction, regulation of gene transcription, and translation regulation; though this is thought to be highly dependent on growth conditions (Ünal and Steinert, 2014). The genome comparisons presented here combined with the previous transcriptome analyses support that PPIase regulation is specific to growth conditions (light vs. dark) and between closely related species. Further study into the expression of *R. lacicola* and *A. photophilum* genes in response to light and dark cycling will better show which genes have light regulated expression.

2.5.4 Shared Genes Related to Metabolism

Ten genes related to metabolism were identified among the 71 shared genes. This group includes *AURMO_00616* Putative competence/damage-inducible protein CinA, which is related to natural competence in bacteria and is even necessary for optimal transformation of *Streptococcus mutans* (Mair et al., 2012). CinA has also been shown to have nicotinamide-nucleotide amidohydrolase and ADP-ribose pyrophosphatase activities in *Thermus thermophilus* indicating that it may be involved in the pyridine nucleotide cycle (Karuppiah et al., 2014). *AURMO_00616* has significantly higher expression in light compared to dark while the *R. lacicola* homolog does not have significantly differential expression (Maresca et al., 2019). This suggests that *A. photophilum* and *R. lacicola* may have different optimal conditions for natural competence.

Additionally, this group includes *Rhola_00011180* phosphomannomutase which has been characterized to convert mannose-6-phosphate to mannose-1-phosphate which is critical for GDP-D-mannose biosynthesis, a reaction used in various processes such as post translational modifications of proteins and glycoconjugate production (Li et al., 2018). While *Rhola_00011180* had higher expression in the dark vs. light, the *A. photophilum* homolog, *AURMO_00383* did not have significant differential expression (Maresca et al., 2019). This suggests that *R. lacicola* and *A. photophilum* may have different regulatory mechanisms for mannose metabolism and *R. lacicola* may prioritize mannose metabolism in the dark.

This group of genes also contains *AURMO_00885* D-inositol 3-phosphate glycosyltransferase which is the first dedicated step in mycothiol biosynthesis. Mycothiol is found in members of the Actinomycetota phylum, and is the major thiol in *Actinobacteria* where it protects against redox stressors and antibiotics (Newton et al., 2008). Specifically, mycothiol has shown to be part of a regulatory circuit that responds to acid stress in *Corynebacterium glutamicum* (Liu et al., 2016). *AURMO_00885* has high expression in dark vs. light while it's homolog in *R. lacicola*, *Rhola_00008110*, did not have significant differential expression; suggesting *A. photophilum* may increase stress response in the dark (Maresca et al., 2019). This further indicates that while *R. lacicola* and *A. photophilum* may have multiple shared predicted metabolic functions, each species may have different regulatory mechanisms.

2.5.5 Unique Genes Related to Transcriptional Regulation

Through genome comparisons, I identified ten putative transcriptional regulators that are unique to *A. photophilum* from *R. lacicola* and *Aurantimicrobium*

sp. strain MWH-UGA1. Among these ten putative transcriptional regulators are *AURMO_00914* FrmR transcriptional repressor and two copies of transcriptional repressor dicA: *AURMO_01696* and *AURMO_01752*. I also identified six putative transcriptional regulators that are unique to *R. lacicola* from *A. photophilum* and *Aurantimicrobium sp.* strain MWH-UGA1. Among those six putative transcriptional regulators are two copies of padR family transcriptional regulator: *Rhola_00001960* and *Rhola_00002790*.

FrmR transcriptional regulator is characterized to sense formaldehyde and regulate a glutathione-dependent formaldehyde detoxification pathway in *E. coli* (Herring and Blattner, 2004; Chen et al., 2016; Denby et al., 2016). *A. photophilum* may encounter formaldehyde from anthropogenic sources, live organisms, and/or decaying organic matter in its surface freshwater environment, therefore it is not surprising that *A. photophilum* encodes a predicted regulator of formaldehyde detoxification. However, previous transcriptome analyses show *AURMO_00914* FrmR transcriptional repressor has higher expression in response to dark vs. light, which indicates *A. photophilum* likely increases formaldehyde detection and detoxification in the dark (Maresca et al., 2019). This leads to many questions that can be addressed in the future including whether *A. photophilum* uses mycothiol, which *A. photophilum* also upregulates in the dark, or a different thiol as the formaldehyde carrier, whether light and/or increased formaldehyde concentration is a signal that regulates *AURMO_00914* FrmR expression, and what is the final oxidation product of formaldehyde detoxification in *A. photophilum* (Chen et al., 2016).

A. photophilum's unique set of genes contains two copies of putative DicA transcriptional repressors. Transcriptional repressor DicA regulates expression of

genes related to cell division and its own expression (Béjar et al., 1986). Additionally, DicA has been shown to be regulated by temperature, however the signal it responds to is not known (Yun et al., 2012). Previous transcriptome analyses show both *AURMO_01696* and *AURMO_01752* DicA has higher expression in light than in dark, suggesting *A. photophilum* likely increases cell division in response to light (Maresca et al., 2019).

R. lacicola's unique set of genes contains two copies of putative PadR transcriptional regulators. PadR transcriptional regulators are a large groups of transcriptional regulators that were first characterized to be repressors of the padA gene which encodes phenolic acid decarboxylase (Gury et al., 2004). Since then, padR-like transcriptional regulators have been identified in multiple other biological processes including stress responses, antibiotic biosynthesis, and carbon metabolism (Nguyen et al., 2011; Flórez et al., 2015; Morabbi Heravi et al., 2015). The two copies of putative PadR transcriptional regulators in the *R. lacicola* unique set of genes had different expression patterns in previous transcriptome analyses where *Rhola_00001960* does not have differential expression light vs dark and *Rhola_00002790* has significantly higher expression in dark vs light (Maresca et al., 2019).

Both *R. lacicola* and *A. photophilum's* group of unique transcriptional regulators contain multiple transcriptional regulators that respond to environmental stimuli. *A. photophilum* encodes a putative protein that responds to exogenous formaldehyde and both groups of unique genes have two copies of different predicted proteins: dicA transcriptional repressor and PadR family transcriptional regulators. Both proteins are characterized to respond to environmental stimuli, suggesting that *R.*

lacicola and *A. photophilum* can very specifically respond to environmental stimuli, using a slightly different set of biological mechanisms.

2.5.6 Concluding Remarks

In conclusion, I hypothesize that closely related freshwater Actinobacteria species with blue light-enhanced growth share mechanism(s) that relay blue-light sensing to increase growth. To identify the mostly likely genes related to the proposed signal cascade, I identified which genes are shared by the three Actinobacteria species with light-enhanced growth. I then combined this with previous transcriptome analyses from constant light vs. constant dark growth conditions to identify shared genes with significant differential expression. I also identified genes shared by and unique to these three species in comparison to *Microbacterium* sp. strain 10M-3C3, which does not have light-enhanced growth as well as genes that are unique to each of the three Actinobacteria species with blue-light enhanced growth in comparison to each other. Furthermore, I annotated GO-slim terms to the predicted proteins of, *R. lacicola* and *A. photophilum* and show their distribution in the shared and unique gene categories. Furthermore, I identified which predicted transcription factors and signal transduction proteins are in these categories of genes. These analyses identify putative genes and predicted functional characteristics that could be related to the light-enhanced growth phenotype and are good candidates for future expression analyses.

Specifically, the twenty-two genes shared by *R. lacicola* and *A. photophilum* that have significant differential expression in light vs dark includes *Rhola_00010430* two-component system, OmpR family, response regulator and *Rhola_00010440* two-component system, OmpR family, sensor kinase (**Table A.1**). Both the *R. lacicola* genes and the *A. photophilum* homologs have higher expression in the dark than in

light. This two-component sensor kinase and response regulator are excellent candidates for further study to determine if and what role they may play in the signal transduction of blue and near-UV light sensing in *R. lacicola* and *A. photophilum.* Unexpectedly, some genes that are shared by *R. lacicola* and *A. photophilum* and not shared with *Microbacterium* sp. strain 10M-3C3 related to transcriptional regulation, protein processing and metabolism do not have similar transcriptional responses to light and dark. This indicates there are likely some differences in which genes are light regulated between *R. lacicola* and *A. photophilum* (**Figure 2.10**). These analyses deliver new insights into which genes are involved in relating blue/near-UVB light sensing to the increased growth phenotype in two freshwater Actinobacteria species. Further studies to determine the presence of the genes identified here in other Actinobacteria as well as the dynamics of transcriptional responses in light and dark cycling will provide more insights into predicted light-regulated mechanisms in freshwater *Microbacteriacea*.

Chapter 3

PANGENOME ANALYSIS OF *MICROBACTERIACEAE*

3.1 Abstract

Members of the *Actinobacteria* phylum can make up 10-60% of the cells found in freshwater bacterioplankton populations (Glöckner et al., 2000; Hahn, 2006; Newton et al., 2011). Though until recently, little was known about the most abundant lineages of freshwater *Actinobacteria* at the species level (Newton et al., 2011). The first of these *Actinobacteria* to have a species description are members of the *Microbacteriaceae* family (Hahn et al., 2014). Since then, more species descriptions have been published. To learn which genes are shared among *Microbacteriaceae* and their distribution in different environments, the genomes of 27 *Microbacteriaceae* originally isolated from marine, freshwater, and soil environments were compared in a pangenome analysis. Overall, I was able to identify trends in the genetic differences between terrestrial *Microbacteriaceae* and marine *Microbacteriaceae*. The marine *Microbacteriaceae* are enriched with genes encoding predicted proteins related to Na+ use, cell division, transcriptional regulation, and signal transduction, while the terrestrial *Microbacteriaceae* are enriched with genes encoding predicted proteins related to signal transduction and combating oxidative stress. Using phylogenetic profiling, I identified COG functions that may be associated with marine, soil, and freshwater *Microbacteriaceae.* I also identified predicted proteins that co-occur with the *R. lacicola* actinorhodopsin, the *R. lacicola* predicted cryptochrome-like protein, and a predicted CryB-type cryptochrome found in some freshwater *Microbacteriaceae*

with light-enhanced growth. The results of the phylogenetic profiling provide insight into the which genes could be related to the enhanced growth phenotype previously observed in some freshwater *Microbacteriaceae*. Overall, this study supports that terrestrial *Microbacteriaceae* have streamlined genomes specialized for their environment.

3.2 Introduction

Many technological advancements in recent years have increased our capabilities to study microorganisms. Specifically, improvements in methodology, cost, and quality of whole genome sequencing have led to an increase in the number of published genomes available in various databases (Kwon and Cox, 2004; Land et al., 2015; Sanders et al., 2022). Databases such as the International Nucleotide Sequence Database Collaboration, the Joint Genome Institute Integrated Microbial Genomes Database (JGI IMG), and the Genome Taxonomy Database (GTDB) have allowed for the study and comparison of microorganisms. Importantly, these databases also contain metadata that describe when and from what kind of environment an organism was isolated. Incorporating metadata to the study of microbial genomes has expanded our ability to determine biogeochemical characteristics within different environments (Newman and Banfield, 2002). This approach can help predict how microorganisms are fit for their environments and what roles they may play in their community.

A family of bacteria that can now be studied in more detail is the *Microbacteriaceae*. *Microbacteriaceae* are found in terrestrial and aquatic ecosystems (Evtushenko and Takeuchi, 2006). The first freshwater members of the class *Actinobacteria* that were isolated are members of the *Microbacteriaceae* family, and include the species *R. lacicola* and *A. photophilum* (Hahn et al., 2003). *Actinobacteria*

are of particular interest because they are known to encode light-sensing proteins, though how *Microbacteriaceae* use light is not completely understood (Sharma et al., 2008; Newton et al., 2011; Ghai et al., 2014; Keffer et al., 2015; Maresca et al., 2019; Chazan et al., 2022). Multiple *Microbacteriaceae* genomes are now available, which makes genome comparisons between species possible.

To learn about genes shared among *Microbacteriaceae* and their distribution in different environments, I have conducted a pangenome analysis of *27 Microbacteriaceae* species. Specifically, my goal is to identify genes that may be related to the unresolved molecular functions of certain light sensors in freshwater *Microbacteriaceae* species with light-enhanced growth. I aim to identify genes enriched in freshwater *Microbacteriaceae* species, since actinorhodopsins are found in Actinobacteria, which are regularly identified in freshwater environments, and the previously observed light-enhanced growth was identified in three closely related freshwater *Microbacteriaceae*. In addition to enrichment analyses, I also used a phylogenetic profiling approach to identify genes that may be involved in signal transduction and transcriptional responses to light.

From the comparison of 27 *Microbacteriaceae* genomes, I found that terrestrial (soil and freshwater) *Microbacteriaceae* genomes are enriched in mechanisms to respond to oxidative stress. The enrichment in predicted genes related to oxidative stress indicates that terrestrial *Microbacteriaceae* may experience more oxidative stress than their marine counterparts. Additionally, I found that genes predicted to encode proteins related to multiple cofactor biosynthesis pathways co-occur with light-sensing proteins found in some freshwater *Microbacteriaceae*. Co-factor biosynthesis may be light-regulated in some freshwater *Microbacteriaceae* and linked

to light-enhanced growth. Based on this evidence, I predict that closely-related *Microbacteriaceae* with light-enhanced growth likely have species specific light-mediated molecular functions.

3.3 Materials and Methods

3.3.1 Genome Selection and Quality Assessment

To form the initial data set, *Microbacteriaceae* genomes were selected using metadata from the Genome Taxonomy Database (GTDB) Release95 and subsequently downloaded from the National Center for Biotechnology Information (NCBI) Genome Database. Only genomes with metadata indicating isolation from marine, freshwater, or soil related environments were selected. Given the previous criterion, strains designated 'representative' by the GTDB were selected where possible. Representative strain designation in the GTDB is determined by considering the type strain of a species, average nucleotide identity (ANI), and alignment fraction (AF) between genomes of a given species (Parks et al., 2020). CheckM metadata from the GTDB was also collected to assess the quality of the isolate genomes. Only genomes with greater than 96% completeness and less than 3% contamination were selected. *Rhodoluna lacicola* strain MWH-Ta8, *Aurantimicrobium photophilum* strain MWH-Mo1, *Aurantimicrobium* sp. strain UGA1, and *Microbacterium* sp. strain 10M-3C3 were also included. The resulting dataset includes 27 genomes (13 isolated from freshwater environments, 7 isolated from marine related environments, and 7 isolated from soil related environments) (**Table 3.1**).

Table 3.1 Metadata of 27 *Microbacteriaceae* species. Environment, latitude, and longitude that organism was isolated from, accession numbers, CheckM completeness and CheckM contamination were collected from the Genome Taxonomy Database (GTDB) Release95.

Genome Name	Accession Number	Environment	Latitude, Longitude	CheckM Completeness (%)	CheckM Contamination (%)
Agrococcus pavilionensis strain RW1	GCF_000400485.1	freshwater	50.86677, -121.74191	100	1.38
Aquiluna sp. strain UB-MaderosW2red	GCF_900100865.1	freshwater	-62.663, -61.1769	98.1	0
Aurantimicrobium minutum	GCF_002355535.1	freshwater	34.28, 132.64	97.47	0
Aurantimicrobium photophilum strain MWH-Mo1	GCF_003194085.1	freshwater	47, 13	97.47	0
Aurantimicrobium sp. strain MWH-Uga1	GCF_003325955.1	freshwater	1.3733, 32.2903	98.4	0
Cryobacterium psychrotolerans strain CGMCC 1.5382	GCF_900101115.1	freshwater	43.05, 86.48	99.49	0
Glaciibacter superstes DSM 21135	GCF_000421145.1	freshwater	64.95, -147.61	99.49	2.02
Glaciihabitans tibetensis strain CGMCC 1.12484 Ga0171600_101	GCF_003003265.1	freshwater	29.469917, 96.500806	99.41	0.51
Leifsonia aquatica strain ATCC 14665	GCF_000469485.1	freshwater	41.8781, -87.6298	97.79	1.14
Microbacterium sp. strain 10M-3C3	GCF_003931875.1	freshwater	-2.46, 121.28	99.49	0.51
Rhodoluna lacicola strain MWH-Ta8	GCA_000699505.1	freshwater	31.258, 120.2051	99.42	0
Subtercola boreus strain K300	GCF_003399685.1	freshwater	37.4563, 126.7052	99.49	0.93
Microterricola viridarii strain ERGS5:02	GCF_001542775.1	freshwater	27.552483, 88.123433	98.91	1.84
Microbacterium sediminis strain YLB-01	GCF_002741995.1	marine	-37.8111, 49.8405	99.44	0

Genome Name	Accession Number	Environment	Latitude, Longitude	CheckM Completeness (%)	CheckM Contamination (%)
Pontimonas salivibrio strain CL-TW6	GCF_002950575.1	marine	34.98, 126.15	97.25	0
Salinibacterium amurskyense strain DSM 16400	GCF_002797685.1	marine	43.0732, 131.7014	98.99	0.51
Microbacterium profundi strain Shh49	GCF_000763375.1	marine	8.377, -145.399	99.49	0.51
*Microbacterium maritypicum*_A UBA6732	GCA_002453945.1	marine	54.341667, -5.183333	96.8	0.67
Microbacterium hydrothermale strain BPSAC84	GCF_004854025.1	marine	23.566667, 92.366667	98.99	0
Microbacterium enclense strain NIO-1002	GCF_001456955.1	marine	15.5428, 73.9208	98.99	0.51
Microcella alkaliphila strain JAM-AC0309	GCF_002355395.1	soil	41.191095, 142.197702	99.38	0.25
Agrococcus carbonis strain DSM 22965	GCF_900104705.1	soil	23.7872198147763, 86.878412915298	99.49	0.17
Leucobacter chromiiresistens strain JG 31	GCF_000231305.1	soil	15.87, 100.9925	96.44	0
Agromyces cerinus subsp. cerinus strain DSM 8595	GCF_900142065.1	soil	55.7558, 37.6173	99.49	0
Pseudoclavibacter soli DSM 23366	GCF_000423505.1	soil	36.3504, 127.3845	99.71	0.19
Yonghaparkia sp. strain Soil809	GCF_001429705.1	soil	50.958, 6.856	99.44	0
Rathayibacter tritici strain NCPPB 1953	GCF_001641005.1	soil	32.4279, 53.688	99.41	2.53

3.3.2 Pangenome Construction

A pangenome of the 27 *Microbacteriaceae* genomes was generated using Anvi'o v6.1 (Eren et al., 2015, 2021). The blastp algorithm at NCBI was used to

calculate amino acid sequence similarity and subsequent gene clustering. All gene calls were included and a minbit parameter (Benedict et al., 2014) of 0.5 was used to filter out weak amino acid matches. An MCL inflation parameter (van Dongen and Abreu-Goodger, 2012) of 4.0 was used to cluster the blastp results, since these genomes share the same family taxonomy. Core, accessory, and unique gene designations were determined for each environment in the Anvi'o interactive interface, calculated from euclidean distance and ward linkage of gene clusters and genomes.

3.3.3 Gene Cluster Enrichment Analysis

The Anvi'o program *anvi-compute-functional-enrichment-in-pan* with the *--annotation source* parameter set to IDENTITY and the *--include-gc-identity-as-function* parameter was used to calculate enrichment of each gene cluster in each environment (soil, marine, freshwater). A gene cluster was labeled associated with an environment or environments if it had an enrichment score greater than 12 and an adjusted p-value (q-value) of the enrichment score is less than 0.05.

3.3.4 Phylogenetic Profiling

The additional parameter, *--functional-occurrence-table-output*, was included during the gene cluster enrichment analysis and was used to count the occurrence of gene clusters in each genome. Gene clusters were then filtered to determine co-occurrence with genes of interest. To determine which gene clusters among the 27 *Microbacteriaceae* have similar co-occurrence with the actinorhodopsins containing gene cluster GC_00002542, gene clusters were filtered for those that occur in *R. lacicola*, *Aurantimicrobium* sp. strain MWH-UGA1 and do not occur in *Microbacterium* sp. strain 10M-3C3. To determine which gene clusters among the 27

Microbacteriaceae have similar co-occurrence with the cryptochrome containing gene clusters GC_00008960 and GC_00001625, gene clusters were filtered for those that occur in *Aquiluna* sp. strain UB-MaderosW2red, *Aurantimicrobium* sp. strain MWH-UGA1, *A. photophilum*, *A. minutum*, *M. alkilipohila* strain JAM-AC0309, *P. salivibrio* strain CL-TW6, *R. tritici* strain NCPPB 1953, *R. lacicola*, *S. boreus* strain K300, *Yonghaparkia* sp. strain Soil809, and not in *Microbacterium* sp. strain 10M-3C3. Absence in *Microbacterium* sp. strain 10M-3C3 was used to filter gene clusters because it does not have the light enhanced growth phenotype. To determine which gene clusters among the 27 *Microbacteriaceae* have similar co-occurrence to the gene cluster GC_00003485, which includes genes that are predicted to encode cryptochrome-like proteins, gene clusters were filtered for those that occur in *Aquiluna* sp. strain UB-MaderosW2red, *P. salivibrio* strain CL-TW6, *R. lacicola*.

3.3.5 COG Function Enrichment Analysis

The 27 *Microbacteriaceae* genomes were categorized by the environment from which they were isolated (freshwater, soil, or marine). The Anvi'o program *anvi-get-enriched-functions-per-pan-group* with the *functional-occurrence-table-output* parameter was used to identify and count COG functions in each genome as well as statistically test for enrichment within freshwater, marine, and/or soil environments. COG functions were considered enriched if the adjusted p-value (q-value) of the enrichment score is lower than 0.05. COG functions were then analyzed for association with each environment. COG functions were labeled with an associated environment if the proportion of genomes in that environment was equal to 1 or the proportion was greater than three times that of other environments. Additionally, a COG function was only labeled as associated with an environment if present in more

than three of the genomes for a given environment. COG functions with a proportion equal to one in all three environments were considered associated with all three. The COG functions associated with each environment were used to assess environmental association of metabolic traits in *Microbacteriaceae*.

3.3.6 Mapping Locus Tags to Gene Clusters

The Anvi'o program *anvi-get-sequences-for-gene-clusters* was used to output the fasta protein sequences in each gene cluster. The output fasta protein sequences were compared to the *R. lacicola* and *A. photophilum* predicted protein sequences using blastp with standard parameters to identify the corresponding locus tags of the sequences in the gene clusters.

3.3.7 Data and Code Availability

Accession numbers, environment, latitude, longitude, CheckM completeness, and CheckM contamination, were collected from the Genome Taxonomy Database (GTDB) Release95 (**Table 3.1**). Genomes were collected from the National Center for Biotechnology (NCBI) Genome Database. Scripts for pangenome generation, analyses, and associated files are available at (https://github.com/MarescaLab/microbacteriaceae-pan-genome).

3.4 Results

3.4.1 Geographic Distribution

In previous work, we compared the genomes of *R. lacicola, A. photophilum, Aurantimicrobium* sp. strain MWH-UGA1, and *Microbacterium* sp. strain 10M-3C3 to each other to identify genes potentially related to the light-enhanced growth phenotype

shared by *R. lacicola* and the two *Aurantimicrobium* species. These four species are related at the family level, belonging to *Microbacteriaceae*, and were isolated from freshwater. To expand our genome comparisons, an additional 23 genomes were selected. Among the total 27 genomes selected for this dataset, 7 were isolated from soil, 7 were isolated from marine environments, and 13 were isolated from freshwater. This subset of *Microbacteriaceae* is geographically diverse (**Figure 3.1**).

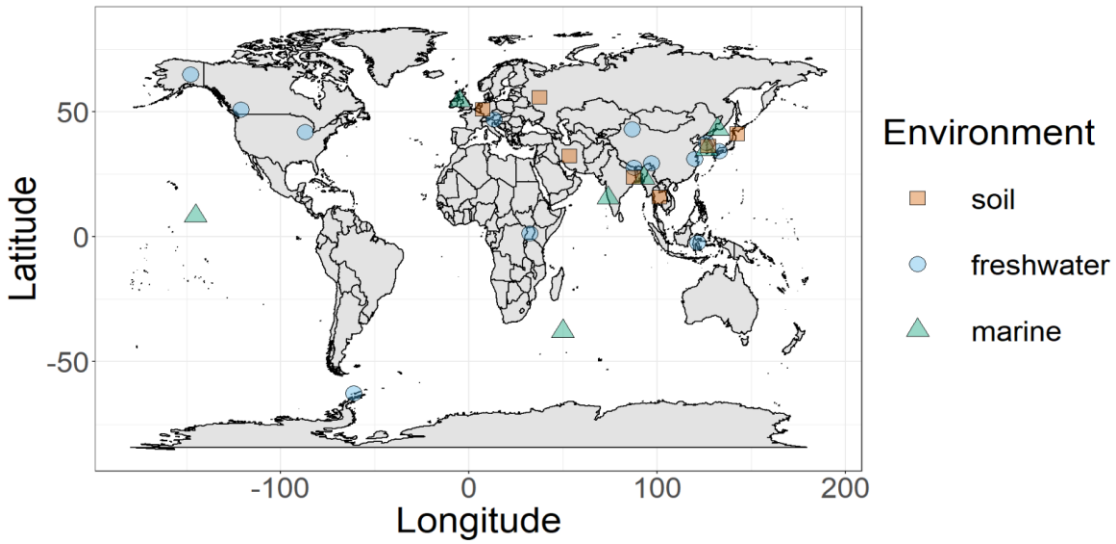

Figure 3.1 Global Distribution of *Microbacteriaceae.* Map of original sampling sites of 27 *Microbacteriaceae* species/strains. Each point represents one species/strain. Squares indicate species/strain was isolated from soil, circles indicate isolation from freshwater, and triangles indicate isolation from marine environments.

3.4.2 *Microbacteriaceae* Pangenome

To detect unique genomic characteristics of freshwater *Microbacteriaceae*, the pangenome analysis compared soil and marine species to freshwater species. First, gene clusters in the core, accessory, and singleton bins of all 27 species were calculated. Gene clusters present in all 27 genomes are labeled “core”, gene clusters present in 1 genome are labeled “singleton”, and gene clusters present in 2-26

genomes are labeled “accessory” (**Figure 3.2**). This resulted in 403 core gene clusters, 8,528 accessory gene clusters, and 22,101 singleton gene clusters. Among the 8,528 accessory gene clusters, are the freshwater, marine, and soil specific gene clusters.

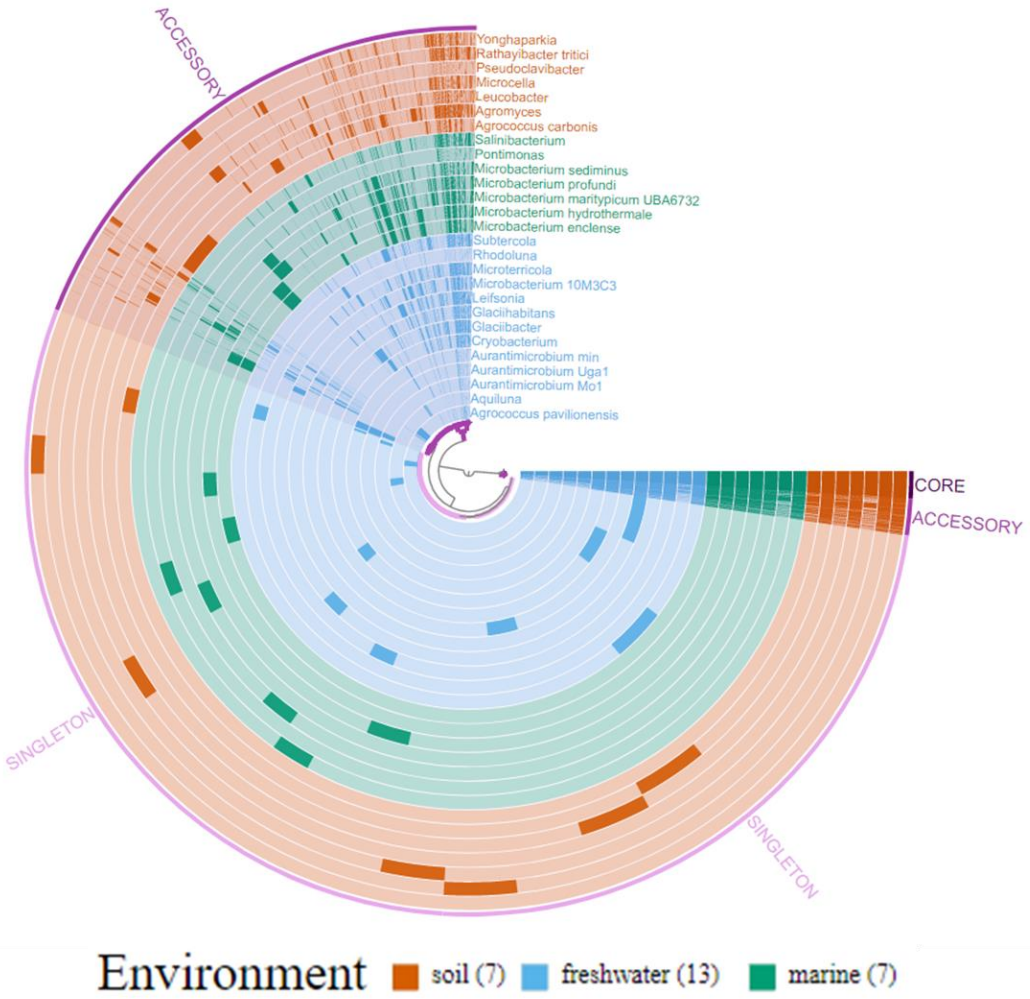

Figure 3.2 Pangenome of 27 *Microbacteriaceae* Circle phylogram shows the presence/absence of gene clusters in each genome. Each layer corresponds to one genome and are colored by their environment. Darker sections indicate gene cluster(s) are present while light sections indicate absence of gene cluster(s). In the outermost layer, gene clusters present in all 27 genomes are labeled the “core” of the pangenome, gene clusters present in a single genome are labeled “singleton”, and gene clusters present in 2-26 genomes are labeled “accessory”.

3.4.3 Gene Cluster Enrichment Analysis

Gene cluster enrichment analysis identified which gene clusters are associated with the freshwater, marine, and/or soil environments assigned to the 27 genomes. In total, 157 gene clusters were associated with one or two environments. 150 of the 157 gene clusters are associated with marine environments, 5 are associated with terrestrial (freshwater and soil) environments, and 2 are associated with soil environments (**Table A.12**). The five gene clusters associated with freshwater and soil environments were assigned the COG functions: 'Peroxiredoxin', 'Glutaredoxin', 'Uncharacterized conserved protein YabN, contains tetrapyrrole methylase and MazG-like pyrophosphatase domain', 'Forkhead associated (FHA) domain, binds pSer, pThr, pTyr' and 'UDP-N-acetylenolpyruvoylglucosamine reductase' (**Table 3.2**).

The *R. lacicola* protein sequences that correspond to four of the five gene clusters associated with freshwater and soil environments are '*Rhola_00006540*: Peroxiredoxin', '*Rhola_00010100*: Protein containing tetrapyrrole methyltransferase domain and MazG-like (Predicted pyrophosphatase) domain', '*Rhola_00001930*: Glutaredoxin-like domain (DUF836)', '*Rhola_00008840*: FHA domain protein'. Each of the four *R. lacicola* proteins have a best reciprocal hit in *A. photophilum*. GC_00000887 contains the *A. photophilum* gene '*AURMO_01480*: UDP-N-acetylenolpyruvoylglucosamine reductas) (**Table 3.2**).

Table 3.2 Significantly enriched gene clusters among terrestrial *Microbacteriaceae.* Gene cluster ID numbers, enrichment score, adjusted p-value, associated groups, corresponding *R. lacicola* locus tags, corresponding *A. photophilum* locus tags, and *R. lacicola* gene annotations that were calculated during construction of the pan-genome of 27 *Microbacteriaceae* and subsequent mapping of locus tags to gene clusters. A gene cluster was labeled enriched in an environment or environments if it had an enrichment score greater than 12 and an adjusted p-value (q-value) less than 0.05.

Gene Cluster IDs	Enrichment score	Adjusted p-value (q-value)	Associated Groups	*R. lacicola* Locus Tag	*A. photophilum* Locus Tag	*R. lacicola* Annotation
GC_00000867	18.98919	0.02773	freshwater, soil	Rhola_00006540	AURMO_00726	Peroxiredoxin
GC_00000822	14.34996	0.02773	freshwater, soil	Rhola_00010100	AURMO_01336	Protein containing tetrapyrrole methyltransferase domain and MazG-like (Predicted pyrophosphatase) domain
GC_00000969	14.07502	0.02773	freshwater, soil	Rhola_00001930	AURMO_01665	Glutaredoxin-like domain (DUF836)
GC_00000736	13.3958	0.02773	freshwater, soil	Rhola_00008840	AURMO_00959	FHA domain protein
GC_00000887	12.75697	0.037919	freshwater, soil	N/A	AURMO_01480	UDP-N-acetylenolpyruvoylglucosamine reductase

3.4.4 COG Function Enrichment Analysis

The COG function enrichment analysis identified which COG functions are associated with freshwater, marine, and/or soil environments assigned to the 27 genomes. For the COG function enrichment analysis, COG functions may have multiple gene clusters assigned to them. No COG functions were identified as enriched within freshwater, marine, and/or soil environments with an adjusted p-value (q-value) lower than 0.05. This result may be because too few genomes were included for a reliable COG function enrichment analysis. Therefore, I identified COG functions that may be associated with a given environment by analyzing the proportion of genomes from each environment with a given COG function. 26 COG functions may be associated with freshwater, 16 COG functions may be associated

with soil, 35 COG functions may be associated with marine, and 32 COG functions may be associated with soil and marine environments (**Table A.13**).

Of the 26 COG functions that may be associated with the *Microbacteriacea* isolated from freshwater, two COG functions are predicted to be in *R. lacicola* and *A. photophilum* and not in *Microbacterium* sp. strain 10M-3C3 (**Table 3.3**). Those COG functions are 'RNA processing exonuclease, beta-lactamase fold, Cft2 family' and 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system'. The COG function 'RNA processing exonuclease, beta-lactamase fold, Cft2 family' is predicted to be in *Aurantimicrobium* sp. strain MWH-UGA1 while 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system' is not. Furthermore, *A. photophilum* is predicted to have two genes with the predicted function 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system' while *R. lacicola* is predicted to have one gene with this function.

Table 3.3 Predicted COG Functions associated with freshwater and found in *R. lacicola* and *A. photophilum*. Predicted COG functions, enrichment score, adjusted p-value, associated groups, assigned gene cluster ids, and occurrence in three genomes that were calculated during construction of the pan-genomes of 27 *Microbacteriaceae* species. A gene cluster was labeled associated with an environment or environments if the proportion of genomes in an environment was equal to 1 or the proportion was greater than three times that of other environments. Additionally, a COG function was only labeled as associated with an environment if present in three or more of the genomes for a given environment.

COG FUNCTION	Enrichment score	Adjusted q-value	Associated Groups	Gene Clusters IDs	Occurrence in *R. lacicola*	Occurrence in *A. photophilum*	Occurrence in *Microbacterium* sp. strain 10M-3C3
mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system	4.746858	0.802067	freshwater	GC_00002073, GC_00006842, GC_00010092, GC_00015244, GC_00020507, GC_00023283	1	2	0

COG FUNCTION	Enrichment score	Adjusted q-value	Associated Groups	Gene Clusters IDs	Occurrence in *R. lacicola*	Occurrence in *A. photophilum*	Occurrence in *Microbacterium* sp. strain 10M-3C3
RNA processing exonuclease, beta-lactamase fold, Cft2 family	3.281557	0.802067	freshwater	GC_00002411, GC_00009994, GC_00019024	1	1	0

3.4.5 COG Function Co-Occurrence with Genes that Encode Actinorhodopsin

The co-occurrence analysis identified gene clusters with a similar distribution pattern to four gene clusters in 27 *Microbacteriaceae* species. The four gene clusters contain genes that encode actinorhodopsins or genes predicted to encode cryptochromes and a cryptochrome-like proteins. Though *A. photophilum* and *Aurantimicrobium* sp. strain MWH-UGA1 do encode predicted heliorhodopsins, heliorhodopsins were not included in this analysis. Gene cluster GC_00002542 contains *Rhola_00012080* and *AURUGA1_00474*, the actinorhodopsin encoding genes from *R. lacicola* and *Aurantimicrobium* sp. strain MWH-UGA1. Gene cluster GC_00008960 contains the predicted CryB-type cryptochrome encoding gene Rhola_00013030 from *R. lacicola* and gene cluster GC_00001625 contains the predicted CryB-type cryptochrome encoding gene *AURMO_00962* from *A. photophilum*. Gene cluster GC_00003485 contains the cryptochrome-like protein encoding gene Rhola_00011000 from *R. lacicola*.

The actinorhodopsins containing gene cluster GC_00002542, contains genes from *Aquiluna* sp. strain UB-MaderosW2red, *Aurantimicrobium* sp. strain MWH-UGA1, *A. minutum*, and *G. tibetensis* strain CGMCC 1.12484 Ga0171600_101 all of which were isolated from freshwater environments (**Table 3.4**). 20 gene clusters were identified with similar co-occurrence to GC_00002542 (**Table 3.4**). 13 of those gene

clusters' predicted functions are related to metabolism, with most related to sugar metabolism. One gene cluster is related to carotenoid biosynthesis (GC_00002203), one gene cluster is related to ubiquinone biosynthesis (GC_00002269), two gene clusters have unknown functions (GC_00002910 and GC_00000467), one gene cluster is related to metal ion transmembrane transport (GC_00003907), and one gene cluster is related to transcriptional regulation (GC_00000900) (**Table 3.4**).

Table 3.4 Presence of Gene Clusters that Co-Occur with Genes that Encode Actinorhodopsin Proteins Among 27 *Microbacteriaceae* Genomes. Shown are gene clusters that co-occur with actinorhodopsin genes and their presence among 27 *Microbacteriaceae*. Gene clusters were first identified in the *Microbacteriaceae* pangenome analysis. Gene clusters were then filtered to determine which co-occur with the actinorhodopsin gene. A gene cluster co-occurs with actinorhodopsin genes if it is present (equal to or greater than 1) in *R. lacicola*, *Aurantimicrobium* sp. strain MWH-UGA1, and not present (equal to 0) in *A. photophilum*. A presence of greater than 1 indicates a genome has more than one predicted gene included in a gene cluster. The gene cluster that contains the *R. lacicola* and *Aurantimicrobium* sp. strain MWH-UGA1 actinorhodopsin genes is GC_00002542 and was assigned the COG function 'Bacteriorhodopsin' from the pangenome analysis. Gene clusters related to carotenoid biosynthesis are highlighted in red. Gene clusters related to ubiquinone biosynthesis are highlighted in green. Gene clusters related to metabolism are highlighted in blue, with dark blue indicated sugar metabolism and light blue indicated other types of metabolism. Gene clusters with unknown functions are highlighted in purple. Gene clusters with miscellaneous functions are not highlighted.

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00002542	Bacteriorhodopsin	0	1	0	1	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GC_00002203	Phytoene dehydrogenase-related protein	0	1	0	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00002269	4-hydroxybenzoate polyprenyltransferase	0	1	0	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GC_00002910	Uncharacterized membrane protein YdfJ, MMPL/SSD domain	0	1	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GC_00000467	#N/A	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GC_00003907	Mn2+ and Fe2+ transporters of the NRAMP family	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GC_00001538	DNA-binding transcriptional regulator, GntR family	0	0	0	1	0	0	1	0	0	2	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0
GC_00002361	Glutamate-1-semialdehyde aminotransferase	0	1	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
GC_00001482	Acyl-CoA hydrolase	0	0	0	1	0	0	0	0	0	2	1	1	0	0	0	1	0	1	0	0	0	0	2	1	0	0	0

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00000311	Aldo/keto reductase, related to diketogulonate reductase	1	0	0	1	1	2	1	1	1	1	2	1	2	1	2	0	1	1	2	1	1	1	0	0	1	2	0
GC_00001692	Fructose-bisphosphate aldolase class Ia, DhnA family	0	0	0	1	0	0	1	0	0	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0
GC_00001736	Sugar or nucleoside kinase, ribokinase family	0	0	0	1	0	0	1	0	0	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0
GC_00002319	5-deoxy-D-glucuronate isomerase	0	0	0	1	0	0	0	0	0	1	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
GC_00002368	TPP-dependent trihydroxycyclohexane-1,2-dione (THcHDO) dehydratase, myo-inositol metabolism	0	0	0	1	0	0	0	0	0	1	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00002646	Sugar phosphate isomerase/epimerase	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GC_00002764	Predicted dehydrogenase	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GC_00002837	Sugar phosphate isomerase/epimerase	0	0	0	1	0	0	0	0	0	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GC_00002950	Sugar phosphate isomerase/epimerase	0	0	0	1	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GC_00003972	ABC-type glycerol-3-phosphate transport system, permease component	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GC_00005238	ABC-type sugar transport system, permease component	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

3.4.6 COG Function Co-Occurrence with Genes that Encode Cryptochromes

The cryptochrome containing gene clusters GC_00001625 and GC_00003485 contain genes from *Aquiluna* sp. strain UB-MaderosW2red, *Aurantimicrobium* sp. strain MWH-UGA1, *A. photophilum*, *A. minutum*, *M. alkilipohila* strain JAM-AC0309, *P. salivibrio* strain CL-TW6, *R. tritici* strain NCPPB 1953, *R. lacicola*, *S. boreus* strain K300, and *Yonghaparkia* sp. strain Soil809 (**Table 3.5**). This group of *Microbacteriacea* includes species isolated from freshwater, soil, and marine environments (**Table 3.5**). 5 gene clusters were identified with similar co-occurrence to the GC_00001625 and GC_00003485 gene clusters. The 5 gene clusters are predicted to encode genes related to transcriptional regulation (GC_00000900), cell wall biosynthesis (GC_00000892), vitamin B5 biosynthesis (GC_00000816), FHA domain functions (GC_00000736), and a NIF3 family protein (GC_00000781) (**Table 3.5**).

Table 3.5 Presence of Gene Clusters that Co-Occur with Genes that Encode Cryptochrome Proteins among 27 *Microbacteriaceae* Genomes. Shown is the presence of gene clusters among 27 *Microbacteriaceae* that co-occur with two gene clusters, GC_00001625 and GC_00008960, which were assigned the COG function 'Uncharacterized protein related to deoxyribodipyrimidine photolyase' from the pangenome analysis and are highlighted in purple. GC_00001625 and GC_00008960 contain genes encoding cryptochrome proteins. Gene clusters were first identified in the *Microbacteriaceae* pangenome analysis. Gene clusters were then filtered to determine which co-occur with two cryptochrome containing gene clusters. A gene cluster co-occurs with the cryptochrome genes if it is present (equal to or greater than 1) in *Aquiluna* sp. strain UB-MaderosW2red, *Aurantimicrobium* sp. strain MWH-UGA1, *A. photophilum*, *A. minutum*, *M. alkilipohila* strain JAM-AC0309, *P. salivibrio* strain CL-TW6, *R. tritici* strain NCPPB 1953, *R. lacicola*, *S. boreus* strain K300, *Yonghaparkia* sp. strain Soil809, and not present (equal to 0) in *Microbacterium* sp. strain 10M-3C3. A presence of greater than 1 indicates a genome has more than one predicted gene included in a gene cluster.

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glaciibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00001625	Uncharacterized protein related to deoxyribodipyrimidine photolyase	0	0	1	1	1	0	0	0	0	0	0	0	1	0	0	0	2	0	1	1	0	0	0	0	0	1	0
GC_00008960	Uncharacterized protein related to deoxyribodipyrimidine photolyase	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00000736	Forkhead associated (FHA) domain, binds pSer, pThr, pTyr	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1
GC_00000781	Putative GTP cyclohydrolase 1 type 2, NIF3 family	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	1	1	0	0	0	0	0	1	1
GC_00000816	Ketopantoate hydroxymethyltransferase	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	1	1	1	1	0	0	0	0	0	1	1
GC_00000892	D-alanine-D-alanine ligase and related ATP-grasp enzymes	0	1	1	1	1	1	1	1	1	0	1	1	1	0	1	0	1	1	1	1	0	0	0	0	0	1	1
GC_00000900	DNA-binding transcriptional regulator, MocR family, contains an aminotransferase domain	0	1	1	1	1	1	1	1	1	0	1	1	1	0	1	0	1	1	1	1	0	0	0	0	0	1	1

The gene cluster GC_00003485 includes genes that are predicted to encode cryptochrome-like proteins and contains genes from *Aquiluna* sp. strain UB-MaderosW2red, *P. salivibrio* strain CL-TW6, and *R. lacicola*. This group of *Microbacteriaceae* includes species isolated from freshwater and marine environments (**Table 3.6**). 9 gene clusters were identified with similar so-occurrence to the gene cluster GC_00003485 (**Table 3.6**). 4 gene clusters are related to metabolism, specifically, the TCA cycle (GC_00001115), the pentose phosphate pathway (GC_00002576), sugar metabolism (GC_00002895), and tryptophan catabolism (GC_00003609). One gene cluster is related to vitamin B6 biosynthesis (GC_00001592), one gene cluster has an unknown function (GC_00001506), and one gene cluster has genes predicted to encode prophage maintenance proteins (GC_00004941) (**Table 3.6**).

Table 3.6 Presence of Gene Clusters that Co-Occur with Genes that Encode Cryptochrome-like Proteins among 27 *Microbacteriaceae* Genomes. Shown is the presence of gene clusters among 27 *Microbacteriaceae* that co-occur with the gene cluster GC_00003485 which as assigned the COG function 'Deoxyribodipyrimidine photolyase' from the pangenome analysis and is highlighted in purple. GC_00003485 contains the *R. lacicola* gene encoding a cryptochrome-like protein. Gene clusters were first identified in the *Microbacteriaceae* pangenome analysis. Gene clusters were then filtered to determine which co-occur with the gene cluster that contains the gene encoding the cryptochrome-like protein. A gene cluster co-occurs with GC_00003485 if it is present (equal to or greater than 1) in *Aquiluna* sp. strain UB-MaderosW2red, *P. salivibrio* strain CL-TW6, *R. lacicola*. A presence of greater than 1 indicates a genome has more than one predicted gene included in a gene cluster. Gene clusters containing genes related to metabolism are highlighted in light blue.

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glaciibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00003485	Deoxyribodipyrimidine photolyase	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
GC_00001506	#N/A	0	1	0	0	0	0	0	0	1	0	0	1	1	0	0	1	0	1	1	0	0	0	0	0	0	1	1
GC_00004941	Prophage maintenance system killer protein	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

		Environment, Genome, # of predicted genes assigned to gene cluster																										
		freshwater													soil							marine						
Gene Cluster ID	**COG Function**	**Agrococcus pavilionensis strain RW1**	**Aquiluna sp. strain UB-MaderosW2red**	**Aurantimicrobium photophilum**	**Aurantimicrobium sp. strain MWH-Uga1**	**Aurantimicrobium minutum**	**Cryobacterium psychrotolerans strain CGMCC 1.5382**	**Glacibacter superstes DSM 21135**	**G. tibetensis strain CGMCC 1.12484 Ga0171600_101**	**Leifsonia aquatica strain ATCC 14665**	**Microbacterium sp. strain 10M-3C3**	**Microterricola viridarii strain ERGS5:02**	**Rhodoluna lacicola strain MWH-Ta8**	**Subtercola boreus strain K300**	**Agrococcus carbonis strain DSM 22965**	**Agromyces cerinus subsp. cerinus strain DSM 8595**	**Leucobacter chromiresistens strain JG 31**	**Microcella alkaliphila strain JAM-AC0309**	**Pseudoclavibacter soli DSM 23366**	**Rathayibacter tritici strain NCPPB 1953**	**Yonghaparkia sp. strain Soil809**	**Microbacterium enclense strain NIO-1002**	**Microbacterium hydrothermale strain BPSAC84**	**Microbacterium maritypicum_A UBA6732**	**Microbacterium profundi strain Shh49**	**Microbacterium sediminis strain YLB-01**	**Pontimonas salivibrio strain CL-TW6**	**Salinibacterium amurskyense strain DSM 16400**
GC_00005241	Permease of the drug/metabolite transporter (DMT) superfamily	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
GC_00001997	Forkhead associated (FHA) domain, binds pSer, pThr, pTyr	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0
GC_00001592	Pyridoxine/pyridoxamine 5'-phosphate oxidase	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	1	1	1	0	0	0	1	1
GC_00001115	Isocitrate dehydrogenase	0	1	0	0	0	1	1	1	1	0	0	1	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1
GC_00002576	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0
GC_00002895	Phosphomannomutase	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
GC_00003609	Kynureninase	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

3.5 Discussion

Among the 27 *Microbacteriaceae* in this dataset, 13 were isolated from freshwater, 7 were isolated from soil, and 7 were isolated from marine environments. The 27 species have been isolated from across the globe (**Figure 3.1**). Additionally, many *Microbacteriaceae* have streamlined genomes thought to be specialized for their environments (Cho et al., 2018). To explore which predicted cellular functions may be specialized to terrestrial *Microbacteriaceae* vs. marine *Microbacteriaceae,* I compared the presence of predicted genes in terrestrial vs. marine *Microbacteriaceae* genomes. To do this, I generated a pan-genome of 27 freshwater, soil and marine *Microbacteriaceae* and identified genes enriched and/or shared by *Microbacteriaceae* isolated from terrestrial environments vs. marine environments (**Figure 3.2**).

In the gene cluster enrichment analysis, I identified 150 gene clusters enriched in the marine genomes, 2 enriched in soil genomes, and 5 enriched in terrestrial (freshwater and soil) environments (**Table A.12**). The larger number of enriched gene clusters in marine environments compared to terrestrial is not surprising, given that marine ecosystems are geochemically distinct from terrestrial ecosystems and thus adaptations to marine environments requires certain genetics. (Wang et al., 2012; Sharoni and Halevy, 2022). For example, marine ecosystems have high salinity and thus the multiple predicted Na+/H+ antiporters among the marine enriched gene clusters are expected (**Table A.12**). Na+/H+ antiporters are known to have several functions in bacterial cells that includes Na+/solute symport, Na+-driven flagellar rotation, and cell volume regulation (Tsuchiya et al., 1977; Tsuchiya and Wilson, 1978; Chen et al., 1985; Hama et al., 1987; Imae and Atsumi, 1989; Padan and Schuldiner, 1994; Grinstein, 2017). Additionally, the large number of enriched gene

clusters in the marine genomes includes several predicted regulatory proteins, signal transduction related proteins, and cell division related protein clusters. Together, this indicates the marine *Microbacteriaceae* are distinctly adapted to high salinity environments compared to terrestrial *Microbacteriaceae*, specifically among some Na+ usage, transcriptional regulation, signal transduction, and cell division related pathways.

The gene clusters enriched in terrestrial environments included predicted genes that encode peroxiredoxins, predicted glutaredoxins, and forkhead associated domain (FHA) containing proteins (**Table 3.2**). Given that glutaredoxins are found in most organisms, it is not surprising to find them within this pangenome. It is interesting that this particular gene cluster is significantly enriched among terrestrial *Microbacteriacea* species but not in marine *Microbacteriaceae* species. Glutaredoxins reduce protein disulfides and GSH-mixed disulfides, compared to thioredoxins which reduce protein disulfides (Fernandes and Holmgren, 2004). Significant enrichment of glutaredoxin-like proteins in terrestrial vs. marine *Microbacteriaceae* may be a result of higher GSH-mixed disulfide concentrations in terrestrial environments compared to marine environments. Alternatively, terrestrial *Microbacteriaceae* may be more competitive for disulfides compared to marine *Microbacteriaceae.* Both glutaredoxins and peroxiredoxins are integral to combating oxidative stress (Cabiscol Català et al., 2000; Perkins et al., 2015). The significant enrichment of both a peroxiredoxin and glutaredoxin-like gene cluster in terrestrial *Microbacteriaceae* shows that terrestrial *Microbactericeae* have additional peroxiredoxin and glutaredoxin encoding genes, indicating they may undergo more oxidative stress than marine *Microbacteriaceae.*

FHA domain proteins are a large group of proteins found in both prokaryotic and eukaryotic organisms that contain a conserved phosphopeptide recognition domain and control various cellular processes, including phosphatases, kinases, and transcription factors (Durocher and Jackson, 2002). Significant enrichment of a gene cluster predicted to encode FHA proteins in terrestrial vs. marine *Microbacteriaceae* suggests that terrestrial *Microbacteriaceae* likely have additional signal transduction pathways that use FHA domain proteins. Different signal transduction pathways and more molecular mechanisms to respond to oxidative stress are two ways in which terrestrial *Microbacteriaceae* may be specialized for their environment compared to marine *Microbacteriaceae.*

R. lacicola and *A. photophilum*, two freshwater *Microbacteriaceae* species that have unexplained faster growth in light than in dark, encode four (*R. lacicola*) and five (*A. photophilum*) of the five predicted genes that are enriched in the terrestrial set of genomes (**Table 3.2**). Whether *R. lacicola* and *A. photophilum* are using light as a signal to regulate these "terrestrial enriched" genes that results in the light-enhanced growth phenotype is an intriguing possibility. Future analyses on the relationship between the presence of light and the expression of these genes will indicate which are regulated by light and thus may be part of the hypothesized light regulated biological functions in *R. lacicola* and *A. photophilum*.

In the COG function enrichment analyses, no COG functions were identified as enriched with statistical significance, therefore, I identified COG functions that may be associated with freshwater, soil, and marine environments. The results show there are 26 COG functions associated with the freshwater genomes, 16 COG functions associated with the soil genomes, 35 COG functions associated with the marine

genomes, 32 COG functions associated with soil and marine *Microbacteriaceae* species, and no COG functions that are associated with either (freshwater and soil) or (freshwater and marine) species (**Table A.13**). Many of the COG functions identified in this analysis are related to transmembrane transport, signaling, transcriptional regulation, and RNA processing. This indicates that *Microbacteriaceae* from marine and soil environments have more shared biological functions related to transmembrane transport, signaling, transcriptional regulation, and RNA processing than *Microbacteriaceae* from freshwater environments. However, these biological functions are likely carried out via different molecular pathways, since there are few significantly enriched gene clusters common to soil and marine genomes. Additionally, the percentage of genomes predicted to encode a COG function that may be associated with a given environment varies greatly from 23% to 100%. Therefore, the results from the COG function enrichment analysis, combined with the observations that *Microbacteriaceae* have very streamlined genomes thought to be specialized for their environments (Cho et al., 2018), may identify COG functions that are specific to the biogeochemical properties of an environment.

To better understand if *Microbacteriaceae* with light-enhanced growth have COG functions that may be associated with freshwater *Microbacteriaceae*, I identified which of the potentially freshwater associated COG functions are present in *R. lacicola* and *A. photophilum* and not in *Microbacterium* sp. strain 10M-3C3. Those two COG functions are: 'RNA processing exonuclease, beta-lactamase fold, Cft2 family' and 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system' (**Table 3.3**). Interestingly, both are nucleases generally related to RNA processing. Enzymes in the metallo-β-lactamase family that also function as

nucleases have been identified in a range of prokaryotes where various enzymatic and non-enzymatic activities related to different biological pathways have been characterized (Garces et al., 2010; Chang et al., 2016; Diene et al., 2020, 2021; Au et al., 2021). Identifying homologous sequences of members within this large protein family using classical BLAST analyses has proven to be difficult, due to low sequence similarity (Garau et al., 2004). However, efforts in comparative sequence analyses suggests that proteins within this protein family are highly specialized to the organisms and/or environments they are in (Thornton, 2004; Baier and Tokuriki, 2014; Keshri et al., 2018). Here I show the COG function 'RNA processing exonuclease, beta-lactamase fold, Cft2 family', which was identified in *R. lacicola* and *A. photophilum* and not in *Microbacterium* sp. strain 10M-3C3, are found at a higher rate in freshwater *Microbacteriaceae* species vs. marine or soil *Microbacteriaceae* species. Given the current observations of nuclease/β-lactamase enzymes as a large group of proteins with multiple specialized functions, it is reasonable to hypothesize that certain members of this protein family are specialized to certain species in freshwater environments. This brings up questions including whether larger pan-genome(s) and/or other comparative sequence analyses support this hypothesis, what are the molecular and biological functions of the predicted exonuclease/β-lactamase, and if its functions support faster growth in response to light.

The mRNA-degrading endonuclease RelE protein is activated during nutrient limitation and ultimately cleaves mRNA during translation, which globally downregulates translation (Griffin et al., 2013). Here, I found that *A. photophilum* is predicted to have two genes with the predicted function 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system' while *R.*

lacicola is predicted to have one gene with this function. Together, the presence of 'RNA processing exonuclease, beta-lactamase fold, Cft2 family' and 'mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system' COG functions in freshwater *Microbacteriaceae* with light-enhanced growth, suggests that the pathways to control mRNA processing are species-specific in freshwater *Microbacteriaceae.* In cultivated marine bacteria, different strategies for nucleic acid processing are observed even among even closely related taxa, which suggests that biogeochemical cycling may be connected to the presence of microbes with different nucleic acid processing capabilities (Lennon, 2007). Therefore, I hypothesize that specific biogeochemical properties of freshwater environments are associated with differences in mRNA processing pathways among freshwater *Microbacteriaceae* with light-enhanced growth.

The predicted genes encoding light sensing proteins were identified in multiple other genomes, though their distribution in types of environments differed. The gene cluster containing the *R. lacicola* and *Aurantimicrobium* sp. strain MWH-UGA1 actinorhodopsin genes was only identified in three other species that were isolated from freshwater (**Table 3.4**). The gene clusters containing genes that encode cryptochrome and cryptochrome-like proteins were also found in *Microbacteriaceae* species isolated from freshwater, soil, and marine environments (**Table 3.5** & **Table 3.6**). These results are expected, given that actinorhodopsins are found in Actinobacteria, which are regularly found in freshwater environments while cryptochrome proteins are found in a diverse set of organisms (Sharma et al., 2009; Maresca et al., 2019).

Identifying genes that co-occur with predicted light sensing proteins found in *Microbacteriaceae* could identify genes in light-regulated pathways. The comparative analysis among four *Microbacteriacea*, presented in Chapter 2, showed that closely related *Microbacteriaceae* with unexplained light-enhanced growth share a large proportion of their genes. To expand upon that analysis, I did a phylogenetic profiling analysis among 27 *Microbacteriacea*. This analysis includes more genomes and thus has more points of comparison when identifying genes with a similar distribution to genes encoding actinorhodopsins, cryptochrome, and cryptotchrome-like proteins.

Interestingly, each of the three predicted light sensors co-occurs with a gene predicted to encode proteins related to various cofactor biosynthesis. Gene cluster GC_00002203 co-occurs with the actinorhodopsins containing gene cluster, GC_00002542 (**Table 3.4**). GC_00002203 contains genes predicted to encode phytoene dehydrogenase related proteins, which are involved in carotenoid biosynthesis (Liang et al., 2020). Carotenoids are cofactors of some rhodopsins and in *Myxococcus xanthus* carotenoid biosynthesis is vitamin B12 regulated (Padmanabhan et al., 2017; Chuon et al., 2021). GC_00002269 contains genes predict to encode 4-hydroxybenzoate polyprenyltransferases, which are involved in ubiquinone biosynthesis. Ubiquinone biosynthesis has also been shown to be regulated by a light-sensing vitamin B12-binding transcriptional regulator (Romine et al., 2017).

Gene cluster GC_00000816 co-occurs with the cryptochrome containing gene clusters, GC_00001625 and GC_00003485 (**Table 3.5**). GC_00000816 contains genes predicted to encode ketopantoate hydroxymethyltransferases, which are involved in vitamin B5 synthesis (Ottenhof et al., 2004). Gene cluster GC_00001592 co-occurs with the gene cluster GC_00003485 which includes genes that are predicted to encode

cryptochrome-like proteins (**Table 3.6**). GC_00001592 contains genes predicted to encode pyridoxine/pyridoxamine 5'-phosphate oxidases, which are involved in vitamin B6 biosynthesis (di Salvo et al., 2003). B vitamins are water-soluble vitamins and can be a precursor to synthesizing coenzyme A, as is the case for vitamin B5, but are mostly used as co-factors for various enzymes broadly related to metabolism, as is the case for vitamin B6 (Yang et al., 2022). For example, cryptochromes are known to use a vitamin B2 based cofactor, $FADH^-$ (Hitomi et al., 2000). These results lead to questions of if vitamin B5 and/or vitamin B6 are light-regulated in *Microbacteriaceae* species with unexplained light-enhanced growth.

To conclude, this study provides insight into which predicted molecular and cellular functions may be specialized to terrestrial *Microbacteriaceae* vs. marine *Microbacteriaceae* and which predicted molecular and cellular functions are shared among species with the same predicted light-sensing proteins. This information provides a larger context for identifying genes that may be related to previously observed unexplained light-enhanced growth in some freshwater *Microbacteriaceae* species. It also contributes to our understanding of how *Microbacteriaceae* species are specialized for their environment.

Chapter 4

CHARACTERIZING THE TRANSCRIPTION OF MODEL FRESHWATER ACTINOBACTERIA THROUGHOUT A LIGHT-DARK CYCLE

Some of the work in this chapter is published in *Frontiers in Microbiology*.

RNA-Seq Reveals that Light and Darkness Are Different Stimuli in Freshwater Heterotrophic Actinobacteria

Hempel PP, Keffer JL, Maresca JA. 2021. Frontiers in Microbiology, 12, p.739005. https://doi.org/10.3389/fmicb.2021.739005.

4.1 Abstract

Light is a ubiquitous source of both energy and information in surface environments, and regulates gene expression not only in photosynthetic microorganisms, but in a broad range of photoheterotrophic and heterotrophic microbes as well. Actinobacteria are keystone species in surface freshwater environments, where the ability to sense light could allow them to coordinate periods of nutrient uptake and metabolic activity with primary production. The model freshwater Actinobacteria *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium photophilum* strain MWH-Mo1 grow faster in the light than in the dark, but do not use light energy to support growth. In this chapter, I characterize transcription throughout a light-dark cycle in *R. lacicola* and *A. photophilum*. In both species, some genes encoding carbohydrate metabolism and storage are upregulated in the light. However, expression of genes of the TCA cycle is only coordinated with

light availability in *R. lacicola*. In fact, the majority of genes that respond to light and darkness in these two species are different, even though their light-responsive phenotypes are similar. The ability to respond to light and darkness may be widespread in freshwater Actinobacteria, but the genetic networks controlled by these two stimuli may vary significantly.

4.2 Introduction

Light is a ubiquitous resource in surface environments, and widely used by microbes. In fact, light-sensing proteins that control gene expression are common in photosynthetic microbes, photoheterotrophs, and non-phototrophic heterotrophs (Eelderink-Chen et al., 2021). The organisms that do not use light energy for carbon fixation can use it for supplementary energy (Calisto et al., 2021), phototaxis (Wilde and Mullineaux, 2017), or to entrain circadian rhythms (Sartor et al., 2019). In non-phototrophic bacteria, light regulates multiple biological processes, including motility, pigment production, and stress responses (Burchard and Dworkin, 1966; Bhaya, 2004; Ziegelhoffer and Donohue, 2009). In photoheterotrophs, light often regulates expression of the photosystems, but may also regulate expression of the biosynthetic pathways of pigments or other photoactive cofactors, electron transport pathways, and the metabolic pathways that intersect with those (Frühwirth et al., 2012; Kumka et al., 2017; Navid et al., 2019). These pathways can also be regulated by oxygen tension, nutrient availability, and other environmental factors, resulting in complex regulatory networks in photoheterotrophs.

In illuminated freshwater environments, Actinobacteria in the *Microbacteriaceae* family are ubiquitous and abundant keystone species which mediate fluxes of organic carbon and nitrogen, reduced sulfur, and vitamins (Eiler et

al., 2012; Garcia et al., 2018; Linz et al., 2018). The freshwater clades have in common small genomes (<2 Mbp) with low GC content compared to other Actinobacteria (~50% GC), and a variety of auxotrophies (Neuenschwander et al., 2018). Both environmental metagenomic analyses and laboratory studies suggest that many members of these clades may be photoheterotrophs: actinorhodopsins and heliorhodopsins are common in their genomes, and both rhodopsin types can act as light-activated proton pumps (Ghai et al., 2014; Keffer et al., 2015; Dwulit-Smith et al., 2018; Pushkarev et al., 2018; Maresca et al., 2019).

Previous work demonstrated that two species of these freshwater Actinobacteria, *Rhodoluna lacicola* strain MWH-Ta8 and *Aurantimicrobium photophilum* strain MWH-Mo1, grow faster in blue light than in the dark, even though neither has a functional rhodopsin under laboratory conditions (Maresca et al., 2019). Both species are free-living heterotrophs (Hahn et al., 2014, 2021). Their growth rate phenotype strongly implies either that the cells have different activities in these two conditions, or that metabolic rates increase in the light. RNA-seq analysis of gene expression in stationary-phase cells grown in constant light or darkness further indicated that cells of both strains grown in constant light had higher expression of carbohydrate transport and metabolism pathways, while cells grown in constant darkness expressed more genes related to protein production and oxidative stress (Maresca et al., 2019). These transcriptional differences suggest that different metabolic pathways are active in light and darkness, and that they are transcriptionally regulated in response to light.

To begin to characterize the genetic and regulatory networks underlying the light-enhanced growth phenotype, *R. lacicola* and *A. photophilum* were grown in a 12-

hour light/12-hour dark cycle and sequenced RNA from samples collected throughout the cycle. *R. lacicola* is representative of the Luna-1 clade of freshwater Actinobacteria, and *A. photophilum* is representative of the Luna-2 clade (Newton et al., 2011). The *R. lacicola* genome is smaller (∼1.4 Mbp as compared to ∼1.8 Mbp), and the two genomes share 879 genes, representing 65% of the *R. lacicola* genome and 50% of the *A. photophilum* genome (Maresca et al., 2019). Initially, I predicted that the transcriptional responses of the two strains to light and darkness would be similar, because they belong to the same family (*Microbacteriaceae*), their genomes are so similar, and their light-enhanced growth phenotypes are similar. Here, I show that light and darkness alter transcription of distinct suites of genes in *R. lacicola* and *A. photophilum*, that approximately half of the genes in both are regulated in response to light or darkness, and that although the growth rate phenotypes of these strains are similar, their transcriptional responses to light and darkness are quite different.

4.3 Materials and Methods

4.3.1 Strains and Growth Conditions

A. photophilum strain MWH-Mo1 and *R. lacicola* strain MWH-Ta8 were grown as described previously in 0.3% NSY medium (Hahn et al., 2004) at room temperature (Maresca et al., 2019). For the light/dark cycling experiment, for each sample to be collected, cells were diluted into 50 mL of fresh media (the starting OD600nm was 0.003 for *R. lacicola* and 0.008 for *A. photophilum*) and placed on an orbital shaker in a dark room. White light was provided by four 13-watt compact fluorescent bulbs (each providing ∼30–40 μmol photons m–2 s–1) arranged approximately 30 cm above the cultures, on a 12-h ON/12-h OFF cycle. The cultures

acclimated to the light/dark cycle for 24 h before sampling began. The first sample was taken in the dark, ∼5 min before the light turned on (t_0). Then, samples were taken 15 min (t_1, 0.25 h), 1 h (t_2), and 6 h (t_3) after the light turned on, and 15 min (t_4, 12.25 h), 1 h (t_5, 13 h), and 6 h (t_6, 18 h) after the light turned off. For each time point and each strain, the entire culture (50 mL) was centrifuged at 4,500 × g for 30 min at room temperature. The supernatant was removed and the cell pellet was resuspended in 1 mL RNAlater (Invitrogen) and stored at −20ºC until processing. Biological replicates were obtained by repeating the experiment 3 times for a total of 4 replicates, ensuring that the initial concentration of cells remained the same. Dr. Jessica Keffer prepared the samples and collected day-time samples. Priscilla Hempel collected night-time samples.

4.3.2 RNA Extraction and cDNA Library Preparation

The archived cell suspensions were separated into four aliquots, and RNA was extracted from one aliquot of each *R. lacicola* sample and from two pooled aliquots of *A. photophilum* samples. The remainder of the material was archived at −80ºC.

Total RNA from *R. lacicola* was extracted as described previously (Maresca et al., 2019). RNA yield from *A. photophilum* was too low when cells were lysed with the enzymatic digestion protocol alone, so cells were lysed by sonication. Cells were centrifuged to remove the RNAlater solution, then resuspended in lysis buffer (30 mM Tris-HCl, 1 mM EDTA, pH 8.0) with lysozyme (15 mg mL^{-1}) and proteinase K (2 mg mL^{-1}). Immediately prior to sonication, Buffer RLT (Qiagen) was added. Cells were then lysed using a Branson Sonifier 450 equipped with a microtip (10 cycles, 60% duty cycle). After sonication, 500 µL 100% ethanol was added, and purification of

total RNA continued using the RNeasy Mini Kit (Qiagen 74104) as described previously (Maresca et al., 2019).

For both strains, residual DNA was removed by treatment with TURBO DNase (Ambion AM1907) and RNA quality was assessed using an AATI fragment analyzer. RNA was concentrated using the RNeasy MinElute Cleanup kit (Qiagen 74204) and quantified using the Qubit RNA BR assay kit (Invitrogen Q10210). The samples sent to the Joint Genome Institute (JGI) for library preparation and sequencing were 25 μL each, containing 25–359 ng RNA μL^{-1}. Dr. Jessica Keffer did the RNA extraction and cDNA library preparation.

4.3.3 Library Preparation and Illumina Sequencing

For each sample, rRNA was removed from 100 ng of total RNA using the Ribo-Zero Bacterial rRNA Removal Kit (Illumina). Stranded cDNA libraries were generated using the Illumina Truseq Stranded mRNA Library Prep Kit. The rRNA-depleted RNA was fragmented and reverse transcribed using random hexamers and SSII (Invitrogen) followed by second strand synthesis. The fragmented cDNA was treated with end-repair, A-tailing, adapter ligation, and 10 cycles of PCR. The prepared libraries were quantified using KAPA Biosystem's next-generation sequencing library qPCR kit and run on a Roche LightCycler 480 real-time PCR instrument. Sequencing of the flowcell was performed on the Illumina HiSeq2500 sequencer using HiSeq TruSeq SBS sequencing kits, v4, following a 2 × 150 nt indexed run recipe. Library preparation and sequencing was carried out at the Joint Genome Institute (JGI).

4.3.4 Read Preprocessing and Filtering

Raw fastq file reads were filtered and processed using BBDuk (Bushnell, 2014a) and its microbial transcriptome filtering options to remove calibration reads, trim reads that contained adapter sequences, trim reads where quality drops to 0, and remove any reads from contaminants. Raw reads were evaluated for artifact sequence by kmer matching (kmer = 25), allowing 1 mismatch, and detected artifacts were trimmed from the 3′ end of the reads. Reads that contained 1 or more 'N' bases, had an average quality score across the read less than 10 or had a minimum length ≤ 51 bp or 33% of the full read length, were removed. Reads mapped with BBMap (Bushnell, 2014b) to masked human, cat, dog and mouse references at 93% identity were removed. Reads aligned to common microbial contaminants and rRNA were also removed. Pre-processing and filtering were done at the JGI using standard JGI pipelines.

4.3.5 Read Mapping, Counting, and Replicate Analysis

The raw reads from each library were aligned to the reference genomes using BBMap (Bushnell, 2014b) with only unique mappings allowed. If a read mapped to more than one location, it was ignored. To generate the raw gene counts, featureCounts was used (Liao et al., 2014). Counts refer to paired reads, so in cases where both reads aligned to the same feature in the reference genome, it was represented as a count of 1 in the gene counts table. These raw gene counts were normalized to gene length and library size. The normalized counts were then used to evaluate the level of correlation between biological samples using Pearson's correlation, but these normalized counts were not used for other downstream analyses. Four of the 28 *A. photophilum* samples (one each from t_0, t_1, t_2, and t_5) were excluded

from downstream analyses because they did not correlate well with their replicate group, as determined by a Pearson correlation calculation. Read mapping, counting, and replicate analysis were done at the JGI.

4.3.6 Principal Component Analysis

To evaluate the similarity of the replicate samples, the plotPCA function of the BiocGenerics R package version 0.34.0 (Huber et al., 2015) was used for principal component analysis. Raw count data was regularized logarithm (rlog) transformed via the rlog function of the DESeq2 R package, version 1.28.1 (Love et al., 2014) and used as input for the PCA analysis. The rlog transformation was applied to the count data to normalize with respect to library size and to decrease differences between samples for genes with low counts. In *A. photophilum*, this analysis showed that 4 samples from different treatment groups separated from all other samples. These four samples (one each from t_3, t_4, t_5, and t_6) were located in the same column of the sequencing plate, and data from these samples was also excluded from further analysis. With the 4 samples removed in the earlier stage, this resulted in exclusion of a total of 8 samples, leaving 20 samples from *A. photophilum* for downstream analysis.

4.3.7 Differential Expression Analysis

For differential expression analysis, raw gene counts were input to the DESeq2 R package, version 1.28.1 (Love et al., 2014), which fits a negative binomial model for abundance of each transcript. A likelihood ratio test (LRT) with a full model design of ~ condition (condition = sampling time) was used to identify genes for which time explains a significant amount of variation in the data. The full model was

compared to a reduced model in which sampling time was not included as a variable. The p-values were adjusted using the Benjamini and Hochberg (BH) method in DESeq2, and the significance threshold for differential gene expression was an adjusted p-value ≤ 0.015.

4.3.8 Gene Expression Pattern Clustering

To group genes by expression patterns throughout the time series, rlog-transformed count values of differentially expressed genes were input to the degPatterns function of the DEGreport R package, version 1.24.1 (Pantano, 2017). The degPatterns function with the ConsensusCluster parameter set to false applies the DIANA (DIvisive ANAlysis) hierarchical clustering-based approach to generate clusters of genes with similar expression patterns. Each replicate was input as an individual sample. All clusters with at least two genes were included in the output. The DIANA hierarchical clustering method provides the divisive coefficient which measures the strength of the cluster structure on a scale from zero to one, with a higher value indicating stronger cluster structure.

4.3.9 Gene Ontology (GO) Enrichment Analysis

Gene Ontology (GO) annotations were assigned to identify functions in gene clusters according the GO database, which is the key functional classification of the National Center for Biotechnology Information (NCBI) (Gene Ontology Consortium, 2004). Protein sequences from both species were annotated with the Blast2GO (version 5.2.5) suite of tools (Götz et al., 2008), using BLASTP against the non-redundant protein database with an E-value cutoff of 1×10^{-3}. The GO-slim function was applied to generate general GO-slim terms to obtain an overview of the biological

processes, cellular locations, and molecular functions of predicted proteins. Gene groups were merged based on their mean expression pattern.

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To determine enrichment of a GO-slim term in a merged gene group, odds ratios were calculated as the ratios of representation of a GO term within a merged group to the representation of the same term in the genome ([A/B]/[C/D], where A is the number of genes with a given GO-slim term in a group, B is the total number of genes assigned any GO-slim term in a group, C is the number of genes assigned the given GO-slim term in the genome, and D is the total number of genes assigned any GO-slim term in the genome.) The stats (version 4.0.4) R package was used to calculate the odds ratios and do a one-sided Fisher's exact test (using the fisher.test function) to test for significance. Ratio p-values were corrected using the Benjamini-Hochberg procedure (using the p.adjust function) to correct for false positives. Results were then filtered with criteria odds ratio > 1, a count in the merged group > 1, and a count in the whole genome ≥ 10.

4.3.10 Plotting

Gene expression patterns were plotted as Z-score transformed transcript abundances. Z-score transformation standardizes data across sampling time points and allows for analysis that is independent of the raw count transcript abundance. Z-score were calculated by subtracting a gene's mean transcript abundance across all timepoints from each sample, then dividing by the standard deviation of all timepoints. Z-scores for timepoint replicates were then averaged. The Z-score represents the number of standard deviations away from the mean transcript abundance across all timepoints. Rlog transformed transcript abundance values above the mean have a positive Z-score while rlog transformed transcript abundance values below the mean have a negative Z-score. All plots were generated using the ggplot2 R package, version 3.3.3 (Wickham, 2009) and the patchwork R package, version 1.1.1 (Pedersen, 2020).

4.3.11 Data and Code Availability

The datasets presented in this study can be found in online at the NCBI sequencing read archive under the Bioproject Numbers PRJNA454999–PRJNA455026 for *R. lacicola* and PRJNA500876–PRJNA500902 for *A. photophilum*. R scripts for all bioinformatic analyses are available on Github (https://github.com/MarescaLab/Transcriptome-Analysis).

4.4 Results

4.4.1 Sequence Data

A total of 56 cDNA samples (2 strains × 7 time points × 4 replicates per time point) were sequenced by the JGI using an Illumina HiSeq system, paired-end 150-nt

reads. For R. lacicola, we obtained a total of 718,789,878 raw reads (range 18,305,388–34,132,688 per sample) and 653,982,504 reads passed quality filtering (range 13,215,036–33,300,442 per sample), resulting in 326,991,252 total fragments (range 6,607,518–16,650,221) (**Table A.6**). 326,304,878 fragments were mapped to the reference genome (range 6,593,343–16,614,066) and 238,500,825 fragments were assigned to genes (range 4,488,560–12,174,032). Pearson correlations were calculated between all samples, and all replicates grouped together as expected.

For *A. photophilum*, we obtained 547,198,496 raw reads (17,947,434–34,160,484 per sample) and 455,067,112 reads (7,766,636–32,336,932 per sample) passed quality filtering, resulting in 227,533,556 total fragments (3,883,318–16,168,466 per sample) (**Table A.7**). A total of 222,502,773 fragments (3,800,635–15,523,899 per sample) were mapped to the reference genome and 167,358,807 (range 2,459,643–12,059,277) fragments were assigned to genes.

4.4.2 Principal Component Analysis

Regularized logarithmic (rlog) transformed count data was analyzed via a principal component analysis to compare treatment groups. In *R. lacicola*, PC1 best captures variance among light timepoints (**Figure 4.1A**). The first two dark timepoints, t_4 and t_5, group closely on both PC1 and PC2. However, PC1 captures variance between the first two dark timepoints and t_6. Interestingly, t_6 (6 h in the dark) groups closest to the first two light timepoints, possibly indicating a cyclical expression pattern. The replicates roughly group together and lie closest to their neighboring timepoints. In *A. photophilum*, PC1 captures the variance between light and dark timepoints (**Figure 4.1B**), indicating light and dark samples are quite different from each other, and PC2 captures variance between the early and late dark

samples. Four samples from the *A. photophilum* dataset were removed due to the PCA analysis. These four samples were in the same column of the sequencing plate, from different timepoints (t_3, t_4, t_5, t_6) and grouped together along both PC1 and PC2, rather than with their timepoint replicates. Removing those samples left three replicates for each timepoint, except for t_5, which had two replicates in downstream analyses. The two remaining t_5 replicates cluster tightly together along PC1 and PC2 that collectively represent 76% of the variance. Of the top 100 genes with the highest loading values in PC1 and PC2, PC2 loading values were the most affected by removing the four samples. Nevertheless, PC2 captures variance between the early and late dark samples both before and after removing the outlying samples.

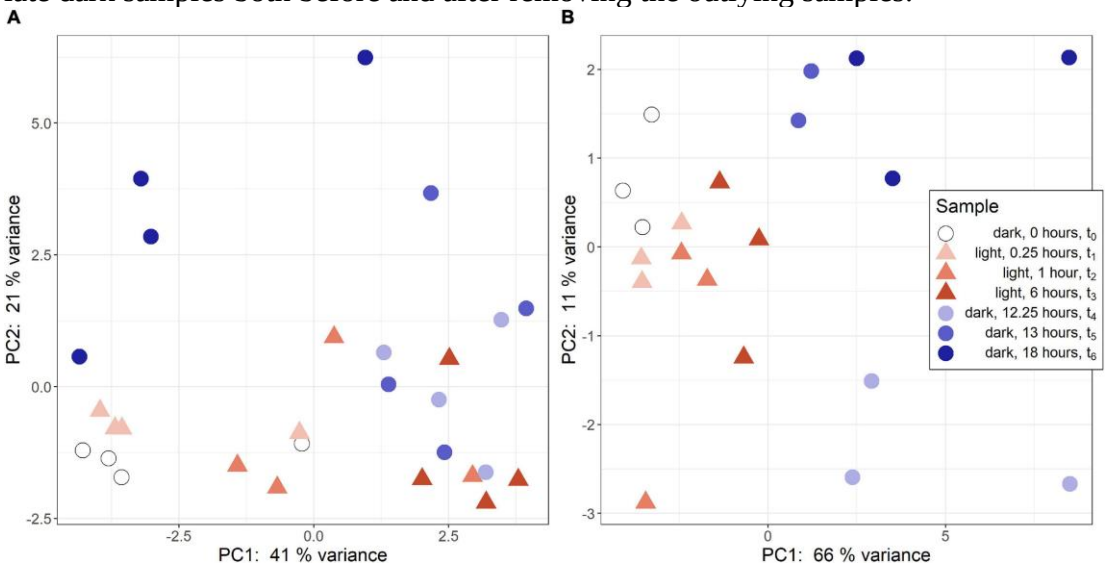

Figure 4.1 Principal component analysis (PCA) of RNA-seq samples. (A) PCA of rlog scaled count data from *R. lacicola*. The steady-state light and early dark timepoints are quite similar in *R. lacicola*, as are steady-state dark and early light timepoints. (B) PCA analysis of *A. photophilum*. Light and dark samples are distinct from each other along PC1. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

4.4.3 Expression Group Analysis

Hierarchical clustering was used to identify groups of differentially expressed genes whose expression patterns were similar across all time points. The divisive coefficient, which indicates the strength of the cluster structure, is 0.998 for *R. lacicola* and 0.995 for *A. photophilum*, indicating very strong cluster structures in both species (maximum value = 1). Fourteen expression groups were identified in each strain (**Figure 4.2**). In *R. lacicola*, 729 genes representing ~54% of all genes were clustered into three categories of expression groups: putative light-responsive groups (8), putative dark-responsive groups (2), and 4 groups which may respond to all changes in light availability **(Figure 4.3**). In *A. photophilum*, the transcripts of 40% of all genes appear to respond to light, darkness, or both (**Figure 4.2B**). In contrast to the patterns in *R. lacicola*, the largest change in transcript abundance occurs after the transition to darkness for nearly all of the genes (**Figure 4.4**).

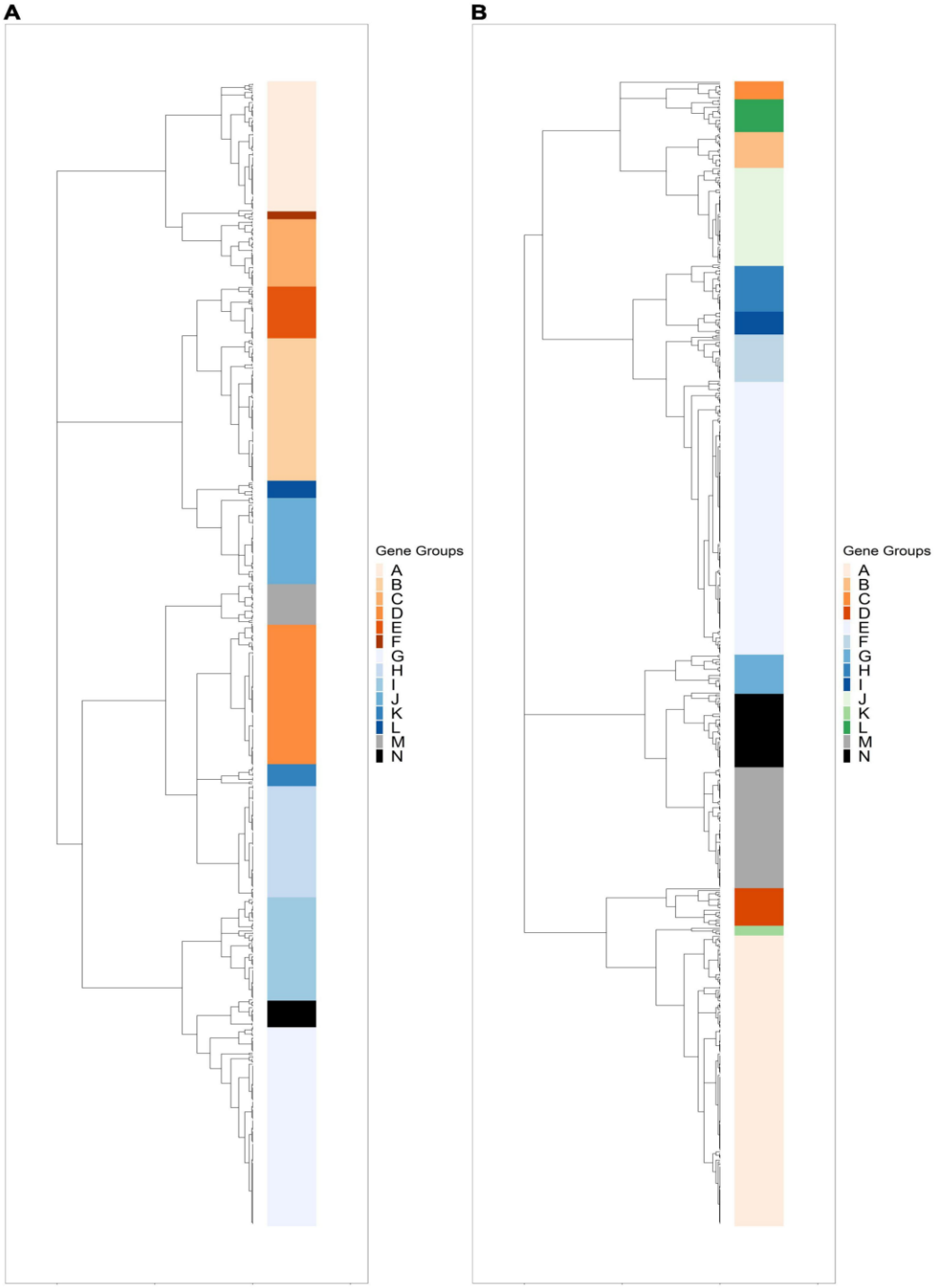

Figure 4.2 Hierarchical clustering of rlog scaled count data through the light-dark cycle. Differentially expressed genes were clustered based on expression patterns through time, and any cluster with fewer than two genes was excluded. (A) Dendrogram of hierarchically clustered differentially expressed genes in *R. lacicola*.

Putative light-responsive genes whose transcript abundance increases during the first hour in the light and decreases between one hour and six hours in the dark are colored in orange shades. Putative light-responsive genes whose transcript abundance generally decreases during the first hour in the light and increases between one hour and six hours in the dark are colored in blue shades. The groups colored black and gray appear to respond to darkness. (B) Dendrogram of hierarchically clustered differentially expressed genes in *A. photophilum*. Colors indicate gene groups with similar expression profiles. Orange shades indicate genes whose expression increases within one hour in the light and decreases within one hour in the dark. Blue shades indicate genes whose expression decreases within one hour in the light and increases within one hour in the dark. Green indicates genes whose expression increases within one hour in the light and decreases within 15 min in the dark. Black and gray indicates genes whose expression decreases within one hour in the light and increases within 15 min in the dark. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

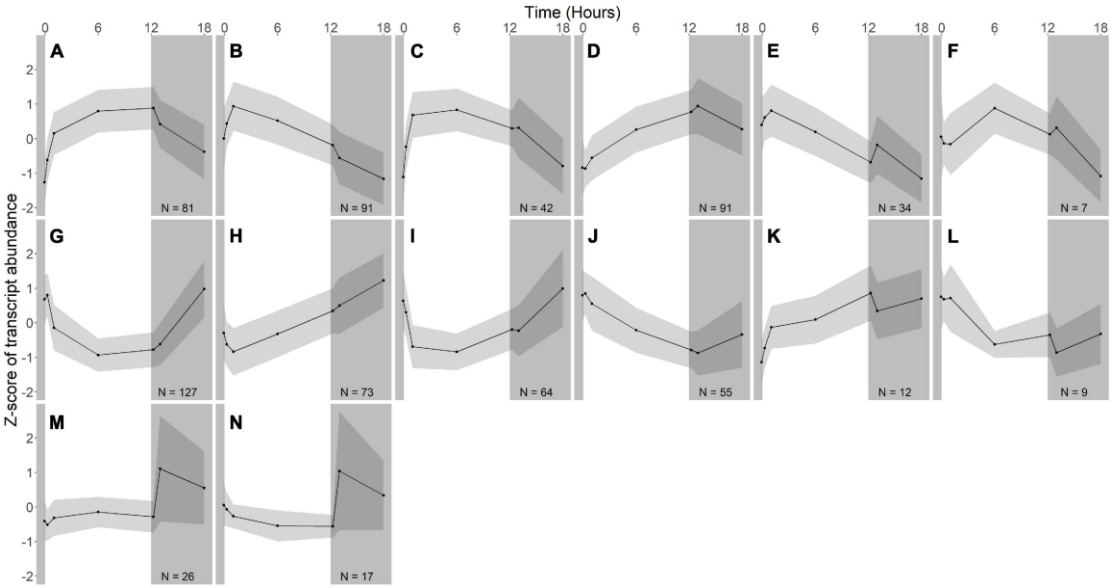

Figure 4.3 Gene expression groups in *R. lacicola*. Groups of genes with similar expression patterns were identified using hierarchical clustering. Means of the z-scores for all genes are plotted, with one standard deviation indicated by the gray shading. N indicates number of genes in each group. (A–F) Groups of light-responsive genes whose expression increases in the light and decreases in the dark. (G–L) Groups of light-responsive genes whose expression decreases in the light and increases in the dark. (M,N) Groups of genes whose expression is consistent until the light turns off, then increases sharply. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

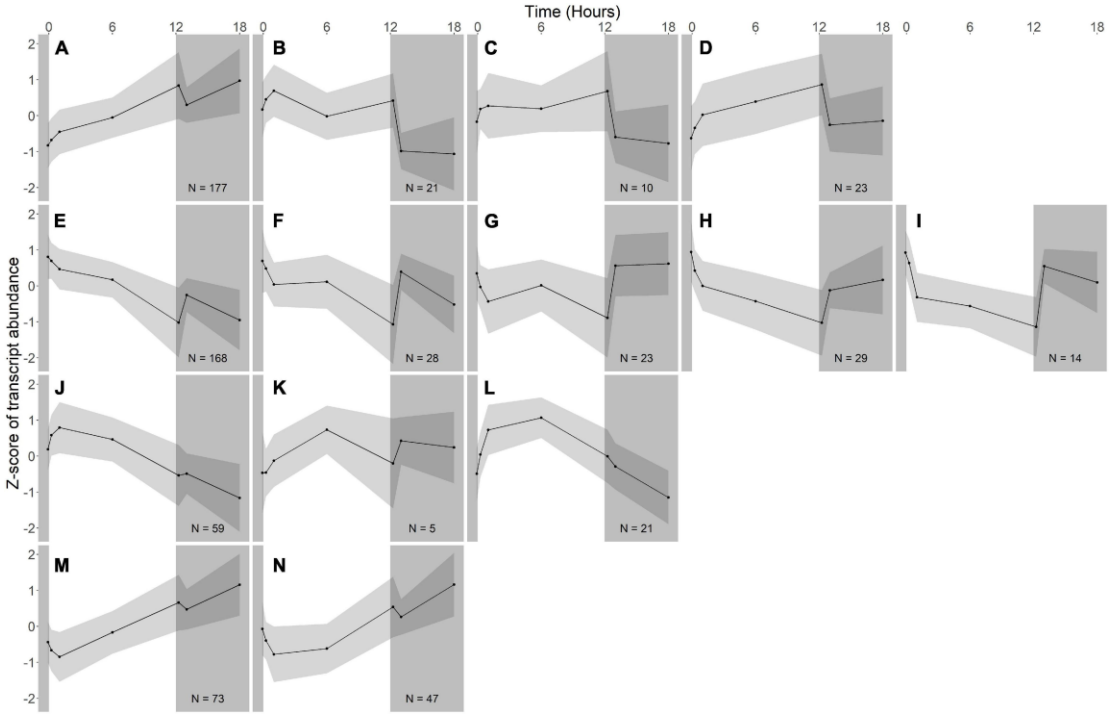

Figure 4.4 Gene expression groups in *A. photophilum*. Groups of genes with similar expression patterns were identified using hierarchical clustering. Means of the z-scores for all genes are plotted, with one standard deviation indicated by the gray shading. N indicates number of genes in each group. In this species, most genes respond more strongly to darkness than to light. (A–D) Groups of genes whose expression increases in the light and rapidly decreases in the dark. (E–I) Groups of genes whose expression decreases in the light and rapidly increases in the dark. (J–L) Groups of genes whose expression increases early during the light period, then decreases. (M,N) Groups of genes whose expression decreases early during the light period, then increases. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

In *R. lacicola*, the genes in the putative light-responsive groups either increase (**Figure 4.3A–D**) or decrease (**Figure 4.3G–J**) in expression level consistently during the light period, then decrease or increase during the dark time points, respectively. The genes in the putative dark-responsive group (~3% of all genes) have fairly consistent expression levels throughout the light period, then increase sharply in the

dark (**Figure 4.3M,N**). Four small groups of genes appear to change in transcript abundance in response to both light and darkness (**Figure 4.3E,F,K,L**).

To identify broad categories of functional genes in the expression groups, generic GO-slim terms (Götz et al., 2011) were mapped to the *R. lacicola* and *A. photophilum* genomes, which have similar content and distribution of GO-slim terms (**Figure 4.5**). The biological process GO-slim terms present at a higher proportion in the expression groups than in the genome were then identified using an odds ratio calculation. In *R. lacicola*, putatively light-responsive groups whose expression increases in the light were enriched in genes associated with cell cycle/cell division, cell wall and morphogenesis processes, precursor metabolite production, DNA metabolic processes, and carbohydrate metabolic processes (**Figure 4.6A**), including two putative starch synthases (**Table A.8**) and most of the genes in the TCA cycle (**Figure 4.7A**). The putatively light-responsive groups of genes whose transcript abundance decreases during the light period, then increases in the dark (**Figure 4.3G–J**) were enriched in functions related to nitrogen metabolic processes, translation, and signal transduction. This group also includes the actinorhodopsin, DNA photolyase, and an uncharacterized cryptochrome-photolyase family protein (CPF2), as well as a peroxiredoxin (*Rhola_00006540*). A second peroxiredoxin, *Rhola_00011030*, does not fall into an expression group, but its expression clearly follows a light-dark cycle (**Figure 4.8A**). Similarly, some components of the ATP synthase fall into group J, but all components have a similar expression pattern, and their transcription in *R. lacicola* is clearly stimulated by light and repressed in the dark (**Figure 4.9A**). Interestingly, sulfur metabolic processes are even more enriched in this group than in the other (**Figure 4.6A** and). The group of potentially dark-responsive genes is enriched in

transport, stress responses, carbohydrate metabolism, and DNA metabolism (**Figure 4.6A** and **Table A.10**).

In *R. lacicola*, the relatively small group of putatively dark-regulated genes (**Figure 4.3M,N**) is enriched in transmembrane transport and carbohydrate metabolism (**Figure 4.6A**). These groups also include genes encoding DNA uptake (*comEC* and *dprA*) and putative components of a *tad/flp* pilus (two homologs of *tadA* and one *tadBC* homolog). Although not all of the genes putatively encoding components of the *tad/flp* pilus in *R. lacicola* fall into specific expression groups, expression of all except *comEA* increases sharply within 1 h of the light turning off (**Figure 4.10A**). Although the genome of *A. photophilum* has homologs to all of these genes, none of them have expression patterns that imply that they respond to light or darkness or that they are coordinately regulated (**Figure 4.10B** and **Table A.9**).

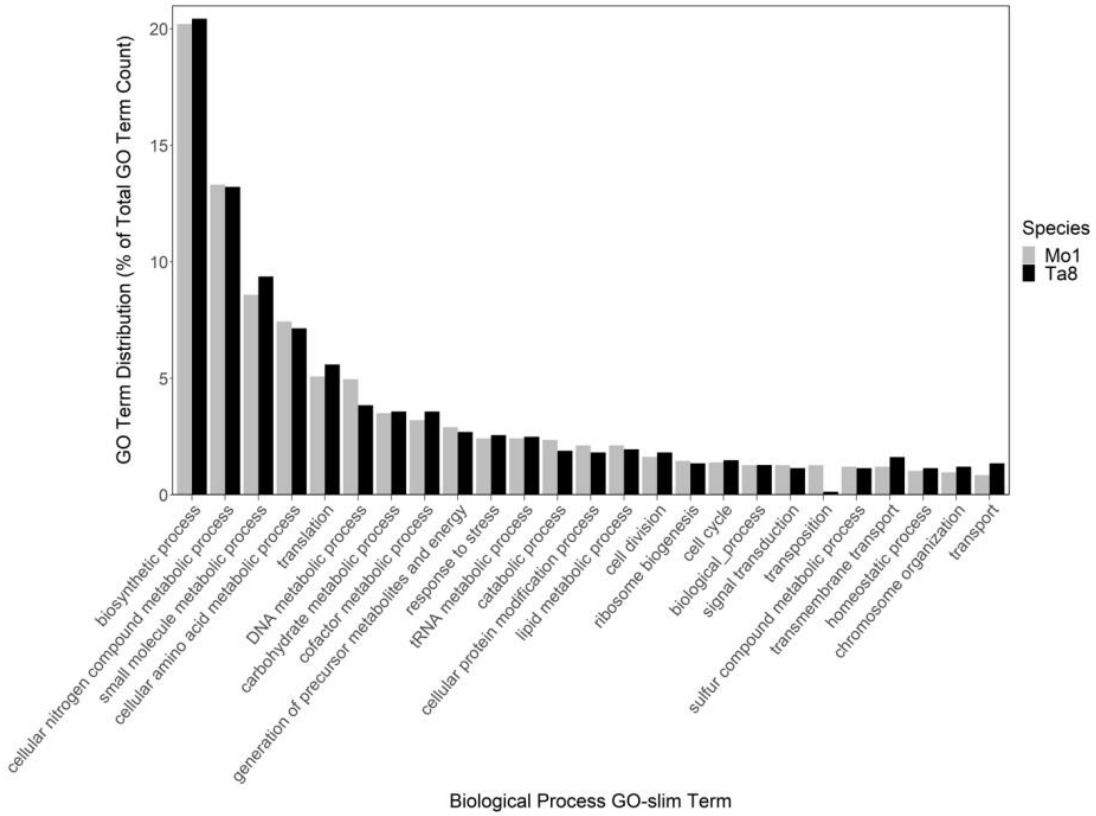

Figure 4.5 Representation of GO-slim terms in the genomes of *R. lacicola* and *A. photophilum*. All terms except transposition are present at similar proportions in the two genomes. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

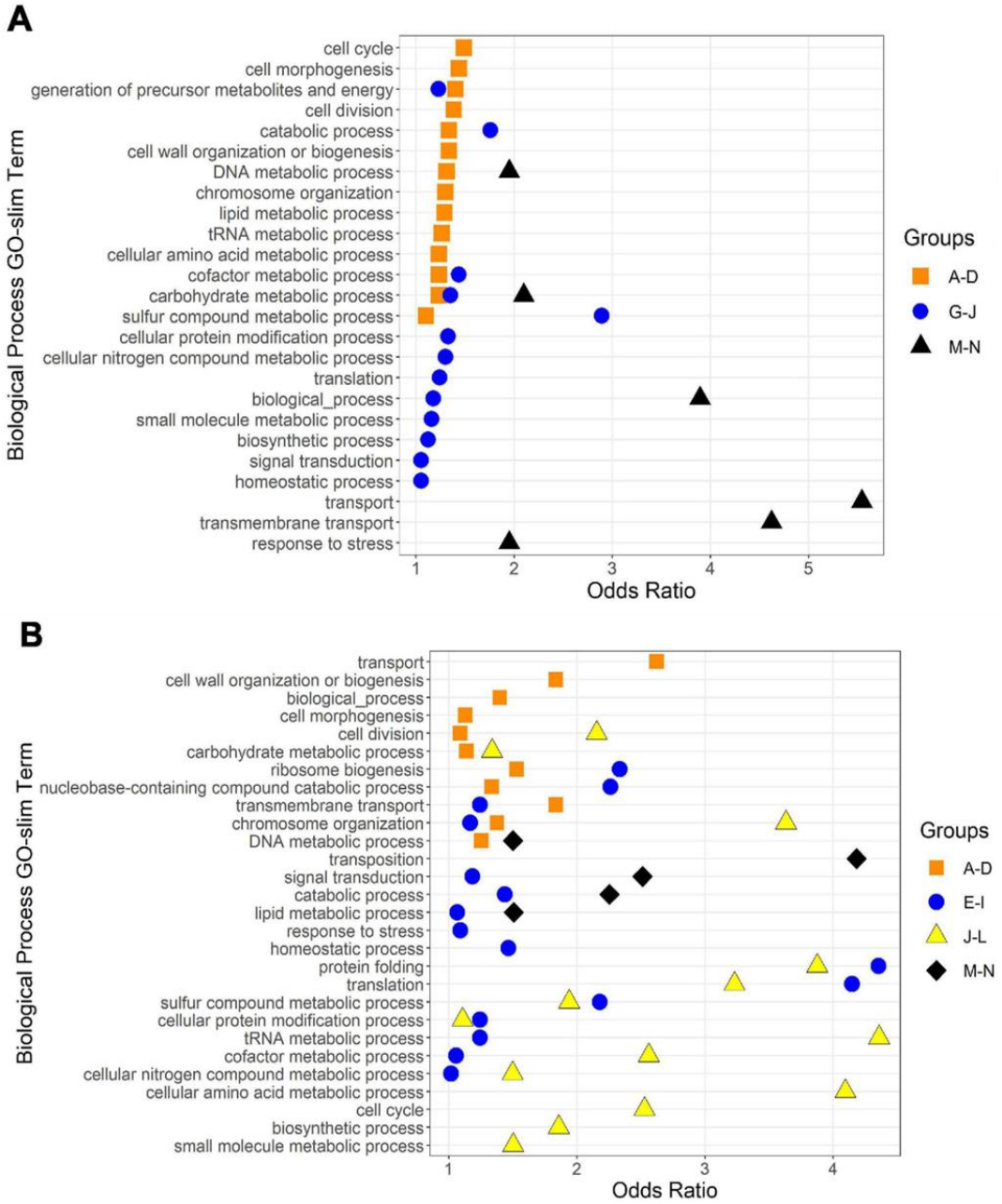

Figure 4.6 Biological Process GO-Slim Terms with significant enrichment in expression groups. Group letters correspond to those in **Figure 4.3** & **Figure 4.4**. Odds ratios were calculated as the ratio of a term's representation in a merged group to its representation in the whole genome; any odds ratios presented here have a ratio > 1, a count in the merged group > 1, and a count in the whole genome ≥ 10. (A) GO-slim terms enriched in *R. lacicola* expression groups. (B) GO-slim terms enriched in *A. photophilum* expression groups. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

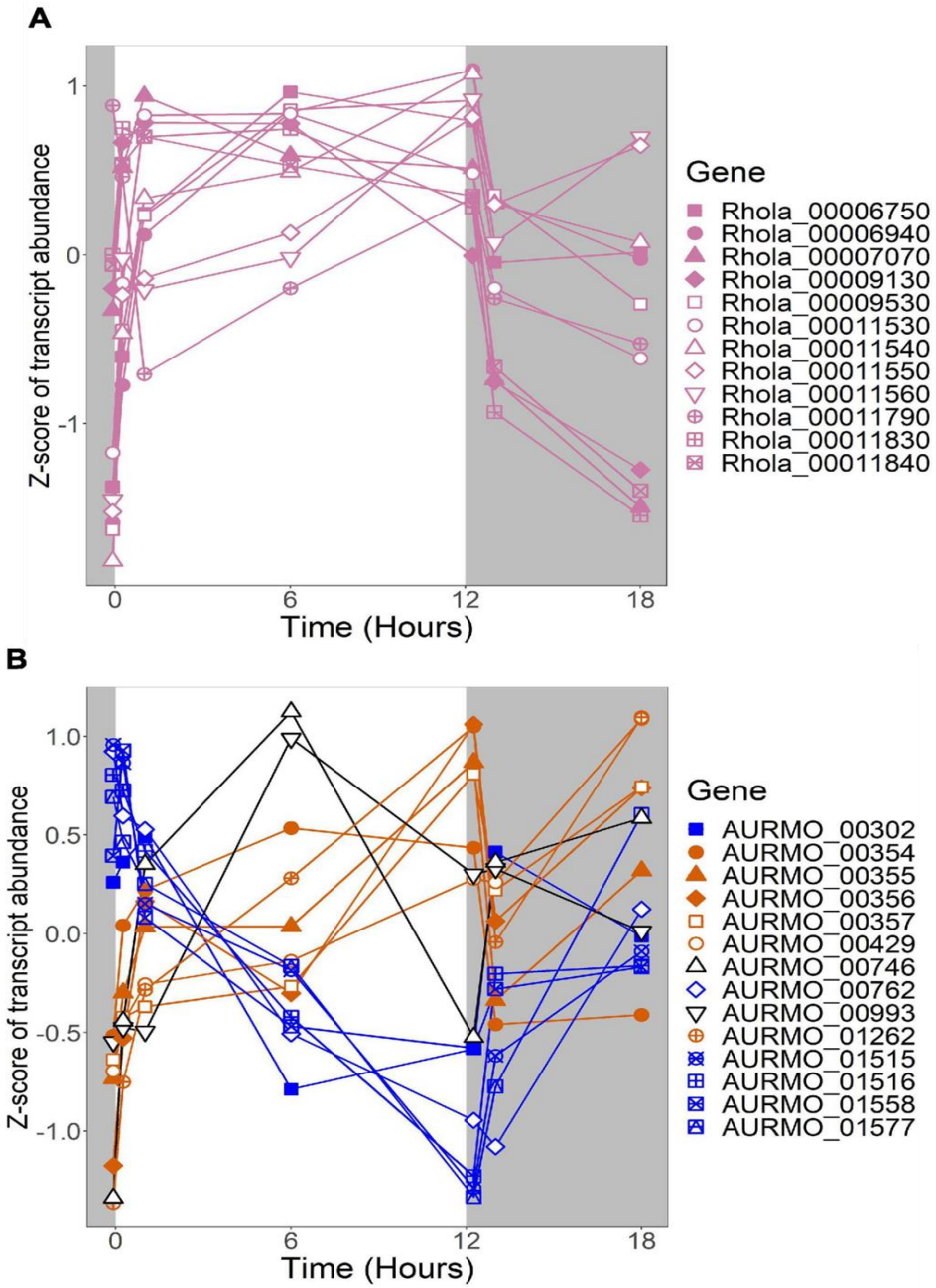

Figure 4.7 Expression of putative TCA cycle genes. Putative TCA genes were identified by comparing the amino acid sequences of known components of the E. coli TCA cycle against the genomes of *R. lacicola* and *A. photophilum* using BLAST. Expression is plotted as z-score of each transcript. (A) Putative TCA cycle genes in *R. lacicola* have higher transcript levels in the light. (B) Putative TCA cycle genes in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

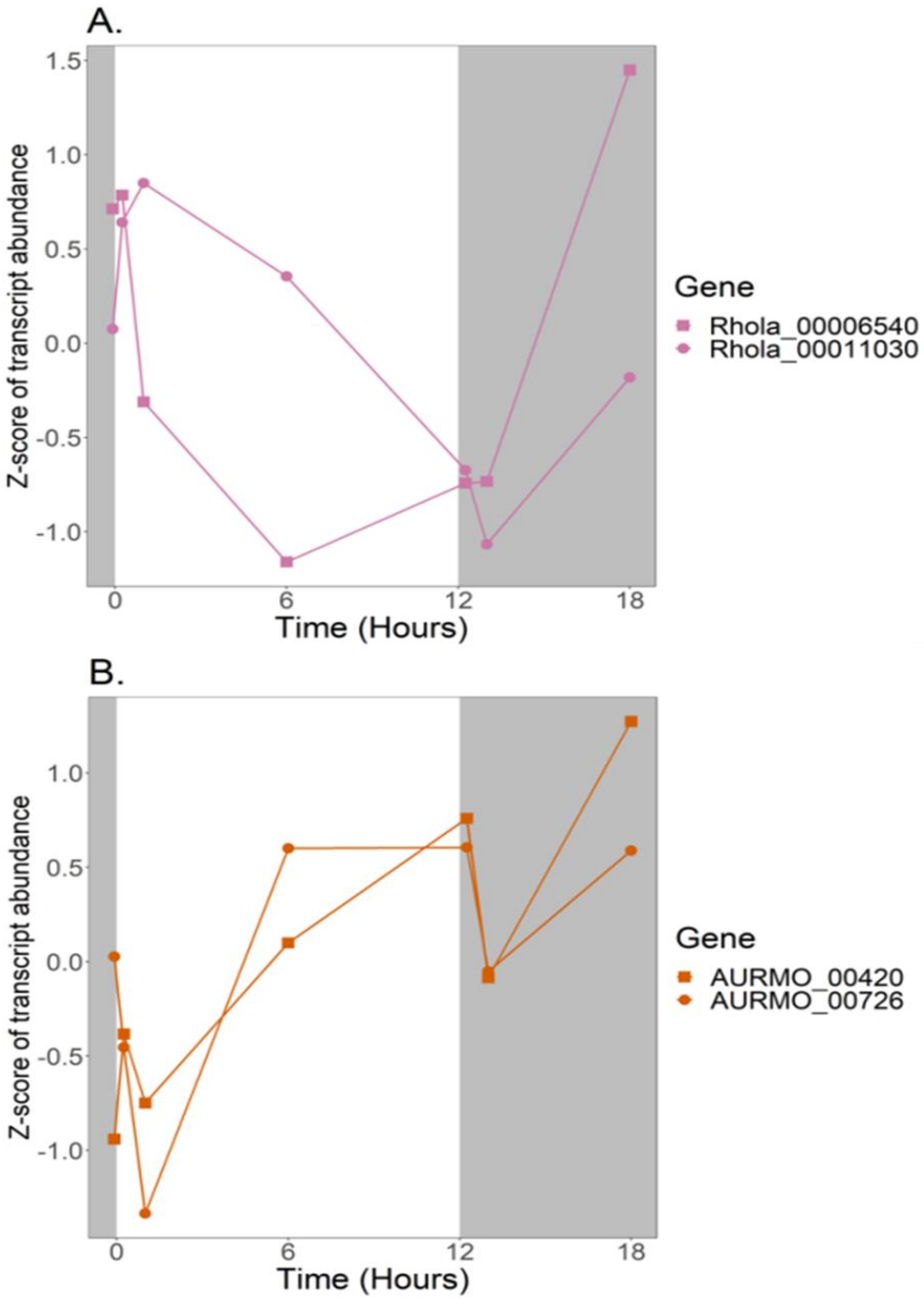

Figure 4.8 Expression of peroxiredoxin genes. Expression is plotted as z-score of each transcript. (A) Putative peroxiredoxins in *R. lacicola*. (B) Putative peroxiredoxins in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

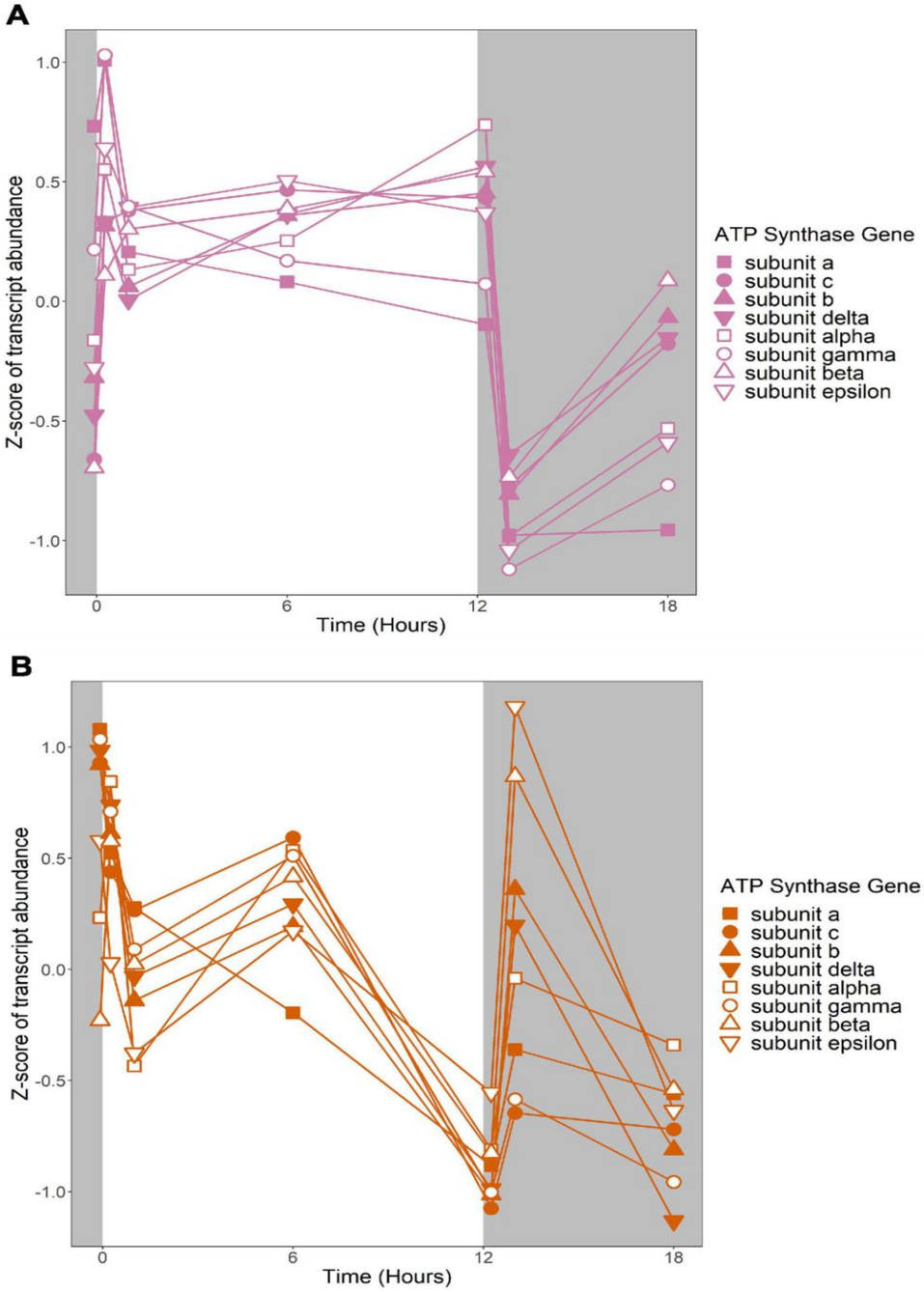

Figure 4.9 Expression of putative ATP synthase genes. Expression is plotted as z-score of each transcript. (A) Putative ATP synthase genes in *R. lacicola*. (B) Putative ATP synthase genes in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

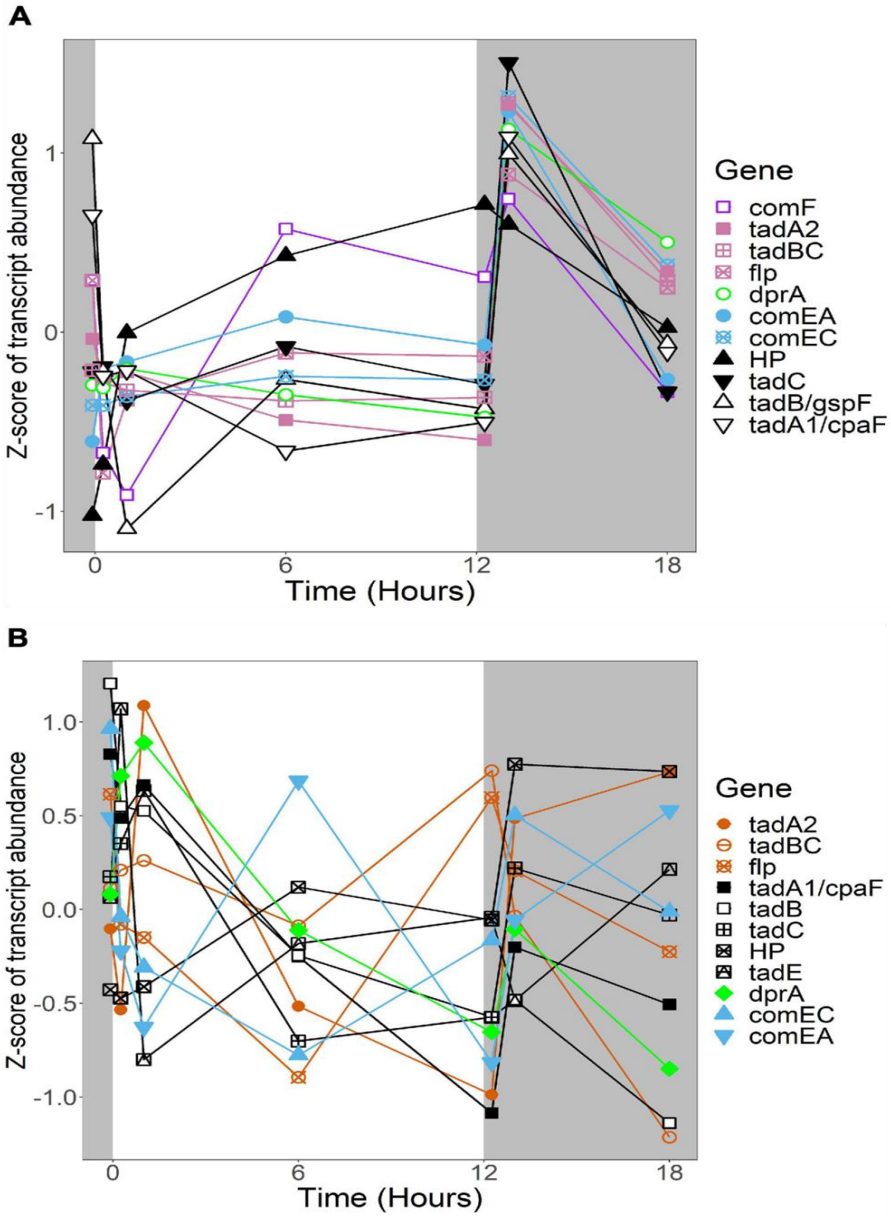

Figure 4.10 Expression of putative competence genes. Putative competence genes were identified by comparing the amino acid sequences of known components of the Com operon and tad/flp pilus from *Micrococcus luteus* against the genomes of *R. lacicola* and *A. photophilum* using BLAST. In both strains, components of the putative tad/flp pilus are organized into two operons, and comEC and comEA form a separate putative operon. Expression is plotted as z-score of each transcript. (A) Putative competence genes in *R. lacicola*. (B) Putative competence genes in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

Fourteen groups of genes with similar expression patterns were identified in *A. photophilum*, but the patterns are quite different from those observed in *R. lacicola* (**Figure 4.4**). The abundance of nearly all transcripts within the expression groups appears to change – sometimes dramatically – in response to darkness (Figure **4.4**). The abundance of ~80 transcripts in *A. photophilum* increases consistently in the light, then decreases (**Figure 4.4J,L**); these groups include functions related to carbohydrate metabolism, cell division, cell cycle, and biosynthesis (**Figure 4.6B**). In four *A. photophilum* expression groups, transcript abundance increases for the first hour in the light, and rapidly decreases between 15 min and 1 h in the dark (**Figure 4.4A–D**). These groups are enriched in functions related to transport, cell wall and morphogenesis, cell division, and carbohydrate metabolism (**Figure 4.6B**), and also include one of the two peroxiredoxins in the *A. photophilum* genome (*AURMO_00420*; **Figure 4.8B** and **Table A.9**) and one of the two putative starch synthases (*AURMO_01094*;**Table A.9**). In five groups, transcript abundance decreases during the first hour in the light, stabilizes or increases through 6 h in the light, then increases between 15 min and 1 h in the dark (**Figure 4.4E–I**). These groups are enriched in functions including ribosome biogenesis, translation, protein folding, protein modification, sulfur metabolism, and signal transduction (**Figure 4.6B** and **Table A.11**), and the superoxide dismutase and phytoene synthase are in Group H (**Table A.9**). Expression patterns of the genes encoding components of the F_1F_0 ATP synthase, though they did not cluster with any of these groups, are most similar to the pattern of group 4F (**Figure 4.9B**). Last, two groups of genes decrease during the first hour in the light, then consistently increase throughout the rest of the experiment, with transient decreases in transcript abundance during the first hour in the dark (**Figure**

4.4M,N). These two groups are enriched in signal transduction, catabolism, lipid metabolism, and transposition (**Figure 4.6B** and **Table A.11**). Of the 120 genes in these two groups, 80 have no homolog in the R. lacicola genome.

In prior work, genes related to carbohydrate metabolism had significantly higher expression in the light than in the dark in both strains (Maresca et al., 2019). In this experiment, in R. lacicola, carbohydrate metabolic processes were enriched in all three merged expression groups. Groups A-D, in which transcript abundances increase in light and decrease in dark, contain genes related to gluconeogenesis, lipid metabolism, and synthesis of sugars. Groups G-J, in which transcript abundances decrease in light and decrease in dark, include genes related to glycolysis and the pentose phosphate pathway. Groups M-N, which drastically increase in the dark, contain 3 genes related to activating or isomerizing sugars for degradation (**Table A.8**). Genes in the TCA cycle fall into all three of these groups, and thus the pathway as a whole does not seem to be co-regulated (**Figure 4.7B**). In *A. photophilum*, only 13 carbohydrate metabolism genes clustered with expression groups. Carbohydrate metabolic processes were enriched in groups A-D and J-L, in which transcription increases for the first hour after the light turns on. Groups A-D include genes related to glycogen metabolism and glycogenesis. Groups J-L include 4 genes related to glycolysis, the pentose phosphate pathway, and a gene related to nucleotide-sugar biosynthesis.

4.4.4 Expression of Putative Light Sensors

Several *R. lacicola* gene products were previously identified as either capable or potentially capable of light sensing: the actinorhodopsin, encoded by *actR* (*Rhola_00012080*), *phrB* (*Rhola_00007890*), *cryB* (*Rhola_00013030*), and *cpf2*

(*Rhola_00011000*), encoding a putative DNA photolyase, cryptochrome, and cryptochrome-photolyase family protein, respectively (Maresca et al., 2019). In *R. lacicola*, *actR* belongs to a group of genes whose transcript abundance is high early in the light period, decreases after 1 h in the light, and increases throughout the dark period (**Figure 4.11A**). The DNA photolyase and CPF2 have the same transcript abundance pattern, and are in the same expression group (**Figure 4.11A** and **Table A.8**). The *cryB* transcript abundance increases slightly throughout the light period, and decreases during the dark (**Figure 4.11A**), but this pattern does not cluster with any other genes. Notably, transcription of all of the putative light sensors in both strains increases immediately after the light turns on, and also increases within an hour of the light turning off.

The homologs to these potential light sensors in *A. photophilum* include *phrB*, *cryB*, and *heR*, a putative heliorhodopsin (Pushkarev et al., 2018; Maresca et al., 2019), encoded by *AURMO_01673*, *AURMO_00962*, and *AURMO_01564*, respectively. Transcript abundance of the putative heliorhodopsin in *A. photophilum* is fairly stable throughout the light period, then increases in the dark (**Figure 4.11B**). Transcription of the *cryB* and *phrB* homologs decreases through the light period and increases early in the dark period, then decreases at 6 h in the dark (**Figure 4.11B**).

The products of *phrB*, *cryB*, and *cpf2* are all either known or predicted to be flavoproteins (Kobayashi et al., 1989; Geisselbrecht et al., 2012; Maresca et al., 2019). The riboflavin biosynthetic genes *ribAB*, *ribD*, *ribH*, and *ribE* (García-Angulo, 2017) are organized into clusters in both the *R. lacicola* and *A. photophilum* genomes (*Rhola_0011600-Rhola_0011630* and *AURMO_00338-AURMO_00341*, respectively). In *R. lacicola*, *ribAB*, *ribD*, and *ribE* fall into expression group J, and although *ribH* is

not in that group, it shares the same expression pattern: transcript abundance increases between t_0 and 15 min in the light, then decreases until 1 h in the dark, then increases again (**Figure 4.12A**). This group also includes a number of genes involved in amino acid and carbohydrate metabolic processes. The riboflavin biosynthetic genes in *A. photophilum* are in expression groups E and J and have a very similar expression pattern: increasing for 1 h in the light, then decreasing until the light turns off, then a transient increase (**Figure 4.12B**). Expression group E also includes the putative DNA photolyase *phrB*, which would require the flavin cofactors synthesized by this pathway (**Table A.9**).

Carotenoid compounds also absorb visible light. Expression of carotenoid biosynthetic genes in *A. photophilum* decreases in the light and increases in the dark, though there is considerable variability in their expression patterns (**Figure 4.13B**). In *R. lacicola*, the putative phytoene synthase (*Rhola_010860*) increases early in the light period, then decreases until the light turns off, then increases again. In contrast, a cluster of three genes encoding a phytoene desaturase and two putative lycopene cyclases decreases in the light, increases in the dark, and a second cluster with a second putative phytoene destaturase and a prenyltransferase increases early in the light period, then decreases for the rest of the experiment, with a transient increase early in the dark period (**Figure 4.13A**).

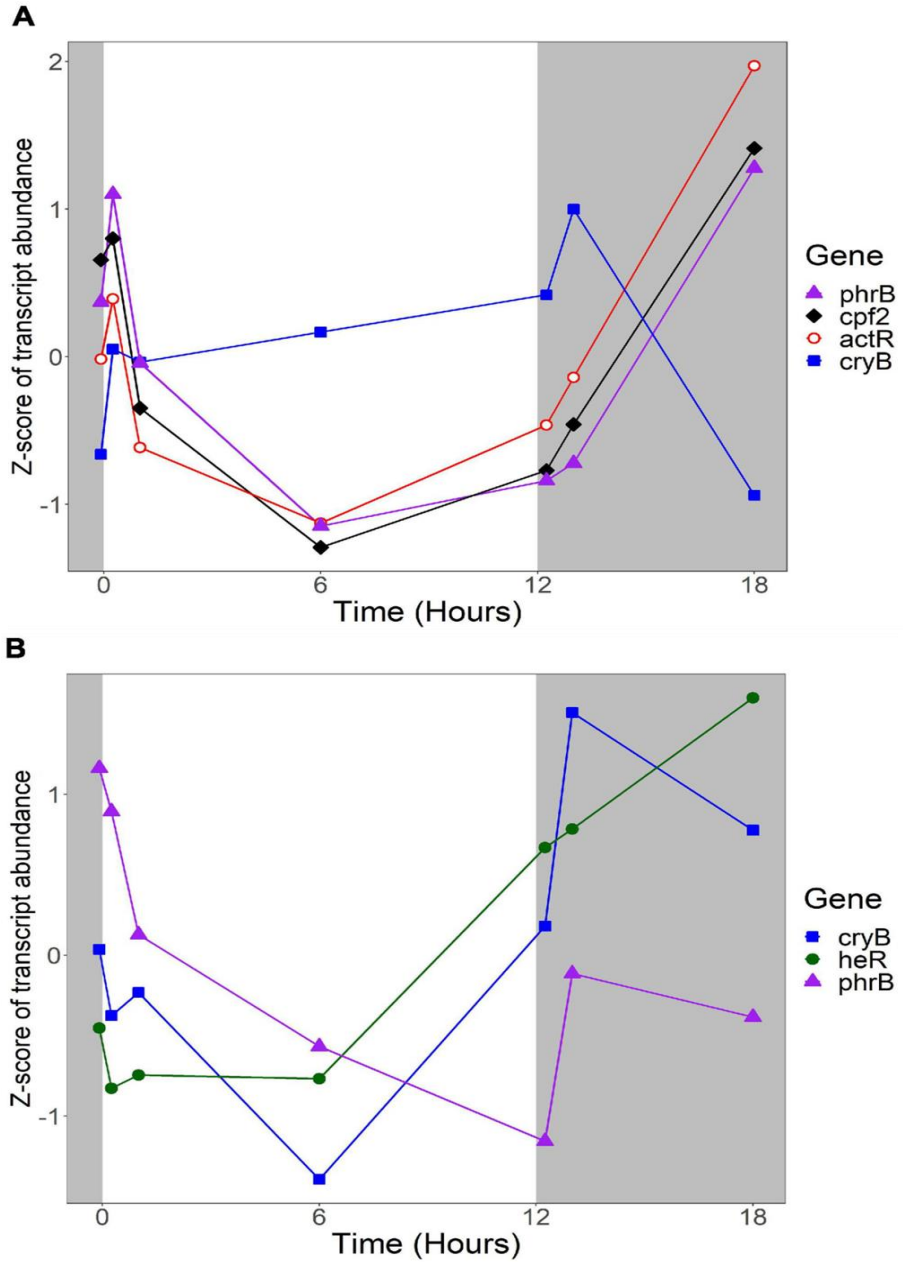

Figure 4.11 Expression of putative light sensors. Expression is plotted as z-score of each transcript. (A) Expression of potential light sensors in *R. lacicola*, which include an actinorhodopsin (*actR*), a DNA photolyase (*phrB*), a CryB-type cryptochrome (*cryB*), and another member of the cryptochrome-photolyase superfamily of proteins (*cpf2*). (B) Expression of potential light sensors in *A. photophilum*, which has a heliorhodopsin (*heR*), a DNA photolyase (*phrB*), and a CryB-type cryptochrome (*cryB*). Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

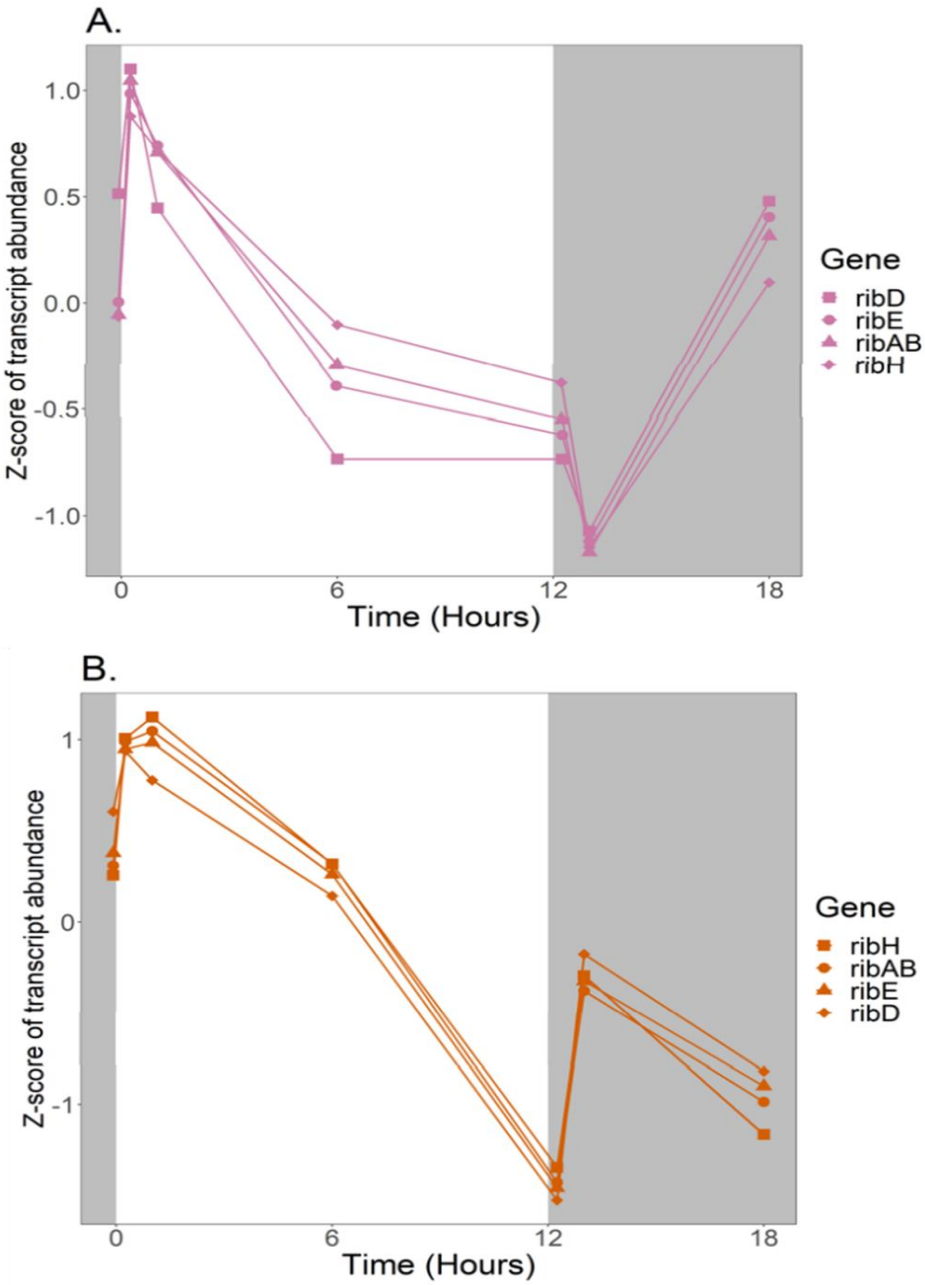

Figure 4.12 Expression of putative riboflavin biosynthesis genes. In both strains, *ribH*, *ribAB*, *ribE*, and *ribD* are organized in a cluster. Expression is plotted as z-score of each transcript. (A) Putative riboflavin biosynthesis genes in *R. lacicola*. (B) Putative riboflavin biosynthesis genes in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

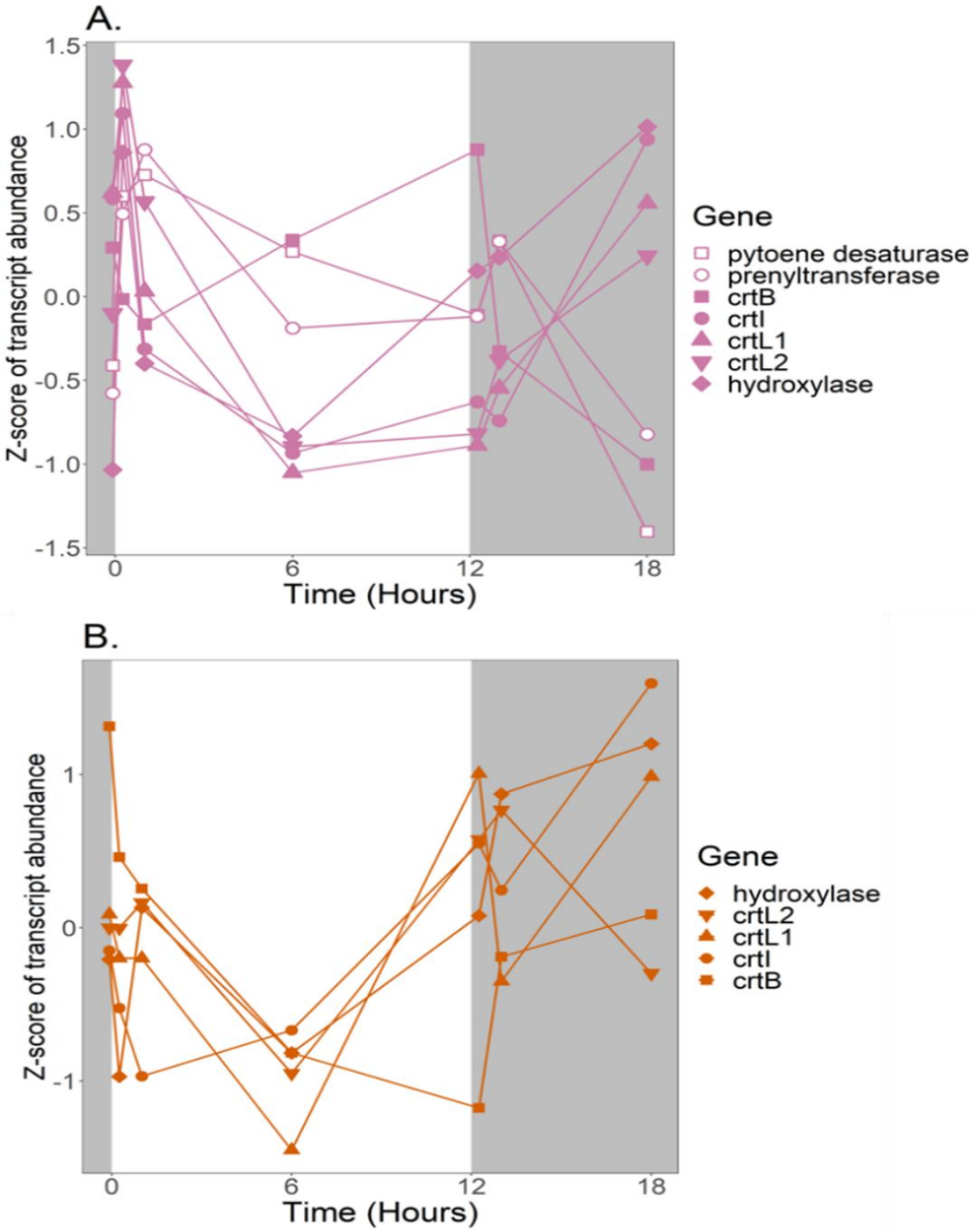

Figure 4.13 Expression of carotenoid biosynthesis genes. Expression is plotted as z-score of each transcript. (A) Putative carotenoid biosynthesis genes in *R. lacicola*. (B) Putative carotenoid biosynthesis genes in *A. photophilum*. Figure reproduced from (Hempel et al., 2021) with permission from Frontiers in Microbiology.

4.4.5 Expression of Putative Transcriptional Regulators of Interest

Multiple predicted transcription factors were previously identified in Chapter 2 and Chapter 3 for their possibility as step(s) in the proposed signal transduction cascade. In Chapter 2, I identified a putative two-component response regulator, ompR gene among the twenty-two genes shared by *R. lacicola* and *A. photophilum* that have significant differential expression in light vs dark. Here, I show the *R. lacicola* putative two-component response regulator, OmpR family (*Rhola_00010430*) and the adjacent sensor kinase (*Rhola_00010440*) have low transcript abundance in the light that generally increases over the 18-hour light/dark cycle with a large increase between 1 hour and 6 hours in the dark (**Figure 4.14A**). While they both share an overall similar expression pattern, *Rhola_00010430* falls into expression group H and *Rhola_00010440* was not assigned an expression group. *R. lacicola's* expression group H contains predicted genes related to stress response, translation, protein modification, sulfur metabolism, and transcriptional regulation (**Figure 4.6A** & **Table A.8**).

The *A. photophilum* best reciprocal hits to *Rhola_00010430* and *Rhola_00010440* are a putative transcriptional regulatory protein TcrX (*AURMO_01425*) and a putative sensor histidine kinase TcrX (*AURMO_01426*), respectively. *AURMO_01425* and *AURMO_01426* have similar expression patterns to each other, where transcript abundance for both decreases immediately in response to light, is stable between 1 hour and 6 hours in light, greatly decreases after 15 minutes in the dark, greatly increases after 1 hour in the dark, and then decreases after 6 hours in the dark (**Figure 4.14B**). Between 15 minutes and 1 hour in the light, *AURMO_01425* decreases while *AURMO_01426* increases transcriptional abundance. While both share an overall similar expression pattern, *AURMO_01425* is included in

expression group F and *AURMO_01426* was not assigned an expression group. *A. photophilum's* expression group F contains predicted genes related to translation, protein degradation, and transmembrane uptake of phosphate and ammonium **Figure 4.6B** & **Table A.9**).

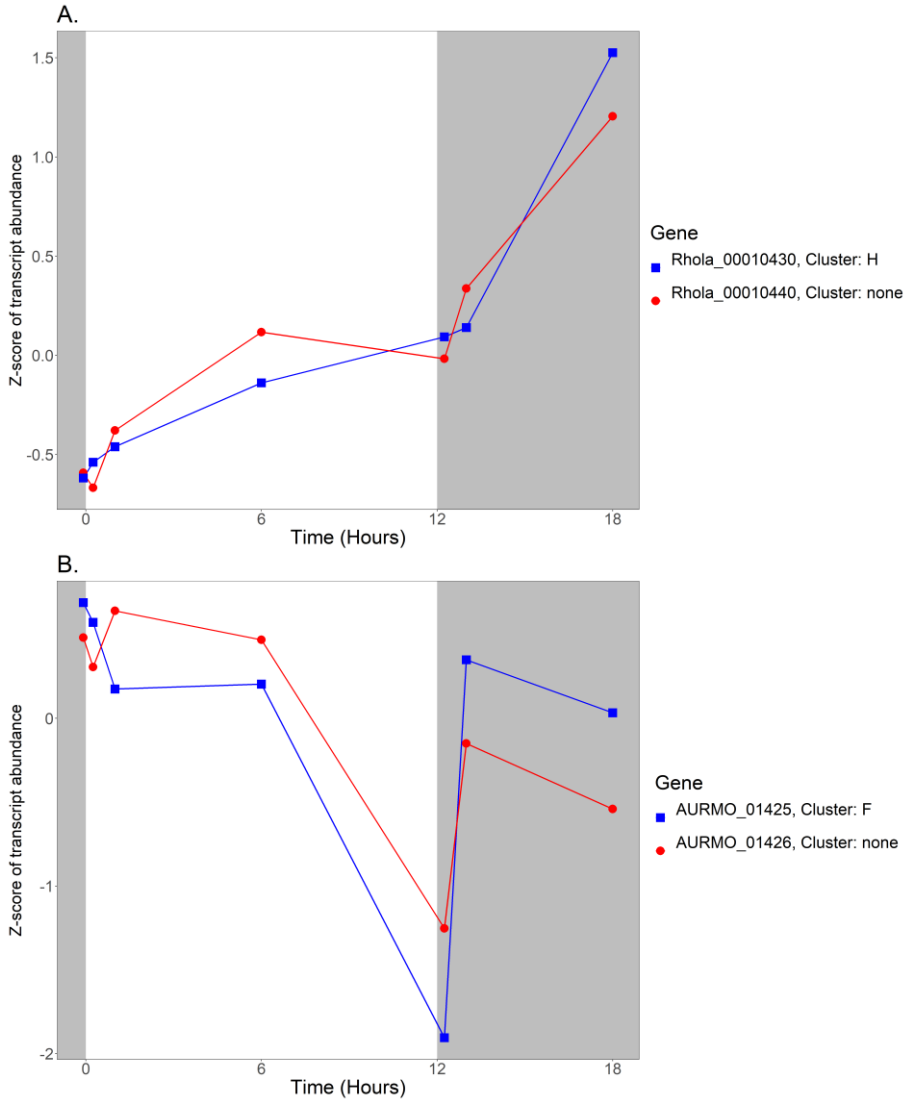

Figure 4.14 Expression of putative two-component response regulator and sensor kinase genes. Expression is plotted as z-score of each transcript. (A) Putative two-component response regulator and sensor kinase genes in *R. lacicola*. (B) Putative two-component response regulator and sensor kinase genes in *A. photophilum*.

In Chapter 3, the *R. lacicola* putative transcriptional regulator, MocR (*Rhola_00013990*) was assigned to gene cluster GC_00000900, which co-occurred with both actinorhodopsin and cryptochrome containing gene clusters. Here I show *Rhola_00013990* has decreasing transcript abundance immediately in response to light until 6 hours, where transcript abundance then increases between 6 and 12 hours in the light and continues to increase throughout the dark. (**Figure 4.15A**). *Rhola_00013990* does not fall within an expression group. However, the genes *Rhola_00013970*, *Rhola_00013980*, and *Rhola_00014000* are located next to *Rhola_00013990* in the genome and fall into expression group G. Furthermore, *Rhola_00013990* has a similar expression pattern to Group G (**Figure 4.6A**). Group G contains *phrB* (*Rhola_00007890*), *cpf2* (*Rhola_00011000*), and predicted genes related to stress response, signal transduction, carotenoid biosynthesis (**Table A.8**).

The *A. photophilum* best reciprocal hit to *Rhola_00013990*, is putative 2-aminoadipate transaminase (*AURMO_00011*). *AURMO_00011* has decreasing transcript abundance through 15 minutes in the light, a small increase through 1 hour in the light, decreases until 15 minutes in the dark, increases until 1 hour in the dark, and then decreases through 6 hours in the dark (**Figure 4.15B**). *AURMO_00011* falls into expression group E, which contains *phrB* (*AURMO_01673*) and predicted genes related to translation, protein folding, riboflavin biosynthesis, and signal transduction (**Table A.9**).

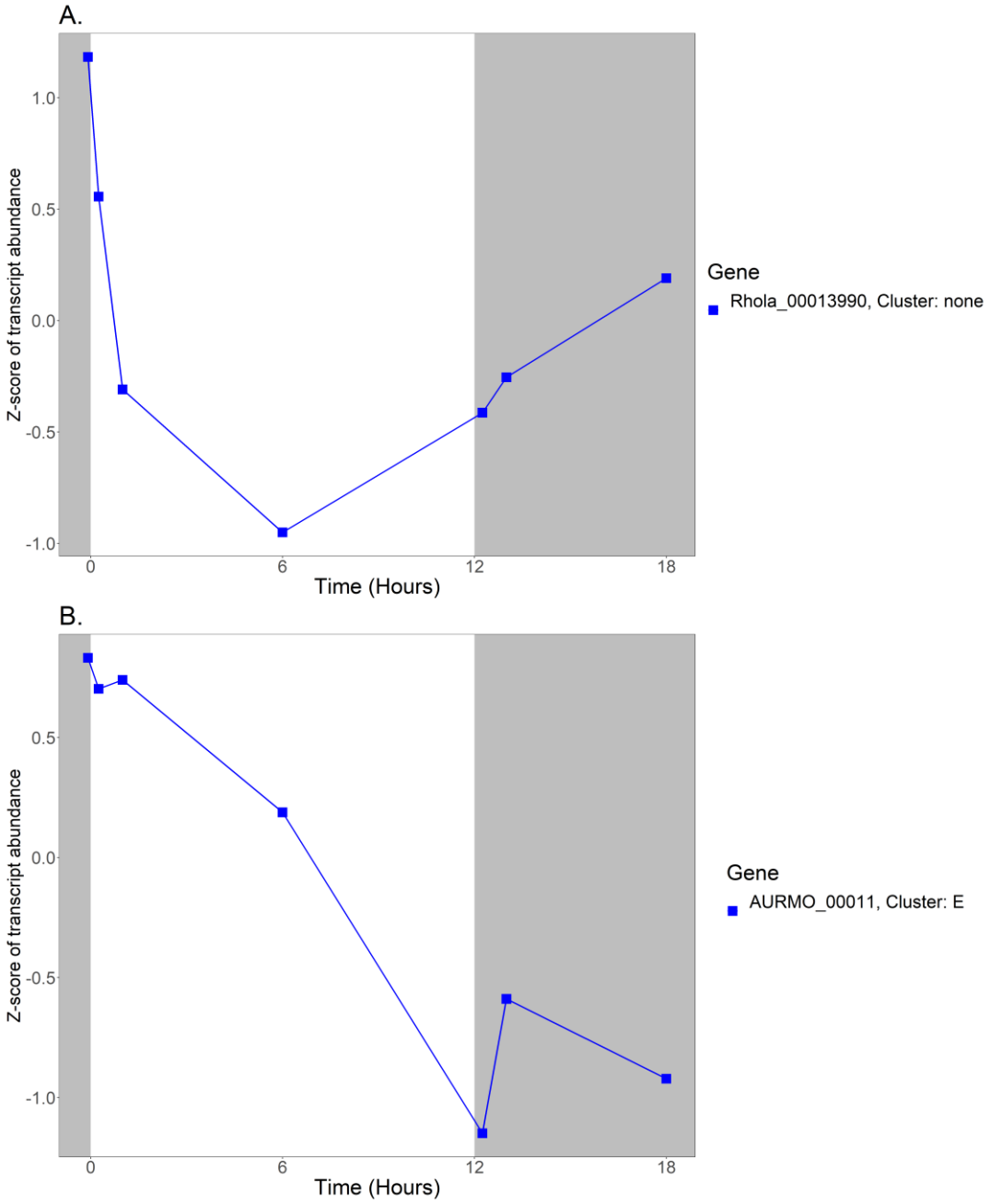

Figure 4.15 Expression of 'putative transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)' genes. Expression is plotted as z-score of each transcript. (A) Putative transcriptional regulator, MocR gene in *R. lacicola*. (B) Putative 2-aminoadipate transaminase in *A. photophilum*.

In the genome comparison presented in Chapter 2, multiple putative transcriptional regulators were identified as unique among the three species *R. lacicola*, *A. photophilum*, and *Aurantimicrobium* sp. strain MWH-UGA1. Among those unique putative transcriptional regulators are: transcriptional regulator (*Rhola_00000060*), Lrp/AsnC family transcriptional regulator (*Rhola_00002820*), WhiB family transcriptional regulator (*Rhola_00011050*), PadR transcriptional regulator (*Rhola_00002790*), transcriptional repressor FrmR (*AURMO_00914*), and transcriptional repressor (*AURMO_01752*).

Rhola_00000060, *Rhola_00002820*, *Rhola_00011050* fall into expression group I. Generally, transcript abundance decreases through six hours in the light and increases between 1 hour and 6 hours in the dark (**Figure 4.16A**). *R. lacicola's* expression group I contains *actR* (*Rhola_00012080*), and predicted genes related to translation and ubiquinone biosynthesis (**Table A.8**).

Rhola_00002790 falls into expression group G. During 15 minutes in the light, transcript abundance increases, then decreases through 6 hours in the light, then increases through 12 hours in the light, and increases throughout 6 hours in the dark (**Figure 4.16B**). *R. lacicola's* expression group G contains *phrB* (*Rhola_00007890*), *cpf2* (*Rhola_00011000*), and predicted genes related to stress response, signal transduction, carotenoid biosynthesis (**Table A.8**).

AURMO_00914 and *AURMO_01752* fall into *A. photophilum's* expression group G. Through 1 hour in the light, they have decreasing transcript abundance which then increases through 6 hours in light, remains constant (*AURMO_01752*) or slightly decreases (*AURMO_00914*) through 15 minutes in the dark, and increases during 1 hour in the dark. *AURMO_00914* increases through 6 hours in the dark and

AURMO_01752 decreases through 6 hours in the dark (**Figure 4.16C**). *A. photophilum's* expression group G contains multiple predicted chaperone proteins, heat-shock proteins, and a BAX inhibitor-1 like protein (*AURMO_01520*) (**Table A.8**).

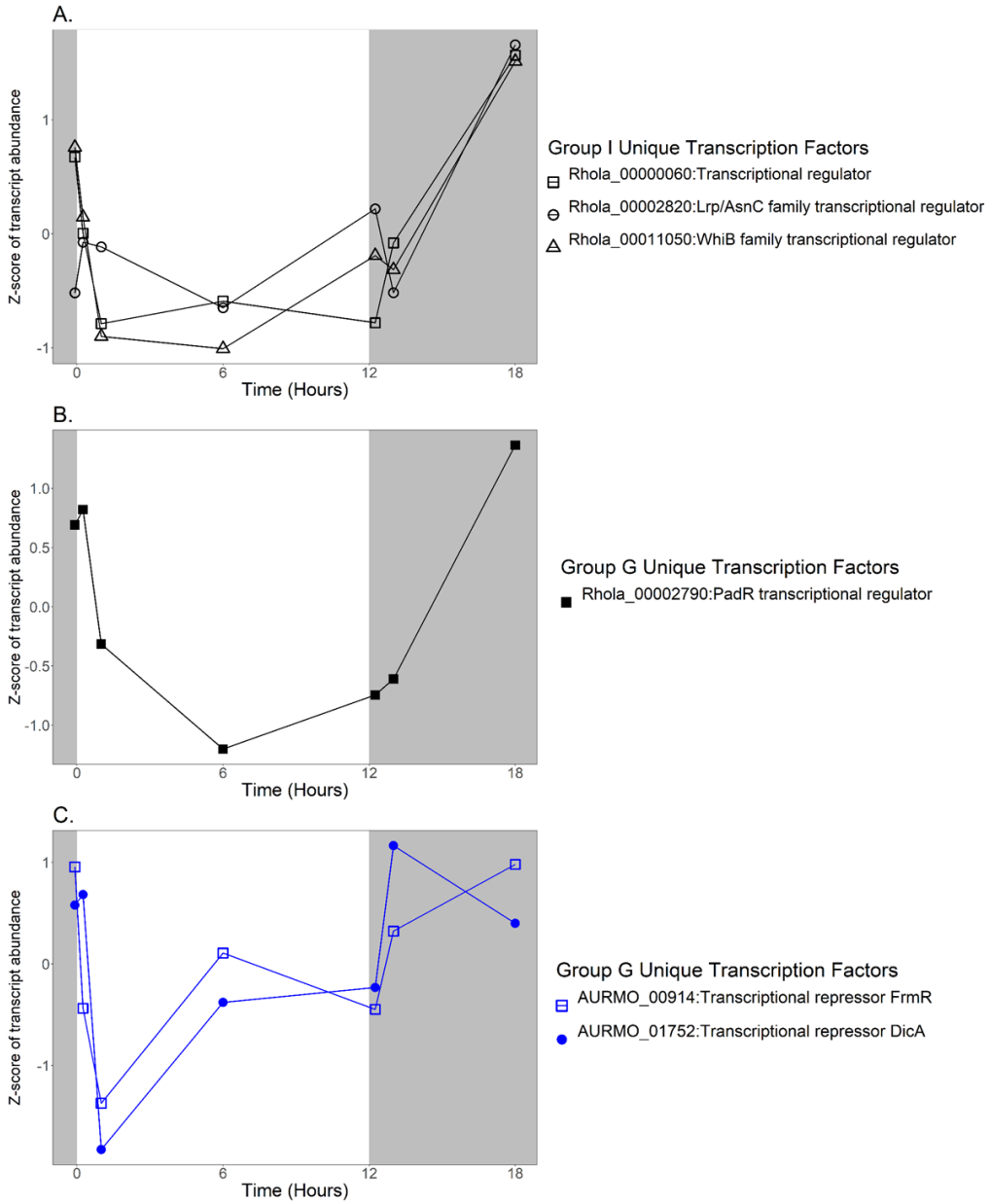

Figure 4.16 Expression of putative transcription factor genes unique to *R. lacicola* and *A. photophilum*. Expression is plotted as z-score of each transcript. (A) *R. lacicola* putative transcriptional regulator genes in expression group I that do not have a best reciprocal BLAST hit in *A. photophilum*. (B) *R. lacicola* putative

transcriptional regulator genes in expression group G that do not have a best reciprocal BLAST hit in *A. photophilum*. (C) *A. photophilum* putative transcriptional regulator genes in expression group G that do not have a best reciprocal BLAST hit in *R. lacicola*.

4.5 Discussion

I hypothesized that R. lacicola and A. photophilum would have similar responses to light, because they belong to the same family (*Microbacteriaceae*) and their genomes are broadly similar. Additionally, I expected that light would stimulate or repress expression of specific genes, and that the effect would decay over time. Instead, I found that different pathways respond to light in *R. lacicola* and *A. photophilum*, and that light and darkness alter transcription differently in each strain

An important difference between the two strains is in energy-conserving pathways: the TCA cycle and the F_1F_0 ATP synthase. In *R. lacicola*, expression of the genes of the TCA cycle and the ATP synthase clearly increases in the light and decreases in response to darkness. Further, the expression patterns of carbohydrate metabolism genes suggest that *R. lacicola* may prioritize early steps of carbohydrate metabolism (glycolysis) in the dark and the TCA cycle as well as synthesis of carbohydrates and storage molecules such as starch in the light. In *A. photophilum*, there are three different expression patterns among the TCA cycle genes, but only one (*AURMO_01262*, encoding a class II fumarate hydratase) was included in an expression group (**Table A.9**), and transcription of genes encoding the ATP synthase appears to increase in response to both light and darkness (**Figure 4.9**). Higher expression of the TCA cycle genes in the light would likely contribute to the faster growth observed in the light in *R. lacicola*; the fact that *A. photophilum* has the same

phenotype without the same gene expression patterns suggests that a different mechanism may be responsible for its increased growth rate in the light.

An intriguing difference between the two strains is the expression of genes encoding a putative *tad/flp* pilus and other putative competence genes. Both strains have two putative operons encoding components of the pilus, as well as the *com* system for competence. In *A. photophilum*, these genes are not coordinately expressed; in *R. lacicola*, expression of all of them clearly increases in response to darkness (**Figure 4.10**). The ways that genetic repair and exchange by these two species are regulated seem to be so different that they may have very different mechanisms for environmental adaptation and diversification. Rapid microdiversification in related freshwater Actinobacteria has been hypothesized previously (Mehrshad et al., 2018), and consistent, daily uptake and incorporation of exogenous DNA could provide a mechanism for these rapid changes in genetic makeup.

Some interesting similarities between the two strains occur in expression of potential light-sensitive proteins and the genes with similar patterns. Expression of the rhodopsin in both strains increases greatly in the dark, and the heliorhodopsin (*heR*) in *A. photophilum* has a similar expression pattern to the carotenoid biosynthetic genes (**Figure 4.11B, Figure 4.13B**). In *R. lacicola*, *actR* expression is similar to expression of about half of the carotenoid biosynthetic genes; the different expression patterns observed in this pathway suggests that different carotenoid products may be produced at different times (**Figure 4.11A, Figure 4.13A**).

The protein that senses light and signals the cells to change their activity has not yet been identified, though based on the growth rate data, it would likely be a blue-light sensing protein (Maresca et al., 2019). A new type of blue light sensor was

identified in *Leptospirillum* (Xu et al., 2021), but no homologs to this gene were found in the genomes of *R. lacicola* or *A. photophilum*. Previously, it was hypothesized that the putative CryB-type cryptochrome both strains have could be the light sensor (Maresca et al., 2019). Here, I show that in *R. lacicola*, transcription of *cryB* increases during the light period, increases transiently when the light turns off, then decreases during the rest of the dark period. In contrast, transcription of *cryB* in *A. photophilum* appears to decrease through the light period, then increase greatly at the beginning of the dark period (**Figure 4.11**). If the CryB homologs in *R. lacicola* and *A. photophilum* regulate the light response, this difference in expression could explain why the transcriptional responses in the two strains have such different dynamics.

The transcription dynamics observed here raise questions about circadian rhythms. It previously observed that both R. lacicola and A. photophilum lack homologs of the core clock proteins (KaiA, KaiB, and KaiC) that control circadian rhythms in cyanobacteria, and that the only predicted proteins with homology to light-sensing domains such as PAS, GAF, and BLUF domains are the photolyases and cryptochromes (Maresca et al., 2019). The genomes likewise lack homologs to YtvA, a putative blue-light sensor, and the histidine kinase *KinC*, both of which have PAS domains and are expressed with circadian patterns in Bacillus subtilis (Eelderink-Chen et al., 2021). Although it is tempting to speculate about circadian rhythms in freshwater bacteria that inhabit surface waters and would therefore consistently be exposed to sunlight, evidence of circadian rhythms would have to come from observing an entrained pattern of activity in the absence of the light signal (Sartor et al., 2019). The oxidation state of peroxiredoxin activity has been suggested to be an indicator of circadian cycles in eukaryotes, bacteria, and archaea (Edgar et al., 2012).

In Chapter 3, the peroxiredoxin (*Rhola_00006540*) and its homolog (*AURMO_00726*), were identified within a gene cluster enriched in terrestrial *Microbacteriaceae*. Both strains studied here have two peroxiredoxins in their genomes. Transcription of both peroxiredoxins in *A. photophilum* increases from 1 h after the light turns on until the light turns off, then drops sharply (**Figure 4.8B**). In contrast, in *R. lacicola*, the peroxiredoxins have inverse transcription patterns, with one increasing early in the light period and the other decreasing, then reversal of those trends (**Figure 4.8A**). Although peroxiredoxin oxidation state was not quantified here, peroxiredoxin transcription in both strains appears to vary in coordination with light availability. This may reflect changes in oxidative stress in the light – other genes in this category have similar transcriptional profiles – but is intriguing, given the observed enrichment in terrestrial *Microbacteriaceae* and the consistent association of peroxiredoxin activity with circadian rhythms (Edgar et al., 2012).

In *R. lacicola*, light stimulates or represses expression of most light-responsive genes, and that effect decays over time, leading to curved gene expression profiles with different maxima or minima. The relatively small number of dark-responsive genes, however, suggest that to this strain, darkness is not just an absence of light, but a different stimulus altogether (**Figure 4.3M, N**). This is observed even more strongly in *A. photophilum*, where both light and darkness induce transient changes in gene expression (**Figure 4.4**). It is possible here, as in *Rhodobacter sphaeroides*, a light sensitive protein is a master regulator, and any change in light availability disrupts expression of a variety of genes (Frühwirth et al., 2012). Regardless, it suggests that *R. lacicola* and *A. photophilum* may have different signal transduction pathways and/or

regulatory proteins that respond to light and darkness. Since they clearly have different networks of light- and dark-responsive genes, this is not surprising.

Here I have identified which shared regulatory proteins are light regulated in both strains and which unique regulatory proteins are light regulated. In both strains, the two-component ompR response regulator have a similar expression pattern to genes related to translation and protein modification (**Figure 4.14** & **Table A.8**, **Table A.9**). However, the patterns differed greatly between the two strains, where the *R. lacicola ompR* response regulator's expression increases throughout the light and the dark periods, the *A. photophilum ompR* response regulator's expression decreases throughout the light, has a large increase immediately to dark, and then decreases through the rest of the dark period. It is possible that this two-component ompR response regulator is part of a light-sensitive two-component system (Drepper et al., 2011). Nevertheless, the differences in expression patterns observed here indicates that the *R. lacicola* and the *A. photophilum* two-component ompR genes may be regulated by different pathways and are good candidates for further study to determine their role in the light-enhanced growth phenotype.

In both strains, the putative MocR transcriptional regulator has a similar expression pattern to *phrB* and genes related to signal transduction (**Figure 4.15** & **Table A.8**, **Table A.9**). Again, the expression patterns differed between the two strains, where *R. lacicola* gene decreases in expression through the light and then increases in response to dark while the *A. photophilum* gene decreases through the light, increases between 15 minutes and 1 hour in the dark, and then decreases through 6 hours in the dark. In both strains, the similarities in genes that are grouped together by expression pattern, yet having different expression patterns between strains,

supports that *R. lacicola* and *A. photophilum* have different regulatory mechanisms that respond to light and dark.

I identified four putative transcriptional regulators unique to *R.lacicola* and two unique to *A. photophilum* that have light regulated expression (**Figure 4.16** & **Table A.8**, **Table A.9**). Three of the four *R. lacicola* transcriptional regulators have similar expression patterns to *actR* and genes related to translation and ubiquinone biosynthesis. The fourth *R. lacicola* transcriptional regulator has a similar expression pattern to both *phrB, cpf2,* and genes related to stress response, signal transduction, carotenoid biosynthesis. Both of the *A. photophilum* transcriptional regulators have similar expression patterns to predicted genes related to stress response. These results suggest that *R. lacicola* and *A. photophilum* experience higher stress in the dark, but use different sets of transcriptional regulators for their stress responses. These transcriptional regulators likely contribute to the different networks of light- and dark-responsive genes in *R. lacicola* and *A. photophilum* and are good candidates for future study to determine their role in the light-enhanced growth phenotype. These data lay the groundwork for experiments testing the effects of light on physiological and biochemical properties of freshwater Actinobacteria, and identifying the cellular activities that correspond to light-induced transcriptional changes in these organisms.

Chapter 5

CONCLUDING REMARKS AND FUTURE DIRECTIONS

5.1 Conclusions

Light is a critical component of many living organisms' daily functions and is Earth's most vital energy source. Earth's most abundant organisms, bacteria, have evolved multiple ways to sense light. Although multiple ways of sensing light have been identified, light's role in heterotrophic nutrient cycling within surface environments is not widely characterized. The work presented here uses a bioinformatics approach to identify the biological activities that respond to light and dark in two model freshwater *Microbacteriaceae* species and provides a foundation to test the physiological and biochemical properties of freshwater Actinobacteria.

Previous to this work, three freshwater *Microbacteriaceae* species that grow faster specifically in blue/near-UV light, were identified. Based on their phenotypes, I hypothesized that closely related Actinobacterial species with light-enhanced growth share a blue light sensor and mechanism(s) that relay blue light sensing to increased growth. To test this, I first annotated the genomes of *A. photophilum* and *Aurantimicrobium* sp. strain MWH-Uga1, both of which have light-enhanced growth, as well as the genome of *Microbacterium* sp. strain 10M-3C3 which does not have light enhanced growth (Chapter 2). I then compared the genomes of three strains with light-enhanced growth, *R. lacicola, A. photophilum, Aurantimicrobium* sp. strain MWH-Uga1, and one strain without light-enhanced growth, *Microbacterium* sp. strain 10M-3C3. I found that closely related freshwater *Actinobacteria* share a large

proportion (between 48%-62%) of their genomes and have similar predicted biochemical functions.

Next, I built upon the genome comparisons in Chapter 2 by using the results of a pangenome analysis of 27 *Microbacteriaceae* to identify genes that may be related to the unresolved molecular functions of certain light sensors in freshwater *Microbacteriaceae* species with light-enhanced growth (Chapter 3). Additionally, I identified genes that are more likely to be found in terrestrial vs. marine *Microbacteriaceae* which provides insight on how *Microbacteriaceae* species are specialized for their environment. I found that marine *Microbacteriaceae* are enriched with Na+ usage, transcriptional regulation, signal transduction, and cell division related pathways, which is unsurprising given the high salinity of marine environments. For *Microbacteriaceae* in terrestrial environments, I identified a significant enrichment of both a peroxiredoxin and glutaredoxin-like genes, which suggests that terrestrial *Microbacteriaceae* may undergo more oxidative stress than marine *Microbacteriaceae.* These results provide evidence and support that *Microbacteriaceae* are highly specialized for their environments.

Finally, I analyzed the transcriptomes of two freshwater *Microbacteriaceae* species, *R. lacicola* and *A. photophilum*. Using pathways and genes identified in Chapter 2 and Chapter 3, I showed that both shared and unique genes between the two species can be light-regulated and furthermore, have different expression patterns through a light/dark cycle. Among shared genes, those involved in the TCA cycle within *R. lacicola* have a coordinated increased transcription in the light, while *A. photophilum* TCA cycle genes follow three different expression patterns. And although ATP synthesis genes in both species respond to light, their expression

patterns differ greatly. With such large differences in their transcriptional responses, this work supports that light mediated signal cascades in *R. lacicola* and *A. photophilum*, that result in increased growth, likely have different (**Figure 5.1 B, C, & D**) downstream effector molecules, transcription factors, and transcribed genes. This is contrary to our initial hypothesis that closely related freshwater Actinobacteria species with blue light-enhanced growth share mechanism(s) that relay blue-light sensing to increase growth.

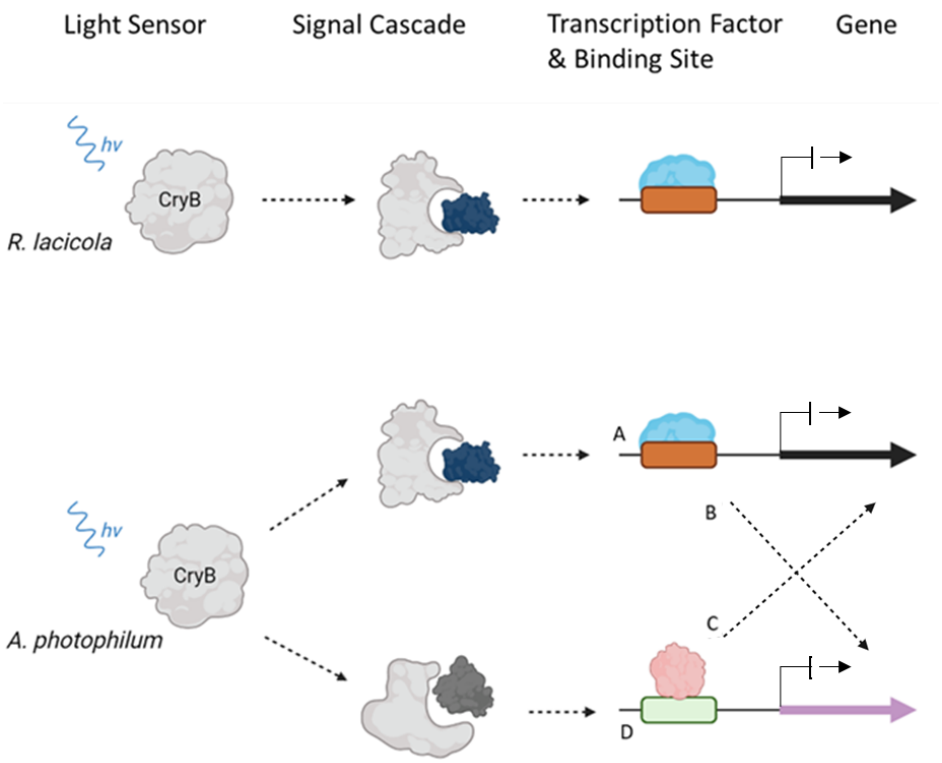

Figure 5.1 Updated putative signal transduction cascade steps in *R. lacicola* vs. *A. photophilum* blue-light mediated growth. Blue light sensing may induce a conformational change in CryB protein, the likely blue-light sensor, that subsequently induces binding to other molecule(s), initiates different signal transduction cascades in *R. lacicola* and *A. photophilum* that causes transcription factors to bind to DNA, which then promote or repress the transcription rate of both shared and unique genes. *R. lacicola* and *A. photophilum* blue light mediated signal cascades likely have different (B, C, & D) downstream effector molecules, transcription factors, and transcribed genes.

Overall, this work has expanded understanding of freshwater Actinobacteria's genetics and their transcriptional response to light and dark cycling. Though freshwater Actinobacteria that have similar growth phenotypes share a large proportion of the genomes, their transcriptional responses vary greatly. The differences in their transcriptional responses indicate that different mechanism(s) may be responsible for the increased growth rates in the light. Therefore, *R. lacicola* and *A. photophilum* may have different signal transduction pathways and/or regulatory proteins that respond to light and darkness. A better understanding of light-regulated freshwater Actinobacteria genetics and transcriptomics has many potential uses and benefits, including engineering light-sensor system71s, construction of efficient light-regulated control of gene expression, identifying new light-sensors, and better understanding of nutrient cycling in freshwater ecosystems.

5.2 Future Work

Within this work, multiple genes of interest were identified as good candidates for future experiments that would test the effects of light and dark on physiological and biochemical properties of freshwater Actinobacteria. These future experiments would work towards identifying and measuring the cellular activities that correspond to light-induced transcriptional changes in these organisms. Genes of interest include those that encode the light-sensors, riboflavin biosynthetic pathway, and transcriptional regulators. The transcriptional regulators include a 'putative two-component response regulator, OmpR family' and a 'putative transcriptional regulator, MocR' which are shared by *R.lacicola* and *A. photophilum*, yet have light-regulated transcription that differs between the two species. These transcriptional regulators,

plus the light-regulated transcriptional regulators that are unique to each species, are entry points in identifying which transcriptional regulators and biological pathways contribute to the light-enhanced growth phenotype. Using genetic engineering techniques, including gene knockouts and/or mutagenesis, may identify the roles of these genes of interest.

Thus far, the transcriptomics analyzed here have provided insight into freshwater Actinobacteria's response to a 24-hour light/dark cycle. This generates questions about whether the transcription dynamics observed here are related to circadian rhythms. While no known mechanisms of circadian rhythms were identified in the species described here, evidence for circadian rhythms should be observed from experiments measuring entrained pattern(s) of activity in the absence of the light signal. These experiments may identify presently unknown circadian rhythm mechanisms.

Additionally, efforts in sampling, isolating, and sequencing Actinobacteria from various environments may identify more strains with light-regulated biological pathways. Also, measuring biological activity under varying environmental conditions may provide new insight on light-regulated bacterial mechanisms. Clearly, bacterial light-sensing is more complex than previously understood and there is much to characterize about how bacteria use light.

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Appendix

RESULTS OF GENOME COMPARISONS AND TRANSCRIPTOMIC ANALYSES

Table A.1 Genes shared by *R. lacicola* and *A. photophilum* that have significant differential expression in constant light vs. constant dark. Genes in each row are best reciprocal BLAST hits. Fold change data was obtained from previous transcriptome studies (Maresca et al., 2019). A negative log2 foldchange indicates expression is higher in the dark than light. Similarity column indicates if log2 foldchange is negative or positive in both *R. lacicola* and *A. photophilum.* Twenty-two genes are shared by *R. lacicola* and *A. photophilum* and have similar responses to light vs. dark. Four genes are shared by *R. lacicola* and *A. photophilum* and have opposing responses to light vs. dark. All twenty-two genes are also shared with *Microbacterium* sp. strain 10M-3C3.

***A. photophilum* Locus Tag**	**Log2 fold change**	***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Log2 fold change**	**Log2 fold change similar?**
AURMO_00336	0.447033	RHOLA_RS05790	*Rhola*_00011660	-1.81625	FALSE
AURMO_00108	-0.457407	RHOLA_RS01425	*Rhola*_00002860	0.324831	FALSE
AURMO_01483	-0.283193	RHOLA_RS02780	*Rhola*_00005600	0.320836	FALSE
AURMO_01543	-0.318609	RHOLA_RS01320	*Rhola*_00002650	1.68523	FALSE
AURMO_00029	0.406398	RHOLA_RS06850	*Rhola*_00013800	0.444892	TRUE
AURMO_00362	0.372785	RHOLA_RS05655	*Rhola*_00011390	0.852225	TRUE
AURMO_01180	0.308576	RHOLA_RS01915	*Rhola*_00003860	0.33556	TRUE
AURMO_01191	0.578797	RHOLA_RS02160	*Rhola*_00004350	0.786643	TRUE
AURMO_01262	0.276182	RHOLA_RS04925	*Rhola*_00009900	0.573257	TRUE
AURMO_01288	0.636671	RHOLA_RS01665	*Rhola*_00003350	0.677553	TRUE
AURMO_00002	-1.06649	RHOLA_RS06990	*Rhola*_00014080	-1.61038	TRUE
AURMO_00018	-0.271988	RHOLA_RS06895	*Rhola*_00013900	-0.779072	TRUE
AURMO_00212	-0.680425	RHOLA_RS06050	Rhola_00012170	-0.975662	TRUE
AURMO_00473	-0.200412	RHOLA_RS02090	Rhola_00004210	-0.368164	TRUE
AURMO_00772	-0.271438	RHOLA_RS03485	Rhola_00007020	-0.296517	TRUE

A. photophilum Locus Tag	Log2 fold change	*R. lacicola* New Locus Tag	*R. lacicola* Old Locus Tag	Log2 fold change	Log2 fold change similar?
AURMO_00932	-0.357985	RHOLA_RS02920	Rhola_00005880	-0.839025	TRUE
AURMO_01020	-0.213302	RHOLA_RS02450	Rhola_00004930	-1.14866	TRUE
AURMO_01160	-0.777481	RHOLA_RS04520	Rhola_00009080	-1.02985	TRUE
AURMO_01212	-0.299521	RHOLA_RS04565	Rhola_00009170	-0.963339	TRUE
AURMO_01225	-0.741211	RHOLA_RS05445	Rhola_00010960	-1.19655	TRUE
AURMO_01227	-0.364064	RHOLA_RS05455	Rhola_00010980	-1.19655	TRUE
AURMO_01375	-0.330325	RHOLA_RS01490	Rhola_00002990	-1.75806	TRUE
AURMO_01425	-0.630193	RHOLA_RS05190	Rhola_00010430	-1.60797	TRUE
AURMO_01426	-0.407186	RHOLA_RS05195	Rhola_00010440	-1.23996	TRUE
AURMO_01594	-0.43756	RHOLA_RS02245	Rhola_00004520	-0.680248	TRUE
AURMO_01726	-0.47633	RHOLA_RS06815	Rhola_00013730	-1.809	TRUE

Table A.2 The 842 genes shared by *A. photophilum*, *Aurantimicrobium* sp. strain MWH-UGA1, and *R. lacicola*. Locus tags for each of the three genomes compared, including both the old and new locus tags for *R. lacicola*, as well as the *R. lacicola* annotations for each gene.

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_01594	AURUGA1_01468	RHOLA_RS02245	Rhola_00004520	phosphate ABC transporter permease subunit PstC
AURMO_00092	AURUGA1_00083	RHOLA_RS01230		ATP-dependent helicase
AURMO_01180	AURUGA1_00512	RHOLA_RS01915	Rhola_00003860	ATP-dependent helicase
AURMO_01593	AURUGA1_01467	RHOLA_RS02250		phosphate ABC transporter permease PtsA
AURMO_00490	AURUGA1_00526	RHOLA_RS02190	Rhola_00004410	4-aminobutyrate--2-oxoglutarate transaminase
AURMO_01193	AURUGA1_00498	RHOLA_RS02150	Rhola_00004330	aspartate aminotransferase family protein
AURMO_01472	AURUGA1_00260	RHOLA_RS01685	Rhola_00003390	heavy metal translocating P-type ATPase
AURMO_00385	AURUGA1_01278	RHOLA_RS05540	Rhola_00011160	DNA-binding response regulator
AURMO_01425	AURUGA1_00300	RHOLA_RS05190	Rhola_00010430	DNA-binding response regulator
AURMO_01598	AURUGA1_01472	RHOLA_RS01835	Rhola_00003700	DNA-binding response regulator
AURMO_00336	AURUGA1_01324	RHOLA_RS05790	Rhola_00011660	ABC transporter ATP-binding protein
AURMO_00635	AURUGA1_01016	RHOLA_RS04345	Rhola_00008730	Stk1 family PASTA domain-containing Ser/Thr kinase
AURMO_01768	AURUGA1_00019	RHOLA_RS00195	Rhola_00000390	serine/threonine-protein kinase
AURMO_01767	AURUGA1_00020	RHOLA_RS00200	Rhola_00000400	serine/threonine protein kinase
AURMO_00506	AURUGA1_01153	RHOLA_RS04635	Rhola_00009310	cell division ATP-binding protein FtsE
AURMO_00917	AURUGA1_00753	RHOLA_RS05240	Rhola_00010530	sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_01592	AURUGA1_01466	RHOLA_RS02255	Rhola_00004540	phosphate ABC transporter ATP-binding protein
AURMO_00333	AURUGA1_01325	RHOLA_RS01715	Rhola_00003450	NAD-dependent succinate-semialdehyde dehydrogenase
AURMO_01191	AURUGA1_00500	RHOLA_RS02160	Rhola_00004350	gamma-aminobutyraldehyde dehydrogenase
AURMO_01245	AURUGA1_00438	RHOLA_RS04810	Rhola_00009670	methylmalonate-semialdehyde dehydrogenase (CoA acylating)
AURMO_01543	AURUGA1_01381	RHOLA_RS01320	Rhola_00002650	sugar ABC transporter ATP-binding protein
AURMO_01535	AURUGA1_01373	RHOLA_RS05710	Rhola_00011500	ABC transporter ATP-binding protein
AURMO_00587	AURUGA1_01072	RHOLA_RS04500		signal recognition particle-docking protein FtsY
AURMO_00588	AURUGA1_01071	RHOLA_RS04495	Rhola_00009030	signal recognition particle protein
AURMO_00733	AURUGA1_00931	RHOLA_RS03285	Rhola_00006620	type I methionyl aminopeptidase
AURMO_00209	AURUGA1_00187	RHOLA_RS06060	Rhola_00012190	type I methionyl aminopeptidase
AURMO_01359	AURUGA1_00342	RHOLA_RS05060	Rhola_00010180	ABC transporter ATP-binding protein
AURMO_00685	AURUGA1_00969	RHOLA_RS03960	Rhola_00007970	ABC transporter ATP-binding protein
AURMO_01065	AURUGA1_00610	RHOLA_RS02805	Rhola_00005650	energy-dependent translational throttle protein EttA
AURMO_01248	AURUGA1_00433	RHOLA_RS06630	Rhola_00013360	fructose-bisphosphatase class II
AURMO_00868	AURUGA1_00802	RHOLA_RS04225	Rhola_00008490	DNA polymerase III subunit alpha
AURMO_00411	AURUGA1_01255	RHOLA_RS04705	Rhola_00009460	bifunctional o-acetylhomoserine/o-acetylserine sulfhydrylase
AURMO_01133	AURUGA1_01499	RHOLA_RS05105	Rhola_00010270	aldo/keto reductase
AURMO_01538	AURUGA1_00450	RHOLA_RS00130	Rhola_00000260	gfo/Idh/MocA family oxidoreductase
AURMO_00239	AURUGA1_00212	RHOLA_RS05945	Rhola_00011960	hypothetical protein
AURMO_01614	AURUGA1_01259	RHOLA_RS06435	Rhola_00012960	UTP--glucose-1-phosphate uridylyltransferase
AURMO_00932	AURUGA1_00735	RHOLA_RS02920	Rhola_00005880	ribonuclease E/G
AURMO_00740	AURUGA1_00925	RHOLA_RS03320	Rhola_00006690	type I glutamate--ammonia ligase
AURMO_00738	AURUGA1_00927	RHOLA_RS03310	Rhola_00006670	type I glutamate--ammonia ligase
AURMO_00928	AURUGA1_00742	RHOLA_RS02940	Rhola_00005920	glutamate 5-kinase
AURMO_00638	AURUGA1_01013	RHOLA_RS04330	Rhola_00008700	polyprenyl synthetase family protein
AURMO_01207	AURUGA1_00488	RHOLA_RS04545	Rhola_00009130	citrate synthase
AURMO_01527	AURUGA1_01367	RHOLA_RS05665	Rhola_00011410	purine-nucleoside phosphorylase
AURMO_00375	AURUGA1_01286	RHOLA_RS05580	Rhola_00011240	O-antigen ligase family protein
AURMO_00108	AURUGA1_00102	RHOLA_RS01425	Rhola_00002860	glutamate-1-semialdehyde-21-aminomutase
AURMO_01483	AURUGA1_01403	RHOLA_RS02780	Rhola_00005600	aminotransferase class V-fold PLP-dependent enzyme
AURMO_01550	AURUGA1_01387	RHOLA_RS04885	Rhola_00009810	hypothetical protein
AURMO_01338	AURUGA1_00358	RHOLA_RS07175	Rhola_00001340	phosphoenolpyruvate carboxykinase (GTP)
AURMO_00663	AURUGA1_00990	RHOLA_RS03860	Rhola_00007770	type I glyceraldehyde-3-phosphate dehydrogenase
AURMO_00111	AURUGA1_00105	RHOLA_RS07195	Rhola_00002880	hydroxymethylbilane synthase
AURMO_00315	AURUGA1_01341	RHOLA_RS01590	Rhola_00003200	acetate--CoA ligase
AURMO_00103	AURUGA1_00096	RHOLA_RS04595	Rhola_00009220	hypothetical protein
AURMO_01764	AURUGA1_00023	RHOLA_RS00215	Rhola_00000430	serine/threonine-protein phosphatase

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_00386	AURUGA1_01277	RHOLA_RS05535	Rhola_00011150	sensor histidine kinase
AURMO_01426	AURUGA1_00299	RHOLA_RS05195	Rhola_00010440	HAMP domain-containing protein
AURMO_01788	AURUGA1_00006	RHOLA_RS00040	Rhola_00000080	DNA gyrase subunit A
AURMO_00754	AURUGA1_00912	RHOLA_RS03405	Rhola_00006860	DNA topoisomerase 4 subunit A
AURMO_00772	AURUGA1_00893	RHOLA_RS03485	Rhola_00007020	ammonium transporter
AURMO_00773	AURUGA1_00894	RHOLA_RS03490	Rhola_00007030	ammonium transporter
AURMO_00361	AURUGA1_01301	RHOLA_RS03355	Rhola_00006760	dihydrolipoyl dehydrogenase
AURMO_00747	AURUGA1_00918	RHOLA_RS05660	Rhola_00011400	NAD(P)H-quinone dehydrogenase
AURMO_00985	AURUGA1_01611	RHOLA_RS06960	Rhola_00014030	ParA family protein
AURMO_00008	AURUGA1_00681	RHOLA_RS04445	Rhola_00008930	ParA family protein
AURMO_00824	AURUGA1_00842	RHOLA_RS03750	Rhola_00007550	anthranilate synthase component I
AURMO_00633	AURUGA1_01018	RHOLA_RS03010	Rhola_00006060	aminodeoxychorismate synthase component I
AURMO_01037	AURUGA1_00629	RHOLA_RS02870	Rhola_00005780	ATP-dependent Clp protease proteolytic subunit
AURMO_01036	AURUGA1_00630	RHOLA_RS02875	Rhola_00005790	ATP-dependent Clp protease proteolytic subunit
AURMO_01341	AURUGA1_00355	RHOLA_RS05025	Rhola_00010110	transcription-repair coupling factor
AURMO_00585	AURUGA1_01074	RHOLA_RS04535	Rhola_00009110	ATP-dependent DNA helicase RecG
AURMO_00986	AURUGA1_00680	RHOLA_RS04450	Rhola_00008940	site-specific tyrosine recombinase XerD
AURMO_00600	AURUGA1_01052	RHOLA_RS02575	Rhola_00005190	tyrosine recombinase XerC
AURMO_00142	AURUGA1_00133	RHOLA_RS00875	Rhola_00001760	ATP-dependent Clp protease ATP-binding subunit
AURMO_01698	AURUGA1_01575	RHOLA_RS06735	Rhola_00013570	ATP-dependent chaperone ClpB
AURMO_01262	AURUGA1_00424	RHOLA_RS04925	Rhola_00009900	class II fumarate hydratase
AURMO_01135	AURUGA1_00545	RHOLA_RS00445	Rhola_00000890	aspartate ammonia-lyase
AURMO_00482	AURUGA1_01186	RHOLA_RS04675	Rhola_00009400	CpaF family protein
AURMO_00316	AURUGA1_01340	RHOLA_RS01595	Rhola_00003210	hypothetical protein
AURMO_01092	AURUGA1_00586	RHOLA_RS02670	Rhola_00005380	cysteine desulfurase
AURMO_01227	AURUGA1_00466	RHOLA_RS05455	Rhola_00010980	cysteine desulfurase
AURMO_01518	AURUGA1_01441	RHOLA_RS05890	Rhola_00011850	ATP-dependent DNA helicase PcrA
AURMO_00550	AURUGA1_01107	RHOLA_RS01955	Rhola_00003940	ATP-dependent helicase
AURMO_00955	AURUGA1_00712	RHOLA_RS04380	Rhola_00008800	pyruvate carboxylase
AURMO_00362	AURUGA1_01300	RHOLA_RS05655	Rhola_00011390	ATP-grasp domain-containing protein
AURMO_00459	AURUGA1_01206	RHOLA_RS02060	Rhola_00004150	peptide chain release factor 1
AURMO_00560	AURUGA1_01101	RHOLA_RS04640	Rhola_00009320	peptide chain release factor 2
AURMO_00613	AURUGA1_01038	RHOLA_RS01330	Rhola_00002670	alpha-amylase
AURMO_01619	AURUGA1_01491	RHOLA_RS01110	Rhola_00002250	alpha-amylase
AURMO_01570	AURUGA1_01451	RHOLA_RS01115	Rhola_00002260	alpha-amylase
AURMO_00688	AURUGA1_00965	RHOLA_RS03110	Rhola_00006260	isoprenyl transferase
AURMO_01315	AURUGA1_00394	RHOLA_RS04945	Rhola_00009950	isoprenyl transferase
AURMO_01225	AURUGA1_00468	RHOLA_RS05445	Rhola_00010960	L-aspartate oxidase

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_00355	AURUGA1_01307	RHOLA_RS05735	Rhola_00011550	succinate dehydrogenase flavoprotein subunit
AURMO_01212	AURUGA1_00483	RHOLA_RS04565	Rhola_00009170	translational GTPase TypA
AURMO_00907	AURUGA1_00763	RHOLA_RS03045	Rhola_00006130	elongation factor 4
AURMO_01789	AURUGA1_00005	RHOLA_RS00035	Rhola_00000070	DNA topoisomerase (ATP-hydrolyzing) subunit B
AURMO_00753	AURUGA1_00913	RHOLA_RS03400	Rhola_00006850	type IIA DNA topoisomerase subunit B
AURMO_00746	AURUGA1_00919	RHOLA_RS03350	Rhola_00006750	2-oxoglutarate dehydrogenase E2 component dihydrolipoamide succinyltransferase
AURMO_00029	AURUGA1_00061	RHOLA_RS06850	Rhola_00013800	2-oxo acid dehydrogenase subunit E2
AURMO_00403	AURUGA1_01262	RHOLA_RS04730	Rhola_00009510	HlyC/CorC family transporter
AURMO_00402	AURUGA1_01263	RHOLA_RS04735	Rhola_00009520	HlyC/CorC family transporter
AURMO_00575	AURUGA1_01084	RHOLA_RS02720	Rhola_00005480	TerC family protein
AURMO_01566	AURUGA1_01445	RHOLA_RS01090	Rhola_00002210	TerC family protein
AURMO_01174	AURUGA1_00517	RHOLA_RS00080	Rhola_00000160	ABC transporter ATP-binding protein
AURMO_00447	AURUGA1_01232	RHOLA_RS06395	Rhola_00012870	ABC transporter ATP-binding protein
AURMO_00001	AURUGA1_00001	RHOLA_RS00005	Rhola_00000010	chromosomal replication initiator protein DnaA
AURMO_00005	AURUGA1_01614	RHOLA_RS06975	Rhola_00014060	membrane protein insertase YidC
AURMO_00006	AURUGA1_01613	RHOLA_RS06970	Rhola_00014050	DNA-binding protein
AURMO_00012	AURUGA1_01607	RHOLA_RS06935	Rhola_00013980	thioredoxin
AURMO_00013	AURUGA1_01606	RHOLA_RS06930	Rhola_00013970	thioredoxin-disulfide reductase
AURMO_00015	AURUGA1_01603	RHOLA_RS06910	Rhola_00013930	CCA tRNA nucleotidyltransferase
AURMO_00016	AURUGA1_01602	RHOLA_RS06905	Rhola_00013920	30S ribosomal protein S6
AURMO_00019	AURUGA1_01599	RHOLA_RS06890	Rhola_00013890	50S ribosomal protein L9
AURMO_00020	AURUGA1_01598	RHOLA_RS06885	Rhola_00013880	replicative DNA helicase
AURMO_00028	AURUGA1_00060	RHOLA_RS06855	Rhola_00013810	alpha-ketoacid dehydrogenase subunit beta
AURMO_00084	AURUGA1_00075	RHOLA_RS00325	Rhola_00000650	alpha-D-glucose phosphate-specific phosphoglucomutase
AURMO_00087	AURUGA1_00078	RHOLA_RS00355	Rhola_00000710	Cof-type HAD-IIB family hydrolase
AURMO_00124	AURUGA1_00116	RHOLA_RS00790	Rhola_00001590	tRNA lysidine(34) synthetase TilS
AURMO_00134	AURUGA1_00126	RHOLA_RS00840	Rhola_00001690	lysine--tRNA ligase
AURMO_00141	AURUGA1_00132	RHOLA_RS06175	Rhola_00012420	pirin family protein
AURMO_00143	AURUGA1_00134	RHOLA_RS00880	Rhola_00001770	amino-acid N-acetyltransferase
AURMO_00178	AURUGA1_00157	RHOLA_RS06210	Rhola_00012490	DNA-directed RNA polymerase subunit beta'
AURMO_00180	AURUGA1_00159	RHOLA_RS06205	Rhola_00012480	30S ribosomal protein S12
AURMO_00182	AURUGA1_00161	RHOLA_RS06195	Rhola_00012460	elongation factor G
AURMO_00183	AURUGA1_00162	RHOLA_RS06190	Rhola_00012450	elongation factor Tu
AURMO_00191	AURUGA1_00169	RHOLA_RS06150	Rhola_00012370	50S ribosomal protein L2
AURMO_00192	AURUGA1_00170	RHOLA_RS06145	Rhola_00012360	30S ribosomal protein S19
AURMO_00193	AURUGA1_00171	RHOLA_RS06140	Rhola_00012350	50S ribosomal protein L22
AURMO_00194	AURUGA1_00172	RHOLA_RS06135	Rhola_00012340	30S ribosomal protein S3

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00195	AURUGA1_00173	RHOLA_RS06130	Rhola_00012330	50S ribosomal protein L16
AURMO_00203	AURUGA1_00181	RHOLA_RS06090	Rhola_00012250	50S ribosomal protein L18
AURMO_00204	AURUGA1_00182	RHOLA_RS06085	Rhola_00012240	30S ribosomal protein S5
AURMO_00206	AURUGA1_00184	RHOLA_RS06075		50S ribosomal protein L15
AURMO_00207	AURUGA1_00185	RHOLA_RS06070	Rhola_00012210	preprotein translocase subunit SecY
AURMO_00215	AURUGA1_00192	RHOLA_RS06035	Rhola_00012140	DNA-directed RNA polymerase subunit alpha
AURMO_00222	AURUGA1_00197	RHOLA_RS06010	Rhola_00012090	phosphoglucosamine mutase
AURMO_00234	AURUGA1_00208	RHOLA_RS05960	Rhola_00011990	SAM-dependent methyltransferase
AURMO_00237	AURUGA1_00210	RHOLA_RS05950	Rhola_00011970	EamA family transporter RarD
AURMO_00242	AURUGA1_00217	RHOLA_RS05900	Rhola_00011870	glutamine-hydrolyzing GMP synthase
AURMO_00282	AURUGA1_01360	RHOLA_RS01355	Rhola_00002720	hypothetical protein
AURMO_00298	AURUGA1_01354	RHOLA_RS01555	Rhola_00003120	recombination protein RecR
AURMO_00311	AURUGA1_01345	RHOLA_RS01575	Rhola_00003160	metallophosphoesterase
AURMO_00312	AURUGA1_01344	RHOLA_RS01580	Rhola_00003170	PASTA domain-containing protein
AURMO_00314	AURUGA1_01342	RHOLA_RS01585	Rhola_00003190	RidA family protein
AURMO_00321	AURUGA1_01335	RHOLA_RS01620	Rhola_00003260	type I DNA topoisomerase
AURMO_00322	AURUGA1_01334	RHOLA_RS01625	Rhola_00003270	dTMP kinase
AURMO_00339	AURUGA1_01321	RHOLA_RS05770	Rhola_00011620	GTP cyclohydrolase II
AURMO_00341	AURUGA1_01319	RHOLA_RS05760	Rhola_00011600	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD
AURMO_00344	AURUGA1_01317	RHOLA_RS05750	Rhola_00011580	exodeoxyribonuclease III
AURMO_00363	AURUGA1_01299	RHOLA_RS05650	Rhola_00011380	septum formation inhibitor Maf
AURMO_00366	AURUGA1_01295	RHOLA_RS05620	Rhola_00011320	acyl-CoA carboxylase subunit beta
AURMO_00367	AURUGA1_01294	RHOLA_RS05615	Rhola_00011310	biotin--[acetyl-CoA-carboxylase] ligase
AURMO_00371	AURUGA1_01290	RHOLA_RS05605	Rhola_00011290	5-(carboxyamino)imidazole ribonucleotide synthase
AURMO_00372	AURUGA1_01289	RHOLA_RS05600	Rhola_00011280	5-(carboxyamino)imidazole ribonucleotide mutase
AURMO_00377	AURUGA1_01285	RHOLA_RS05575	Rhola_00011230	mannose-6-phosphate isomerase class I
AURMO_00379	AURUGA1_01283	RHOLA_RS05565	Rhola_00011210	glycosyltransferase family 2 protein
AURMO_00398	AURUGA1_01267	RHOLA_RS05495		hypothetical protein
AURMO_00415	AURUGA1_01251	RHOLA_RS04695	Rhola_00009440	N-acetyltransferase
AURMO_00421	AURUGA1_01245	RHOLA_RS00100	Rhola_00000200	dTDP-glucose 46-dehydratase
AURMO_00425	AURUGA1_01243	RHOLA_RS04760	Rhola_00009570	3-phosphoshikimate 1-carboxyvinyltransferase
AURMO_00426	AURUGA1_01242	RHOLA_RS04755	Rhola_00009560	RNA polymerase subunit sigma
AURMO_00454	AURUGA1_01211	RHOLA_RS02040	Rhola_00004110	homoserine dehydrogenase
AURMO_00455	AURUGA1_01210	RHOLA_RS02045	Rhola_00004120	threonine synthase
AURMO_00466	AURUGA1_01200	RHOLA_RS02065	Rhola_00004160	peptide chain release factor N(5)-glutamine methyltransferase
AURMO_00469	AURUGA1_01197	RHOLA_RS02075	Rhola_00004180	undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00474	AURUGA1_01193	RHOLA_RS02095	Rhola_00004220	F0F1 ATP synthase subunit B
AURMO_00477	AURUGA1_01190	RHOLA_RS02110	Rhola_00004250	F0F1 ATP synthase subunit gamma
AURMO_00489	AURUGA1_00525	RHOLA_RS06185	Rhola_00012440	hypothetical protein
AURMO_00497	AURUGA1_00532	RHOLA_RS02215	Rhola_00004460	transcription termination/antitermination protein NusA
AURMO_00508	AURUGA1_01151	RHOLA_RS04625	Rhola_00009280	SsrA-binding protein SmpB
AURMO_00520	AURUGA1_01135	RHOLA_RS00145	Rhola_00000290	imidazolonepropionase
AURMO_00521	AURUGA1_01134	RHOLA_RS00150	Rhola_00000300	urocanate hydratase
AURMO_00522	AURUGA1_01133	RHOLA_RS00140	Rhola_00000280	histidine ammonia-lyase
AURMO_00548	AURUGA1_01109	RHOLA_RS01945	Rhola_00003920	hypothetical protein
AURMO_00549	AURUGA1_01108	RHOLA_RS01950	Rhola_00003930	NAD(+) diphosphatase
AURMO_00553	AURUGA1_01104	RHOLA_RS01970	Rhola_00003970	PDZ domain-containing protein
AURMO_00559	AURUGA1_01102	RHOLA_RS04645	Rhola_00009330	MFS transporter
AURMO_00565	AURUGA1_01095	RHOLA_RS05375	Rhola_00010810	ketol-acid reductoisomerase
AURMO_00568	AURUGA1_01092	RHOLA_RS05370	Rhola_00010800	phosphoglycerate dehydrogenase
AURMO_00571	AURUGA1_01089	RHOLA_RS05340	Rhola_00010740	glutamate--tRNA ligase
AURMO_00578	AURUGA1_01081	RHOLA_RS05290	Rhola_00010640	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
AURMO_00579	AURUGA1_01080	RHOLA_RS05285	Rhola_00010630	1-acyl-sn-glycerol-3-phosphate acyltransferase
AURMO_00583	AURUGA1_01076	RHOLA_RS05265	Rhola_00010590	thiamine-phosphate kinase
AURMO_00589	AURUGA1_01067	RHOLA_RS05220	Rhola_00010490	peptide-methionine (R)-S-oxide reductase
AURMO_00594	AURUGA1_01058	RHOLA_RS02535	Rhola_00005110	tRNA (guanosine(37)-N1)-methyltransferase TrmD
AURMO_00595	AURUGA1_01057	RHOLA_RS02540	Rhola_00005120	50S ribosomal protein L19
AURMO_00597	AURUGA1_01055	RHOLA_RS02550	Rhola_00005140	ribonuclease HII
AURMO_00598	AURUGA1_01054	RHOLA_RS02555	Rhola_00005150	DUF2469 domain-containing protein
AURMO_00599	AURUGA1_01053	RHOLA_RS02570	Rhola_00005180	DNA-protecting protein DprA
AURMO_00601	AURUGA1_01051	RHOLA_RS02840	Rhola_00005720	cation:proton antiporter
AURMO_00603	AURUGA1_01049	RHOLA_RS05110	Rhola_00010280	TIGR01777 family protein
AURMO_00634	AURUGA1_01017	RHOLA_RS03015	Rhola_00006070	leucine--tRNA ligase
AURMO_00644	AURUGA1_01008	RHOLA_RS04305	Rhola_00008650	penicillin-binding protein 2
AURMO_00646	AURUGA1_01007	RHOLA_RS04295	Rhola_00008630	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
AURMO_00648	AURUGA1_01005	RHOLA_RS04285	Rhola_00008610	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
AURMO_00649	AURUGA1_01004	RHOLA_RS04280	Rhola_00008600	cell division protein FtsW
AURMO_00654	AURUGA1_00999	RHOLA_RS04255	Rhola_00008550	YggS family pyridoxal phosphate-dependent enzyme
AURMO_00662	AURUGA1_00991	RHOLA_RS03855	Rhola_00007760	superoxide dismutase
AURMO_00665	AURUGA1_00988	RHOLA_RS03870	Rhola_00007790	triose-phosphate isomerase
AURMO_00667	AURUGA1_00986	RHOLA_RS07225	Rhola_00007810	RNA polymerase-binding protein RbpA
AURMO_00670	AURUGA1_00985	RHOLA_RS03885	Rhola_00007820	6-phosphogluconolactonase

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_00672	AURUGA1_00983	RHOLA_RS03895	Rhola_00007840	glucose-6-phosphate dehydrogenase
AURMO_00677	AURUGA1_00977	RHOLA_RS03925	Rhola_00007900	heme A synthase
AURMO_00682	AURUGA1_00972	RHOLA_RS03950	Rhola_00007950	metal-sulfur cluster assembly factor
AURMO_00691	AURUGA1_00962	RHOLA_RS03120	Rhola_00006280	tRNA dihydrouridine synthase DusB
AURMO_00694	AURUGA1_00959	RHOLA_RS03135	Rhola_00006310	hypothetical protein
AURMO_00696	AURUGA1_00957	RHOLA_RS03155	Rhola_00006350	branched-chain amino acid ABC transporter permease
AURMO_00698	AURUGA1_00955	RHOLA_RS03165	Rhola_00006370	peptide deformylase
AURMO_00720	AURUGA1_00944	RHOLA_RS03220	Rhola_00006480	beta-ketoacyl-[acyl-carrier-protein] synthase family protein
AURMO_00721	AURUGA1_00943	RHOLA_RS03225	Rhola_00006490	acyl carrier protein
AURMO_00723	AURUGA1_00941	RHOLA_RS03235	Rhola_00006510	ACP S-malonyltransferase
AURMO_00731	AURUGA1_00933	RHOLA_RS03275	Rhola_00006590	bifunctional RNase H/acid phosphatase
AURMO_00736	AURUGA1_00929	RHOLA_RS03295	Rhola_00006640	3-methyl-2-oxobutanoate hydroxymethyltransferase
AURMO_00742	AURUGA1_00923	RHOLA_RS03330	Rhola_00006710	DUF4191 domain-containing protein
AURMO_00749	AURUGA1_00916	RHOLA_RS03365	Rhola_00006780	PAC2 family protein
AURMO_00750	AURUGA1_00915	RHOLA_RS03380	Rhola_00006810	RNA polymerase sigma factor
AURMO_00755	AURUGA1_00911	RHOLA_RS03410	Rhola_00006870	hypothetical protein
AURMO_00760	AURUGA1_00906	RHOLA_RS03435	Rhola_00006920	DUF3710 domain-containing protein
AURMO_00763	AURUGA1_00903	RHOLA_RS03450	Rhola_00006950	1-deoxy-D-xylulose-5-phosphate synthase
AURMO_00765	AURUGA1_00901	RHOLA_RS06545	Rhola_00013190	acetyl-CoA C-acyltransferase
AURMO_00770	AURUGA1_00896	RHOLA_RS03475	Rhola_00007000	sulfurtransferase
AURMO_00777	AURUGA1_00889	RHOLA_RS03520	Rhola_00007090	threonine--tRNA ligase
AURMO_00791	AURUGA1_00875	RHOLA_RS03585	Rhola_00007220	peptidylprolyl isomerase
AURMO_00792	AURUGA1_00874	RHOLA_RS03590	Rhola_00007230	replication-associated recombination protein A
AURMO_00795	AURUGA1_00871	RHOLA_RS03610	Rhola_00007270	alanine--tRNA ligase
AURMO_00802	AURUGA1_00864	RHOLA_RS03645	Rhola_00007340	3-dehydroquinate dehydratase
AURMO_00814	AURUGA1_00852	RHOLA_RS03705	Rhola_00007460	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC
AURMO_00815	AURUGA1_00851	RHOLA_RS06950	Rhola_00014010	methionine adenosyltransferase
AURMO_00821	AURUGA1_00845	RHOLA_RS03735	Rhola_00007520	ATP phosphoribosyltransferase
AURMO_00822	AURUGA1_00844	RHOLA_RS03740	Rhola_00007530	imidazole glycerol phosphate synthase subunit HisF
AURMO_00828	AURUGA1_00838	RHOLA_RS03770	Rhola_00007590	tryptophan synthase subunit beta
AURMO_00829	AURUGA1_00837	RHOLA_RS03775	Rhola_00007600	tryptophan synthase subunit alpha
AURMO_00832	AURUGA1_00834	RHOLA_RS03790	Rhola_00007630	glutamate synthase subunit beta
AURMO_00835	AURUGA1_00831	RHOLA_RS03805	Rhola_00007660	ANTAR domain-containing protein
AURMO_00836	AURUGA1_00830	RHOLA_RS03810	Rhola_00007670	hotdog fold thioesterase
AURMO_00837	AURUGA1_00829	RHOLA_RS03815	Rhola_00007680	DNA polymerase I
AURMO_00839	AURUGA1_00827	RHOLA_RS03825	Rhola_00007700	dephospho-CoA kinase

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00863	AURUGA1_00807	RHOLA_RS04195	Rhola_00008430	dipeptidase
AURMO_00865	AURUGA1_00805	RHOLA_RS04205	Rhola_00008450	quinone-dependent dihydroorotate dehydrogenase
AURMO_00867	AURUGA1_00803	RHOLA_RS04215	Rhola_00008470	histidinol dehydrogenase
AURMO_00870	AURUGA1_00800	RHOLA_RS04110	Rhola_00008260	RNA helicase
AURMO_00873	AURUGA1_00797	RHOLA_RS04090	Rhola_00008220	WYL domain-containing protein
AURMO_00874	AURUGA1_00796	RHOLA_RS04085		WYL domain-containing protein
AURMO_00875	AURUGA1_00795	RHOLA_RS04080		hypothetical protein
AURMO_00878	AURUGA1_00792	RHOLA_RS04065	Rhola_00008170	PAC2 family protein
AURMO_00884	AURUGA1_00786	RHOLA_RS04045	Rhola_00008130	NAD-dependent protein deacetylase
AURMO_00889	AURUGA1_00781	RHOLA_RS04005	Rhola_00008050	ABC transporter ATP-binding protein
AURMO_00902	AURUGA1_00768	RHOLA_RS03070	Rhola_00006180	16S rRNA (uracil(1498)-N(3))-methyltransferase
AURMO_00909	AURUGA1_00761	RHOLA_RS03030	Rhola_00006100	DNA polymerase III subunit delta
AURMO_00911	AURUGA1_00759	RHOLA_RS03020	Rhola_00006080	hypothetical protein
AURMO_00916	AURUGA1_00754	RHOLA_RS06455	Rhola_00013000	LLM class flavin-dependent oxidoreductase
AURMO_00918	AURUGA1_00752	RHOLA_RS05245	Rhola_00010540	DUF4032 domain-containing protein
AURMO_00927	AURUGA1_00745	RHOLA_RS02945	Rhola_00005930	glutamate-5-semialdehyde dehydrogenase
AURMO_00930	AURUGA1_00738	RHOLA_RS02930	Rhola_00005900	50S ribosomal protein L27
AURMO_00944	AURUGA1_00724	RHOLA_RS02790	Rhola_00005620	thiol reductase thioredoxin
AURMO_00951	AURUGA1_00717	RHOLA_RS04360	Rhola_00008760	glucokinase
AURMO_00953	AURUGA1_00715	RHOLA_RS04370	Rhola_00008780	peptide deformylase
AURMO_00954	AURUGA1_00714	RHOLA_RS04375	Rhola_00008790	MinD/ParA family protein
AURMO_00956	AURUGA1_00711	RHOLA_RS04385		ParA family protein
AURMO_00979	AURUGA1_00687	RHOLA_RS04410	Rhola_00008860	ribosome biogenesis GTPase Der
AURMO_00980	AURUGA1_00686	RHOLA_RS04415	Rhola_00008870	(d)CMP kinase
AURMO_00983	AURUGA1_00683	RHOLA_RS04435	Rhola_00008910	SMC-Scp complex subunit ScpB
AURMO_00984	AURUGA1_00682	RHOLA_RS04440	Rhola_00008920	segregation/condensation protein A
AURMO_00988	AURUGA1_00678	RHOLA_RS04460	Rhola_00008960	CTP synthase
AURMO_00989	AURUGA1_00677	RHOLA_RS04465	Rhola_00008970	DNA repair protein RecN
AURMO_00999	AURUGA1_00667	RHOLA_RS01645	Rhola_00003310	cation acetate symporter
AURMO_01026	AURUGA1_00639	RHOLA_RS02435	Rhola_00004900	SseB family protein
AURMO_01027	AURUGA1_00638	RHOLA_RS02430	Rhola_00004890	bifunctional 1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4- carboxamide isomerase/phosphoribosylanthranilate isomerase PriA
AURMO_01033	AURUGA1_00632	RHOLA_RS04020	Rhola_00008080	hypothetical protein
AURMO_01034	AURUGA1_00631	RHOLA_RS02880	Rhola_00005800	ATP-dependent Clp protease ATP-binding subunit ClpX
AURMO_01059	AURUGA1_00616	RHOLA_RS02830	Rhola_00005700	hypothetical protein
AURMO_01062	AURUGA1_00613	RHOLA_RS02815	Rhola_00005670	acyl-CoA thioesterase II

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_01068	AURUGA1_00607	RHOLA_RS02795	Rhola_00005630	peptide-methionine (S)-S-oxide reductase
AURMO_01076	AURUGA1_00603	RHOLA_RS02710	Rhola_00005460	oligoribonuclease
AURMO_01087	AURUGA1_00592	RHOLA_RS02695	Rhola_00005430	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA
AURMO_01091	AURUGA1_00587	RHOLA_RS02675	Rhola_00005390	tRNA 2-thiouridine(34) synthase MnmA
AURMO_01094	AURUGA1_00584	RHOLA_RS02660	Rhola_00005360	alpha-14-glucan--maltose-1-phosphate maltosyltransferase
AURMO_01097	AURUGA1_00581	RHOLA_RS02645	Rhola_00005330	hypothetical protein
AURMO_01099	AURUGA1_00579	RHOLA_RS02635	Rhola_00005310	AI-2E family transporter
AURMO_01100	AURUGA1_00578	RHOLA_RS02630	Rhola_00005300	alpha/beta hydrolase
AURMO_01108	AURUGA1_00570	RHOLA_RS02585	Rhola_00005210	30S ribosomal protein S2
AURMO_01115	AURUGA1_00564	RHOLA_RS02300	Rhola_00004630	insulinase family protein
AURMO_01117	AURUGA1_00562	RHOLA_RS02295	Rhola_00004620	polyribonucleotide nucleotidyltransferase
AURMO_01143	AURUGA1_01159	RHOLA_RS02765	Rhola_00005570	alanine dehydrogenase
AURMO_01179	AURUGA1_00513	RHOLA_RS01920	Rhola_00003870	hypothetical protein
AURMO_01183	AURUGA1_00508	RHOLA_RS01905	Rhola_00003840	PHP domain-containing protein
AURMO_01184	AURUGA1_00507	RHOLA_RS01900	Rhola_00003830	peptidase M24 family protein
AURMO_01189	AURUGA1_00502	RHOLA_RS01885	Rhola_00003800	DUF1003 domain-containing protein
AURMO_01190	AURUGA1_00501	RHOLA_RS01880	Rhola_00003790	MRP family ATP-binding protein
AURMO_01208	AURUGA1_00487	RHOLA_RS04550	Rhola_00009140	succinyldiaminopimelate transaminase
AURMO_01213	AURUGA1_00478	RHOLA_RS04575	Rhola_00009180	CPBP family intramembrane metalloprotease
AURMO_01223	AURUGA1_00470	RHOLA_RS05435	Rhola_00010940	NUDIX hydrolase
AURMO_01226	AURUGA1_00467	RHOLA_RS05450	Rhola_00010970	carboxylating nicotinate-nucleotide diphosphorylase
AURMO_01229	AURUGA1_00465	RHOLA_RS00945	Rhola_00001900	heme-binding protein
AURMO_01236	AURUGA1_00460	RHOLA_RS02740	Rhola_00005520	KR domain-containing protein
AURMO_01246	AURUGA1_00435	RHOLA_RS04880	Rhola_00009800	DNA recombination protein RmuC
AURMO_01249	AURUGA1_00432	RHOLA_RS04895	Rhola_00009830	class II fructose-bisphosphate aldolase
AURMO_01257	AURUGA1_00430	RHOLA_RS04900	Rhola_00009850	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
AURMO_01258	AURUGA1_00429	RHOLA_RS04905	Rhola_00009860	exodeoxyribonuclease VII large subunit
AURMO_01261	AURUGA1_00425	RHOLA_RS04920	Rhola_00009890	carbonic anhydrase
AURMO_01317	AURUGA1_00393	RHOLA_RS04950	Rhola_00009960	hemolysin III
AURMO_01321	AURUGA1_00389	RHOLA_RS04965	Rhola_00009990	transcription elongation factor GreA
AURMO_01322	AURUGA1_00388	RHOLA_RS04970	Rhola_00010000	threonine ammonia-lyase
AURMO_01323	AURUGA1_00387	RHOLA_RS04975	Rhola_00010010	protease
AURMO_01330	AURUGA1_00366	RHOLA_RS04990	Rhola_00010040	NAD(P)/FAD-dependent oxidoreductase
AURMO_01335	AURUGA1_00361	RHOLA_RS05015	Rhola_00010090	histidine--tRNA ligase
AURMO_01336	AURUGA1_00360	RHOLA_RS05020	Rhola_00010100	nucleoside triphosphate hydrolase
AURMO_01340	AURUGA1_00356	RHOLA_RS06700	Rhola_00013500	Na+/H+ antiporter NhaA
AURMO_01344	AURUGA1_00352	RHOLA_RS05035	Rhola_00010130	50S ribosomal protein L25

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_01345	AURUGA1_00351	RHOLA_RS01310	Rhola_00002630	phosphogluconate dehydrogenase (NADP(+)-dependent decarboxylating)
AURMO_01351	AURUGA1_00345	RHOLA_RS05050	Rhola_00010160	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU
AURMO_01360	AURUGA1_00341	RHOLA_RS05065	Rhola_00010190	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase
AURMO_01361	AURUGA1_00340	RHOLA_RS05075	Rhola_00010210	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))- dimethyltransferase RsmA
AURMO_01363	AURUGA1_00338	RHOLA_RS05085	Rhola_00010230	methionine--tRNA ligase
AURMO_01366	AURUGA1_00334	RHOLA_RS05090	Rhola_00010240	16S rRNA (cytidine(1402)-2'-O)-methyltransferase
AURMO_01383	AURUGA1_00326	RHOLA_RS00860	Rhola_00001730	class 1b ribonucleoside-diphosphate reductase subunit alpha
AURMO_01403	AURUGA1_00319	RHOLA_RS05130	Rhola_00010320	5-formyltetrahydrofolate cyclo-ligase
AURMO_01416	AURUGA1_00309	RHOLA_RS05150	Rhola_00010350	HNH endonuclease
AURMO_01421	AURUGA1_00304	RHOLA_RS05170	Rhola_00010390	cold-shock protein
AURMO_01423	AURUGA1_00302	RHOLA_RS05180	Rhola_00010410	hypothetical protein
AURMO_01424	AURUGA1_00301	RHOLA_RS05185	Rhola_00010420	helicase
AURMO_01464	AURUGA1_00267	RHOLA_RS05835	Rhola_00011750	serine hydroxymethyltransferase
AURMO_01465	AURUGA1_00266	RHOLA_RS05840	Rhola_00011770	formyltetrahydrofolate deformylase
AURMO_01473	AURUGA1_01393	RHOLA_RS01175	Rhola_00002380	50S ribosomal protein L1
AURMO_01482	AURUGA1_01402	RHOLA_RS01135	Rhola_00002300	MaoC family dehydratase
AURMO_01484	AURUGA1_01404	RHOLA_RS02770	Rhola_00005580	agmatine deiminase family protein
AURMO_01497	AURUGA1_01409	RHOLA_RS05345	Rhola_00010750	DUF2437 domain-containing protein
AURMO_01508	AURUGA1_01434	RHOLA_RS05865	Rhola_00011800	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase PurH
AURMO_01512	AURUGA1_01436	RHOLA_RS05875	Rhola_00011820	hypothetical protein
AURMO_01523	AURUGA1_01363	RHOLA_RS06250	Rhola_00012570	uracil phosphoribosyltransferase
AURMO_01529	AURUGA1_01369	RHOLA_RS05690	Rhola_00011460	thymidine phosphorylase
AURMO_01532	AURUGA1_01372	RHOLA_RS05705	Rhola_00011490	ABC transporter permease
AURMO_01536	AURUGA1_01374	RHOLA_RS05715	Rhola_00011510	BMP family ABC transporter substrate-binding protein
AURMO_01539	AURUGA1_01377	RHOLA_RS01290	Rhola_00002590	ROK family protein
AURMO_01541	AURUGA1_01379	RHOLA_RS01280	Rhola_00002570	xylulokinase
AURMO_01549	AURUGA1_01386	RHOLA_RS01235	Rhola_00002500	50S ribosomal protein L10
AURMO_01582	AURUGA1_01461	RHOLA_RS01070	Rhola_00002170	YajQ family cyclic di-GMP-binding protein
AURMO_01596	AURUGA1_01470	RHOLA_RS01825	Rhola_00003680	phosphate transport system regulatory protein PhoU
AURMO_01597	AURUGA1_01471	RHOLA_RS01830	Rhola_00003690	GHKL domain-containing protein
AURMO_01600	AURUGA1_01474	RHOLA_RS01365	Rhola_00002740	hypothetical protein
AURMO_01603	AURUGA1_01477	RHOLA_RS00675	Rhola_00001360	phosphoribosylamine--glycine ligase
AURMO_01608	AURUGA1_01481	RHOLA_RS00680	Rhola_00001370	DUF305 domain-containing protein
AURMO_01620	AURUGA1_01492	RHOLA_RS05825	Rhola_00011730	tryptophan 23-dioxygenase
AURMO_01625	AURUGA1_01497	RHOLA_RS01340	Rhola_00002690	DUF3817 domain-containing protein

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_01626	AURUGA1_01498	RHOLA_RS00615	Rhola_00001230	phosphoribosylformylglycinamidine synthase subunit PurL
AURMO_01632	AURUGA1_01507	RHOLA_RS05360		SAM-dependent methyltransferase
AURMO_01635	AURUGA1_01511	RHOLA_RS01770	Rhola_00003560	EamA/RhaT family transporter
AURMO_01636	AURUGA1_01512	RHOLA_RS02715	Rhola_00005470	AcrB/AcrD/AcrF family protein
AURMO_01642	AURUGA1_01518	RHOLA_RS00700	Rhola_00001410	phosphoribosylformylglycinamidine cyclo-ligase
AURMO_01647	AURUGA1_01523	RHOLA_RS01055	Rhola_00002140	demethylmenaquinone methyltransferase
AURMO_01654	AURUGA1_01530	RHOLA_RS01015	Rhola_00002060	14-dihydroxy-2-naphthoyl-CoA synthase
AURMO_01658	AURUGA1_01534	RHOLA_RS00995	Rhola_00002020	cytochrome C biogenesis protein CcdA
AURMO_01660	AURUGA1_01536	RHOLA_RS00985	Rhola_00002000	histidine phosphatase family protein
AURMO_01667	AURUGA1_01543	RHOLA_RS01675	Rhola_00003370	ATPase
AURMO_01671	AURUGA1_01547	RHOLA_RS06245	Rhola_00012560	nucleoside deaminase
AURMO_01686	AURUGA1_01566	RHOLA_RS06720	Rhola_00013540	exodeoxyribonuclease III
AURMO_01690	AURUGA1_01570	RHOLA_RS01400	Rhola_00002810	hypothetical protein
AURMO_01693	AURUGA1_01573	RHOLA_RS06270	Rhola_00012620	hypothetical protein
AURMO_01700	AURUGA1_01578	RHOLA_RS04935	Rhola_00009930	hypothetical protein
AURMO_01702	AURUGA1_01580	RHOLA_RS06740	Rhola_00013580	MerR family DNA-binding transcriptional regulator
AURMO_01703	AURUGA1_01581	RHOLA_RS06745	Rhola_00013590	molecular chaperone DnaJ
AURMO_01705	AURUGA1_01583	RHOLA_RS06755	Rhola_00013610	molecular chaperone DnaK
AURMO_01714	AURUGA1_01590		Rhola_00010860	Phytoene/squalene synthetase
AURMO_01740	AURUGA1_00035	RHOLA_RS03115	Rhola_00006270	glycine--tRNA ligase
AURMO_01741	AURUGA1_00034	RHOLA_RS00240	Rhola_00000480	peptidase M13
AURMO_01744	AURUGA1_00031	RHOLA_RS06300	Rhola_00012680	endonuclease NucS
AURMO_01762	AURUGA1_00025	RHOLA_RS00225	Rhola_00000450	DUF2662 domain-containing protein
AURMO_01790	AURUGA1_00004	RHOLA_RS00020	Rhola_00000040	DUF721 domain-containing protein
AURMO_01791	AURUGA1_00003	RHOLA_RS00015	Rhola_00000030	DNA replication and repair protein RecF
AURMO_00009	AURUGA1_01610	RHOLA_RS06955	Rhola_00014020	ParB/RepB/Spo0J family partition protein
AURMO_00010	AURUGA1_01609	RHOLA_RS06945	Rhola_00014000	D-alanine--D-alanine ligase
AURMO_00011	AURUGA1_01608	RHOLA_RS06940	Rhola_00013990	PLP-dependent aminotransferase family protein
AURMO_00017	AURUGA1_01601	RHOLA_RS06900	Rhola_00013910	single-stranded DNA-binding protein
AURMO_00023	AURUGA1_00055	RHOLA_RS06875	Rhola_00013850	adenylosuccinate lyase
AURMO_00027	AURUGA1_00059	RHOLA_RS06860	Rhola_00013820	thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha
AURMO_00064	AURUGA1_00068	RHOLA_RS00270	Rhola_00000540	alpha/beta hydrolase
AURMO_00066	AURUGA1_00070	RHOLA_RS00300	Rhola_00000600	site-specific DNA-methyltransferase
AURMO_00081	AURUGA1_00072	RHOLA_RS00315	Rhola_00000630	MFS transporter
AURMO_00086	AURUGA1_00077	RHOLA_RS00350	Rhola_00000700	serine--tRNA ligase
AURMO_00094	AURUGA1_00085	RHOLA_RS06550	Rhola_00013200	acyl-CoA dehydrogenase
AURMO_00097	AURUGA1_00089	RHOLA_RS06450	Rhola_00012990	hypothetical protein

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_00100	AURUGA1_00093	RHOLA_RS04025	Rhola_00008090	methionine synthase
AURMO_00109	AURUGA1_00103	RHOLA_RS01430	Rhola_00002870	porphobilinogen synthase
AURMO_00112	AURUGA1_00106	RHOLA_RS01440	Rhola_00002890	glutamyl-tRNA reductase
AURMO_00113	AURUGA1_00107	RHOLA_RS01445	Rhola_00002900	uroporphyrinogen decarboxylase
AURMO_00114	AURUGA1_00108	RHOLA_RS01450	Rhola_00002910	protoporphyrinogen oxidase
AURMO_00116	AURUGA1_00110	RHOLA_RS01460	Rhola_00002930	ferrochelatase
AURMO_00128	AURUGA1_00120	RHOLA_RS00810	Rhola_00001630	dihydropteroate synthase
AURMO_00150	AURUGA1_00139	RHOLA_RS00920	Rhola_00001850	DNA repair protein RadA
AURMO_00169	AURUGA1_00147	RHOLA_RS06780	Rhola_00013660	DUF2834 domain-containing protein
AURMO_00173	AURUGA1_00152	RHOLA_RS02685	Rhola_00005410	hypothetical protein
AURMO_00177	AURUGA1_00156	RHOLA_RS06215	Rhola_00012500	DNA-directed RNA polymerase subunit beta
AURMO_00181	AURUGA1_00160	RHOLA_RS06200	Rhola_00012470	30S ribosomal protein S7
AURMO_00186	AURUGA1_00164	RHOLA_RS02330	Rhola_00004690	SulP family inorganic anion transporter
AURMO_00187	AURUGA1_00165	RHOLA_RS06170		30S ribosomal protein S10
AURMO_00201	AURUGA1_00179	RHOLA_RS06100	Rhola_00012270	30S ribosomal protein S8
AURMO_00208	AURUGA1_00186	RHOLA_RS06065	Rhola_00012200	adenylate kinase
AURMO_00211	AURUGA1_00189	RHOLA_RS06055	Rhola_00012180	translation initiation factor IF-1
AURMO_00214	AURUGA1_00191	RHOLA_RS06040	Rhola_00012150	30S ribosomal protein S11
AURMO_00216	AURUGA1_00193	RHOLA_RS06030	Rhola_00012130	50S ribosomal protein L17
AURMO_00220	AURUGA1_00195	RHOLA_RS06020	Rhola_00012110	50S ribosomal protein L13
AURMO_00221	AURUGA1_00196	RHOLA_RS06015	Rhola_00012100	30S ribosomal protein S9
AURMO_00226	AURUGA1_00201	RHOLA_RS05985	Rhola_00012040	alanine racemase
AURMO_00227	AURUGA1_00202	RHOLA_RS05980	Rhola_00012030	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE
AURMO_00230	AURUGA1_00205	RHOLA_RS05970		tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD
AURMO_00251	AURUGA1_00226	RHOLA_RS05940	Rhola_00011950	ABC transporter ATP-binding protein
AURMO_00301	AURUGA1_01352	RHOLA_RS01565	Rhola_00003140	aspartate-semialdehyde dehydrogenase
AURMO_00324	AURUGA1_01332	RHOLA_RS01635	Rhola_00003290	alpha/beta hydrolase
AURMO_00328	AURUGA1_01328	RHOLA_RS06765	Rhola_00013630	hypothetical protein
AURMO_00340	AURUGA1_01320	RHOLA_RS05765	Rhola_00011610	riboflavin synthase
AURMO_00343	AURUGA1_01318	RHOLA_RS05755	Rhola_00011590	tryptophan--tRNA ligase
AURMO_00353	AURUGA1_01309	RHOLA_RS06420	Rhola_00012930	phosphoenolpyruvate--protein phosphotransferase
AURMO_00356	AURUGA1_01306	RHOLA_RS05730	Rhola_00011540	succinate dehydrogenase
AURMO_00384	AURUGA1_01279	RHOLA_RS05545	Rhola_00011170	adenosylhomocysteinase
AURMO_00390	AURUGA1_01273	RHOLA_RS05515	Rhola_00011110	preprotein translocase subunit SecA
AURMO_00401	AURUGA1_01264	RHOLA_RS05490	Rhola_00011060	ATPase
AURMO_00405	AURUGA1_01260	RHOLA_RS04715	Rhola_00009480	DUF2029 domain-containing protein

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00406	AURUGA1_01258	RHOLA_RS04710	Rhola_00009470	homoserine O-acetyltransferase
AURMO_00407	AURUGA1_01257	RHOLA_RS06555	Rhola_00013210	enoyl-CoA hydratase
AURMO_00414	AURUGA1_01252	RHOLA_RS04700	Rhola_00009450	uracil-DNA glycosylase
AURMO_00420	AURUGA1_01246	RHOLA_RS05475	Rhola_00011030	thioredoxin-dependent thiol peroxidase
AURMO_00443	AURUGA1_01223	RHOLA_RS07125	Rhola_00011250	LysM domain-containing protein
AURMO_00452	AURUGA1_01236	RHOLA_RS02030	Rhola_00004090	arginine--tRNA ligase
AURMO_00456	AURUGA1_01209	RHOLA_RS02050	Rhola_00004130	homoserine kinase
AURMO_00458	AURUGA1_01207	RHOLA_RS02055	Rhola_00004140	transcription termination factor Rho
AURMO_00465	AURUGA1_01201	RHOLA_RS04835	Rhola_00009710	cysteine synthase A
AURMO_00472	AURUGA1_01195	RHOLA_RS02085	Rhola_00004200	ATP synthase F0 subunit A
AURMO_00476	AURUGA1_01191	RHOLA_RS02105	Rhola_00004240	F0F1 ATP synthase subunit alpha
AURMO_00478	AURUGA1_01189	RHOLA_RS02115	Rhola_00004260	F0F1 ATP synthase subunit beta
AURMO_00491	AURUGA1_00527	RHOLA_RS02195	Rhola_00004420	1-deoxy-D-xylulose-5-phosphate reductoisomerase
AURMO_00495	AURUGA1_00530	RHOLA_RS05305	Rhola_00010670	MFS transporter
AURMO_00496	AURUGA1_00531	RHOLA_RS02210	Rhola_00004450	proline--tRNA ligase
AURMO_00499	AURUGA1_00534	RHOLA_RS02225	Rhola_00004480	translation initiation factor IF-2
AURMO_00500	AURUGA1_00535	RHOLA_RS02230	Rhola_00004490	30S ribosome-binding factor RbfA
AURMO_00504	AURUGA1_01155	RHOLA_RS01190	Rhola_00002410	hypothetical protein
AURMO_00507	AURUGA1_01152	RHOLA_RS04630	Rhola_00009300	ABC transporter permease
AURMO_00512	AURUGA1_01143	RHOLA_RS02750	Rhola_00005540	glutathione peroxidase
AURMO_00515	AURUGA1_01140	RHOLA_RS04770	Rhola_00009590	histidinol-phosphatase
AURMO_00517	AURUGA1_01138	RHOLA_RS01690	Rhola_00003400	MBL fold metallo-hydrolase
AURMO_00527	AURUGA1_01128	RHOLA_RS01775	Rhola_00003570	SDR family NAD(P)-dependent oxidoreductase
AURMO_00546	AURUGA1_01111	RHOLA_RS01935	Rhola_00003900	ATP-dependent helicase
AURMO_00563	AURUGA1_01097	RHOLA_RS05385	Rhola_00010830	acetolactate synthase large subunit
AURMO_00576	AURUGA1_01083	RHOLA_RS05300	Rhola_00010660	3-isopropylmalate dehydratase large subunit
AURMO_00577	AURUGA1_01082	RHOLA_RS05295	Rhola_00010650	3-isopropylmalate dehydratase small subunit
AURMO_00581	AURUGA1_01078	RHOLA_RS05275	Rhola_00010610	D-alanine--D-alanine ligase
AURMO_00582	AURUGA1_01077	RHOLA_RS05270	Rhola_00010600	DUF3515 domain-containing protein
AURMO_00584	AURUGA1_01075	RHOLA_RS04540	Rhola_00009120	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD
AURMO_00586	AURUGA1_01073	RHOLA_RS04530	Rhola_00009100	pantetheine-phosphate adenylyltransferase
AURMO_00591	AURUGA1_01061	RHOLA_RS04490		30S ribosomal protein S16
AURMO_00593	AURUGA1_01059	RHOLA_RS04480	Rhola_00009000	ribosome maturation factor RimM
AURMO_00596	AURUGA1_01056	RHOLA_RS02545	Rhola_00005130	signal peptidase I
AURMO_00606	AURUGA1_01046	RHOLA_RS02325	Rhola_00004680	thymidylate synthase (FAD)
AURMO_00614	AURUGA1_01037	RHOLA_RS02345	Rhola_00004720	DNA translocase FtsK
AURMO_00616	AURUGA1_01035	RHOLA_RS02355	Rhola_00004740	CinA family protein

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00623	AURUGA1_01028	RHOLA_RS02385	Rhola_00004800	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
AURMO_00624	AURUGA1_01027	RHOLA_RS02390	Rhola_00004810	diaminopimelate epimerase
AURMO_00641	AURUGA1_01011	RHOLA_RS04320	Rhola_00008680	transcriptional regulator MraZ
AURMO_00652	AURUGA1_01001	RHOLA_RS07230	Rhola_00008570	hypothetical protein
AURMO_00659	AURUGA1_00994	RHOLA_RS04230	Rhola_00008500	RluA family pseudouridine synthase
AURMO_00660	AURUGA1_00993	RHOLA_RS03845	Rhola_00007740	RNase adapter RapZ
AURMO_00661	AURUGA1_00992	RHOLA_RS03850	Rhola_00007750	DNA-binding protein WhiA
AURMO_00664	AURUGA1_00989	RHOLA_RS03865	Rhola_00007780	phosphoglycerate kinase
AURMO_00671	AURUGA1_00984	RHOLA_RS03890	Rhola_00007830	OpcA protein
AURMO_00674	AURUGA1_00981	RHOLA_RS03905	Rhola_00007860	transaldolase
AURMO_00675	AURUGA1_00980	RHOLA_RS03910	Rhola_00007870	transketolase
AURMO_00676	AURUGA1_00978	RHOLA_RS03915	Rhola_00007880	protoheme IX farnesyltransferase
AURMO_00681	AURUGA1_00973	RHOLA_RS03945	Rhola_00007940	Fe-S cluster assembly ATPase SufC
AURMO_00692	AURUGA1_00961	RHOLA_RS03125	Rhola_00006290	deoxyguanosinetriphosphate triphosphohydrolase
AURMO_00700	AURUGA1_00953	RHOLA_RS03175	Rhola_00006390	glycosyltransferase family 4 protein
AURMO_00722	AURUGA1_00942	RHOLA_RS03230	Rhola_00006500	ketoacyl-ACP synthase III
AURMO_00724	AURUGA1_00940	RHOLA_RS03240	Rhola_00006520	PucR family transcriptional regulator
AURMO_00725	AURUGA1_00939	RHOLA_RS03245	Rhola_00006530	pyruvate dehydrogenase (acetyl-transferring) homodimeric type
AURMO_00737	AURUGA1_00928	RHOLA_RS03305	Rhola_00006660	NAD+ synthase
AURMO_00739	AURUGA1_00926	RHOLA_RS03315	Rhola_00006680	bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase
AURMO_00743	AURUGA1_00922	RHOLA_RS03335	Rhola_00006720	lipoyl synthase
AURMO_00744	AURUGA1_00921	RHOLA_RS03340	Rhola_00006730	lipoyl(octanoyl) transferase LipB
AURMO_00748	AURUGA1_00917	RHOLA_RS03360	Rhola_00006770	leucyl aminopeptidase
AURMO_00761	AURUGA1_00905	RHOLA_RS03440	Rhola_00006930	DUF3159 domain-containing protein
AURMO_00762	AURUGA1_00904	RHOLA_RS03445	Rhola_00006940	aconitate hydratase AcnA
AURMO_00778	AURUGA1_00888	RHOLA_RS03525	Rhola_00007100	HIT domain-containing protein
AURMO_00779	AURUGA1_00887	RHOLA_RS03530	Rhola_00007110	pyridoxal 5'-phosphate synthase lyase subunit PdxS
AURMO_00782	AURUGA1_00884	RHOLA_RS03545	Rhola_00007140	crossover junction endodeoxyribonuclease RuvC
AURMO_00783	AURUGA1_00883	RHOLA_RS03550	Rhola_00007150	Holliday junction branch migration protein RuvA
AURMO_00787	AURUGA1_00879	RHOLA_RS03570	Rhola_00007190	protein translocase subunit SecF
AURMO_00790	AURUGA1_00876	RHOLA_RS03580	Rhola_00007210	DUF349 domain-containing protein
AURMO_00796	AURUGA1_00870	RHOLA_RS03615	Rhola_00007280	Holliday junction resolvase RuvX
AURMO_00799	AURUGA1_00867	RHOLA_RS03630	Rhola_00007310	chorismate synthase
AURMO_00804	AURUGA1_00862	RHOLA_RS03655	Rhola_00007360	transcription antitermination factor NusB
AURMO_00806	AURUGA1_00860	RHOLA_RS03665	Rhola_00007380	aspartate carbamoyltransferase catalytic subunit
AURMO_00809	AURUGA1_00857	RHOLA_RS03680	Rhola_00007410	carbamoyl-phosphate synthase small subunit
AURMO_00812	AURUGA1_00854	RHOLA_RS03695	Rhola_00007440	guanylate kinase

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_00816	AURUGA1_00850	RHOLA_RS03710	Rhola_00007470	hypothetical protein
AURMO_00817	AURUGA1_00849	RHOLA_RS03715	Rhola_00007480	methionyl-tRNA formyltransferase
AURMO_00818	AURUGA1_00848	RHOLA_RS03720	Rhola_00007490	hypothetical protein
AURMO_00827	AURUGA1_00839	RHOLA_RS03765	Rhola_00007580	indole-3-glycerol phosphate synthase TrpC
AURMO_00830	AURUGA1_00836	RHOLA_RS03780	Rhola_00007610	prolipoprotein diacylglyceryl transferase
AURMO_00831	AURUGA1_00835	RHOLA_RS03785	Rhola_00007620	glutamate synthase large subunit
AURMO_00840	AURUGA1_00826	RHOLA_RS03830	Rhola_00007710	excinuclease ABC subunit UvrB
AURMO_00841	AURUGA1_00825	RHOLA_RS03835	Rhola_00007720	excinuclease ABC subunit UvrA
AURMO_00843	AURUGA1_00823	RHOLA_RS04125	Rhola_00008290	glycerophosphodiester phosphodiesterase
AURMO_00850	AURUGA1_00819	RHOLA_RS01545	Rhola_00003100	MFS transporter
AURMO_00853	AURUGA1_00816	RHOLA_RS04140	Rhola_00008320	anthranilate phosphoribosyltransferase
AURMO_00854	AURUGA1_00815	RHOLA_RS04145	Rhola_00008330	heme-copper oxidase subunit III
AURMO_00855	AURUGA1_00814	RHOLA_RS04150	Rhola_00008340	cystathionine beta-lyase
AURMO_00856	AURUGA1_00813	RHOLA_RS04155	Rhola_00008350	ubiquinol-cytochrome C reductase
AURMO_00860	AURUGA1_00810	RHOLA_RS04180	Rhola_00008400	cytochrome c oxidase subunit I
AURMO_00861	AURUGA1_00809	RHOLA_RS04185	Rhola_00008410	cytochrome c oxidase subunit II
AURMO_00866	AURUGA1_00804	RHOLA_RS04210	Rhola_00008460	transcriptional repressor NrdR
AURMO_00887	AURUGA1_00783	RHOLA_RS04015	Rhola_00008070	DNA polymerase III subunit epsilon
AURMO_00888	AURUGA1_00782	RHOLA_RS04010	Rhola_00008060	type B 50S ribosomal protein L31
AURMO_00892	AURUGA1_00778	RHOLA_RS03990	Rhola_00008020	phosphoserine phosphatase SerB
AURMO_00895	AURUGA1_00775	RHOLA_RS03965	Rhola_00007980	SURF1 family protein
AURMO_00898	AURUGA1_00772	RHOLA_RS03090		HlyC/CorC family transporter
AURMO_00903	AURUGA1_00767	RHOLA_RS03065	Rhola_00006170	molecular chaperone DnaJ
AURMO_00915	AURUGA1_00755	RHOLA_RS00650	Rhola_00001300	CoA-disulfide reductase
AURMO_00933	AURUGA1_00733	RHOLA_RS02915	Rhola_00005870	hypothetical protein
AURMO_00950	AURUGA1_00718	RHOLA_RS04355	Rhola_00008750	1-acyl-sn-glycerol-3-phosphate acyltransferase
AURMO_00952	AURUGA1_00716	RHOLA_RS04365	Rhola_00008770	long-chain fatty acid--CoA ligase
AURMO_00957	AURUGA1_00710	RHOLA_RS04390	Rhola_00008820	transcriptional regulator
AURMO_00959	AURUGA1_00708	RHOLA_RS04400	Rhola_00008840	FHA domain-containing protein
AURMO_00962	AURUGA1_00706	RHOLA_RS06470	Rhola_00013030	deoxyribodipyrimidine photo-lyase
AURMO_00966	AURUGA1_00702	RHOLA_RS01300	Rhola_00002610	EamA/RhaT family transporter
AURMO_00982	AURUGA1_00684	RHOLA_RS04430	Rhola_00008900	rRNA pseudouridine synthase
AURMO_00987	AURUGA1_00679	RHOLA_RS04455	Rhola_00008950	NUDIX hydrolase
AURMO_00991	AURUGA1_00675	RHOLA_RS04475	Rhola_00008990	TlyA family rRNA (cytidine-2'-O)-methyltransferase
AURMO_01002	AURUGA1_00666	RHOLA_RS02530	Rhola_00005090	HAD-IIA family hydrolase
AURMO_01003	AURUGA1_00665	RHOLA_RS02520	Rhola_00005070	hypothetical protein
AURMO_01007	AURUGA1_00657	RHOLA_RS02500	Rhola_00005030	tyrosine--tRNA ligase

A. photophilum **Locus Tag**	***Aurantimicrobium*** **sp. strain MWH-UGA1 Locus Tag**	***R. lacicola*** **New Locus Tags**	***R. lacicola*** **Old Locus Tags**	***R. lacicola*** **Annotation**
AURMO_01010	AURUGA1_00653	RHOLA_RS02485	Rhola_00005000	acetylglutamate kinase
AURMO_01011	AURUGA1_00652	RHOLA_RS02480	Rhola_00004990	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ
AURMO_01012	AURUGA1_00651	RHOLA_RS02475	Rhola_00004980	N-acetyl-gamma-glutamyl-phosphate reductase
AURMO_01015	AURUGA1_00648	RHOLA_RS02465	Rhola_00004960	phenylalanine--tRNA ligase subunit alpha
AURMO_01019	AURUGA1_00646	RHOLA_RS02455	Rhola_00004940	50S ribosomal protein L20
AURMO_01021	AURUGA1_00644	RHOLA_RS02445	Rhola_00004920	translation initiation factor IF-3
AURMO_01029	AURUGA1_00636	RHOLA_RS02420	Rhola_00004870	imidazoleglycerol-phosphate dehydratase HisB
AURMO_01030	AURUGA1_00635	RHOLA_RS02415	Rhola_00004860	histidinol-phosphate transaminase
AURMO_01039	AURUGA1_00627	RHOLA_RS00120	Rhola_00000240	amino acid transporter
AURMO_01056	AURUGA1_00619	RHOLA_RS02850	Rhola_00005740	Fpg/Nei family DNA glycosylase
AURMO_01060	AURUGA1_00615	RHOLA_RS02825	Rhola_00005690	globin
AURMO_01086	AURUGA1_00593	RHOLA_RS02700	Rhola_00005440	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB
AURMO_01090	AURUGA1_00588	RHOLA_RS02680	Rhola_00005400	NAD-dependent DNA ligase LigA
AURMO_01096	AURUGA1_00582	RHOLA_RS02650	Rhola_00005340	hypothetical protein
AURMO_01105	AURUGA1_00573	RHOLA_RS02600	Rhola_00005240	ribosome recycling factor
AURMO_01106	AURUGA1_00572	RHOLA_RS02595	Rhola_00005230	UMP kinase
AURMO_01107	AURUGA1_00571	RHOLA_RS02590	Rhola_00005220	elongation factor Ts
AURMO_01138	AURUGA1_00542	RHOLA_RS02275	Rhola_00004580	bifunctional riboflavin kinase/FAD synthetase
AURMO_01141	AURUGA1_00539	RHOLA_RS02235	Rhola_00004500	tRNA pseudouridine(55) synthase TruB
AURMO_01153	AURUGA1_01169	RHOLA_RS04505	Rhola_00009050	chromosome segregation protein SMC
AURMO_01159	AURUGA1_01173	RHOLA_RS04515	Rhola_00009070	ribonuclease III
AURMO_01164	AURUGA1_01177	RHOLA_RS06265	Rhola_00012610	DedA family protein
AURMO_01165	AURUGA1_01178	RHOLA_RS02015	Rhola_00004060	hypothetical protein
AURMO_01167	AURUGA1_00524	RHOLA_RS01750	Rhola_00003520	SDR family oxidoreductase
AURMO_01169	AURUGA1_00522	RHOLA_RS02005	Rhola_00004040	ribonuclease PH
AURMO_01170	AURUGA1_00521	RHOLA_RS02000	Rhola_00004030	glutamate racemase
AURMO_01192	AURUGA1_00499	RHOLA_RS02155	Rhola_00004340	Lrp/AsnC family transcriptional regulator
AURMO_01202	AURUGA1_00490	RHOLA_RS05255	Rhola_00010570	2345-tetrahydropyridine-26-dicarboxylate N-succinyltransferase
AURMO_01224	AURUGA1_00469	RHOLA_RS05440	Rhola_00010950	quinolinate synthase NadA
AURMO_01237	AURUGA1_00459	RHOLA_RS04865	Rhola_00009770	SRPBCC domain-containing protein
AURMO_01324	AURUGA1_00386	RHOLA_RS04980	Rhola_00010020	LemA family protein
AURMO_01325	AURUGA1_00385	RHOLA_RS04685	Rhola_00009420	MFS transporter
AURMO_01331	AURUGA1_00365	RHOLA_RS04995	Rhola_00010050	peptidase S8
AURMO_01332	AURUGA1_00364	RHOLA_RS05000	Rhola_00010060	DUF501 domain-containing protein
AURMO_01334	AURUGA1_00362	RHOLA_RS05010	Rhola_00010080	phosphopyruvate hydratase
AURMO_01343	AURUGA1_00353	RHOLA_RS05030	Rhola_00010120	aminoacyl-tRNA hydrolase
AURMO_01346	AURUGA1_00350	RHOLA_RS01200	Rhola_00002430	carbohydrate kinase

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_01350	AURUGA1_00346	RHOLA_RS05045	Rhola_00010150	ribose-phosphate diphosphokinase
AURMO_01362	AURUGA1_00339	RHOLA_RS05080	Rhola_00010220	TatD family deoxyribonuclease
AURMO_01385	AURUGA1_00324	RHOLA_RS01740	Rhola_00003500	hypothetical protein
AURMO_01386	AURUGA1_00323	RHOLA_RS06500	Rhola_00013090	pyridoxamine 5'-phosphate oxidase
AURMO_01402	AURUGA1_00320	RHOLA_RS05125	Rhola_00010310	N-acetyltransferase
AURMO_01429	AURUGA1_00296	RHOLA_RS06365		DUF3048 domain-containing protein
AURMO_01436	AURUGA1_00289	RHOLA_RS01855	Rhola_00003740	cysteine--tRNA ligase
AURMO_01440	AURUGA1_00284	RHOLA_RS01820	Rhola_00003670	phosphoglyceromutase
AURMO_01445	AURUGA1_00279	RHOLA_RS01785	Rhola_00003590	RNA degradosome polyphosphate kinase
AURMO_01446	AURUGA1_00278	RHOLA_RS01780	Rhola_00003580	NUDIX hydrolase
AURMO_01474	AURUGA1_01394	RHOLA_RS01170	Rhola_00002370	50S ribosomal protein L11
AURMO_01475	AURUGA1_01395	RHOLA_RS01165	Rhola_00002360	transcription termination/antitermination protein NusG
AURMO_01478	AURUGA1_01398	RHOLA_RS01150	Rhola_00002330	pyridoxal phosphate-dependent aminotransferase
AURMO_01481	AURUGA1_01401	RHOLA_RS01140	Rhola_00002310	acyl dehydratase
AURMO_01515	AURUGA1_01438	RHOLA_RS05880	Rhola_00011830	succinate--CoA ligase subunit alpha
AURMO_01516	AURUGA1_01439	RHOLA_RS05885	Rhola_00011840	ADP-forming succinate--CoA ligase subunit beta
AURMO_01519	AURUGA1_01442	RHOLA_RS05895	Rhola_00011860	hypothetical protein
AURMO_01528	AURUGA1_01368	RHOLA_RS05670	Rhola_00011420	phospho-sugar mutase
AURMO_01531	AURUGA1_01371	RHOLA_RS05700	Rhola_00011480	ABC transporter permease
AURMO_01542	AURUGA1_01380	RHOLA_RS01315	Rhola_00002640	sugar ABC transporter substrate-binding protein
AURMO_01601	AURUGA1_01475	RHOLA_RS00935	Rhola_00001880	arsenate reductase ArsC
AURMO_01622	AURUGA1_01494	RHOLA_RS05820	Rhola_00011720	aminotransferase class V-fold PLP-dependent enzyme
AURMO_01634	AURUGA1_01510	RHOLA_RS06715	Rhola_00013530	orotate phosphoribosyltransferase
AURMO_01648	AURUGA1_01524	RHOLA_RS01045	Rhola_00002120	isochorismate synthase
AURMO_01649	AURUGA1_01525	RHOLA_RS01040	Rhola_00002110	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase
AURMO_01652	AURUGA1_01528	RHOLA_RS01025	Rhola_00002080	14-dihydroxy-2-naphthoate polyprenyltransferase
AURMO_01653	AURUGA1_01529	RHOLA_RS01020		hypothetical protein
AURMO_01655	AURUGA1_01531	RHOLA_RS01010	Rhola_00002050	O-succinylbenzoate synthase
AURMO_01657	AURUGA1_01533	RHOLA_RS01000	Rhola_00002030	cytochrome c biogenesis protein ResB
AURMO_01659	AURUGA1_01535	RHOLA_RS00990	Rhola_00002010	TlpA family protein disulfide reductase
AURMO_01661	AURUGA1_01537	RHOLA_RS00980	Rhola_00001990	aspartate--tRNA(Asn) ligase
AURMO_01670	AURUGA1_01546	RHOLA_RS06240	Rhola_00012550	cation transporter
AURMO_01680	AURUGA1_01558	RHOLA_RS01385	Rhola_00002780	AarF/ABC1/UbiB kinase family protein
AURMO_01706	AURUGA1_01584	RHOLA_RS06760	Rhola_00013620	MFS transporter
AURMO_01707	AURUGA1_01585	RHOLA_RS04725	Rhola_00009500	NADH:flavin oxidoreductase/NADH oxidase
AURMO_01710	AURUGA1_01586	RHOLA_RS05415	Rhola_00010900	prenyltransferase
AURMO_01721	AURUGA1_00053	RHOLA_RS06790	Rhola_00013680	helicase

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AURMO_01723	AURUGA1_00051	RHOLA_RS06795	Rhola_00013690	copper transporter
AURMO_01725	AURUGA1_00049	RHOLA_RS06810	Rhola_00013720	30S ribosomal protein S14
AURMO_01729	AURUGA1_00046	RHOLA_RS06825	Rhola_00013750	transcriptional repressor
AURMO_01765	AURUGA1_00022	RHOLA_RS00210	Rhola_00000420	FtsW/RodA/SpoVE family cell cycle protein
AURMO_01774	AURUGA1_00013	RHOLA_RS00165	Rhola_00000330	peptidylprolyl isomerase
AURMO_00332	AURUGA1_01457	RHOLA_RS01105	Rhola_00002240	MMPL family transporter
AURMO_01510	AURUGA1_01435	RHOLA_RS05870	Rhola_00011810	phosphoribosylglycinamide formyltransferase
AURMO_00197	AURUGA1_00175	RHOLA_RS06120	Rhola_00012310	30S ribosomal protein S17
AURMO_00083	AURUGA1_00074	RHOLA_RS00320		D-alanyl-D-alanine carboxypeptidase family protein
AURMO_00085	AURUGA1_00076	RHOLA_RS00330	Rhola_00000660	prephenate dehydratase
AURMO_00089	AURUGA1_00080	RHOLA_RS00365	Rhola_00000730	LytR family transcriptional regulator
AURMO_00095	AURUGA1_00086	RHOLA_RS00750	Rhola_00001510	MFS transporter
AURMO_00099	AURUGA1_00092	RHOLA_RS00470	Rhola_00000940	dienelactone hydrolase family protein
AURMO_00125	AURUGA1_00117	RHOLA_RS00795	Rhola_00001600	hypoxanthine phosphoribosyltransferase
AURMO_00126	AURUGA1_00118	RHOLA_RS00800	Rhola_00001610	ATP-dependent zinc metalloprotease FtsH
AURMO_00127	AURUGA1_00119	RHOLA_RS00805	Rhola_00001620	GTP cyclohydrolase I FolE
AURMO_00130	AURUGA1_00122	RHOLA_RS00820	Rhola_00001650	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase
AURMO_00175	AURUGA1_00154	RHOLA_RS05420		sprT domain-containing protein
AURMO_00198	AURUGA1_00176	RHOLA_RS06115	Rhola_00012300	50S ribosomal protein L14
AURMO_00199	AURUGA1_00177	RHOLA_RS06110	Rhola_00012290	50S ribosomal protein L24
AURMO_00217	AURUGA1_00194	RHOLA_RS06025	Rhola_00012120	tRNA pseudouridine(38-40) synthase TruA
AURMO_00223	AURUGA1_00198	RHOLA_RS06000	Rhola_00012070	type I pantothenate kinase
AURMO_00224	AURUGA1_00199	RHOLA_RS05995	Rhola_00012060	glutamine--fructose-6-phosphate transaminase (isomerizing)
AURMO_00247	AURUGA1_00222	RHOLA_RS05920	Rhola_00011910	IMP dehydrogenase
AURMO_00250	AURUGA1_00225	RHOLA_RS05935	Rhola_00011940	ABC transporter ATP-binding protein
AURMO_00283	AURUGA1_00951	RHOLA_RS01360	Rhola_00002730	catalase/peroxidase HPI
AURMO_00309	AURUGA1_01605	RHOLA_RS06925	Rhola_00013960	murein biosynthesis integral membrane protein MurJ
AURMO_00349	AURUGA1_01312	RHOLA_RS06410	Rhola_00012910	PTS fructose transporter subunit IIA
AURMO_00357	AURUGA1_01305	RHOLA_RS05725	Rhola_00011530	succinate dehydrogenase cytochrome b556 subunit
AURMO_00373	AURUGA1_01288	RHOLA_RS05595	Rhola_00011270	hypothetical protein
AURMO_00387	AURUGA1_01276	RHOLA_RS05530	Rhola_00011140	hypothetical protein
AURMO_00424	AURUGA1_01244	RHOLA_RS04765	Rhola_00009580	ribosome small subunit-dependent GTPase A
AURMO_00445	AURUGA1_01218	RHOLA_RS00095	Rhola_00000190	glucose-1-phosphate thymidylyltransferase
AURMO_00453	AURUGA1_01212	RHOLA_RS02035	Rhola_00004100	diaminopimelate decarboxylase
AURMO_00468	AURUGA1_01198	RHOLA_RS02070	Rhola_00004170	threonylcarbamoyl-AMP synthase
AURMO_00519	AURUGA1_01136	RHOLA_RS00135	Rhola_00000270	hypothetical protein
AURMO_00523	AURUGA1_01132	RHOLA_RS00155	Rhola_00000310	IclR family transcriptional regulator

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AURMO_00530	AURUGA1_01125	RHOLA_RS04850	Rhola_00009740	acyl-CoA desaturase
AURMO_00540	AURUGA1_01117	RHOLA_RS06725	Rhola_00013550	DNA alkylation repair protein
AURMO_00542	AURUGA1_01115	RHOLA_RS06390	Rhola_00012860	glycosyltransferase family 2 protein
AURMO_00547	AURUGA1_01110	RHOLA_RS01940	Rhola_00003910	ATP-dependent helicase
AURMO_00552	AURUGA1_01105	RHOLA_RS01965	Rhola_00003960	hypothetical protein
AURMO_00569	AURUGA1_01091	RHOLA_RS05355	Rhola_00010770	3-isopropylmalate dehydrogenase
AURMO_00626	AURUGA1_01025	RHOLA_RS02395	Rhola_00004820	methyltransferase domain-containing protein
AURMO_00631	AURUGA1_01020	RHOLA_RS03000	Rhola_00006040	DedA family protein
AURMO_00645	AURUGA1_01100	RHOLA_RS04300	Rhola_00008640	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2 6-diaminopimelate ligase
AURMO_00650	AURUGA1_01003	RHOLA_RS04275	Rhola_00008590	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
AURMO_00673	AURUGA1_00978	RHOLA_RS03900	Rhola_00007850	glucose-6-phosphate isomerase
AURMO_00679	AURUGA1_00975	RHOLA_RS03935	Rhola_00007920	Fe-S cluster assembly protein SufD
AURMO_00687	AURUGA1_00966	RHOLA_RS03105	Rhola_00006250	DNA repair protein RecO
AURMO_00689	AURUGA1_00964	RHOLA_RS06345	Rhola_00012770	hypothetical protein
AURMO_00732	AURUGA1_00932	RHOLA_RS03280	Rhola_00006610	ROK family protein
AURMO_00756	AURUGA1_00910	RHOLA_RS03415	Rhola_00006880	DUF3071 domain-containing protein
AURMO_00759	AURUGA1_00907	RHOLA_RS03430	Rhola_00006910	dUTP diphosphatase
AURMO_00764	AURUGA1_00902	RHOLA_RS06540	Rhola_00013180	3-hydroxyacyl-CoA dehydrogenase
AURMO_00766	AURUGA1_00900	RHOLA_RS03455	Rhola_00006960	ribonuclease D
AURMO_00769	AURUGA1_00897	RHOLA_RS03470	Rhola_00006990	SufE family protein
AURMO_00780	AURUGA1_00886	RHOLA_RS03535	Rhola_00007120	pyridoxal 5'-phosphate synthase glutaminase subunit PdxT
AURMO_00781	AURUGA1_00885	RHOLA_RS03540	Rhola_00007130	YebC/PmpR family DNA-binding transcriptional regulator
AURMO_00786	AURUGA1_00880	RHOLA_RS03565	Rhola_00007180	protein translocase subunit SecD
AURMO_00801	AURUGA1_00865	RHOLA_RS03640	Rhola_00007330	3-dehydroquinate synthase
AURMO_00807	AURUGA1_00859	RHOLA_RS03670	Rhola_00007390	dihydroorotase
AURMO_00819	AURUGA1_00847	RHOLA_RS03725	Rhola_00007500	ribulose-phosphate 3-epimerase
AURMO_00842	AURUGA1_00824	RHOLA_RS03840	Rhola_00007730	excinuclease ABC subunit UvrC
AURMO_00844	AURUGA1_00822	RHOLA_RS03985	Rhola_00008010	short chain dehydrogenase
AURMO_00857	AURUGA1_00812	RHOLA_RS04160	Rhola_00008360	cytochrome bc complex cytochrome b subunit
AURMO_00864	AURUGA1_00806	RHOLA_RS04200	Rhola_00008440	DUF3043 domain-containing protein
AURMO_00869	AURUGA1_00801	RHOLA_RS04115	Rhola_00008270	apolipoprotein N-acyltransferase
AURMO_00876	AURUGA1_00794	RHOLA_RS04075	Rhola_00008190	tRNA (adenine-N1)-methyltransferase
AURMO_00886	AURUGA1_00784	RHOLA_RS04030	Rhola_00008100	alpha/beta hydrolase
AURMO_00890	AURUGA1_00780	RHOLA_RS04000	Rhola_00008040	glycogen synthase
AURMO_00896	AURUGA1_00774	RHOLA_RS03100	Rhola_00006240	2-isopropylmalate synthase
AURMO_00900	AURUGA1_00770	RHOLA_RS03080	Rhola_00006200	PhoH family protein
AURMO_00904	AURUGA1_00766	RHOLA_RS03060	Rhola_00006160	heat-inducible transcriptional repressor HrcA

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00905	AURUGA1_00765	RHOLA_RS03050	Rhola_00006140	coproporphyrinogen III oxidase
AURMO_00910	AURUGA1_00760	RHOLA_RS03025	Rhola_00006090	DNA internalization-related competence protein ComEC/Rec2
AURMO_00923	AURUGA1_00749	RHOLA_RS02965	Rhola_00005970	ribosome silencing factor
AURMO_00929	AURUGA1_00740	RHOLA_RS02935	Rhola_00005910	GTPase ObgE
AURMO_00939	AURUGA1_00727	RHOLA_RS02890	Rhola_00005820	valine--tRNA ligase
AURMO_00981	AURUGA1_00685	RHOLA_RS04420	Rhola_00008880	prephenate dehydrogenase
AURMO_00990	AURUGA1_00676	RHOLA_RS04470	Rhola_00008980	NAD kinase
AURMO_01008	AURUGA1_00656	RHOLA_RS02495	Rhola_00005020	argininosuccinate lyase
AURMO_01024	AURUGA1_00641	RHOLA_RS01335	Rhola_00002680	hypothetical protein
AURMO_01028	AURUGA1_00637	RHOLA_RS02425	Rhola_00004880	imidazole glycerol phosphate synthase subunit HisH
AURMO_01104	AURUGA1_00574	RHOLA_RS02605	Rhola_00005250	CDP-archaeol synthase
AURMO_01158	AURUGA1_01172	RHOLA_RS04510	Rhola_00009060	bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase
AURMO_01161	AURUGA1_01175	RHOLA_RS04525	Rhola_00009090	hypothetical protein
AURMO_01168	AURUGA1_00523	RHOLA_RS02010	Rhola_00004050	non-canonical purine NTP pyrophosphatase RdgB/HAM1 family
AURMO_01172	AURUGA1_00519	RHOLA_RS06380	Rhola_00012840	phosphocholine cytidylyltransferase family protein
AURMO_01188	AURUGA1_00503	RHOLA_RS01890	Rhola_00003810	magnesium transporter
AURMO_01241	AURUGA1_00455	RHOLA_RS02995	Rhola_00006030	SOS response-associated peptidase
AURMO_01242	AURUGA1_00453	RHOLA_RS04870	Rhola_00009780	redox-regulated ATPase YchF
AURMO_01314	AURUGA1_00395	RHOLA_RS04940	Rhola_00009940	PhoH family protein
AURMO_01367	AURUGA1_00333	RHOLA_RS05095	Rhola_00010250	phospholipid carrier-dependent glycosyltransferase
AURMO_01379	AURUGA1_00329	RHOLA_RS01345	Rhola_00002700	ATP-dependent RNA helicase HrpA
AURMO_01405	AURUGA1_00317	RHOLA_RS05140	Rhola_00010330	hypothetical protein
AURMO_01441	AURUGA1_00283	RHOLA_RS01815	Rhola_00003660	methylase
AURMO_01442	AURUGA1_00282	RHOLA_RS01805	Rhola_00003640	folate-binding protein
AURMO_01444	AURUGA1_00280	RHOLA_RS01790	Rhola_00003600	DNA-binding response regulator
AURMO_01463	AURUGA1_00268	RHOLA_RS05830	Rhola_00011740	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
AURMO_01530	AURUGA1_01370	RHOLA_RS05695	Rhola_00011470	cytidine deaminase
AURMO_01540	AURUGA1_01378	RHOLA_RS01285	Rhola_00002580	xylose isomerase
AURMO_01544	AURUGA1_01382	RHOLA_RS01325	Rhola_00002660	ABC transporter permease
AURMO_01567	AURUGA1_01446	RHOLA_RS01085	Rhola_00002200	sodium-dependent bicarbonate transport family permease
AURMO_01602	AURUGA1_01476	RHOLA_RS00725	Rhola_00001460	pyridine nucleotide-disulfide oxidoreductase
AURMO_01604	AURUGA1_01478	RHOLA_RS00670	Rhola_00001350	phosphoribosylaminoimidazolesuccinocarboxamide synthase
AURMO_01605	AURUGA1_01479	RHOLA_RS04130	Rhola_00008300	membrane protein
AURMO_01631	AURUGA1_01506	RHOLA_RS06690	Rhola_00013480	adenylosuccinate synthase
AURMO_01656	AURUGA1_01532	RHOLA_RS01005	Rhola_00002040	c-type cytochrome biogenesis protein CcsB

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AURMO_01668	AURUGA1_01544	RHOLA_RS01680	Rhola_00003380	TrkA family potassium uptake protein
AURMO_01669	AURUGA1_01545	RHOLA_RS00925	Rhola_00001860	pyrroline-5-carboxylate reductase
AURMO_01673	AURUGA1_01549	RHOLA_RS03920	Rhola_00007890	deoxyribodipyrimidine photo-lyase
AURMO_01769	AURUGA1_00018	RHOLA_RS00190	Rhola_00000380	glutamine amidotransferase
AURMO_01776	AURUGA1_00011	RHOLA_RS01395	Rhola_00002800	hypothetical protein
AURMO_01766	AURUGA1_00021	RHOLA_RS00205	Rhola_00000410	cell division protein FtsI
AURMO_01734	AURUGA1_00041	RHOLA_RS00235	Rhola_00000470	rhodanese domain-containing protein
AURMO_00115	AURUGA1_00109	RHOLA_RS01455	Rhola_00002920	chlorite dismutase
AURMO_00123	AURUGA1_00115	RHOLA_RS00785	Rhola_00001580	inorganic diphosphatase
AURMO_00132	AURUGA1_00124	RHOLA_RS00830	Rhola_00001670	DUF2520 domain-containing protein
AURMO_00133	AURUGA1_00125	RHOLA_RS00835	Rhola_00001680	pantoate--beta-alanine ligase
AURMO_00188	AURUGA1_00166	RHOLA_RS06165	Rhola_00012400	50S ribosomal protein L3
AURMO_00189	AURUGA1_00167	RHOLA_RS06160	Rhola_00012390	50S ribosomal protein L4
AURMO_00190	AURUGA1_00168	RHOLA_RS06155	Rhola_00012380	50S ribosomal protein L23
AURMO_00200	AURUGA1_00178	RHOLA_RS06105	Rhola_00012280	50S ribosomal protein L5
AURMO_00202	AURUGA1_00180	RHOLA_RS06095	Rhola_00012260	50S ribosomal protein L6
AURMO_00213	AURUGA1_00190	RHOLA_RS06045	Rhola_00012160	30S ribosomal protein S13
AURMO_00235	AURUGA1_00209	RHOLA_RS05955	Rhola_00011980	co-chaperone GroES
AURMO_00246	AURUGA1_00221	RHOLA_RS05915	Rhola_00011900	GuaB3 family IMP dehydrogenase-related protein
AURMO_00248	AURUGA1_00223	RHOLA_RS05925	Rhola_00011920	branched-chain amino acid ABC transporter permease
AURMO_00249	AURUGA1_00224	RHOLA_RS05930	Rhola_00011930	branched-chain amino acid ABC transporter permease
AURMO_01469	AURUGA1_00263	RHOLA_RS00265	Rhola_00000530	hypothetical protein
AURMO_01438	AURUGA1_00287	RHOLA_RS01845	Rhola_00003720	CarD family transcriptional regulator
AURMO_01437	AURUGA1_00288	RHOLA_RS01850	Rhola_00003730	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
AURMO_01435	AURUGA1_00290	RHOLA_RS01860	Rhola_00003750	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB
AURMO_01428	AURUGA1_00297	RHOLA_RS05205	Rhola_00010460	chaperonin GroEL
AURMO_01419	AURUGA1_00306	RHOLA_RS05160	Rhola_00010370	phosphoserine transaminase
AURMO_01406	AURUGA1_00316	RHOLA_RS06460	Rhola_00013010	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN
AURMO_01311	AURUGA1_00398	RHOLA_RS00370	Rhola_00000740	CoA ester lyase
AURMO_01209	AURUGA1_00486	RHOLA_RS04555	Rhola_00009150	ferredoxin family protein
AURMO_01201	AURUGA1_00491	RHOLA_RS05250	Rhola_00010560	succinyl-diaminopimelate desuccinylase
AURMO_01195	AURUGA1_00496	RHOLA_RS02140	Rhola_00004310	DNA-3-methyladenine glycosylase I
AURMO_00492	AURUGA1_00528	RHOLA_RS02200	Rhola_00004430	PDZ domain-containing protein
AURMO_00493	AURUGA1_00529	RHOLA_RS02205	Rhola_00004440	flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
AURMO_01118	AURUGA1_00561	RHOLA_RS02290	Rhola_00004610	30S ribosomal protein S15
AURMO_01113	AURUGA1_00566	RHOLA_RS02305	Rhola_00004640	4-hydroxy-tetrahydrodipicolinate reductase

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_01102	AURUGA1_00576	RHOLA_RS07055	Rhola_00005280	lytic transglycosylase domain-containing protein
AURMO_01095	AURUGA1_00583	RHOLA_RS02655	Rhola_00005350	14-alpha-glucan branching protein GlgB
AURMO_01093	AURUGA1_00585	RHOLA_RS02665	Rhola_00005370	glycogen debranching enzyme GlgX
AURMO_01067	AURUGA1_00608	RHOLA_RS02800		single-stranded DNA-binding protein
AURMO_01058	AURUGA1_00617	RHOLA_RS02835	Rhola_00005710	aminopeptidase N
AURMO_01057	AURUGA1_00618	RHOLA_RS02845	Rhola_00005730	ribose-5-phosphate isomerase
AURMO_01047	AURUGA1_00626	RHOLA_RS02865	Rhola_00005770	trigger factor
AURMO_01032	AURUGA1_00633	RHOLA_RS02405	Rhola_00004840	transcriptional repressor LexA
AURMO_01018	AURUGA1_00647	RHOLA_RS02460	Rhola_00004950	RNA methyltransferase
AURMO_01014	AURUGA1_00649	RHOLA_RS02470	Rhola_00004970	phenylalanine--tRNA ligase subunit beta
AURMO_01009	AURUGA1_00654	RHOLA_RS02490	Rhola_00005010	ornithine carbamoyltransferase
AURMO_00958	AURUGA1_00709	RHOLA_RS04395	Rhola_00008830	MerR family transcriptional regulator
AURMO_00949	AURUGA1_00719	RHOLA_RS04350	Rhola_00008740	3-deoxy-7-phosphoheptulonate synthase class II
AURMO_00938	AURUGA1_00728	RHOLA_RS02895	Rhola_00005830	isoleucine--tRNA ligase
AURMO_00937	AURUGA1_00729	RHOLA_RS02900	Rhola_00005840	bifunctional folylpolyglutamate synthase/dihydrofolate synthase
AURMO_00935	AURUGA1_00731	RHOLA_RS02910	Rhola_00005860	nucleoside-diphosphate kinase
AURMO_00925	AURUGA1_00747	RHOLA_RS02955	Rhola_00005950	nicotinate-nucleotide adenylyltransferase
AURMO_00899	AURUGA1_00771	RHOLA_RS03085	Rhola_00006210	rRNA maturation RNase YbeY
AURMO_00897	AURUGA1_00773	RHOLA_RS03095	Rhola_00006230	GTPase Era
AURMO_00893	AURUGA1_00777	RHOLA_RS03980	Rhola_00008000	beta-ketoacyl-ACP reductase
AURMO_00891	AURUGA1_00779	RHOLA_RS03995	Rhola_00008030	glucose-1-phosphate adenylyltransferase
AURMO_00885	AURUGA1_00785	RHOLA_RS04035	Rhola_00008110	glycosyltransferase family 1 protein
AURMO_00879	AURUGA1_00791	RHOLA_RS04060	Rhola_00008160	undecaprenyl-diphosphate phosphatase
AURMO_00877	AURUGA1_00793	RHOLA_RS04070	Rhola_00008180	hydrolase
AURMO_00871	AURUGA1_00799	RHOLA_RS04105	Rhola_00008250	twin-arginine translocase subunit TatC
AURMO_00862	AURUGA1_00808	RHOLA_RS04190	Rhola_00008420	iron-sulfur cluster insertion protein ErpA
AURMO_00838	AURUGA1_00828	RHOLA_RS03820	Rhola_00007690	30S ribosomal protein S1
AURMO_00833	AURUGA1_00833	RHOLA_RS03795	Rhola_00007640	pyruvate kinase
AURMO_00811	AURUGA1_00855	RHOLA_RS03690	Rhola_00007430	orotidine-5'-phosphate decarboxylase
AURMO_00810	AURUGA1_00856	RHOLA_RS03685	Rhola_00007420	carbamoyl-phosphate synthase large subunit
AURMO_00805	AURUGA1_00861	RHOLA_RS03660	Rhola_00007370	bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR
AURMO_00803	AURUGA1_00863	RHOLA_RS03650	Rhola_00007350	elongation factor P
AURMO_00798	AURUGA1_00868	RHOLA_RS03625	Rhola_00007300	shikimate dehydrogenase
AURMO_00797	AURUGA1_00869	RHOLA_RS03620	Rhola_00007290	endolytic transglycosylase MltG
AURMO_00793	AURUGA1_00873	RHOLA_RS03595	Rhola_00007240	30S ribosomal protein S4
AURMO_00788	AURUGA1_00878	RHOLA_RS03575	Rhola_00007200	bifunctional (p)ppGpp synthetase/guanosine-3'5'-bis(diphosphate) 3'-pyrophosphohydrolase
AURMO_00784	AURUGA1_00882	RHOLA_RS03555	Rhola_00007160	Holliday junction branch migration DNA helicase RuvB

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00771	AURUGA1_00895	RHOLA_RS03480	Rhola_00007010	cell division protein ZapE
AURMO_00767	AURUGA1_00899	RHOLA_RS03460	Rhola_00006970	DUF3000 domain-containing protein
AURMO_00729	AURUGA1_00935	RHOLA_RS03265	Rhola_00006570	Nif3-like dinuclear metal center hexameric protein
AURMO_00726	AURUGA1_00938	RHOLA_RS03250	Rhola_00006540	peroxiredoxin
AURMO_00699	AURUGA1_00954	RHOLA_RS03170	Rhola_00006380	hypothetical protein
AURMO_00693	AURUGA1_00960	RHOLA_RS03130	Rhola_00006300	DNA primase
AURMO_00678	AURUGA1_00976	RHOLA_RS03930	Rhola_00007910	Fe-S cluster assembly protein SufB
AURMO_00657	AURUGA1_00996	RHOLA_RS04240	Rhola_00008520	DivIVA domain-containing protein
AURMO_00651	AURUGA1_01002	RHOLA_RS04270	Rhola_00008580	UDP-N-acetylmuramate--L-alanine ligase
AURMO_00647	AURUGA1_01006	RHOLA_RS04290	Rhola_00008620	phospho-N-acetylmuramoyl-pentapeptide-transferase
AURMO_00642	AURUGA1_01010	RHOLA_RS04315	Rhola_00008670	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
AURMO_00629	AURUGA1_01022	RHOLA_RS02400	Rhola_00004830	GTPase HflX
AURMO_00622	AURUGA1_01029	RHOLA_RS02380	Rhola_00004790	tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB
AURMO_00619	AURUGA1_01032	RHOLA_RS02370	Rhola_00004770	recombinase RecA
AURMO_00617	AURUGA1_01034	RHOLA_RS02360	Rhola_00004750	XRE family transcriptional regulator
AURMO_00615	AURUGA1_01036	RHOLA_RS02350	Rhola_00004730	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
AURMO_00608	AURUGA1_01044	RHOLA_RS02340	Rhola_00004710	RNase J family beta-CASP ribonuclease
AURMO_00607	AURUGA1_01045	RHOLA_RS02335	Rhola_00004700	4-hydroxy-tetrahydrodipicolinate synthase
AURMO_00580	AURUGA1_01079	RHOLA_RS05280	Rhola_00010620	NAD(P)-dependent glycerol-3-phosphate dehydrogenase
AURMO_00573	AURUGA1_01086	RHOLA_RS05315	Rhola_00010690	diacylglycerol kinase family lipid kinase
AURMO_00570	AURUGA1_01090	RHOLA_RS05350	Rhola_00010760	branched-chain amino acid aminotransferase
AURMO_00564	AURUGA1_01096	RHOLA_RS05380	Rhola_00010820	acetolactate synthase small subunit
AURMO_00562	AURUGA1_01098	RHOLA_RS05390	Rhola_00010840	dihydroxy-acid dehydratase
AURMO_00554	AURUGA1_01103	RHOLA_RS01975	Rhola_00003980	UPF0182 family protein
AURMO_00541	AURUGA1_01116	RHOLA_RS01990	Rhola_00004010	PDZ domain-containing protein
AURMO_00514	AURUGA1_01141	RHOLA_RS01655	Rhola_00003330	DUF2236 domain-containing protein
AURMO_00475	AURUGA1_01192	RHOLA_RS02100	Rhola_00004230	F0F1 ATP synthase subunit delta
AURMO_00463	AURUGA1_01202	RHOLA_RS04840	Rhola_00009720	serine O-acetyltransferase
AURMO_00429	AURUGA1_01240	RHOLA_RS04740	Rhola_00009530	multifunctional oxoglutarate decarboxylase/oxoglutarate dehydrogenase thiamine pyrophosphate-binding subunit/dihydrolipoyllysine-residue succinyltransferase subunit
AURMO_00383	AURUGA1_01280	RHOLA_RS05550	Rhola_00011180	phosphomannomutase/phosphoglucomutase
AURMO_00380	AURUGA1_01282	RHOLA_RS07120	Rhola_00011200	hypothetical protein
AURMO_00378	AURUGA1_01284	RHOLA_RS05570	Rhola_00011220	WhiB family transcriptional regulator
AURMO_00369	AURUGA1_01292	RHOLA_RS00720	Rhola_00001450	polyprenol monophosphomannose synthase
AURMO_00364	AURUGA1_01298	RHOLA_RS05645	Rhola_00011370	class I SAM-dependent RNA methyltransferase
AURMO_00359	AURUGA1_01303	RHOLA_RS05685	Rhola_00011450	adenosine deaminase

A. photophilum Locus Tag	*Aurantimicrobium* sp. strain MWH-UGA1 Locus Tag	*R. lacicola* New Locus Tags	*R. lacicola* Old Locus Tags	*R. lacicola* Annotation
AURMO_00358	AURUGA1_01304	RHOLA_RS05720	Rhola_00011520	mannose-1-phosphate guanylyltransferase
AURMO_00354	AURUGA1_01308	RHOLA_RS05740	Rhola_00011560	succinate dehydrogenase iron-sulfur subunit
AURMO_00338	AURUGA1_01322	RHOLA_RS05775	Rhola_00011630	67-dimethyl-8-ribityllumazine synthase
AURMO_00323	AURUGA1_01333	RHOLA_RS01630	Rhola_00003280	DNA polymerase III subunit delta'
AURMO_00306	AURUGA1_01347	RHOLA_RS03215	Rhola_00006470	thymidine kinase
AURMO_00302	AURUGA1_01351	RHOLA_RS03510	Rhola_00007070	malate dehydrogenase (quinone)
AURMO_00300	AURUGA1_01353	RHOLA_RS01560	Rhola_00003130	aspartate kinase
AURMO_00297	AURUGA1_01355	RHOLA_RS01550	Rhola_00003110	DNA polymerase III subunit gamma and tau
AURMO_00288	AURUGA1_01357	RHOLA_RS01380	Rhola_00002770	extradiol dioxygenase
AURMO_01537	AURUGA1_01375	RHOLA_RS02745	Rhola_00005530	argininosuccinate synthase
AURMO_01547	AURUGA1_01384	RHOLA_RS00870	Rhola_00001750	hypothetical protein
AURMO_01480	AURUGA1_01400	RHOLA_RS01145	Rhola_00002320	UDP-N-acetylmuramate dehydrogenase
AURMO_01494	AURUGA1_01406	RHOLA_RS00760	Rhola_00001530	NAD(P)-dependent alcohol dehydrogenase
AURMO_01565	AURUGA1_01444	RHOLA_RS01095	Rhola_00002220	MarR family transcriptional regulator
AURMO_01624	AURUGA1_01496	RHOLA_RS00620	Rhola_00001240	phosphoribosylformylglycinamidine synthase subunit PurQ
AURMO_01633	AURUGA1_01509	RHOLA_RS06695	Rhola_00013490	TrmH family RNA methyltransferase
AURMO_01643	AURUGA1_01519	RHOLA_RS00695	Rhola_00001400	amidophosphoribosyltransferase
AURMO_01646	AURUGA1_01522	RHOLA_RS01060	Rhola_00002150	polyprenyl synthetase family protein
AURMO_01672	AURUGA1_01548	RHOLA_RS06255	Rhola_00012590	winged helix family transcriptional regulator
AURMO_01691	AURUGA1_01571	RHOLA_RS01410	Rhola_00002830	low specificity L-threonine aldolase
AURMO_01713	AURUGA1_01589		Rhola_00010870	phytoene desaturase
AURMO_01719	AURUGA1_01595	RHOLA_RS06775	Rhola_00013650	dCTP deaminase
AURMO_00007	AURUGA1_01612	RHOLA_RS06965	Rhola_00014040	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG

Table A.3 458 genes unique to *R. lacicola* from *A. photophilum* and *Aurantimicrobium* sp. strain MWH-UGA1.

R. lacicola New Locus Tag	*R. lacicola* Old Locus Tag	Annotation
RHOLA_RS00030	Rhola_00000060	transcriptional regulator
RHOLA_RS00045	Rhola_00000090	hypothetical protein
RHOLA_RS00060	Rhola_00000120	hypothetical protein
RHOLA_RS00065	Rhola_00000130	glycosyltransferase family 2 protein
RHOLA_RS00070		hypothetical protein
RHOLA_RS00075	Rhola_00000150	ABC transporter permease
RHOLA_RS00090	Rhola_00000180	dTDP-4-dehydrorhamnose reductase
RHOLA_RS00105	Rhola_00000210	glycosyltransferase family 2 protein
RHOLA_RS00110	Rhola_00000220	hypothetical protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS00115	Rhola_00000230	hypothetical protein
RHOLA_RS00125	Rhola_00000250	hypothetical protein
RHOLA_RS00160	Rhola_00000320	hypothetical protein
RHOLA_RS00170	Rhola_00000340	DUF1751 domain-containing protein
RHOLA_RS00175	Rhola_00000350	hypothetical protein
RHOLA_RS00180	Rhola_00000360	DUF3800 domain-containing protein
RHOLA_RS00185	Rhola_00000370	hypothetical protein
RHOLA_RS00220	Rhola_00000440	FHA domain-containing protein
RHOLA_RS00230	Rhola_00000460	hypothetical protein
RHOLA_RS00245	Rhola_00000490	4-hydroxybenzoyl-CoA thioesterase
RHOLA_RS00250	Rhola_00000500	FAD:protein FMN transferase
RHOLA_RS00255		FMN-binding protein
RHOLA_RS00260	Rhola_00000520	FMN-binding protein
RHOLA_RS00275	Rhola_00000550	N-acetyltransferase
RHOLA_RS00280	Rhola_00000560	hypothetical protein
RHOLA_RS00285	Rhola_00000570	tripartite tricarboxylate transporter TctB family protein
RHOLA_RS00290	Rhola_00000580	tripartite tricarboxylate transporter TctA
RHOLA_RS00295	Rhola_00000590	MFS transporter
RHOLA_RS00305	Rhola_00000610	iron ABC transporter permease
RHOLA_RS00310	Rhola_00000620	thiamine ABC transporter substrate-binding protein
RHOLA_RS00335	Rhola_00000670	hypothetical protein
RHOLA_RS00345	Rhola_00000690	type II toxin-antitoxin system death-on-curing family toxin
RHOLA_RS00380	Rhola_00000760	IclR family transcriptional regulator
RHOLA_RS00385	Rhola_00000770	ABC transporter permease
RHOLA_RS00395	Rhola_00000790	ABC transporter permease
RHOLA_RS00400	Rhola_00000800	glycine/betaine ABC transporter substrate-binding protein
RHOLA_RS00405	Rhola_00000810	formaldehyde-activating enzyme
RHOLA_RS00410	Rhola_00000820	mandelate racemase/muconate lactonizing enzyme family protein
RHOLA_RS00420	Rhola_00000840	NAD(P)-dependent oxidoreductase
RHOLA_RS00425	Rhola_00000850	NAD-dependent alcohol dehydrogenase
RHOLA_RS00450	Rhola_00000900	hypothetical protein
RHOLA_RS00475	Rhola_00000950	ROK family protein
RHOLA_RS00480	Rhola_00000960	sugar phosphate isomerase
RHOLA_RS00485	Rhola_00000970	sugar ABC transporter substrate-binding protein
RHOLA_RS00495	Rhola_00000990	ABC transporter permease
RHOLA_RS00500	Rhola_00001000	hypothetical protein
RHOLA_RS00510	Rhola_00001020	gfo/Idh/MocA family oxidoreductase
RHOLA_RS00515	Rhola_00001030	sugar phosphate isomerase/epimerase

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS00520	Rhola_00001040	antibiotic biosynthesis monooxygenase
RHOLA_RS00530	Rhola_00001060	hypothetical protein
RHOLA_RS00535	Rhola_00001070	hypothetical protein
RHOLA_RS00545	Rhola_00001090	hypothetical protein
RHOLA_RS00550	Rhola_00001100	hypothetical protein
RHOLA_RS00555	Rhola_00001110	NYN domain-containing protein
RHOLA_RS00560	Rhola_00001120	hypothetical protein
RHOLA_RS00565	Rhola_00001130	hypothetical protein
RHOLA_RS00570	Rhola_00001140	type I restriction-modification system subunit M
RHOLA_RS00575	Rhola_00001150	hypothetical protein
RHOLA_RS00580	Rhola_00001160	restriction endonuclease subunit S
RHOLA_RS00585	Rhola_00001170	type I restriction endonuclease subunit R
RHOLA_RS00590	Rhola_00001180	hypothetical protein
RHOLA_RS00595	Rhola_00001190	hypothetical protein
RHOLA_RS00610	Rhola_00001220	hypothetical protein
RHOLA_RS00625	Rhola_00001250	phosphoribosylformylglycinamidine synthase purS protein
RHOLA_RS00630	Rhola_00001260	prevent-host-death family protein
RHOLA_RS00635	Rhola_00001270	type II toxin-antitoxin system RelE/ParE family toxin
RHOLA_RS00640	Rhola_00001280	hypothetical protein
RHOLA_RS00645	Rhola_00001290	ATP-binding protein
RHOLA_RS00655	Rhola_00001310	metal-sensitive transcriptional regulator
RHOLA_RS00660	Rhola_00001320	rhodanese-like domain-containing protein
RHOLA_RS00685	Rhola_00001380	hypothetical protein
RHOLA_RS00690	Rhola_00001390	hypothetical protein
RHOLA_RS00730	Rhola_00001470	N-acetyltransferase
RHOLA_RS00735	Rhola_00001480	DUF3073 domain-containing protein
RHOLA_RS00740		CrcB family protein
RHOLA_RS00755	Rhola_00001520	hypothetical protein
RHOLA_RS00780	Rhola_00001570	hypothetical protein
RHOLA_RS00815	Rhola_00001640	dihydroneopterin aldolase
RHOLA_RS00845	Rhola_00001700	hypothetical protein
RHOLA_RS00850	Rhola_00001710	glutaredoxin-like protein NrdH
RHOLA_RS00855	Rhola_00001720	class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI
RHOLA_RS00865	Rhola_00001740	class 1b ribonucleoside-diphosphate reductase subunit beta
RHOLA_RS00885	Rhola_00001780	hypothetical protein
RHOLA_RS00950	Rhola_00001920	HAD-IB family hydrolase
RHOLA_RS00955	Rhola_00001930	glutaredoxin family protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS00960	Rhola_00001950	PASTA domain-containing protein
RHOLA_RS00965	Rhola_00001960	PadR family transcriptional regulator
RHOLA_RS00970	Rhola_00001970	hypothetical protein
RHOLA_RS00975	Rhola_00001980	type II toxin-antitoxin system VapC family toxin
RHOLA_RS01030	Rhola_00002090	DUF4229 domain-containing protein
RHOLA_RS01035	Rhola_00002100	hypothetical protein
RHOLA_RS01050	Rhola_00002130	hypothetical protein
RHOLA_RS01065	Rhola_00002160	MFS transporter
RHOLA_RS01075	Rhola_00002180	LacI family transcriptional regulator
RHOLA_RS01120	Rhola_00002270	hypothetical protein
RHOLA_RS01160	Rhola_00002350	preprotein translocase subunit SecE
RHOLA_RS01185	Rhola_00002400	MFS transporter
RHOLA_RS01195	Rhola_00002420	TM0106 family RecB-like putative nuclease
RHOLA_RS01205	Rhola_00002440	hypothetical protein
RHOLA_RS01215	Rhola_00002460	glutaredoxin family protein
RHOLA_RS01225	Rhola_00002480	ATP-binding protein
RHOLA_RS01240	Rhola_00002510	50S ribosomal protein L7/L12
RHOLA_RS01255	Rhola_00002530	MFS transporter
RHOLA_RS01260		hypothetical protein
RHOLA_RS01275	Rhola_00002560	hypothetical protein
RHOLA_RS01295	Rhola_00002600	GMC family oxidoreductase
RHOLA_RS01350	Rhola_00002710	hypothetical protein
RHOLA_RS01370	Rhola_00002750	DUF4188 domain-containing protein
RHOLA_RS01375	Rhola_00002760	DUF1801 domain-containing protein
RHOLA_RS01390	Rhola_00002790	PadR family transcriptional regulator
RHOLA_RS01405	Rhola_00002820	Lrp/AsnC family transcriptional regulator
RHOLA_RS01415	Rhola_00002840	hypothetical protein
RHOLA_RS01465	Rhola_00002940	DNA-binding protein
RHOLA_RS01470	Rhola_00002950	hypothetical protein
RHOLA_RS01480	Rhola_00002970	hypothetical protein
RHOLA_RS01495	Rhola_00003000	metal-sensitive transcriptional regulator
RHOLA_RS01510	Rhola_00003030	DUF305 domain-containing protein
RHOLA_RS01515	Rhola_00003040	hypothetical protein
RHOLA_RS01525	Rhola_00003060	hypothetical protein
RHOLA_RS01540	Rhola_00003090	hypothetical protein
RHOLA_RS01570	Rhola_00003150	hypothetical protein
RHOLA_RS01600	Rhola_00003220	hypothetical protein
RHOLA_RS01605	Rhola_00003230	DUF4244 domain-containing protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS01640	Rhola_00003300	DUF485 domain-containing protein
RHOLA_RS01650	Rhola_00003320	hypothetical protein
RHOLA_RS01660	Rhola_00003340	rhizopine-binding protein
RHOLA_RS01670	Rhola_00003360	ABC transporter permease
RHOLA_RS01705	Rhola_00003430	copper resistance protein CopC
RHOLA_RS01720	Rhola_00003460	hypothetical protein
RHOLA_RS01730	Rhola_00003480	hypothetical protein
RHOLA_RS01735	Rhola_00003490	DUF1737 domain-containing protein
RHOLA_RS01760	Rhola_00003540	acyltransferase
RHOLA_RS01795	Rhola_00003610	hypothetical protein
RHOLA_RS01800	Rhola_00003630	FABP family protein
RHOLA_RS01810	Rhola_00003650	FUSC family protein
RHOLA_RS01840	Rhola_00003710	hypothetical protein
RHOLA_RS01865	Rhola_00003760	O-methyltransferase
RHOLA_RS01870	Rhola_00003770	hypothetical protein
RHOLA_RS01895	Rhola_00003820	hypothetical protein
RHOLA_RS01910	Rhola_00003850	DUF4287 domain-containing protein
RHOLA_RS01925	Rhola_00003880	hypothetical protein
RHOLA_RS01930	Rhola_00003890	DUF3107 domain-containing protein
RHOLA_RS01960	Rhola_00003950	hypothetical protein
RHOLA_RS01995	Rhola_00004020	DUF3039 domain-containing protein
RHOLA_RS02080	Rhola_00004190	hypothetical protein
RHOLA_RS02090	Rhola_00004210	ATP synthase F0 subunit C
RHOLA_RS02120	Rhola_00004270	F0F1 ATP synthase subunit epsilon
RHOLA_RS02125	Rhola_00004280	cob(I)yrinic acid ac-diamide adenosyltransferase
RHOLA_RS02130	Rhola_00004290	peroxide stress protein YaaA
RHOLA_RS02135	Rhola_00004300	hypothetical protein
RHOLA_RS02145		methylated-DNA--[protein]-cysteine S-methyltransferase
RHOLA_RS02165	Rhola_00004360	hypothetical protein
RHOLA_RS02170	Rhola_00004370	spermidine/putrescine ABC transporter substrate-binding protein
RHOLA_RS02180	Rhola_00004390	ABC transporter permease
RHOLA_RS02185	Rhola_00004400	ABC transporter permease
RHOLA_RS02220		DUF448 domain-containing protein
RHOLA_RS02240	Rhola_00004510	hypothetical protein
RHOLA_RS02260		hypothetical protein
RHOLA_RS02265	Rhola_00004560	hypothetical protein
RHOLA_RS02270	Rhola_00004570	hypothetical protein
RHOLA_RS02280	Rhola_00004590	hypothetical protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS02285	Rhola_00004600	DUF805 domain-containing protein
RHOLA_RS02310	Rhola_00004650	hypothetical protein
RHOLA_RS02315	Rhola_00004660	DUF4395 domain-containing protein
RHOLA_RS02320	Rhola_00004670	thioredoxin
RHOLA_RS02365	Rhola_00004760	DUF3046 domain-containing protein
RHOLA_RS02375	Rhola_00004780	RecX family transcriptional regulator
RHOLA_RS02410	Rhola_00004850	LysM peptidoglycan-binding domain-containing protein
RHOLA_RS02440	Rhola_00004910	hypothetical protein
RHOLA_RS02450	Rhola_00004930	50S ribosomal protein L35
RHOLA_RS02525	Rhola_00005080	hypothetical protein
RHOLA_RS02560	Rhola_00005160	YraN family protein
RHOLA_RS02565	Rhola_00005170	ATP-binding protein
RHOLA_RS02580		M23 family peptidase
RHOLA_RS02610	Rhola_00005260	DivIVA domain-containing protein
RHOLA_RS02615	Rhola_00005270	HNH endonuclease
RHOLA_RS02625	Rhola_00005290	hypothetical protein
RHOLA_RS02640	Rhola_00005320	hypothetical protein
RHOLA_RS02690	Rhola_00005420	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC
RHOLA_RS02725	Rhola_00005490	membrane protein
RHOLA_RS02735	Rhola_00005510	hypothetical protein
RHOLA_RS02755	Rhola_00005550	heme-degrading domain-containing protein
RHOLA_RS02760	Rhola_00005560	Lrp/AsnC family transcriptional regulator
RHOLA_RS02775	Rhola_00005590	hydrolase
RHOLA_RS02785	Rhola_00005610	hypothetical protein
RHOLA_RS02820	Rhola_00005680	hypothetical protein
RHOLA_RS02885	Rhola_00005810	hypothetical protein
RHOLA_RS02905	Rhola_00005850	DUF4233 domain-containing protein
RHOLA_RS02950	Rhola_00005940	hypothetical protein
RHOLA_RS02960	Rhola_00005960	hypothetical protein
RHOLA_RS02975	Rhola_00005990	DUF167 domain-containing protein
RHOLA_RS02980	Rhola_00006000	deoxyribose-phosphate aldolase
RHOLA_RS02985	Rhola_00006010	hypothetical protein
RHOLA_RS02990		hypothetical protein
RHOLA_RS03005	Rhola_00006050	hypothetical protein
RHOLA_RS03035	Rhola_00006110	MFS transporter
RHOLA_RS03040	Rhola_00006120	30S ribosomal protein S20
RHOLA_RS03055	Rhola_00006150	DUF4870 domain-containing protein
RHOLA_RS03075	Rhola_00006190	HIT domain-containing protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS03160	Rhola_00006360	branched-chain amino acid transporter AzlD
RHOLA_RS03190	Rhola_00006420	amino acid ABC transporter permease
RHOLA_RS03200	Rhola_00006440	ABC transporter substrate-binding protein
RHOLA_RS03205	Rhola_00006450	hypothetical protein
RHOLA_RS03210	Rhola_00006460	o-succinylbenzoate synthase
RHOLA_RS03260	Rhola_00006560	hypothetical protein
RHOLA_RS03270	Rhola_00006580	hypothetical protein
RHOLA_RS03290	Rhola_00006630	hypothetical protein
RHOLA_RS03300	Rhola_00006650	RidA family protein
RHOLA_RS03325	Rhola_00006700	transporter
RHOLA_RS03345		hypothetical protein
RHOLA_RS03370	Rhola_00006790	SDR family oxidoreductase
RHOLA_RS03375	Rhola_00006800	MFS transporter
RHOLA_RS03385	Rhola_00006820	DUF1727 domain-containing protein
RHOLA_RS03390	Rhola_00006830	hypothetical protein
RHOLA_RS03395	Rhola_00006840	hypothetical protein
RHOLA_RS03420	Rhola_00006890	DUF4193 domain-containing protein
RHOLA_RS03425		DUF3093 domain-containing protein
RHOLA_RS03465	Rhola_00006980	hypothetical protein
RHOLA_RS03515		VIT family protein
RHOLA_RS03600	Rhola_00007250	DUF948 domain-containing protein
RHOLA_RS03635	Rhola_00007320	shikimate kinase
RHOLA_RS03700	Rhola_00007450	DNA-directed RNA polymerase subunit omega
RHOLA_RS03730	Rhola_00007510	phosphoribosyl-ATP diphosphatase
RHOLA_RS03745	Rhola_00007540	phosphoribosyl-AMP cyclohydrolase
RHOLA_RS03755	Rhola_00007560	hypothetical protein
RHOLA_RS03760	Rhola_00007570	hypothetical protein
RHOLA_RS03875	Rhola_00007800	preprotein translocase subunit SecG
RHOLA_RS03940	Rhola_00007930	non-heme iron oxygenase ferredoxin subunit
RHOLA_RS03955	Rhola_00007960	biotin transporter BioY
RHOLA_RS03970		hypothetical protein
RHOLA_RS03975	Rhola_00007990	DUF3099 domain-containing protein
RHOLA_RS04040	Rhola_00008120	histidine phosphatase family protein
RHOLA_RS04055	Rhola_00008150	hypothetical protein
RHOLA_RS04095	Rhola_00008230	hypothetical protein
RHOLA_RS04100	Rhola_00008240	twin-arginine translocase TatA/TatE family subunit
RHOLA_RS04120	Rhola_00008280	hypothetical protein
RHOLA_RS04135	Rhola_00008310	NUDIX domain-containing protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS04170	Rhola_00008380	hypothetical protein
RHOLA_RS04175	Rhola_00008390	cytochrome c oxidase subunit 4
RHOLA_RS04220	Rhola_00008480	flavin reductase
RHOLA_RS04235		hypothetical protein
RHOLA_RS04245	Rhola_00008530	YggT family protein
RHOLA_RS04250	Rhola_00008540	DUF552 domain-containing protein
RHOLA_RS04310	Rhola_00008660	hypothetical protein
RHOLA_RS04325	Rhola_00008690	DUF3040 domain-containing protein
RHOLA_RS04335	Rhola_00008710	DNA-binding protein
RHOLA_RS04340		LysM peptidoglycan-binding domain-containing protein
RHOLA_RS04405	Rhola_00008850	CDP-alcohol phosphatidyltransferase family protein
RHOLA_RS04425	Rhola_00008890	chorismate mutase
RHOLA_RS04485	Rhola_00009010	RNA-binding protein
RHOLA_RS04520	Rhola_00009080	50S ribosomal protein L32
RHOLA_RS04570		DUF393 domain-containing protein
RHOLA_RS04600	Rhola_00009230	ECF transporter S component
RHOLA_RS04605		hypothetical protein
RHOLA_RS04610	Rhola_00009250	hypothetical protein
RHOLA_RS04615	Rhola_00009260	trimeric intracellular cation channel family protein
RHOLA_RS04620	Rhola_00009270	hypothetical protein
RHOLA_RS04650	Rhola_00009340	hypothetical protein
RHOLA_RS04655	Rhola_00009350	hypothetical protein
RHOLA_RS04660		hypothetical protein
RHOLA_RS04665		type II secretion system F family protein
RHOLA_RS04670		hypothetical protein
RHOLA_RS04720	Rhola_00009490	MFS transporter
RHOLA_RS04745	Rhola_00009540	hypothetical protein
RHOLA_RS04750	Rhola_00009550	mycothiol system anti-sigma-R factor
RHOLA_RS04790	Rhola_00009630	LacI family transcriptional regulator
RHOLA_RS04825		hypothetical protein
RHOLA_RS04830	Rhola_00009700	hypothetical protein
RHOLA_RS04845	Rhola_00009730	DUF1761 domain-containing protein
RHOLA_RS04855		DUF1801 domain-containing protein
RHOLA_RS04860	Rhola_00009760	hypothetical protein
RHOLA_RS04875	Rhola_00009790	hypothetical protein
RHOLA_RS04910	Rhola_00009870	exodeoxyribonuclease VII small subunit
RHOLA_RS04915		DUF4245 domain-containing protein
RHOLA_RS04930		prepilin peptidase

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS04955	Rhola_00009970	hypothetical protein
RHOLA_RS04960	Rhola_00009980	DUF4307 domain-containing protein
RHOLA_RS05040	Rhola_00010140	amino acid permease
RHOLA_RS05070	Rhola_00010200	hypothetical protein
RHOLA_RS05100	Rhola_00010260	hypothetical protein
RHOLA_RS05115	Rhola_00010290	hypothetical protein
RHOLA_RS05120	Rhola_00010300	hypothetical protein
RHOLA_RS05165	Rhola_00010380	DUF3027 domain-containing protein
RHOLA_RS05175	Rhola_00010400	hypothetical protein
RHOLA_RS05200	Rhola_00010450	WXG100 family type VII secretion target
RHOLA_RS05210	Rhola_00010470	cold-shock protein
RHOLA_RS05215	Rhola_00010480	hypothetical protein
RHOLA_RS05225	Rhola_00010500	hypothetical protein
RHOLA_RS05235	Rhola_00010520	hypothetical protein
RHOLA_RS05260	Rhola_00010580	hypothetical protein
RHOLA_RS05320	Rhola_00010700	hypothetical protein
RHOLA_RS05325	Rhola_00010710	hypothetical protein
RHOLA_RS05330	Rhola_00010720	hypothetical protein
RHOLA_RS05365	Rhola_00010790	rhodanese-like domain-containing protein
RHOLA_RS05405	Rhola_00010880	lycopene cyclase domain-containing protein
RHOLA_RS05410	Rhola_00010890	lycopene cyclase domain-containing protein
RHOLA_RS05425	Rhola_00010920	hypothetical protein
RHOLA_RS05430	Rhola_00010930	nucleoside deaminase
RHOLA_RS05460	Rhola_00010990	glyoxalase
RHOLA_RS05465	Rhola_00011000	deoxyribodipyrimidine photo-lyase
RHOLA_RS05480	Rhola_00011040	hypothetical protein
RHOLA_RS05485	Rhola_00011050	WhiB family transcriptional regulator
RHOLA_RS05500	Rhola_00011080	hypothetical protein
RHOLA_RS05505	Rhola_00011090	hypothetical protein
RHOLA_RS05510	Rhola_00011100	hypothetical protein
RHOLA_RS05520	Rhola_00011120	ribosome-associated translation inhibitor RaiA
RHOLA_RS05525	Rhola_00011130	ComF family protein
RHOLA_RS05555	Rhola_00011190	hypothetical protein
RHOLA_RS05590	Rhola_00011260	hypothetical protein
RHOLA_RS05610	Rhola_00011300	hypothetical protein
RHOLA_RS05625	Rhola_00011330	acyl-CoA carboxylase subunit epsilon
RHOLA_RS05630	Rhola_00011340	hypothetical protein
RHOLA_RS05635	Rhola_00011350	ATP-binding protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS05640	Rhola_00011360	DNA-binding response regulator
RHOLA_RS05675	Rhola_00011430	PTS ascorbate transporter subunit IIB
RHOLA_RS05680	Rhola_00011440	hypothetical protein
RHOLA_RS05745		Rieske (2Fe-2S) protein
RHOLA_RS05780	Rhola_00011640	hypothetical protein
RHOLA_RS05795	Rhola_00011670	DUF4242 domain-containing protein
RHOLA_RS05810	Rhola_00011700	hypothetical protein
RHOLA_RS05815	Rhola_00011710	ABC transporter permease
RHOLA_RS05860	Rhola_00011790	NADP-dependent isocitrate dehydrogenase
RHOLA_RS05905	Rhola_00011880	DUF3817 domain-containing protein
RHOLA_RS05910	Rhola_00011890	hypothetical protein
RHOLA_RS05975		tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB
RHOLA_RS05990	Rhola_00012050	holo-ACP synthase
RHOLA_RS06050	Rhola_00012170	50S ribosomal protein L36
RHOLA_RS06080	Rhola_00012230	50S ribosomal protein L30
RHOLA_RS06125	Rhola_00012320	50S ribosomal protein L29
RHOLA_RS06180	Rhola_00012430	hypothetical protein
RHOLA_RS06220	Rhola_00012510	hypothetical protein
RHOLA_RS06225	Rhola_00012520	hypothetical protein
RHOLA_RS06230		hypothetical protein
RHOLA_RS06260		hypothetical protein
RHOLA_RS06275	Rhola_00012630	hypothetical protein
RHOLA_RS06305	Rhola_00012690	NYN domain-containing protein
RHOLA_RS06310	Rhola_00012700	hypothetical protein
RHOLA_RS06335	Rhola_00012750	hypothetical protein
RHOLA_RS06340	Rhola_00012760	hypothetical protein
RHOLA_RS06350	Rhola_00012780	hypothetical protein
RHOLA_RS06355	Rhola_00012790	hypothetical protein
RHOLA_RS06360	Rhola_00012800	hypothetical protein
RHOLA_RS06385	Rhola_00012850	hypothetical protein
RHOLA_RS06400	Rhola_00012880	ABC transporter permease
RHOLA_RS06415	Rhola_00012920	HPr family phosphocarrier protein
RHOLA_RS06425	Rhola_00012940	L-lactate dehydrogenase
RHOLA_RS06430	Rhola_00012950	glycosyltransferase family 8 protein
RHOLA_RS06440	Rhola_00012970	glycosyltransferase family 2 protein
RHOLA_RS06445	Rhola_00012980	EamA family transporter
RHOLA_RS06465	Rhola_00013020	sucrose phosphorylase

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS06475		class E sortase
RHOLA_RS06480	Rhola_00013050	hypothetical protein
RHOLA_RS06485	Rhola_00013060	hypothetical protein
RHOLA_RS06495	Rhola_00013080	LysE family translocator
RHOLA_RS06520	Rhola_00013130	hypothetical protein
RHOLA_RS06535	Rhola_00013160	hypothetical protein
RHOLA_RS06570	Rhola_00013240	hypothetical protein
RHOLA_RS06575	Rhola_00013250	hypothetical protein
RHOLA_RS06585	Rhola_00013270	ATP-binding protein
RHOLA_RS06590	Rhola_00013280	hypothetical protein
RHOLA_RS06610	Rhola_00013320	sugar ABC transporter substrate-binding protein
RHOLA_RS06625	Rhola_00013350	LacI family transcriptional regulator
RHOLA_RS06635	Rhola_00013370	EamA/RhaT family transporter
RHOLA_RS06640	Rhola_00013380	hydroxypyruvate isomerase
RHOLA_RS06645	Rhola_00013390	hypothetical protein
RHOLA_RS06650	Rhola_00013400	inositol 2-dehydrogenase
RHOLA_RS06655	Rhola_00013410	inosose dehydratase
RHOLA_RS06665	Rhola_00013430	LacI family transcriptional regulator
RHOLA_RS06670	Rhola_00013440	hypothetical protein
RHOLA_RS06685	Rhola_00013470	GNAT family N-acetyltransferase
RHOLA_RS06705	Rhola_00013510	HAD family hydrolase
RHOLA_RS06710	Rhola_00013520	MFS transporter
RHOLA_RS06730	Rhola_00013560	hypothetical protein
RHOLA_RS06750		nucleotide exchange factor GrpE
RHOLA_RS06770		copper chaperone PCu(A)C
RHOLA_RS06785	Rhola_00013670	cytochrome P450
RHOLA_RS06800	Rhola_00013700	isoprenylcysteine carboxylmethyltransferase family protein
RHOLA_RS06805	Rhola_00013710	integration host factor
RHOLA_RS06815	Rhola_00013730	50S ribosomal protein L33
RHOLA_RS06820	Rhola_00013740	50S ribosomal protein L28
RHOLA_RS06830	Rhola_00013760	metal ABC transporter permease
RHOLA_RS06835	Rhola_00013770	metal ABC transporter ATP-binding protein
RHOLA_RS06840	Rhola_00013780	hypothetical protein
RHOLA_RS06845		XRE family transcriptional regulator
RHOLA_RS06865	Rhola_00013830	phage holin family protein
RHOLA_RS06870	Rhola_00013840	hypothetical protein
RHOLA_RS06895	Rhola_00013900	30S ribosomal protein S18
RHOLA_RS06915	Rhola_00013940	NUDIX hydrolase

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS06920	Rhola_00013950	hypothetical protein
RHOLA_RS06990	Rhola_00014080	50S ribosomal protein L34
RHOLA_RS07015	Rhola_00001500	hypothetical protein
RHOLA_RS07020	Rhola_00001660	DUF3180 domain-containing protein
RHOLA_RS07025	Rhola_00001870	TetR/AcrR family transcriptional regulator
RHOLA_RS07030	Rhola_00001890	hypothetical protein
RHOLA_RS07040	Rhola_00003240	hypothetical protein
RHOLA_RS07045	Rhola_00003250	hypothetical protein
RHOLA_RS07050	Rhola_00004000	hypothetical protein
RHOLA_RS07060	Rhola_00006340	DNA-binding response regulator
RHOLA_RS07065	Rhola_00007170	preprotein translocase subunit YajC
RHOLA_RS07070	Rhola_00007400	hypothetical protein
RHOLA_RS07075	Rhola_00008370	hypothetical protein
RHOLA_RS07085	Rhola_00009160	hypothetical protein
RHOLA_RS07090	Rhola_00009200	hypothetical protein
RHOLA_RS07095		hypothetical protein
RHOLA_RS07100	Rhola_00009210	hypothetical protein
RHOLA_RS07105	Rhola_00009430	hypothetical protein
RHOLA_RS07110	Rhola_00010070	septum formation initiator family protein
RHOLA_RS07115	Rhola_00010360	hypothetical protein
RHOLA_RS07130	Rhola_00011650	hypothetical protein
RHOLA_RS07135	Rhola_00011780	hypothetical protein
RHOLA_RS07140	Rhola_00012000	DUF4190 domain-containing protein
RHOLA_RS07145	Rhola_00012730	DNA-binding response regulator
RHOLA_RS07150	Rhola_00012820	hypothetical protein
RHOLA_RS07160	Rhola_00013860	hypothetical protein
RHOLA_RS07165	Rhola_00013870	hypothetical protein
RHOLA_RS07180	Rhola_00001910	AURKAIP1/COX24 domain-containing protein
RHOLA_RS07185		hypothetical protein
RHOLA_RS07205	Rhola_00003070	hypothetical protein
RHOLA_RS07215	Rhola_00006330	hypothetical protein
RHOLA_RS07240	Rhola_00009840	hypothetical protein
RHOLA_RS07245		FmdB family transcriptional regulator
RHOLA_RS07250	Rhola_00010550	DUF3117 domain-containing protein
RHOLA_RS07260		hypothetical protein
RHOLA_RS07265		DUF2256 domain-containing protein
RHOLA_RS07270		DUF2200 domain-containing protein
RHOLA_RS07275		hypothetical protein

***R. lacicola* New Locus Tag**	***R. lacicola* Old Locus Tag**	**Annotation**
RHOLA_RS07290	Rhola_00001330	hypothetical protein
RHOLA_RS07305		membrane protein insertion efficiency factor YidD
RHOLA_RS07310	Rhola_00014070	ribonuclease P protein component
RHOLA_RS07005	Rhola_00001050	hypothetical protein:RHOLA
RHOLA_RS06320	Rhola_00012720	hypothetical protein:RHOLA
RHOLA_RS06280	Rhola_00012640	ATP-binding protein:RHOLA
RHOLA_RS06620	Rhola_00013340	gfo/Idh/MocA family oxidoreductase:RHOLA
RHOLA_RS06660	Rhola_00013420	gfo/Idh/MocA family oxidoreductase:RHOLA
RHOLA_RS01305	Rhola_00002620	EamA/RhaT family transporter:RHOLA
RHOLA_RS06330	Rhola_00012740	hypothetical protein:RHOLA
RHOLA_RS06675	Rhola_00013450	ABC transporter permease:RHOLA
RHOLA_RS00505	Rhola_00001010	gfo/Idh/MocA family oxidoreductase:RHOLA
RHOLA_RS00375	Rhola_00000750	EamA/RhaT family transporter:RHOLA
RHOLA_RS01475	Rhola_00002960	hypothetical protein:RHOLA
RHOLA_RS01710	Rhola_00003440	hypothetical protein:RHOLA
RHOLA_RS06285	Rhola_00012650	ATP-binding protein:RHOLA
RHOLA_RS06605	Rhola_00013310	ABC transporter permease:RHOLA
RHOLA_RS07000	Rhola_00000930	hypothetical protein:RHOLA
RHOLA_RS01700	Rhola_00003420	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase:RHOLA
RHOLA_RS07010	Rhola_00001080	hypothetical protein:RHOLA
RHOLA_RS07035	Rhola_00002520	hypothetical protein:RHOLA
RHOLA_RS07190		hypothetical protein:RHOLA
RHOLA_RS01220	Rhola_00002470	DNA-binding response regulator
RHOLA_RS06290	Rhola_00012660	DNA-binding response regulator
RHOLA_RS01500	Rhola_00003010	heavy metal translocating P-type ATPase
RHOLA_RS02175	Rhola_00004380	ABC transporter ATP-binding protein
RHOLA_RS03195	Rhola_00006430	amino acid ABC transporter ATP-binding protein
RHOLA_RS05805	Rhola_00011690	hypothetical protein
RHOLA_RS01875	Rhola_00003780	hypothetical protein
RHOLA_RS06600	Rhola_00013300	sugar ABC transporter ATP-binding protein
RHOLA_RS04890	Rhola_00009820	fructose-bisphosphatase class II family protein
RHOLA_RS06490	Rhola_00013070	DNA polymerase III subunit alpha
RHOLA_RS01745	Rhola_00003510	O-succinylhomoserine sulfhydrylase

Table A.4 The 420 genes unique to *A. photophilum* from *Aurantimicrobium* sp. strain MWH-UGA1, and *R. lacicola*.

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00030	Fic family protein
AURMO_00034	3-oxoacid CoA-transferase subunit A
AURMO_00035	3-oxoacid CoA-transferase subunit B
AURMO_00036	acetyl-CoA C-acetyltransferase
AURMO_00038	4-cresol dehydrogenase (hydroxylating)
AURMO_00039	hypothetical protein
AURMO_00040	alpha/beta hydrolase family protein DUF1100
AURMO_00041	3alpha(or 20beta)-hydroxysteroid dehydrogenase
AURMO_00042	lactoylglutathione lyase/glyoxylase I family protein
AURMO_00043	DNA-binding transcriptional repressor PuuR
AURMO_00044	2-polyprenyl-6-methoxyphenol hydroxylase-like FAD-dependent oxidoreductase
AURMO_00046	DHA1 family bicyclomycin/chloramphenicol resistance-like MFS transporter
AURMO_00047	catechol-2,3-dioxygenase
AURMO_00049	FAD/FMN-containing dehydrogenase
AURMO_00050	ribose 5-phosphate isomerase B
AURMO_00051	NADPH
AURMO_00052	monosaccharide ABC transporter substrate-binding protein (CUT2 family)
AURMO_00054	monosaccharide ABC transporter membrane protein (CUT2 family)
AURMO_00055	quinol monooxygenase YgiN
AURMO_00056	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase in catechol pathway
AURMO_00059	kynurenine formamidase
AURMO_00060	uncharacterized protein (TIGR02246 family)
AURMO_00068	hypothetical protein
AURMO_00069	hypothetical protein
AURMO_00070	hypothetical protein
AURMO_00071	hypothetical protein
AURMO_00072	hypothetical protein
AURMO_00075	HlyD family secretion protein
AURMO_00076	galactosyltransferase-like protein
AURMO_00077	hypothetical protein
AURMO_00078	glycosyltransferase involved in cell wall biosynthesis
AURMO_00079	Anp1 protein
AURMO_00080	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00091	hypothetical protein
AURMO_00096	hypothetical protein
AURMO_00135	hypothetical protein
AURMO_00139	TfoX/Sxy family transcriptional regulator of competence genes
AURMO_00148	Fic/DOC family protein
AURMO_00149	hypothetical protein
AURMO_00152	LuxR family two component transcriptional regulator
AURMO_00153	signal transduction histidine kinase
AURMO_00155	putative ABC transport system permease protein
AURMO_00159	hypothetical protein
AURMO_00161	signal transduction histidine kinase
AURMO_00162	uncharacterized protein DUF285
AURMO_00163	hypothetical protein
AURMO_00164	hypothetical protein
AURMO_00165	AbrB family transcriptional regulator
AURMO_00167	hypothetical protein
AURMO_00170	hypothetical protein
AURMO_00184	hypothetical protein
AURMO_00205	LSU ribosomal protein L30P
AURMO_00212	LSU ribosomal protein L36P
AURMO_00219	helix-turn-helix protein
AURMO_00231	uncharacterized protein DUF4190
AURMO_00233	uncharacterized protein DUF4190
AURMO_00236	hypothetical protein
AURMO_00240	hypothetical protein
AURMO_00252	excisionase family DNA binding protein
AURMO_00253	hypothetical protein
AURMO_00254	hypothetical protein
AURMO_00255	hypothetical protein
AURMO_00258	restriction endonuclease BglII
AURMO_00259	DNA (cytosine-5)-methyltransferase 1
AURMO_00260	hypothetical protein
AURMO_00261	hypothetical protein
AURMO_00262	PhoH-like protein
AURMO_00263	helicase-like protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00264	uncharacterized protein DUF1998
AURMO_00267	hypothetical protein
AURMO_00269	hypothetical protein
AURMO_00271	hypothetical protein
AURMO_00272	hypothetical protein
AURMO_00273	EndoU nuclease-like protein
AURMO_00274	hypothetical protein
AURMO_00277	hypothetical protein
AURMO_00278	hypothetical protein
AURMO_00280	hypothetical protein
AURMO_00284	hypothetical protein
AURMO_00286	predicted nucleic acid-binding protein
AURMO_00287	hypothetical protein
AURMO_00293	hypothetical protein
AURMO_00295	nucleotidyltransferase AbiEii toxin of type IV toxin-antitoxin system
AURMO_00296	putative AbiEi antitoxin of type IV toxin-antitoxin system
AURMO_00299	acetylornithine deacetylase
AURMO_00308	polysaccharide deacetylase
AURMO_00310	lipid II
AURMO_00313	hypothetical protein
AURMO_00318	uncharacterized protein DUF4244
AURMO_00319	hypothetical protein
AURMO_00320	secretion/DNA translocation related TadE-like protein
AURMO_00342	hypothetical protein
AURMO_00352	hypothetical protein
AURMO_00365	hypothetical protein
AURMO_00382	uncharacterized protein DUF3499
AURMO_00396	excisionase family DNA binding protein
AURMO_00408	mRNA-degrading endonuclease toxin of MazEF toxin-antitoxin module
AURMO_00409	hypothetical protein
AURMO_00410	uncharacterized protein DUF3467
AURMO_00419	DNA-binding XRE family transcriptional regulator
AURMO_00422	dTDP-4-dehydrorhamnose 3,5-epimerase
AURMO_00430	peptidoglycan/LPS O-acetylase OafA/YrhL
AURMO_00432	glycosyl transferase family 2

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00433	hypothetical protein
AURMO_00437	glycosyltransferase involved in cell wall biosynthesis
AURMO_00439	glycosyl transferase family 2
AURMO_00440	predicted dehydrogenase
AURMO_00442	succinyltransferase-like protein
AURMO_00444	hypothetical protein
AURMO_00446	ABC-2 type transport system permease protein
AURMO_00464	AAA ATPase-like protein
AURMO_00471	Fic family protein
AURMO_00473	ATP synthase F0 subcomplex C subunit
AURMO_00479	ATP synthase F1 subcomplex epsilon subunit
AURMO_00481	transcriptional regulator with XRE-family HTH domain
AURMO_00485	hypothetical protein
AURMO_00494	hypothetical protein
AURMO_00505	hypothetical protein
AURMO_00525	hypothetical protein
AURMO_00528	hypothetical protein
AURMO_00536	hypothetical protein
AURMO_00538	hypothetical protein
AURMO_00555	cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein
AURMO_00556	cytochrome bd-I ubiquinol oxidase subunit 2 apoprotein
AURMO_00557	ATP-binding cassette subfamily C protein CydD
AURMO_00590	2-phosphosulfolactate phosphatase
AURMO_00610	raffinose/stachyose/melibiose transport system substrate-binding protein
AURMO_00618	hypothetical protein
AURMO_00621	hypothetical protein
AURMO_00628	hypothetical protein
AURMO_00639	hypothetical protein
AURMO_00640	hypothetical protein
AURMO_00666	preprotein translocase subunit SecG
AURMO_00697	branched-subunit amino acid transport protein AzlD
AURMO_00702	hypothetical protein
AURMO_00703	hypothetical protein
AURMO_00704	bifunctional DNA primase/polymerase-like protein
AURMO_00705	P4 family phage/plasmid primase-like protien

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00706	hypothetical protein
AURMO_00707	hypothetical protein
AURMO_00708	hypothetical protein
AURMO_00709	hypothetical protein
AURMO_00710	uncharacterized protein DUF4352
AURMO_00711	DNA invertase Pin-like site-specific DNA recombinase
AURMO_00712	reverse transcriptase (RNA-dependent DNA polymerase)
AURMO_00713	site-specific recombinase XerD
AURMO_00714	chitinase
AURMO_00728	hypothetical protein
AURMO_00734	hypothetical protein
AURMO_00789	hypothetical protein
AURMO_00794	hypothetical protein
AURMO_00846	uncharacterized membrane protein HdeD (DUF308 family)
AURMO_00847	glycine/D-amino acid oxidase-like deaminating enzyme
AURMO_00848	hypothetical protein
AURMO_00858	hypothetical protein
AURMO_00872	sec-independent protein translocase protein TatA
AURMO_00908	SSU ribosomal protein S20P
AURMO_00914	DNA-binding FrmR family transcriptional regulator
AURMO_00921	ribose 5-phosphate isomerase B
AURMO_00926	hypothetical protein
AURMO_00940	hypothetical protein
AURMO_00941	TM2 domain-containing protein
AURMO_00961	LPXTG-motif cell wall-anchored protein
AURMO_00965	3-oxoacyl-[acyl-carrier protein] reductase
AURMO_00967	hypothetical protein
AURMO_00992	hypothetical protein
AURMO_01016	mRNA interferase MazF
AURMO_01017	hypothetical protein
AURMO_01020	large subunit ribosomal protein L35
AURMO_01035	hypothetical protein
AURMO_01038	hypothetical protein
AURMO_01040	alkylmercury lyase-like protein
AURMO_01042	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01043	hypothetical protein
AURMO_01046	gamma-glutamylcyclotransferase (GGCT)/AIG2-like uncharacterized protein YtfP
AURMO_01052	hypothetical protein
AURMO_01066	hypothetical protein
AURMO_01071	hypothetical protein
AURMO_01078	hypothetical protein
AURMO_01085	hypothetical protein
AURMO_01089	DNA polymerase-3 subunit epsilon
AURMO_01109	hypothetical protein
AURMO_01122	hypothetical protein
AURMO_01126	hypothetical protein
AURMO_01156	mRNA-degrading endonuclease RelE of RelBE toxin-antitoxin system
AURMO_01157	prevent-host-death family protein
AURMO_01160	LSU ribosomal protein L32P
AURMO_01162	peptidoglycan/LPS O-acetylase OafA/YrhL
AURMO_01177	D-amino-acid
AURMO_01178	uncharacterized protein DUF3107
AURMO_01185	uncharacterized membrane protein
AURMO_01196	helix-turn-helix protein
AURMO_01199	uncharacterized protein DUF3117
AURMO_01203	CshA-type fibril repeat protein
AURMO_01204	hypothetical protein
AURMO_01206	hypothetical protein
AURMO_01210	hypothetical protein
AURMO_01217	hypothetical protein
AURMO_01218	uncharacterized protein with HEPN domain
AURMO_01228	polyketide cyclase/dehydrase/lipid transport protein
AURMO_01230	putative MATE family efflux protein
AURMO_01232	uncharacterized protein DUF4287
AURMO_01235	hypothetical protein
AURMO_01240	addiction module HigA family antidote
AURMO_01243	hypothetical protein
AURMO_01259	exodeoxyribonuclease VII small subunit
AURMO_01275	uncharacterized protein with HEPN domain
AURMO_01276	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01280	PadR family transcriptional regulator
AURMO_01281	vanillate demethylase subunit A
AURMO_01282	vanillate demethylase subunit B
AURMO_01283	MarR family transcriptional regulator
AURMO_01285	transketolase subunit A
AURMO_01286	transketolase
AURMO_01289	ribose transport system permease protein
AURMO_01290	monosaccharide ABC transporter substrate-binding protein (CUT2 family)
AURMO_01292	D-tagatose 3-epimerase
AURMO_01293	6-phosphofructokinase
AURMO_01294	muconolactone D-isomerase
AURMO_01295	protocatechuate 4,5-dioxygenase alpha subunit
AURMO_01297	alpha/beta hydrolase family protein
AURMO_01310	hypothetical protein
AURMO_01316	Fic family protein
AURMO_01319	hypothetical protein
AURMO_01327	prevent-host-death family protein
AURMO_01328	mRNA-degrading endonuclease RelE of RelBE toxin-antitoxin system
AURMO_01354	hypothetical protein
AURMO_01355	AbrB family looped-hinge helix DNA binding protein
AURMO_01356	PIN domain nuclease of toxin-antitoxin system
AURMO_01357	hypothetical protein
AURMO_01358	hypothetical protein
AURMO_01364	hypothetical protein
AURMO_01365	EndoU nuclease-like protein
AURMO_01369	homocysteine S-methyltransferase
AURMO_01370	hypothetical protein
AURMO_01371	uncharacterized protein (DUF305 family)
AURMO_01373	AhpD family alkylhydroperoxidase
AURMO_01374	DNA-binding FrmR family transcriptional regulator
AURMO_01376	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin reductase subunit
AURMO_01377	homocysteine S-methyltransferase
AURMO_01380	LPXTG-motif cell wall-anchored protein
AURMO_01382	hypothetical protein
AURMO_01389	LPXTG-site transpeptidase (sortase) family protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01390	hypothetical protein
AURMO_01391	dihydroorotate dehydrogenase (fumarate)
AURMO_01392	hypothetical protein
AURMO_01393	hypothetical protein
AURMO_01394	hypothetical protein
AURMO_01395	hypothetical protein
AURMO_01396	uncharacterized protein DUF4333
AURMO_01397	phosphate ABC transporter substrate-binding protein (PhoT family)
AURMO_01404	hypothetical protein
AURMO_01407	hypothetical protein
AURMO_01408	hypothetical protein
AURMO_01409	cobalt-zinc-cadmium efflux system protein
AURMO_01410	cation efflux family protein
AURMO_01411	ArsR family transcriptional regulator
AURMO_01412	hypothetical protein
AURMO_01413	abortive infection Abi-like protein
AURMO_01414	hypothetical protein
AURMO_01417	cell wall-associated NlpC family hydrolase
AURMO_01422	hypothetical protein
AURMO_01430	putative cold-shock DNA-binding protein
AURMO_01432	uncharacterized protein DUF3263
AURMO_01443	hypothetical protein
AURMO_01448	hypothetical protein
AURMO_01450	hypothetical protein
AURMO_01451	uncharacterized repeat protein (TIGR02543 family)
AURMO_01453	signal transduction histidine kinase
AURMO_01454	hypothetical protein
AURMO_01458	hypothetical protein
AURMO_01459	poly-gamma-glutamate synthesis protein (capsule biosynthesis protein)
AURMO_01467	hypothetical protein
AURMO_01468	hypothetical protein
AURMO_01476	preprotein translocase subunit SecE
AURMO_01485	hypothetical protein
AURMO_01486	TIR-like protein DUF1863
AURMO_01487	lactococcin 972 family bacteriocin

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01488	hypothetical protein
AURMO_01489	hypothetical protein
AURMO_01490	putative ABC transport system ATP-binding protein
AURMO_01491	hypothetical protein
AURMO_01492	uncharacterized protein DUF3800
AURMO_01493	2Fe-2S ferredoxin
AURMO_01496	ferredoxin
AURMO_01503	GMP synthase (glutamine-hydrolysing)
AURMO_01511	hypothetical protein
AURMO_01513	hypothetical protein
AURMO_01522	DoxX-like protein
AURMO_01571	peptidase M23-like protein
AURMO_01574	HEPN domain-containing protein
AURMO_01576	fusaric acid resistance family protein
AURMO_01579	uncharacterized repeat protein (TIGR02543 family)
AURMO_01583	uncharacterized membrane protein
AURMO_01584	DNA-binding Lrp family transcriptional regulator
AURMO_01587	death-on-curing protein
AURMO_01588	hypothetical protein
AURMO_01590	uncharacterized protein DUF1905
AURMO_01606	hypothetical protein
AURMO_01607	hypothetical protein
AURMO_01610	copper ion binding protein
AURMO_01615	hypothetical protein
AURMO_01627	hypothetical protein
AURMO_01629	chorismate mutase
AURMO_01639	camphor resistance protein CrcB
AURMO_01640	hypothetical protein
AURMO_01644	hypothetical protein
AURMO_01650	phospholipase D-like protein
AURMO_01651	uncharacterized protein DUF4229
AURMO_01662	glutaredoxin
AURMO_01663	putative oligomerization/nucleic acid binding protein
AURMO_01665	glutaredoxin-like protein DUF836
AURMO_01678	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01682	GT2 family glycosyltransferase
AURMO_01685	transglutaminase superfamily protein
AURMO_01697	uncharacterized protein DUF3800
AURMO_01701	hypothetical protein
AURMO_01708	helix-turn-helix protein
AURMO_01709	hypothetical protein
AURMO_01717	predicted nucleic acid-binding protein
AURMO_01718	prevent-host-death family protein
AURMO_01726	LSU ribosomal protein L33P
AURMO_01728	Fic/DOC family protein
AURMO_01736	uncharacterized protein DUF3618
AURMO_01748	hypothetical protein
AURMO_01749	hypothetical protein
AURMO_01753	EndoU nuclease-like protein
AURMO_01754	hypothetical protein
AURMO_01756	ferredoxin-NADP reductase
AURMO_01757	thiamine biosynthesis lipoprotein
AURMO_01758	hypothetical protein
AURMO_01759	hypothetical protein
AURMO_01761	signal transduction histidine kinase
AURMO_01770	hypothetical protein
AURMO_01777	lipid II glycine glycyltransferase (peptidoglycan interpeptide bridge formation enzyme)
AURMO_01778	uncharacterized protein with HEPN domain
AURMO_01779	hypothetical protein
AURMO_01780	bacteriocin resistance YdeI/OmpD-like protein
AURMO_01782	fibronectin type III domain protein
AURMO_01783	hypothetical protein
AURMO_01054	carbohydrate ABC transporter membrane protein 1 (CUT1 family)
AURMO_01695	adenine-specific methyltransferase EcoRI-like protein
AURMO_01752	helix-turn-helix protein
AURMO_00438	hypothetical protein
AURMO_00612	raffinose/stachyose/melibiose transport system permease protein
AURMO_01296	protocatechuate 4,5-dioxygenase beta subunit
AURMO_01578	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01683	hypothetical protein
AURMO_01287	(R,R)-butanediol dehydrogenase/meso-butanediol dehydrogenase/diacetyl reductase/L-iditol 2-dehydrogenase
AURMO_00290	FtsP/CotA-like multicopper oxidase with cupredoxin domain
AURMO_00611	raffinose/stachyose/melibiose transport system permease protein
AURMO_00441	dTDP-4-amino-4,6-dideoxygalactose transaminase
AURMO_00121	transposase-like protein
AURMO_00168	hypothetical protein
AURMO_01696	helix-turn-helix protein
AURMO_00450	hypothetical protein
AURMO_00436	hypothetical protein
AURMO_00972	MFS transporter
AURMO_01694	HNH endonuclease
AURMO_01750	HNH endonuclease
AURMO_00735	transposase IS481 family protein
AURMO_00045	DNA-binding transcriptional LysR family regulator
AURMO_00331	transposase InsO family protein
AURMO_01784	hypothetical protein
AURMO_00669	transposase IS481 family protein
AURMO_00058	DNA-binding transcriptional LysR family regulator
AURMO_00435	glycosyltransferase involved in cell wall biosynthesis
AURMO_01266	transposase-like protein
AURMO_01462	transposase IS481 family protein
AURMO_01053	raffinose/stachyose/melibiose transport system permease protein
AURMO_01075	helix-turn-helix protein
AURMO_01120	uncharacterized membrane protein YhaH (DUF805 family)
AURMO_01751	adenine-specific methyltransferase EcoRI-like protein
AURMO_00449	transposase
AURMO_01573	hypothetical protein
AURMO_00428	IS30 family transposase
AURMO_00751	IS30 family transposase
AURMO_01041	IS30 family transposase
AURMO_01591	IS30 family transposase
AURMO_00335	hypothetical protein
AURMO_00718	hypothetical protein

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_00942	transposase-like protein
AURMO_01001	hypothetical protein
AURMO_01233	transposase-like protein
AURMO_01533	transposase-like protein
AURMO_01291	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)
AURMO_00048	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)
AURMO_00037	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)
AURMO_01399	phosphate transport system permease protein
AURMO_00166	ATP-dependent RNA helicase CsdA
AURMO_01398	phosphate ABC transporter membrane protein 2 (PhoT family)
AURMO_00122	transposase InsO family protein
AURMO_00334	transposase InsO family protein
AURMO_00719	transposase InsO family protein
AURMO_00943	transposase InsO family protein
AURMO_01000	transposase InsO family protein
AURMO_01074	putative transposase
AURMO_01234	transposase InsO family protein
AURMO_01265	putative transposase
AURMO_01534	transposase InsO family protein
AURMO_00232	4-aminobutyrate aminotransferase-like enzyme
AURMO_00279	EndoU nuclease-like protein
AURMO_00270	hypothetical protein
AURMO_00158	LuxR family two component transcriptional regulator
AURMO_00160	DNA-binding NarL/FixJ family response regulator
AURMO_00291	Cu2+-exporting ATPase
AURMO_01760	DNA-binding response OmpR family regulator
AURMO_00073	ABC-type bacteriocin/lantibiotic exporter with double-glycine peptidase domain
AURMO_00074	NHLM bacteriocin system ABC transporter peptidase/ATP-binding protein
AURMO_00434	ABC-type bacteriocin/lantibiotic exporter with double-glycine peptidase domain
AURMO_00558	ATP-binding cassette subfamily C protein CydC
AURMO_01400	serine/threonine-protein kinase
AURMO_00154	putative ABC transport system ATP-binding protein
AURMO_01388	phosphate ABC transporter ATP-binding protein (PhoT family)
AURMO_00057	succinate-semialdehyde dehydrogenase/glutarate-semialdehyde dehydrogenase
AURMO_01279	benzaldehyde dehydrogenase (NAD+)

***A. photophilum* Locus Tag**	**Annotation**
AURMO_00002	LSU ribosomal protein L34P
AURMO_00018	SSU ribosomal protein S18P
AURMO_00024	hypothetical protein
AURMO_01284	acyl-CoA reductase-like NAD-dependent aldehyde dehydrogenase

Table A.5 *R. lacicola* genes shared with *A. photophilum*, *Aurantimicrobium* sp. strain MWH-Uga1, and not shared with *Microbacterium* sp. strain 10M-3C3. Genes in each row are best reciprocal BLAST hits. Expression data was obtained from previous transcriptome studies (Maresca et al., 2019). An "L" in the expression data columns indicates significantly higher expression in light vs dark. A "D" in the expression data columns indicates significantly higher expression in dark vs light. An "N/A" in the expression data columns indicates no significant differential expression in light vs dark. A difference between light and dark is significant if the q-value (false discovery rate adjusted p-value) was <0.05. Seventy-one genes are shared by *R. lacicola* and *A. photophilum* and are not found in *Microbacterium* sp. strain 10M-3C3.

***A. photophilum* Locus Tag**	***A. photophilum* Annotation**	**Expression in Light vs. Dark**	***R. lacicola* Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00885	glycosyltransferase involved in cell wall biosynthesis	D	Rhola_00008110	Glycosyltransferase involved in cell wall bisynthesis	F:molecular_function	N/A
AURMO_00010	D-alanine-D-alanine ligase	N/A	Rhola_00014000	D-alanine-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell wall organization or biogenesis	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00523	IclR family transcriptional regulator	D	Rhola_00000310	transcriptional regulator, IclR family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	N/A
AURMO_01565	MarR family protein	L	Rhola_00002220	Winged helix-turn-helix DNA-binding	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	N/A
AURMO_01192	AsnC family transcriptional regulator	L	Rhola_00004340	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	L
AURMO_00726	peroxiredoxin	D	Rhola_00006540	Peroxiredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process	D

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00011	DNA-binding transcriptional MocR family regulator	D	Rhola_00013990	DNA-binding transcriptional regulator, MocR family, contains an aminotransferase domain	F:DNA binding; P:biosynthetic process; F:ion binding	N/A
AURMO_00504	VIT1/CCC1 family predicted Fe2+/Mn2+ transporter	L	Rhola_00002410	Predicted Fe2+/Mn2+ transporter, VIT1/CCC1 family	C:cell; F:transmembrane transporter activity; P:homeostatic process	N/A
AURMO_00966	drug/metabolite transporter (DMT)-like permease	N/A	Rhola_00002610	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	N/A
AURMO_01600	glycerol uptake facilitator-like aquaporin	D	Rhola_00002740	Glycerol uptake facilitator (Major Intrinsic Protein Family)	C:cellular_component; F:transmembrane transporter activity	N/A
AURMO_00850	fucose permease	N/A	Rhola_00003100	Predicted arabinose efflux permease, MFS family	C:cellular_component; P:transmembrane transport	L
AURMO_01635	drug/metabolite transporter (DMT)-like permease	L	Rhola_00003560	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	N/A
AURMO_00186	SulP family sulfate permease	L	Rhola_00004690	sulfate permease, SulP family	C:cellular_component; F:transmembrane transporter activity	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_01059	small conductance mechanosensitive channel	L	Rhola_00005700	small conductance mechanosensitive channel	C:cellular_component; P:transmembrane transport	N/A
AURMO_00601	potassium/proton antiporter membrane subunit (CPA2 family)	L	Rhola_00005720	monovalent cation H+ antiporter-2, CPA2 family	C:cellular_component; F:transmembrane transporter activity	N/A
AURMO_01325	nitrate/nitrite transporter NarK	D	Rhola_00009420	Sugar phosphate permease	C:cellular_component; P:transmembrane transport	N/A
AURMO_01670	cation diffusion facilitator family transporter	N/A	Rhola_00012550	cation diffusion facilitator family transporter	C:cellular_component; F:transmembrane transporter activity	N/A
AURMO_00349	PTS system fructose-specific IIA component	L	Rhola_00012910	PTS system, fructose-specific IIA component	C:cellular_component; F:kinase activity; F:transmembrane transporter activity	L
AURMO_01323	heat shock protein	D	Rhola_00010010	heat shock protein HtpX	C:plasma membrane; F:peptidase activity; F:ion binding	D
AURMO_00519	formiminoglutamase	L	Rhola_00000270	formiminoglutamase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	N/A

***A. photophilum* Locus Tag**	***A. photophilum* Annotation**	**Expression in Light vs. Dark**	***R. lacicola* Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_01469	predicted ferric reductase	D	Rhola_00000530	Predicted ferric reductase	C:cellular_component; F:oxidoreductase activity	D
AURMO_01311	citrate lyase subunit beta/citryl-CoA lyase	N/A	Rhola_00000740	citrate lyase subunit beta / citryl-CoA lyase	F:lyase activity; F:ion binding	N/A
AURMO_00099	carboxymethylenebutenolidase	N/A	Rhola_00000940	carboxymethylenebutenolidase	F:molecular_function	N/A
AURMO_00915	NADPH-dependent 2,4-dienoyl-CoA reductase/sulfur reductase-like enzyme	D	Rhola_00001300	NADPH-dependent 2,4-dienoyl-CoA reductase, sulfur reductase	C:cell; F:oxidoreductase activity; P:homeostatic process; F:ion binding	N/A
AURMO_00369	dolichol-phosphate mannosyltransferase	D	Rhola_00001450	dolichol-phosphate mannosyltransferase	P:biological_process; F:transferase activity, transferring glycosyl groups	N/A
AURMO_01346	fructokinase	N/A	Rhola_00002430	fructokinase	P:carbohydrate metabolic process; F:kinase activity	N/A
AURMO_00114	oxygen-dependent protoporphyrinogen oxidase	D	Rhola_00002910	oxygen-dependent protoporphyrinogen oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00616	competence/ damage-inducible protein cinA	L	Rhola_00004740	nicotinamide-nucleotide amidase	0	N/A
AURMO_01236	short-subunit dehydrogenase	L	Rhola_00005520	Short-chain dehydrogenase	F:oxidoreductase activity	N/A
AURMO_01068	peptide-methionine (S)-S-oxide reductase	N/A	Rhola_00005630	peptide-methionine (S)-S-oxide reductase	P:cellular protein modification process; F:oxidoreductase activity	N/A
AURMO_00694	phosphoglycerate dehydrogenase-like enzyme	L	Rhola_00006310	Phosphoglycerate dehydrogenase	F:molecular_function; P:biological_process	N/A
AURMO_00721	acyl carrier protein	L	Rhola_00006490	acyl carrier protein	F:molecular_function; C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; P:small molecule metabolic process	N/A
AURMO_00731	ribonuclease HI	N/A	Rhola_00006590	probable phosphoglycerate mutase	F:nuclease activity; F:isomerase activity	L

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00736	ketopantoate hydroxymethyltransferase	L	Rhola_00006640	ketopantoate hydroxymethyltransferase	C:cytoplasm; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00737	NAD+ synthase (glutamine-hydrolysing)	L	Rhola_00006660	NAD+ synthase (glutamine-hydrolysing)	C:cytoplasm; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	N/A
AURMO_00791	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	L	Rhola_00007220	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	C:cellular_component; P:cellular protein modification process; F:isomerase activity	N/A
AURMO_00802	3-dehydroquinate dehydratase	L	Rhola_00007340	3-dehydroquinate dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00100	methionine synthase (B12-dependent)	L	Rhola_00008090	methionine synthase (B12-dependent)	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:methyltransferase activity; P:biosynthetic process; F:ion binding	L
AURMO_01550	1-phosphofructokinase	N/A	Rhola_00009810	1-phosphofructokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding	N/A
AURMO_01700	putative lumazine-binding protein	N/A	Rhola_00009930	Putative lumazine-binding	0	N/A
AURMO_00383	phosphomannomutase	N/A	Rhola_00011180	phosphomannomutase	P:carbohydrate metabolic process; F:isomerase activity	D
AURMO_01693	nitroreductase	D	Rhola_00012620	Nitroreductase	F:oxidoreductase activity	D

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_01386	pyridoxamine 5'-phosphate oxidase	L	Rhola_00013090	Pyridoxamine 5'-phosphate oxidase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	L
AURMO_00540	3-methyladenine DNA glycosylase AlkD	N/A	Rhola_00013550	3-methyladenine DNA glycosylase AlkD	0	N/A
AURMO_00384	adenosylhomocysteinase	N/A	Rhola_00011170	adenosylhomocysteinase	F:molecular_function; C:cytoplasm; P:small molecule metabolic process	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_01167	cyclic-di-GMP-binding biofilm dispersal mediator protein	L	Rhola_00003520	cyclic-di-GMP-binding biofilm dispersal mediator protein	P:biosynthetic process; F:oxidoreductase activity; P:secondary metabolic process; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	N/A
AURMO_01484	agmatine deiminase	N/A	Rhola_00005580	agmatine deiminase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process	N/A
AURMO_00911	competence protein ComEA	D	Rhola_00006080	competence protein ComEA	F:DNA binding; C:cellular_component; P:DNA metabolic process; P:response to stress	N/A

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_00783	Holliday junction DNA helicase subunit RuvA	D	Rhola_00007150	Holliday junction DNA helicase subunit RuvA	F:DNA binding; F:helicase activity; C:intracellular; P:DNA metabolic process; P:response to stress; C:protein-containing complex; F:ion binding; P:chromosome organization	N/A
AURMO_01605	hypothetical protein	L	Rhola_00008300	Uncharacterized membrane protein YczE	C:cellular_component	L
AURMO_01734	UPF0176 protein	L	Rhola_00000470	UPF0176 protein	F:molecular_function	N/A
AURMO_01608	uncharacterized protein (DUF305 family)	D	Rhola_00001370	Uncharacterized conserved protein, DUF305 family	0	D
AURMO_01567	hypothetical protein	D	Rhola_00002200	hypothetical protein	C:cellular_component	D
AURMO_00282	hypothetical protein	L	Rhola_00002720	hypothetical protein	0	L
AURMO_00288	hypothetical protein	L	Rhola_00002770	hypothetical protein	F:oxidoreductase activity; F:lyase activity	L
AURMO_00517	metallo-beta-lactamase family protein	L	Rhola_00003400	metallo-beta-lactamase family protein	F:nuclease activity	L
AURMO_01115	predicted Zn-dependent peptidase	N/A	Rhola_00004630	Predicted Zn-dependent peptidase	F:peptidase activity; F:ion binding	D

A. photophilum **Locus Tag**	***A. photophilum*** **Annotation**	**Expression in Light vs. Dark**	***R. lacicola*** **Locus Tag**	**Annotation**	**GO-slim Terms**	**Expression in Light vs Dark**
AURMO_01097	hypothetical protein	N/A	Rhola_00005330	hypothetical protein	C:cellular_component	N/A
AURMO_00173	hypothetical protein	L	Rhola_00005410	DivIVA domain-containing protein	0	D
AURMO_00729	dinuclear metal center YbgI/SA1388 family protein	N/A	Rhola_00006570	dinuclear metal center protein, YbgI/SA1388 family	0	L
AURMO_01237	uncharacterized protein YndB with AHSA1/START domain	L	Rhola_00009770	Uncharacterized conserved protein YndB, AHSA1/START domain	0	N/A
AURMO_00380	hypothetical protein	N/A	Rhola_00011200	hypothetical protein	0	N/A
AURMO_01512	hypothetical protein	N/A	Rhola_00011820	hypothetical protein	C:cellular_component	L
AURMO_01164	membrane-associated protein	N/A	Rhola_00012610	membrane-associated protein	C:cellular_component	D
AURMO_00689	hypothetical protein	D	Rhola_00012770	hypothetical protein	0	D
AURMO_00097	FAR-17a/AIG1-like protein	L	Rhola_00012990	FAR-17a/AIG1-like protein.	C:cellular_component	N/A
AURMO_00916	probable LLM family oxidoreductase	D	Rhola_00013000	probable oxidoreductase, LLM family	F:oxidoreductase activity	D
AURMO_00169	uncharacterized protein DUF2834	L	Rhola_00013660	Protein of unknown function (DUF2834)	C:cellular_component	N/A
#N/A	#N/A	#N/A	RHOLA_RS02800	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	RHOLA_RS05360	#N/A	#N/A	#N/A
#N/A	#N/A	#N/A	RHOLA_RS06365	#N/A	#N/A	#N/A

Table A.6 Sequencing read data for *R. lacicola* MWH-Ta8 light/dark cycling transcriptomics. 28 (7 timepoints x 4 replicates per time point) *R. lacicola* cDNA samples were sequenced using Illumina HiSeq system, paired-end 150-nt reads. Samples for the first timepoint were taken 5 minutes before the light turned on (-0.083 hours). Raw data is available in the Joint Genome Institute Integrated Microbial Genomes & Microbiomes (JGI IMG/M) database, under the sequencing project ID: 1167272.

Library Name	Sample Name	Sample ID	Sampling Time (Hours through the light/dark cycle)	Sampling Time (Light or Dark)	Sample Information Merged: L/D_timepoint_replicate	Raw Reads	Quality Filtered Reads	Total Fragments	Mapped Fragments	Fragments Assigned	Sequencer Type	Run Type	Included in Analyses
CNCCP	TA2	164192	1	Light	L_t2_1	18305388	13215036	6607518	6593343	4605617	HiSeq-2500	2x151	TRUE
CNCCS	TA3	164193	6	Light	L_t3_1	26766940	25944606	12972303	12951354	9584260	HiSeq-2500	2x151	TRUE
CNCCO	TA1	164191	0.25	Light	L_t1_1	22389602	15095248	7547624	7536952	5061167	HiSeq-2500	2x151	TRUE
CNCCY	TB1	164198	0.25	Light	L_t1_2	26358156	25660486	12830243	12806494	9971779	HiSeq-2500	2x151	TRUE
CNCGZ	TE3	164214	6	Light	L_t3_4	29571520	28570290	14285145	14254501	10844603	HiSeq-2500	2x151	TRUE
CNCGP	TC3	164207	6	Light	L_t3_3	25834684	22888236	11444118	11424570	8431733	HiSeq-2500	2x151	TRUE
CNCGT	TC5	164209	13	Dark	D_t5_3	27266694	26811324	13405662	13379157	9424970	HiSeq-2500	2x151	TRUE
CNCGG	TB6	164203	18	Dark	D_t6_2	34132688	33300442	16650221	16614066	12174032	HiSeq-2500	2x151	TRUE
CNCGN	TC1	164205	0.25	Light	L_t1_3	29222570	28618930	14309465	14286347	10948437	HiSeq-2500	2x151	TRUE
CNCCZ	TB2	164199	1	Light	L_t2_2	27397090	26873462	13436731	13411620	10428197	HiSeq-2500	2x151	TRUE
CNCGB	TB4	164201	12.25	Dark	D_t4_2	26065142	25309850	12654925	12619764	9433435	HiSeq-2500	2x151	TRUE
CNCGW	TE0	164211	-0.083	Dark	D_t0_4	27317786	21751614	10875807	10856481	7702326	HiSeq-2500	2x151	TRUE
CNCGY	TE2	164213	1	Light	L_t2_4	30611354	29172936	14586468	14559591	11156273	HiSeq-2500	2x151	TRUE
CNCCW	TA6	164196	18	Dark	D_t6_1	22480946	22074178	11037089	11012706	7572895	HiSeq-2500	2x151	TRUE
CNCCT	TA4	164194	12.25	Dark	D_t4_1	22029072	17926160	8963080	8944629	6010229	HiSeq-2500	2x151	TRUE
CNCCU	TA5	164195	13	Dark	D_t5_1	31711192	22609548	11304774	11283965	7408740	HiSeq-2500	2x151	TRUE
CNCHA	TE4	164215	12.25	Dark	D_t4_4	27879686	26344776	13172388	13150369	9501977	HiSeq-2500	2x151	TRUE

Library Name	Sample Name	Sample ID	Sampling Time (Hours through the light/dark cycle)	Sampling Time (Light or Dark)	Sample Information Merged: L/D_timepoint_replicate	Raw Reads	Quality Filtered Reads	Total Fragments	Mapped Fragments	Fragments Assigned	Sequencer Type	Run Type	Included in Analyses
CNCGA	TB3	164200	6	Light	L_t3_2	22609206	22033054	11016527	10998844	8502997	HiSeq-2500	2x151	TRUE
CNCGO	TC2	164206	1	Light	L_t2_3	26604414	26192760	13096380	13074105	9912435	HiSeq-2500	2x151	TRUE
CNCGH	TC0	164204	-0.083	Dark	D_t0_3	22253810	13713748	6856874	6843932	4488560	HiSeq-2500	2x151	TRUE
CNCGC	TB5	164202	13	Dark	D_t5_2	23923346	23282512	11641256	11622112	8635362	HiSeq-2500	2x151	TRUE
CNCCX	TB0	164197	-0.083	Dark	D_t0_2	28763274	28359188	14179594	14155827	10756517	HiSeq-2500	2x151	TRUE
CNCGX	TE1	164212	0.25	Light	L_t1_4	22070972	21286004	10643002	10626523	8060791	HiSeq-2500	2x151	TRUE
CNCGU	TC6	164210	18	Dark	D_t6_3	18851292	16936264	8468132	8451437	5765649	HiSeq-2500	2x151	TRUE
CNCCN	TA0	164190	-0.083	Dark	D_t0_1	29105796	24837234	12418617	12325541	9094328	HiSeq-2500	2x151	TRUE
CNCGS	TC4	164208	12.25	Dark	D_t4_3	20904052	20108880	10054440	10033420	7201735	HiSeq-2500	2x151	TRUE
CNCHC	TE6	164217	18	Dark	D_t6_4	27718458	24787786	12393893	12368037	8479221	HiSeq-2500	2x151	TRUE
CNCHB	TE5	164216	13	Dark	D_t5_4	20644748	20277952	10138976	10119191	7342560	HiSeq-2500	2x151	TRUE

Table A.7 Sequencing read data for *A. photophilum* MWH-Mo1 light/dark cycling transcriptomics. 28 (7 timepoints x 4 replicates per time point) *A. photophilum* cDNA samples were sequenced using Illumina HiSeq system, paired-end 150-nt reads. Samples for the first timepoint were taken 5 minutes before the light turned on (-0.083 hours). Raw data is available in the Joint Genome Institute Integrated Microbial Genomes & Microbiomes (JGI IMG/M) database, under the sequencing project ID: 1167273. Four samples (MX0, MX1, MZ5, MX2) were removed from the final deliverable of the sequencing project by JGI due to low similarity to their replates. Four samples (MX4, MX6, MX3, MX5) were not included in downstream analyses due to low similarity to their replicates as determined via principal component analysis.

Library Name	Sample Name	Sample ID	Sampling Time (Hours through the light/dark cycle)	Sampling Time (Light or Dark)	Sample Information Merged: L/D_timepoint_replicate	Raw Reads	Quality Filtered Reads	Total Fragments	Mapped Fragments	Fragments Assigned to Genes	Sequencer Type	Run Type	Included in Analyses
CNCHZ	MX4	164229	12.25	Dark	#N/A	23537238	20802236	10401118	10340229	7899323	HiSeq-2500 1TB	2x151	Removed due to PCA
CNCNG	MY1	164233	0.25	Light	L_t1_2	23912892	13028218	6514109	6421477	4543488	HiSeq-2500 1TB	2x151	TRUE
CNCNB	MX6	164231	18	Dark	#N/A	23933930	17702182	8851091	8799518	6284869	HiSeq-2500 1TB	2x151	Removed due to PCA
CNCHY	MX3	164228	6	Light	#N/A	16938524	14419956	7209978	7173573	5603342	HiSeq-2500 1TB	2x151	Removed due to PCA
CNCNA	MX5	164230	13	Dark	#N/A	20080288	17891404	8945702	8892119	6918037	HiSeq-2500 1TB	2x151	Removed due to PCA
CNCNW	MZ2	164241	1	Light	L_t2_3	34160484	32336932	16168466	15523899	12059277	HiSeq-2500 1TB	2x151	TRUE
CNCNT	MZ0	164239	-0.083	Dark	D_t0_3	23222224	19360406	9680203	9234710	6956202	HiSeq-2500 1TB	2x151	TRUE
CNCOA	MZ6	164245	18	Dark	D_t6_3	27827978	23707242	11853621	11474394	8379342	HiSeq-2500 1TB	2x151	TRUE
CNCNY	MZ4	164243	12.25	Dark	D_t4_3	24820842	22949684	11474842	10807434	7659269	HiSeq-2500 1TB	2x151	TRUE
CNCHG	MW0	164218	-0.083	Dark	D_t0_1	19213060	17634596	8817298	8729598	6865874	HiSeq-2500 1TB	2x151	TRUE
CNCNP	MY5	164237	13	Dark	D_t5_2	31018470	28270838	14135419	13735237	10393556	HiSeq-2500 1TB	2x151	TRUE

Library Name	Sample Name	Sample ID	Sampling Time (Hours through the light/dark cycle)	Sampling Time (Light or Dark)	Sample Information Merged: L/D_timepoint_replicate	Raw Reads	Quality Filtered Reads	Total Fragments	Mapped Fragments	Fragments Assigned to Genes	Sequencer Type	Run Type	Included in Analyses
CNCNN	MY3	164235	6	Light	L_t3_2	28551170	20627584	10313792	10280103	7706599	HiSeq-2500 1TB	2x151	TRUE
CNCHH	MW1	164219	0.25	Light	L_t1_1	27574486	23214478	11607239	11523543	8842139	HiSeq-2500 1TB	2x151	TRUE
CNCHO	MW3	164221	6	Light	L_t3_1	27753616	25591988	12795994	12723663	9975555	HiSeq-2500 1TB	2x151	TRUE
CNCHS	MW5	164223	13	Dark	D_t5_1	27346598	25565684	12782842	12561037	9536641	HiSeq-2500 1TB	2x151	TRUE
CNCHN	MW2	164220	1	Light	L_t2_1	14419498	11148764	5574382	5498094	4164371	HiSeq-2500 1TB	2x151	TRUE
CNCNX	MZ3	164242	6	Light	L_t3_3	18943598	7766636	3883318	3800635	2459643	HiSeq-2500 1TB	2x151	TRUE
CNCHP	MW4	164222	12.25	Dark	D_t4_1	21043766	18427228	9213614	9068974	6865369	HiSeq-2500 1TB	2x151	TRUE
CNCNH	MY2	164234	1	Light	L_t2_2	18419162	17267664	8633832	8460136	6387915	HiSeq-2500 1TB	2x151	TRUE
CNCNC	MY0	164232	-0.083	Dark	D_t0_2	17947434	15973648	7986824	7918009	6288247	HiSeq-2500 1TB	2x151	TRUE
CNCNS	MY6	164238	18	Dark	D_t6_2	19718160	18423886	9211943	8876721	6443096	HiSeq-2500 1TB	2x151	TRUE
CNCNO	MY4	164236	12.25	Dark	D_t4_2	18874052	17037474	8518737	8401750	6395484	HiSeq-2500 1TB	2x151	TRUE
CNCHT	MW6	164224	18	Dark	D_t6_1	19463304	11698462	5849231	5721516	3832211	HiSeq-2500 1TB	2x151	TRUE
CNCNU	MZ1	164240	0.25	Light	L_t1_3	18477722	14219922	7109961	6536404	4898958	HiSeq-2500 1TB	2x151	TRUE
	MX0		-0.083	Dark	#N/A						HiSeq-2500 1TB	2x151	Removed by JGI
	MX1		0.25	Light	#N/A						HiSeq-2500 1TB	2x151	Removed by JGI
	MZ5		13	Dark	#N/A						HiSeq-2500 1TB	2x151	Removed by JGI
	MX2		1	Light	#N/A						HiSeq-2500 1TB	2x151	Removed by JGI

Table A.8 Expression data and groups for each *R.lacicola* gene. For each gene in *Rhodoluna lacicola*: Locus tag, annotation, GO-slim term(s) assigned (#N/A indicates that no GO-slim term was assigned to this gene), homolog in *A. photophilum* (#N/A indicates that no homolog exists in that genome), expression group (#N/A indicates that the gene did not group with any other genes), and Benjamini and Hochberg-adjusted p-value indicating probability of belonging to that expression group.

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000010	chromosomal replication initiator protein	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:ion binding	AURMO_00001	#N/A	0.01806
Rhola_00000020	DNA polymerase-3 subunit beta	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex	#N/A	D	0.001665
Rhola_00000030	DNA replication and repair protein RecF	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ion binding	AURMO_01791	#N/A	0.053849
Rhola_00000040	Predicted nucleic acid-binding protein, contains Zn-ribbon domain (includes truncated derivatives)		AURMO_01790	D	3.34E-08
Rhola_00000050	serine/threonine-protein kinase HipA	F:molecular_function	AURMO_00218	I	2.14E-08
Rhola_00000060	transcriptional regulator, y4mF family	F:DNA binding	#N/A	I	4.11E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000070	DNA gyrase subunit B	F:DNA binding; C:chromosome; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	AURMO_01789	#N/A	0.01549
Rhola_00000080	DNA gyrase subunit A	F:DNA binding; C:chromosome; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	AURMO_01788	#N/A	0.726493
Rhola_00000090	Transmembrane protein of unknown function (DUF3566)	C:cellular_component	#N/A	H	0.010516
Rhola_00000120	Glycosyltransferase involved in cell wall bisynthesis	F:molecular_function	#N/A	#N/A	0.042079
Rhola_00000130	Glycosyl transferase family 2.	F:molecular_function	#N/A	H	0.010444
Rhola_00000140	Glycosyltransferase, GT2 family	#N/A	#N/A	#N/A	0.793001
Rhola_00000150	lipopolysaccharide transport system permease protein	C:plasma membrane	#N/A	#N/A	0.671876
Rhola_00000160	lipopolysaccharide transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_01174	#N/A	0.211127
Rhola_00000170	dTDP-4-dehydrorhamnose 3,5-epimerase	F:isomerase activity	#N/A	#N/A	0.691315

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000180	dTDP-4-dehydrorhamnose reductase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.033709
Rhola_00000190	glucose-1-phosphate thymidylyltransferase	P:carbohydrate metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; F:ion binding	AURMO_00445	J	2.04E-06
Rhola_00000200	dTDP-glucose 4,6-dehydratase	F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00421	#N/A	0.07987
Rhola_00000210	Glycosyltransferase involved in cell wall bisynthesis	F:molecular_function; C:cellular_component	#N/A	#N/A	0.021079
Rhola_00000220	Dolichyl-phosphate-mannose-protein mannosyltransferase	C:cellular_component	#N/A	#N/A	0.035336
Rhola_00000230	Glycosyltransferase, GT2 family	F:molecular_function	#N/A	#N/A	0.170157
Rhola_00000240	L-lysine exporter family protein LysE/ArgO	C:plasma membrane; P:transport	AURMO_01039	#N/A	0.942717
Rhola_00000250	hypothetical protein	C:cellular_component	#N/A	#N/A	0.048678
Rhola_00000260	Predicted dehydrogenase	F:oxidoreductase activity	AURMO_01538	#N/A	0.027707
Rhola_00000270	formiminoglutamase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	AURMO_00519	D	6.32E-25

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000280	histidine ammonia-lyase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00522	H	6.69E-13
Rhola_00000290	imidazolonepropionase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00520	H	4.81E-31
Rhola_00000300	urocanate hydratase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00521	H	2.85E-10
Rhola_00000310	transcriptional regulator, IclR family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00523	#N/A	0.178453
Rhola_00000320	hypothetical protein	P:biological_process; F:methyltransferase activity	#N/A	#N/A	0.163476

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000330	peptidyl-prolyl cis-trans isomerase A (cyclophilin A)	P:protein folding; P:cellular protein modification process; F:isomerase activity	AURMO_01774	B	8.10E-06
Rhola_00000340	Membrane associated serine protease, rhomboid family	C:cellular_component; F:peptidase activity	#N/A	E	3.38E-06
Rhola_00000350	hypothetical protein	0	#N/A	#N/A	0.885518
Rhola_00000360	Protein of unknown function (DUF3800)	0	#N/A	#N/A	0.083699
Rhola_00000370	Uncharacterised protein family (UPF0233)	C:plasma membrane; P:cell cycle; P:cell division	#N/A	E	1.52E-06
Rhola_00000380	para-aminobenzoate synthetase component 2	F:molecular_function; P:cellular amino acid metabolic process	AURMO_01769	#N/A	0.76005
Rhola_00000390	serine/threonine protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	AURMO_01768	H	2.19E-05
Rhola_00000400	serine/threonine protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	AURMO_01767	C	0.003596
Rhola_00000410	peptidoglycan glycosyltransferase	F:transferase activity, transferring glycosyl groups; F:ion binding; P:cell division	AURMO_01766	C	0.010656
Rhola_00000420	cell elongation-specific peptidoglycan biosynthesis regulator RodA	C:cellular_component; P:cell division	AURMO_01765	#N/A	0.099606

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000430	protein phosphatase	C:cellular_component; P:cellular protein modification process; F:phosphatase activity	AURMO_01764	#N/A	0.096519
Rhola_00000440	Forkhead associated (FHA) domain, binds pSer, pThr, pTyr	C:cellular_component	#N/A	E	5.10E-09
Rhola_00000450	FOG FHA domain	0	AURMO_01762	J	6.04E-05
Rhola_00000460	hypothetical protein	0	#N/A	H	2.49E-05
Rhola_00000470	UPF0176 protein	F:molecular_function	AURMO_01734	I	1.26E-06
Rhola_00000480	putative endopeptidase	F:peptidase activity	AURMO_01741	#N/A	0.037717
Rhola_00000490	Acyl-CoA thioesterase FadM	0	#N/A	B	3.96E-09
Rhola_00000500	thiamine biosynthesis lipoprotein	P:cellular protein modification process; F:ion binding	#N/A	H	0.012959
Rhola_00000510	Uncharacterized protein conserved in bacteria	#N/A	#N/A	#N/A	0.042136
Rhola_00000520	FMN-binding domain-containing protein	C:cellular_component; F:ion binding	#N/A	#N/A	0.095791
Rhola_00000530	Predicted ferric reductase	C:cellular_component; F:oxidoreductase activity	AURMO_01469	H	0.005411
Rhola_00000540	Lysophospholipase, alpha-beta hydrolase superfamily	0	AURMO_00064	D	2.50E-07
Rhola_00000550	hypothetical protein	F:molecular_function	#N/A	#N/A	0.096519
Rhola_00000560	putative tricarboxylic transport membrane protein	0	#N/A	#N/A	0.795659
Rhola_00000570	putative tricarboxylic transport membrane protein	C:cellular_component	#N/A	#N/A	0.709546
Rhola_00000580	putative tricarboxylic transport membrane protein	C:cellular_component	#N/A	#N/A	0.740551

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000590	Predicted arabinose efflux permease, MFS family	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.470815
Rhola_00000600	site-specific DNA-methyltransferase (adenine-specific)	F:DNA binding; P:DNA metabolic process; F:methyltransferase activity	AURMO_00066	#N/A	0.323916
Rhola_00000610	thiamine transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	N	0.001222
Rhola_00000620	thiamine transport system substrate-binding protein	F:molecular_function; P:transport	#N/A	N	9.51E-06
Rhola_00000630	drug resistance transporter, EmrB/QacA subfamily	C:plasma membrane; F:transmembrane transporter activity	AURMO_00081	G	1.41E-16
Rhola_00000640	D-alanyl-D-alanine carboxypeptidase	#N/A	#N/A	#N/A	0.072969
Rhola_00000650	phosphoglucomutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	AURMO_00084	H	7.34E-07
Rhola_00000660	prephenate dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:isomerase activity	AURMO_00085	#N/A	0.945167
Rhola_00000670	Diacylglycerol kinase family enzyme	F:kinase activity	#N/A	M	0.0008
Rhola_00000680	Ribbon-helix-helix protein, copG family.	#N/A	#N/A	H	5.64E-05
Rhola_00000690	death on curing protein	F:kinase activity	#N/A	M	8.09E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000700	seryl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00086	#N/A	0.861649
Rhola_00000710	Cof subfamily of IIB subfamily of haloacid dehalogenase superfamily	F:molecular_function	AURMO_00087	E	0.010723
Rhola_00000730	transcriptional attenuator, LytR family	C:cellular_component	AURMO_00089	I	0.000612
Rhola_00000740	citrate lyase subunit beta / citryl-CoA lyase	F:lyase activity; F:ion binding	AURMO_01311	D	3.88E-07
Rhola_00000750	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	#N/A	D	0.005542
Rhola_00000760	transcriptional regulator, IclR family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.412394
Rhola_00000770	osmoprotectant transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	M	0.000352
Rhola_00000780	osmoprotectant transport system ATP-binding protein	C:cellular_component; P:transport; F:ATPase activity; F:ion binding	#N/A	M	0.008447
Rhola_00000790	osmoprotectant transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	M	0.006263
Rhola_00000800	osmoprotectant transport system substrate-binding protein	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	K	0.009567

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000810	5,6,7,8-tetrahydromethanopterin hydro-lyase	P:carbohydrate metabolic process; P:biosynthetic process; F:lyase activity	#N/A	#N/A	0.487745
Rhola_00000820	L-alanine-DL-glutamate epimerase	F:isomerase activity	#N/A	#N/A	0.611042
Rhola_00000830	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase	F:oxidoreductase activity	#N/A	G	7.13E-16
Rhola_00000840	3-hydroxyisobutyrate dehydrogenase	F:oxidoreductase activity	#N/A	G	2.85E-10
Rhola_00000850	alcohol dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	G	3.23E-16
Rhola_00000860	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	G	1.75E-16
Rhola_00000870	phytoene desaturase	P:signal transduction; F:oxidoreductase activity; F:enzyme regulator activity	#N/A	#N/A	0.018242
Rhola_00000880	4-hydroxybenzoate polyprenyltransferase	C:cellular_component; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	#N/A	#N/A	0.373149
Rhola_00000890	aspartate ammonia-lyase	P:generation of precursor metabolites and energy; F:lyase activity	AURMO_01135	D	2.89E-07
Rhola_00000900	Listeria/Bacterioides repeat-containing protein	0	#N/A	D	0.000351
Rhola_00000910	Signal transduction histidine kinase	C:cellular_component; F:kinase activity	AURMO_01045	M	0.000555
Rhola_00000920	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01044	M	0.003593

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00000930	Listeria/Bacterioides repeat-containing protein	C:membrane; C:integral component of membrane	#N/A	N	5.39E-05
Rhola_00000940	carboxymethylenebutenolidase	F:molecular_function	AURMO_00099	H	2.26E-05
Rhola_00000950	Sugar kinase of the NBD/HSP70 family, may contain an N-terminal HTH domain	F:kinase activity	#N/A	#N/A	0.33183
Rhola_00000960	inosose dehydratase	F:lyase activity; F:isomerase activity	#N/A	J	0.002693
Rhola_00000970	monosaccharide ABC transporter substrate-binding protein, CUT2 family	P:transport	#N/A	#N/A	0.02368
Rhola_00000980	monosaccharide ABC transporter ATP-binding protein, CUT2 family	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_00053_	#N/A	0.114075
Rhola_00000990	ribose transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.025801
Rhola_00001000	hypothetical protein	0	#N/A	J	0.001974
Rhola_00001010	Predicted dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.025323
Rhola_00001020	Predicted dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.134316
Rhola_00001030	Sugar phosphate isomerase/epimerase	F:DNA binding; F:nuclease activity; F:isomerase activity	#N/A	#N/A	0.359601
Rhola_00001040	Quinol monooxygenase YgiN	F:monooxygenase activity; P:oxidation-reduction process	#N/A	#N/A	0.307379
Rhola_00001050	hypothetical protein	C:cellular_component	#N/A	#N/A	0.505238
Rhola_00001060	carboxymethylenebutenolidase	F:molecular_function	#N/A	M	2.69E-05
Rhola_00001070	OmpA family protein	C:cellular_component; F:ion binding	#N/A	E	0.000952

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001080	hypothetical protein	C:cellular_component	#N/A	D	1.06E-05
Rhola_00001090	hypothetical protein	0	#N/A	F	0.000412
Rhola_00001100	carboxymethylenebutenolidase	F:molecular_function	#N/A	#N/A	0.059256
Rhola_00001110	NYN domain-containing protein	0	#N/A	G	0.00936
Rhola_00001120	hypothetical protein	0	#N/A	D	1.04E-10
Rhola_00001130	hypothetical protein	0	#N/A	#N/A	0.132576
Rhola_00001140	type I restriction enzyme M protein	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:methyltransferase activity	#N/A	#N/A	0.023688
Rhola_00001150	hypothetical protein	C:cellular_component	#N/A	A	0.00044
Rhola_00001160	type I restriction enzyme, S subunit	F:DNA binding; F:nuclease activity; P:DNA metabolic process	#N/A	A	4.36E-11
Rhola_00001170	type I restriction enzyme, R subunit	F:DNA binding; F:helicase activity; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding	#N/A	C	1.52E-05
Rhola_00001180	hypothetical protein	0	#N/A	C	0.000334
Rhola_00001190	hypothetical protein	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	M	0.001218

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001200	hypothetical protein	F:DNA binding; P:regulation of transcription, DNA-templated	AURMO_00394	G	3.83E-06
Rhola_00001210	Nucleotidyltransferase	F:transferase activity	AURMO_00395	G	0.001506
Rhola_00001220	hypothetical protein	0	#N/A	#N/A	0.182459
Rhola_00001230	phosphoribosylformylglycinamidine synthase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01626	#N/A	0.234992
Rhola_00001240	phosphoribosylformylglycinamidine synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_01624	B	1.02E-07
Rhola_00001250	phosphoribosylformylglycinamidine synthase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	J	2.39E-13

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001260	antitoxin YefM	0	#N/A	M	0.00624
Rhola_00001270	Cytotoxic translational repressor of toxin-antitoxin stability system	F:endonuclease activity; P:nucleic acid phosphodiester bond hydrolysis	#N/A	#N/A	0.097553
Rhola_00001280	hypothetical protein	0	#N/A	F	0.005657
Rhola_00001290	ATPases of the AAA+ class	F:transferase activity, transferring acyl groups; F:ion binding	#N/A	I	6.99E-15
Rhola_00001300	NADPH-dependent 2,4-dienoyl-CoA reductase, sulfur reductase	C:cell; F:oxidoreductase activity; P:homeostatic process; F:ion binding	AURMO_00915	#N/A	0.06524
Rhola_00001310	DNA-binding transcriptional regulator, FrmR family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	J	0.002174
Rhola_00001320	Rhodanese-related sulfurtransferase	F:molecular_function	#N/A	G	1.98E-07
Rhola_00001330	hypothetical protein	0	#N/A	G	5.35E-08
Rhola_00001340	phosphoenolpyruvate carboxykinase (GTP)	C:cytoplasm; P:carbohydrate metabolic process; P:biosynthetic process; F:kinase activity; F:oxidoreductase activity; F:lyase activity; F:ion binding; P:small molecule metabolic process	AURMO_01338	D	0.000309

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001350	phosphoribosylaminoimidazole-succinocarboxamide synthase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01604	#N/A	0.033243
Rhola_00001360	phosphoribosylamine--glycine ligase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01603	#N/A	0.089293
Rhola_00001370	Uncharacterized conserved protein, DUF305 family	0	AURMO_01608	H	0.000206
Rhola_00001380	hypothetical protein	0	#N/A	#N/A	0.081782
Rhola_00001390	hypothetical protein	C:cellular_component	#N/A	G	5.64E-10
Rhola_00001400	amidophosphoribosyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_01643	H	1.68E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001410	phosphoribosylformylglycinamidine cyclo-ligase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01642	H	5.60E-06
Rhola_00001420	iron(III) transport system ATP-binding protein	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; C:protein-containing complex; F:ion binding	#N/A	G	1.41E-09
Rhola_00001430	iron(III) transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	G	2.88E-29
Rhola_00001440	iron(III) transport system substrate-binding protein	F:ion binding	#N/A	G	1.47E-23
Rhola_00001450	dolichol-phosphate mannosyltransferase	P:biological_process; F:transferase activity, transferring glycosyl groups	AURMO_00369	#N/A	0.530197
Rhola_00001460	ferredoxin--NADP+ reductase	F:oxidoreductase activity	AURMO_01602	E	8.23E-13
Rhola_00001470	Acetyltransferases	F:transferase activity, transferring acyl groups	#N/A	#N/A	0.035847
Rhola_00001480	Protein of unknown function (DUF3073)	0	#N/A	B	0.000351
Rhola_00001490	camphor resistance protein CrcB	#N/A	#N/A	#N/A	0.031771
Rhola_00001500	CrcB protein	C:plasma membrane	#N/A	#N/A	0.149218
Rhola_00001510	drug resistance transporter, EmrB/QacA subfamily	C:plasma membrane; F:transmembrane transporter activity	AURMO_00095	D	3.64E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001520	Uncharacterized membrane protein	C:cellular_component	#N/A	C	0.012692
Rhola_00001530	uncharacterized zinc-type alcohol dehydrogenase-like protein	F:oxidoreductase activity; F:ion binding	AURMO_01494	#N/A	0.09642
Rhola_00001570	Cell wall-associated hydrolase, NlpC family	F:molecular_function	#N/A	H	3.43E-05
Rhola_00001580	inorganic pyrophosphatase	C:cytoplasm; P:biological_process; F:ion binding	AURMO_00123	#N/A	0.057803
Rhola_00001590	tRNA(Ile)-lysidine synthase	C:cytoplasm; P:tRNA metabolic process; F:ligase activity; F:ion binding	AURMO_00124	#N/A	0.134608
Rhola_00001600	hypoxanthine phosphoribosyltransferase	C:cytoplasm; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00125	#N/A	0.808493
Rhola_00001610	cell division protease FtsH	C:plasma membrane; F:peptidase activity; P:catabolic process; F:ATPase activity; F:ion binding; P:cell division	AURMO_00126	#N/A	0.067679

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001620	GTP cyclohydrolase I	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00127	#N/A	0.561371
Rhola_00001630	dihydropteroate synthase	P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00128	#N/A	0.179725
Rhola_00001640	dihydroneopterin aldolase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	#N/A	0.538492

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001650	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00130	C	0.009584
Rhola_00001660	Protein of unknown function (DUF3180)	C:cellular_component	#N/A	A	0.001973
Rhola_00001670	Predicted oxidoreductase, contains short-chain dehydrogenase (SDR) and DUF2520 domains	0	AURMO_00132	#N/A	0.029382
Rhola_00001680	pantoate--beta-alanine ligase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00133	#N/A	0.067513
Rhola_00001690	lysyl-tRNA synthetase, class II	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00134	B	6.54E-11
Rhola_00001700	hypothetical protein	C:cellular_component	#N/A	#N/A	0.16835

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001710	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process	#N/A	I	0.00924
Rhola_00001720	protein involved in ribonucleotide reduction	P:cellular protein modification process; F:ion binding	#N/A	I	0.001571
Rhola_00001730	ribonucleoside-diphosphate reductase alpha chain	P:biosynthetic process; F:oxidoreductase activity; F:ion binding	AURMO_01383	I	5.25E-11
Rhola_00001740	ribonucleoside-diphosphate reductase beta chain	C:cytosol; P:biosynthetic process; F:oxidoreductase activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	G	1.48E-09
Rhola_00001750	manganese transport protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_01547	I	1.16E-13
Rhola_00001760	ATP-dependent Clp protease ATP-binding subunit ClpC	P:biological_process; F:ion binding	AURMO_00142	G	1.09E-10

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001770	amino-acid N-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_00143	#N/A	0.790658
Rhola_00001780	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.598535
Rhola_00001790	AraC-type DNA-binding protein	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01256	#N/A	0.059422
Rhola_00001800	sorbitol/mannitol transport system substrate-binding protein	P:transport	AURMO_01255	#N/A	0.016068
Rhola_00001810	sorbitol/mannitol transport system permease protein	C:plasma membrane; P:transmembrane transport	AURMO_01254	#N/A	0.10336
Rhola_00001820	sorbitol/mannitol transport system permease protein	C:plasma membrane; P:transmembrane transport	AURMO_01253	#N/A	0.092676
Rhola_00001830	mannitol 2-dehydrogenase	P:carbohydrate metabolic process; F:oxidoreductase activity; P:small molecule metabolic process	AURMO_01252	#N/A	0.052411
Rhola_00001840	L-iditol 2-dehydrogenase	F:oxidoreductase activity; F:ion binding	AURMO_01251	A	0.013716

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001850	DNA repair protein RadA/Sms	F:DNA binding; P:DNA metabolic process; P:response to stress; F:peptidase activity; F:ATPase activity; F:ion binding	AURMO_00150	D	1.55E-06
Rhola_00001860	pyrroline-5-carboxylate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_01669	#N/A	0.598535
Rhola_00001870	transcriptional regulator, TetR family	F:DNA binding	#N/A	I	6.73E-24
Rhola_00001880	arsenate reductase	F:oxidoreductase activity	AURMO_01601	#N/A	0.350885
Rhola_00001890	Glycerol uptake facilitator (Major Intrinsic Protein Family)	C:cellular_component; F:transmembrane transporter activity	#N/A	A	0.002358
Rhola_00001900	SOUL heme-binding protein	F:ATP binding	AURMO_01229	#N/A	0.750867
Rhola_00001910	protein of unknown function (DUF1713)	0	#N/A	#N/A	0.731351
Rhola_00001920	HAD-superfamily subfamily IB hydrolase, TIGR01490	F:molecular_function	#N/A	#N/A	0.136092
Rhola_00001930	Glutaredoxin-like domain (DUF836)	0	#N/A	#N/A	0.598535
Rhola_00001940	hypothetical protein	#N/A	#N/A	#N/A	0.105755
Rhola_00001950	PASTA domain-containing protein	C:cellular_component	#N/A	D	0.002876
Rhola_00001960	PadR family transcriptional regulator, regulatory protein PadR	0	#N/A	D	0.004273
Rhola_00001970	antitoxin VapB	F:DNA binding	#N/A	#N/A	0.1591
Rhola_00001980	tRNA(fMet)-specific endonuclease VapC	F:nuclease activity; F:ion binding	#N/A	#N/A	0.279643

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00001990	aspartyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01661	B	4.94E-06
Rhola_00002000	Broad specificity phosphatase PhoE	0	AURMO_01660	J	2.36E-06
Rhola_00002010	Thiol-disulfide isomerase or thioredoxin	C:cell; F:oxidoreductase activity; F:isomerase activity; P:homeostatic process	AURMO_01659	#N/A	0.618504
Rhola_00002020	cytochrome c-type biogenesis protein	C:cellular_component; P:protein-containing complex assembly	AURMO_01658	C	0.01439
Rhola_00002030	cytochrome c biogenesis protein	C:cellular_component	AURMO_01657	#N/A	0.016607
Rhola_00002040	cytochrome c-type biogenesis protein CcsB	F:molecular_function; C:cellular_component; P:protein-containing complex assembly	AURMO_01656	G	3.53E-10
Rhola_00002050	O-succinylbenzoate synthase	P:biosynthetic process; F:lyase activity; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01655	#N/A	0.041468
Rhola_00002060	1,4-Dihydroxy-2-naphthoyl-CoA synthase	P:biosynthetic process; F:lyase activity; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01654	G	0.000238

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002070	O-succinylbenzoic acid--CoA ligase	#N/A	#N/A	I	1.19E-08
Rhola_00002080	1,4-dihydroxy-2-naphthoate prenyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01652	#N/A	0.023276
Rhola_00002090	Protein of unknown function (DUF4229)	C:cellular_component	#N/A	B	3.91E-13
Rhola_00002100	hypothetical protein	0	#N/A	G	5.21E-18
Rhola_00002110	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	P:biosynthetic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01649	G	4.39E-16
Rhola_00002120	isochorismate synthase	P:biosynthetic process; F:isomerase activity	AURMO_01648	G	1.52E-18
Rhola_00002130	hypothetical protein	C:cellular_component	#N/A	#N/A	0.205434
Rhola_00002140	demethylmenaquinone methyltransferase / 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	F:methyltransferase activity; P:biosynthetic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01647	J	0.001051

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002150	heptaprenyl diphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_01646	J	1.20E-06
Rhola_00002160	Sugar phosphate permease	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.217245
Rhola_00002170	hypothetical protein	0	AURMO_01582	#N/A	0.177667
Rhola_00002180	transcriptional regulator, LacI family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.156504
Rhola_00002200	hypothetical protein	C:cellular_component	AURMO_01567	#N/A	0.03545
Rhola_00002210	tellurite resistance protein TerC	C:cellular_component	AURMO_01566	#N/A	0.236265
Rhola_00002220	Winged helix-turn-helix DNA-binding	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01565	E	0.004368
Rhola_00002230	Acyl-CoA hydrolase	F:molecular_function	#N/A	#N/A	0.042486
Rhola_00002240	putative drug exporter of the RND superfamily	C:cellular_component	AURMO_00332	I	7.70E-16
Rhola_00002250	alpha-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	AURMO_01619	B	9.18E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002260	alpha-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	AURMO_01570	B	2.97E-11
Rhola_00002270	carbohydrate ABC transporter substrate-binding protein, CUT1 family	P:carbohydrate transport; F:carbohydrate transmembrane transporter activity; P:carbohydrate transmembrane transport	#N/A	#N/A	0.7728
Rhola_00002300	Acyl dehydratase	0	AURMO_01482	#N/A	0.698112
Rhola_00002310	Acyl dehydratase	0	AURMO_01481	#N/A	0.918523
Rhola_00002320	UDP-N-acetylmuramate dehydrogenase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	AURMO_01480	#N/A	0.104182
Rhola_00002330	aspartate aminotransferase	P:biosynthetic process; F:ion binding	AURMO_01478	#N/A	0.188842
Rhola_00002350	preprotein translocase subunit SecE	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	#N/A	#N/A	0.196583
Rhola_00002360	transcription antitermination protein nusG	P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01475	#N/A	0.323916

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002370	LSU ribosomal protein L11P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_01474	#N/A	0.037995
Rhola_00002380	large subunit ribosomal protein L1	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_01473	#N/A	0.195028
Rhola_00002390	lysine decarboxylase	F:lyase activity	#N/A	#N/A	0.018455
Rhola_00002400	MFS transporter, DHA3 family, macrolide efflux protein	C:cellular_component; P:transmembrane transport	#N/A	H	0.004368
Rhola_00002410	Predicted Fe2+/Mn2+ transporter, VIT1/CCC1 family	C:cell; F:transmembrane transporter activity; P:homeostatic process	AURMO_00504	#N/A	0.052411
Rhola_00002420	uncharacterized protein	0	#N/A	N	0.000373
Rhola_00002430	fructokinase	P:carbohydrate metabolic process; F:kinase activity	AURMO_01346	#N/A	0.185881
Rhola_00002440	hypothetical protein	C:cellular_component	#N/A	D	0.000131
Rhola_00002450	sugar-phosphatase	F:molecular_function	AURMO_00668	D	0.005411
Rhola_00002460	Glutaredoxin	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process	#N/A	#N/A	0.234992

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002470	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.202615
Rhola_00002480	Signal transduction histidine kinase	C:cellular_component	#N/A	#N/A	0.042587
Rhola_00002490	Superfamily II DNA and RNA helicase	#N/A	#N/A	I	2.88E-07
Rhola_00002500	LSU ribosomal protein L10P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex; P:ribosome biogenesis	AURMO_01549	#N/A	0.274468
Rhola_00002510	large subunit ribosomal protein L7/L12	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	#N/A	0.310676
Rhola_00002520	Listeria/Bacterioides repeat-containing protein	C:cellular_component	#N/A	#N/A	0.108232
Rhola_00002530	MFS transporter, DHA1 family, bicyclomycin/chloramphenicol resistance protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.029762
Rhola_00002540	hypothetical protein	#N/A	#N/A	I	2.60E-10
Rhola_00002550	Saccharopine dehydrogenase, NADP-dependent	F:oxidoreductase activity; F:ion binding	AURMO_01546	H	9.17E-23
Rhola_00002560	aldose 1-epimerase	P:carbohydrate metabolic process; F:isomerase activity	#N/A	M	0.002394

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002570	xylulokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	AURMO_01541	H	1.33E-06
Rhola_00002580	xylose isomerase	C:cytoplasm; P:carbohydrate metabolic process; F:isomerase activity; F:ion binding; P:small molecule metabolic process	AURMO_01540	H	4.11E-05
Rhola_00002590	Sugar kinase of the NBD/HSP70 family, may contain an N-terminal HTH domain	F:kinase activity	AURMO_01539	#N/A	0.289321
Rhola_00002600	cholesterol oxidase	F:oxidoreductase activity; F:ion binding	#N/A	D	0.001736
Rhola_00002610	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	AURMO_00966	#N/A	0.074265
Rhola_00002620	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	#N/A	#N/A	0.439467
Rhola_00002630	6-phosphogluconate dehydrogenase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:small molecule metabolic process	AURMO_01345	J	1.82E-06
Rhola_00002640	D-xylose transport system substrate-binding protein	0	AURMO_01542	D	0.007612
Rhola_00002650	D-xylose transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_01543	D	0.008559

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002660	D-xylose transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_01544	D	0.000934
Rhola_00002670	alpha-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	AURMO_00613	#N/A	0.037637
Rhola_00002680	putative drug exporter of the RND superfamily	C:cellular_component	AURMO_01024	G	9.17E-31
Rhola_00002690	integral membrane protein	C:cellular_component	AURMO_01625	G	3.77E-31
Rhola_00002700	ATP-dependent helicase HrpA	F:helicase activity; F:ion binding	AURMO_01379	#N/A	0.222187
Rhola_00002710	Uncharacterized conserved protein YdhG, YjbR/CyaY-like superfamily, DUF1801 family	0	#N/A	#N/A	0.663183
Rhola_00002720	hypothetical protein	0	AURMO_00282	#N/A	0.02085
Rhola_00002730	catalase-peroxidase	P:response to stress; P:catabolic process; F:oxidoreductase activity; F:ion binding; P:cofactor metabolic process	AURMO_00283	G	5.09E-17
Rhola_00002740	Glycerol uptake facilitator (Major Intrinsic Protein Family)	C:cellular_component; F:transmembrane transporter activity	AURMO_01600	#N/A	0.054634
Rhola_00002750	protein of unknown function (DUF4188)	0	#N/A	D	1.56E-07
Rhola_00002760	protein of unknown function (DU1801)	F:aminoacyl-tRNA ligase activity	#N/A	A	1.63E-07
Rhola_00002770	hypothetical protein	F:oxidoreductase activity; F:lyase activity	AURMO_00288	#N/A	0.040872

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002780	Predicted unusual protein kinase regulating ubiquinone biosynthesis, AarF/ABC1/UbiB family	C:cellular_component; F:kinase activity	AURMO_01680	G	2.06E-20
Rhola_00002790	Predicted transcriptional regulators	F:DNA binding	#N/A	G	7.30E-19
Rhola_00002800	hypothetical protein	F:peptidase activity	AURMO_01776	#N/A	0.505684
Rhola_00002810	hypothetical protein	0	AURMO_01690	G	2.92E-06
Rhola_00002820	transcriptional regulator, AsnC family	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	I	0.000171
Rhola_00002830	L-threonine aldolase	P:cellular amino acid metabolic process; F:lyase activity	AURMO_01691	I	0.00001
Rhola_00002840	hypothetical protein	C:cellular_component	#N/A	#N/A	0.1591
Rhola_00002850	hypothetical protein	#N/A	#N/A	H	0.014148
Rhola_00002860	glutamate-1-semialdehyde 2,1-aminomutase	C:cytoplasm; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_00108	A	7.14E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002870	porphobilinogen synthase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_00109	#N/A	0.189278
Rhola_00002880	hydroxymethylbilane synthase	P:cellular protein modification process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:lyase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00111	C	0.004656
Rhola_00002890	glutamyl-tRNA reductase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00112	#N/A	0.978458
Rhola_00002900	uroporphyrinogen decarboxylase	C:cytoplasm; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00113	B	3.10E-18

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00002910	oxygen-dependent protoporphyrinogen oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00114	#N/A	0.095924
Rhola_00002920	chlorite dismutase	F:peroxidase activity; P:cellular oxidant detoxification	AURMO_00115	#N/A	0.492974
Rhola_00002930	ferrochelatase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_00116	G	9.56E-11
Rhola_00002940	DNA binding domain-containing protein, excisionase family	F:DNA binding	#N/A	G	1.41E-09
Rhola_00002950	putative DNA primase/helicase	P:biological_process	#N/A	G	0.00624
Rhola_00002960	hypothetical protein	0	#N/A	#N/A	0.121486
Rhola_00002970	Predicted ATPase	0	#N/A	B	0.007167
Rhola_00002980	Polyketide cyclase / dehydrase and lipid transport.	0	AURMO_00292	G	8.15E-07
Rhola_00002990	Cu2+-exporting ATPase	C:plasma membrane; F:oxidoreductase activity; F:transmembrane transporter activity; F:ion binding	AURMO_01375_	G	0.003249

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003000	DNA-binding transcriptional regulator, FrmR family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	G	0.005411
Rhola_00003010	cation-transporting ATPase G	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	#N/A	H	0.000202
Rhola_00003020	Multicopper oxidase with three cupredoxin domains (includes cell division protein FtsP and spore coat protein CotA)	C:cellular_component; F:oxidoreductase activity; F:ion binding	AURMO_01609	I	1.68E-05
Rhola_00003030	Uncharacterized conserved protein, DUF305 family	0	#N/A	I	1.19E-06
Rhola_00003040	hypothetical protein	C:cellular_component	#N/A	#N/A	0.292401
Rhola_00003050	BNR/Asp-box repeat.	0	AURMO_01372	#N/A	0.902929
Rhola_00003060	hypothetical protein	0	#N/A	#N/A	0.828572
Rhola_00003070	Site-specific recombinase XerD	F:DNA binding; P:DNA metabolic process	#N/A	M	0.000167
Rhola_00003090	membrane protein, MarC family	C:plasma membrane	#N/A	B	0.004293
Rhola_00003100	Predicted arabinose efflux permease, MFS family	C:cellular_component; P:transmembrane transport	AURMO_00850	#N/A	0.240662

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003110	DNA polymerase-3 subunit gamma/tau	F:DNA binding; C:intracellular; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex; F:ion binding	AURMO_00297	#N/A	0.040266
Rhola_00003120	DNA replication and repair protein RecR	F:DNA binding; P:DNA metabolic process; P:response to stress; F:ion binding	AURMO_00298	D	1.46E-11
Rhola_00003130	aspartate kinase	P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	AURMO_00300	#N/A	0.32219
Rhola_00003140	aspartate-semialdehyde dehydrogenase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00301	#N/A	0.349002
Rhola_00003150	hypothetical protein	0	#N/A	K	0.000555
Rhola_00003160	Predicted phosphohydrolase, MPP superfamily	F:molecular_function; C:cellular_component	AURMO_00311	D	7.38E-08
Rhola_00003170	Membrane carboxypeptidase (penicillin-binding protein)	F:peptidase activity; F:ion binding	AURMO_00312	#N/A	0.015115
Rhola_00003180	protein of unknown function (DUF4177)	#N/A	#N/A	#N/A	0.171519

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003190	Enamine deaminase RidA, house cleaning of reactive enamine intermediates, YjgF/YER057c/UK114 family	0	AURMO_00314	#N/A	0.036047
Rhola_00003200	acetyl-CoA synthetase	P:sulfur compound metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00315	D	8.54E-06
Rhola_00003210	pilus assembly protein CpaF	0	AURMO_00316	N	2.16E-06
Rhola_00003220	tight adherence protein B	C:cellular_component	#N/A	N	0.000108
Rhola_00003230	Protein of unknown function (DUF4244)	C:cellular_component	#N/A	#N/A	0.308015
Rhola_00003240	hypothetical protein	C:cellular_component	#N/A	#N/A	0.033656
Rhola_00003250	hypothetical protein	0	#N/A	M	0.0051
Rhola_00003260	DNA topoisomerase I	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ion binding; P:chromosome organization	AURMO_00321	A	3.88E-07
Rhola_00003270	dTMP kinase	P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00322	#N/A	0.053935

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003280	DNA polymerase-3 subunit delta'	P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	AURMO_00323	D	3.58E-07
Rhola_00003290	alpha/beta hydrolase fold	F:molecular_function	AURMO_00324	D	8.55E-12
Rhola_00003300	Uncharacterized membrane protein, DUF485 family	C:cellular_component	#N/A	D	0.000314
Rhola_00003310	cation/acetate symporter	C:cellular_component; F:transmembrane transporter activity	AURMO_00999	D	0.011669
Rhola_00003320	hypothetical protein	C:cellular_component	#N/A	B	0.002304
Rhola_00003330	Uncharacterized conserved protein, DUF2236 family	0	AURMO_00514	G	7.67E-19
Rhola_00003340	inositol transport system substrate-binding protein	P:transport	#N/A	#N/A	0.980669
Rhola_00003350	inositol transport system ATP-binding protein	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_01288_	#N/A	0.790703
Rhola_00003360	inositol transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.611042
Rhola_00003370	Trk-type K+ transport system, membrane component	C:cellular_component; F:transmembrane transporter activity	AURMO_01667	#N/A	0.447979
Rhola_00003380	trk system potassium uptake protein TrkA	F:transmembrane transporter activity	AURMO_01668	#N/A	0.233048

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003390	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	AURMO_01472	#N/A	0.142823
Rhola_00003400	metallo-beta-lactamase family protein	F:nuclease activity	AURMO_00517	D	7.85E-15
Rhola_00003410	hypothetical protein	#N/A	#N/A	D	0.009303
Rhola_00003420	D-alanyl-D-alanine carboxypeptidase / D-alanyl-D-alanine-endopeptidase (penicillin-binding protein 4)	F:peptidase activity	#N/A	#N/A	0.118776
Rhola_00003430	hypothetical protein	C:cellular_component; P:transport; F:ion binding	#N/A	#N/A	0.488027
Rhola_00003440	D-alanyl-D-alanine carboxypeptidase / D-alanyl-D-alanine-endopeptidase (penicillin-binding protein 4)	C:cellular_component; F:peptidase activity	#N/A	#N/A	0.393865
Rhola_00003450	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase	F:oxidoreductase activity	AURMO_00333	D	5.23E-10
Rhola_00003460	hypothetical protein	0	#N/A	D	2.13E-09
Rhola_00003470	inorganic phosphate transporter, PiT family	C:cellular_component; F:transmembrane transporter activity	AURMO_00535	#N/A	0.667537
Rhola_00003480	hypothetical protein	C:cellular_component	#N/A	#N/A	0.721957
Rhola_00003490	hypothetical protein	0	#N/A	#N/A	0.953223
Rhola_00003500	cystathione beta-lyase	P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_01385	D	0.00477

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003510	O-succinylhomoserine sulfhydrylase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	#N/A	H	1.60E-08
Rhola_00003520	cyclic-di-GMP-binding biofilm dispersal mediator protein	P:biosynthetic process; F:oxidoreductase activity; P:secondary metabolic process; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_01167	D	0.00118
Rhola_00003530	Protein of unknown function (DUF998)	C:cellular_component	AURMO_01456	#N/A	0.028017
Rhola_00003540	Peptidoglycan/LPS O-acetylase OafA/YrhL, contains acyltransferase and SGNH-hydrolase domains	C:cellular_component; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.298879
Rhola_00003560	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	AURMO_01635	#N/A	0.54395
Rhola_00003570	Uncharacterized conserved protein YbjT, contains NAD(P)-binding and DUF2867 domains	0	AURMO_00527	D	8.41E-06
Rhola_00003580	8-oxo-dGTP diphosphatase	F:molecular_function	AURMO_01446	#N/A	0.40601
Rhola_00003590	polyphosphate kinase	P:biosynthetic process; F:kinase activity; C:protein-containing complex; F:ion binding; P:small molecule metabolic process	AURMO_01445	H	0.013387

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003600	DNA-binding response regulator, OmpR family, contains REC and winged-helix (wHTH) domain	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01444	#N/A	0.382396
Rhola_00003610	hypothetical protein	C:cellular_component	#N/A	#N/A	0.027059
Rhola_00003620	hypothetical protein	#N/A	#N/A	#N/A	0.886452
Rhola_00003630	protein of unknown function (DUF1794)	P:transport	#N/A	B	0.000127
Rhola_00003640	hypothetical protein	F:molecular_function	AURMO_01442	A	0.000232
Rhola_00003650	Uncharacterized membrane protein YgaE, UPF0421/DUF939 family	C:cellular_component	#N/A	C	0.000164
Rhola_00003660	hypothetical protein	P:biological_process; F:methyltransferase activity	AURMO_01441	#N/A	0.094714
Rhola_00003670	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01440	#N/A	0.663183
Rhola_00003680	phosphate uptake regulator, PhoU	C:cell; C:cytoplasm; P:transport; P:homeostatic process	AURMO_01596	M	0.000952

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003690	two-component system, OmpR family, sensor histidine kinase SenX3	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	AURMO_01597	#N/A	0.333875
Rhola_00003700	two-component system, OmpR family, response regulator RegX3	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01598	#N/A	0.919343
Rhola_00003710	hypothetical protein	0	#N/A	#N/A	0.211337
Rhola_00003720	transcriptional regulator, CarD family	0	AURMO_01438	J	0.012546
Rhola_00003730	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; F:lyase activity; F:ion binding; P:small molecule metabolic process	AURMO_01437	G	7.72E-05
Rhola_00003740	cysteinyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01436	H	0.001461
Rhola_00003750	23S rRNA (guanosine2251-2'-O)-methyltransferase	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_01435	H	3.88E-17

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003760	Predicted O-methyltransferase YrrM	P:biological_process; F:methyltransferase activity	#N/A	#N/A	0.132845
Rhola_00003770	sec-independent protein translocase protein TatB	C:cellular_component	#N/A	#N/A	0.10721
Rhola_00003780	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	C	2.10E-06
Rhola_00003790	ATP-binding protein involved in chromosome partitioning	F:ATPase activity; F:ion binding	AURMO_01190	H	4.02E-05
Rhola_00003800	Predicted membrane protein	C:cellular_component	AURMO_01189	#N/A	0.076727
Rhola_00003810	Mg/Co/Ni transporter MgtE (contains CBS domain)	C:cellular_component; F:transmembrane transporter activity	AURMO_01188	G	0.00918
Rhola_00003820	hypothetical protein	C:cellular_component	#N/A	H	0.002843
Rhola_00003830	Xaa-Pro aminopeptidase	F:peptidase activity; F:ion binding	AURMO_01184	D	0.014465
Rhola_00003840	hypothetical protein	F:molecular_function	AURMO_01183	#N/A	0.121719
Rhola_00003850	protein of unknown function (DUF4287)	0	#N/A	#N/A	0.052733
Rhola_00003860	Superfamily II DNA and RNA helicase	F:helicase activity; F:ion binding	AURMO_01180	#N/A	0.015574
Rhola_00003870	tRNA-(MS[2]IO[6]A)-hydroxylase (MiaE)-like	0	AURMO_01179	#N/A	0.018242
Rhola_00003880	hypothetical protein	C:cellular_component	#N/A	B	1.59E-06
Rhola_00003890	Protein of unknown function (DUF3107)	F:ion binding	#N/A	B	0.009994
Rhola_00003900	Superfamily I DNA or RNA helicase	F:DNA binding; F:helicase activity; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	AURMO_00546	M	0.004453

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00003910	DNA helicase-2 / ATP-dependent DNA helicase PcrA	F:DNA binding; F:helicase activity; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	AURMO_00547	D	0.006938
Rhola_00003920	Predicted kinase, aminoglycoside phosphotransferase (APT) family	F:molecular_function	AURMO_00548	#N/A	0.016104
Rhola_00003930	NAD+ diphosphatase	F:ion binding	AURMO_00549	D	8.63E-14
Rhola_00003940	ATP-dependent DNA helicase, Rep family	F:DNA binding; F:helicase activity; F:ion binding; P:chromosome organization	AURMO_00550	#N/A	0.049087
Rhola_00003950	hypothetical protein	F:ligase activity	#N/A	N	0.000162
Rhola_00003960	putative hydrolase	F:molecular_function	AURMO_00552	G	1.55E-25
Rhola_00003970	PDZ domain-containing protein	C:cellular_component; F:peptidase activity; P:catabolic process; F:ATPase activity; F:ion binding	AURMO_00553	G	1.88E-05
Rhola_00003980	hypothetical protein	C:plasma membrane	AURMO_00554	J	3.85E-18
Rhola_00004000	PKD domain.	0	#N/A	N	0.001324
Rhola_00004010	putative serine protease PepD	C:cellular_component; F:peptidase activity	AURMO_00541	H	0.002616
Rhola_00004020	Protein of unknown function (DUF3039)	0	#N/A	H	1.37E-05
Rhola_00004030	glutamate racemase	P:cell morphogenesis; P:biosynthetic process; F:isomerase activity; P:cell wall organization or biogenesis	AURMO_01170	#N/A	0.05325

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004040	ribonuclease PH	F:RNA binding; F:nuclease activity; P:tRNA metabolic process; F:nucleotidyltransferase activity; P:nucleobase-containing compound catabolic process; P:ribosome biogenesis	AURMO_01169	#N/A	0.338019
Rhola_00004050	XTP/dITP diphosphohydrolase	P:biosynthetic process; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01168	A	5.62E-05
Rhola_00004060	membrane-associated protein	C:cellular_component	AURMO_01165	#N/A	0.585789
Rhola_00004080	beta-fructofuranosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	#N/A	D	2.22E-07
Rhola_00004090	arginyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00452	I	0.000852
Rhola_00004100	diaminopimelate decarboxylase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_00453	#N/A	0.030119

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004110	homoserine dehydrogenase	P:cellular amino acid metabolic process; F:oxidoreductase activity	AURMO_00454	#N/A	0.868583
Rhola_00004120	threonine synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_00455	#N/A	0.76005
Rhola_00004130	homoserine kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	AURMO_00456	B	0.000765
Rhola_00004140	transcription termination factor Rho	F:RNA binding; F:helicase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00458	#N/A	0.087217
Rhola_00004150	peptide chain release factor 1	C:cytoplasm; F:translation factor activity, RNA binding	AURMO_00459	#N/A	0.051272
Rhola_00004160	release factor glutamine methyltransferase	P:cellular protein modification process; F:methyltransferase activity	AURMO_00466	#N/A	0.75521
Rhola_00004170	tRNA threonylcarbamoyl adenosine modification protein, Sua5/YciO/YrdC/YwlC family	F:RNA binding	AURMO_00468	#N/A	0.238394
Rhola_00004180	UDP-GlcNAc	F:molecular_function; C:cellular_component	AURMO_00469	C	0.012468
Rhola_00004190	hypothetical protein	C:cellular_component	#N/A	A	4.08E-14

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004200	F-type H+-transporting ATPase subunit a	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00472	J	0.00512
Rhola_00004210	F-type H+-transporting ATPase subunit c	C:intracellular; C:plasma membrane; F:lipid binding; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.319088
Rhola_00004220	ATP synthase F0 subcomplex B subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00474	#N/A	0.610618

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004230	ATP synthase F1 subcomplex delta subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00475	#N/A	0.594672
Rhola_00004240	ATP synthase F1 subcomplex alpha subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00476	#N/A	0.165328
Rhola_00004250	ATP synthase F1 subcomplex gamma subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00477	J	0.009567

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004260	F-type H+-transporting ATPase subunit beta	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00478	#N/A	0.359601
Rhola_00004270	ATP synthase F1 subcomplex epsilon subunit	C:intracellular; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.077399
Rhola_00004280	cob(I)alamin adenosyltransferase	P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	#N/A	0.612841
Rhola_00004290	hypothetical protein	0	#N/A	E	0.00608

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004300	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	H	2.56E-05
Rhola_00004310	DNA-3-methyladenine glycosylase I	P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds	AURMO_01195	#N/A	0.03682
Rhola_00004320	methylated-DNA-[protein]-cysteine S-methyltransferase	#N/A	#N/A	H	3.05E-11
Rhola_00004330	hypothetical protein	F:ion binding	AURMO_01193	D	4.22E-07
Rhola_00004340	Lrp/AsnC family transcriptional regulator, regulator for asnA, asnC and gidA	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01192	D	4.13E-06
Rhola_00004350	betaine-aldehyde dehydrogenase	F:oxidoreductase activity	AURMO_01191	D	1.08E-11
Rhola_00004360	DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family	F:DNA binding; F:ion binding	#N/A	H	0.000165
Rhola_00004370	spermidine/putrescine transport system substrate-binding protein	F:molecular_function; C:cellular_component; P:transport	#N/A	K	6.61E-06
Rhola_00004380	spermidine/putrescine transport system ATP-binding protein	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; C:protein-containing complex; F:ion binding	#N/A	A	8.73E-16
Rhola_00004390	spermidine/putrescine transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	C	3.79E-06

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004400	spermidine/putrescine transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	A	1.13E-08
Rhola_00004410	4-aminobutyrate aminotransferase / (S)-3-amino-2-methylpropionate transaminase	P:cellular amino acid metabolic process; F:ion binding	AURMO_00490	#N/A	0.108921
Rhola_00004420	1-deoxy-D-xylulose 5-phosphate reductoisomerase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:isomerase activity; F:ion binding; P:small molecule metabolic process	AURMO_00491	#N/A	0.544563
Rhola_00004430	RIP metalloprotease RseP	C:cellular_component; F:peptidase activity; F:ion binding	AURMO_00492	H	2.98E-05
Rhola_00004440	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	AURMO_00493	#N/A	0.01819
Rhola_00004450	prolyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00496	#N/A	0.314686
Rhola_00004460	NusA antitermination factor	F:DNA-binding transcription factor activity; C:cytoplasm; F:translation factor activity, RNA binding	AURMO_00497	#N/A	0.220938

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004470	hypothetical protein	#N/A	#N/A	G	0.005175
Rhola_00004480	translation initiation factor IF-2	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	AURMO_00499	G	1.98E-06
Rhola_00004490	ribosome-binding factor A	C:cytoplasm; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00500	G	1.09E-05
Rhola_00004500	tRNA pseudouridine synthase B	F:RNA binding; P:tRNA metabolic process; F:isomerase activity	AURMO_01141	G	6.77E-11
Rhola_00004510	hypothetical protein	C:cellular_component	#N/A	#N/A	0.226885
Rhola_00004520	phosphate transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_01594	N	0.006785
Rhola_00004530	phosphate transport system permease protein	#N/A	#N/A	M	0.000197
Rhola_00004540	phosphate transport system ATP-binding protein	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_01592	#N/A	0.019185
Rhola_00004550	phosphate transport system substrate-binding protein	#N/A	#N/A	M	0.012468
Rhola_00004560	phosphate transport system substrate-binding protein	0	#N/A	#N/A	0.093657
Rhola_00004570	hypothetical protein	C:cellular_component	#N/A	#N/A	0.234992

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004580	riboflavin kinase / FMN adenylyltransferase	P:biosynthetic process; F:kinase activity; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01138	#N/A	0.213362
Rhola_00004590	hypothetical protein	C:cellular_component	#N/A	H	0.000185
Rhola_00004600	Uncharacterized membrane protein YhaH, DUF805 family	C:cellular_component	#N/A	C	0.003811
Rhola_00004610	small subunit ribosomal protein S15	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_01118	#N/A	0.587882
Rhola_00004620	polyribonucleotide nucleotidyltransferase	F:RNA binding; C:cytoplasm; F:nucleotidyltransferase activity; P:nucleobase-containing compound catabolic process; F:ion binding	AURMO_01117	I	1.20E-09
Rhola_00004630	Predicted Zn-dependent peptidase	F:peptidase activity; F:ion binding	AURMO_01115	I	1.87E-13
Rhola_00004640	dihydrodipicolinate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_01113	J	0.00126

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004650	hypothetical protein	C:cellular_component	#N/A	#N/A	0.508599
Rhola_00004660	protein of unknown function (DUF4395)	C:cellular_component	#N/A	I	5.81E-06
Rhola_00004670	Thioredoxin	C:cell; P:homeostatic process	#N/A	G	0.000204
Rhola_00004680	thymidylate synthase (FAD)	F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00606	#N/A	0.602564
Rhola_00004690	sulfate permease, SulP family	C:cellular_component; F:transmembrane transporter activity	AURMO_00186	D	7.74E-06
Rhola_00004700	4-hydroxy-tetrahydrodipicolinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	AURMO_00607	#N/A	0.349872
Rhola_00004710	ribonuclease J	F:RNA binding; F:nuclease activity; C:cytoplasm; P:ribosome biogenesis; F:ion binding	AURMO_00608	#N/A	0.018474
Rhola_00004720	DNA segregation ATPase FtsK/SpoIIIE, S-DNA-T family	F:DNA binding; C:plasma membrane; P:cell cycle; P:chromosome segregation; F:ion binding; P:cell division	AURMO_00614	E	0.005098

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004730	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	F:molecular_function; C:cellular_component; P:lipid metabolic process; P:biosynthetic process	AURMO_00615	E	0.00134
Rhola_00004740	nicotinamide-nucleotide amidase	0	AURMO_00616	#N/A	0.273844
Rhola_00004750	Helix-turn-helix domain-containing protein	F:DNA binding	AURMO_00617	G	1.48E-36
Rhola_00004760	Protein of unknown function (DUF3046)	0	#N/A	G	3.29E-13
Rhola_00004770	recombination protein RecA	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; F:ion binding	AURMO_00619	K	8.92E-06
Rhola_00004780	regulatory protein	C:cytoplasm; P:DNA metabolic process; P:response to stress	#N/A	#N/A	0.567259
Rhola_00004790	tRNA-2-methylthio-N6-dimethylallyladenosine synthase	C:cytoplasm; P:tRNA metabolic process; F:ion binding	AURMO_00622	#N/A	0.022913
Rhola_00004800	tRNA dimethylallyltransferase	P:tRNA metabolic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	AURMO_00623	#N/A	0.410884
Rhola_00004810	diaminopimelate epimerase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity	AURMO_00624	#N/A	0.116119

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004820	16S rRNA m(2)G 1207 methyltransferase	P:biological_process; F:methyltransferase activity	AURMO_00626	H	1.25E-08
Rhola_00004830	GTP-binding protein HflX	F:GTPase activity; C:cytoplasm; F:ion binding	AURMO_00629	#N/A	0.624271
Rhola_00004840	SOS-response transcriptional repressor, LexA	F:DNA binding; P:DNA metabolic process; P:response to stress; F:peptidase activity; P:biosynthetic process	AURMO_01032	H	4.96E-07
Rhola_00004850	LysM domain-containing protein	C:cellular_component; P:biological_process	#N/A	H	4.58E-12
Rhola_00004860	histidinol-phosphate aminotransferase	P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_01030	#N/A	0.559319
Rhola_00004870	imidazoleglycerol-phosphate dehydratase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_01029	J	0.000204

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004880	glutamine amidotransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_01028	#N/A	0.437575
Rhola_00004890	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process	AURMO_01027	#N/A	0.465745
Rhola_00004900	SseB protein N-terminal domain-containing protein	0	AURMO_01026	#N/A	0.276804
Rhola_00004910	hypothetical protein	0	#N/A	#N/A	0.097521
Rhola_00004920	translation initiation factor IF-3	C:cytoplasm; F:translation factor activity, RNA binding	AURMO_01021	#N/A	0.120609
Rhola_00004930	large subunit ribosomal protein L35	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	#N/A	0.059256

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004940	large subunit ribosomal protein L20	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; P:ribonucleoprotein complex assembly; P:ribosome biogenesis	AURMO_01019	#N/A	0.134383
Rhola_00004950	RNA methyltransferase, TrmH family	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_01018	#N/A	0.031184
Rhola_00004960	phenylalanyl-tRNA synthetase, alpha subunit	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01015	L	0.000439
Rhola_00004970	phenylalanyl-tRNA synthetase beta subunit	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01014	#N/A	0.882554
Rhola_00004980	N-acetyl-gamma-glutamyl-phosphate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_01012	D	3.15E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00004990	glutamate N-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_01011	#N/A	0.015293
Rhola_00005000	N-acetylglutamate kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	AURMO_01010	C	1.01E-05
Rhola_00005010	ornithine carbamoyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; F:ion binding	AURMO_01009	A	1.49E-07
Rhola_00005020	argininosuccinate lyase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	AURMO_01008	C	0.010536
Rhola_00005030	tyrosyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01007	C	4.24E-08
Rhola_00005070	hypothetical protein	0	AURMO_01003	J	1.55E-05
Rhola_00005080	hypothetical protein	0	#N/A	#N/A	0.986301
Rhola_00005090	HAD-superfamily subfamily IIA hydrolase, TIGR01457	F:molecular_function	AURMO_01002	#N/A	0.302389
Rhola_00005100	hypothetical protein	#N/A	#N/A	#N/A	0.033812

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005110	tRNA (guanine37-N1)-methyltransferase	C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity	AURMO_00594	#N/A	0.047967
Rhola_00005120	large subunit ribosomal protein L19	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00595	G	5.79E-05
Rhola_00005130	signal peptidase I	C:cellular_component; F:peptidase activity	AURMO_00596	#N/A	0.221904
Rhola_00005140	RNase HII	F:RNA binding; F:nuclease activity; C:cytoplasm; F:ion binding	AURMO_00597	#N/A	0.038856
Rhola_00005150	Protein of unknown function (DUF2469)	0	AURMO_00598	B	2.50E-07
Rhola_00005160	putative endonuclease	F:nuclease activity	#N/A	#N/A	0.750429
Rhola_00005170	magnesium chelatase family protein	F:ATP binding	#N/A	#N/A	0.042486
Rhola_00005180	DNA processing protein	P:biological_process	AURMO_00599	N	0.008401
Rhola_00005190	integrase/recombinase XerC	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:cell cycle; P:chromosome segregation; P:transposition; P:cell division	AURMO_00600	#N/A	0.030005
Rhola_00005200	Membrane proteins related to metalloendopeptidases	#N/A	#N/A	D	0.000171
Rhola_00005210	small subunit ribosomal protein S2	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	AURMO_01108	#N/A	0.018203

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005220	elongation factor Ts	C:cytoplasm; F:translation factor activity, RNA binding	AURMO_01107	I	0.000122
Rhola_00005230	uridylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01106	#N/A	0.457132
Rhola_00005240	ribosome recycling factor	C:cytoplasm; P:translation	AURMO_01105	#N/A	0.420476
Rhola_00005250	phosphatidate cytidylyltransferase	C:cellular_component; P:lipid metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01104	#N/A	0.197264
Rhola_00005260	DivIVA domain-containing protein	0	#N/A	A	0.000232
Rhola_00005270	Protein of unknown function (DUF1524)	F:endonuclease activity; P:nucleic acid phosphodiester bond hydrolysis	#N/A	A	0.002484
Rhola_00005280	Transglycosylase SLT domain-containing protein	C:cellular_component	AURMO_01102	#N/A	0.391378
Rhola_00005290	hypothetical protein	0	#N/A	I	0.005069
Rhola_00005300	hypothetical protein	F:molecular_function	AURMO_01100	H	2.96E-14
Rhola_00005310	Predicted PurR-regulated permease PerM	C:cellular_component	AURMO_01099	#N/A	0.052383

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005320	DivIVA protein	0	#N/A	J	5.04E-09
Rhola_00005330	hypothetical protein	C:cellular_component	AURMO_01097	#N/A	0.022857
Rhola_00005340	putative thioredoxin	C:cell; P:homeostatic process	AURMO_01096	#N/A	0.366181
Rhola_00005350	1,4-alpha-glucan branching enzyme	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on glycosyl bonds; F:ion binding	AURMO_01095	#N/A	0.058558
Rhola_00005360	starch synthase (maltosyl-transferring)	P:carbohydrate metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on glycosyl bonds	AURMO_01094	D	0.003883
Rhola_00005370	glycogen operon protein	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:hydrolase activity, acting on glycosyl bonds	AURMO_01093	#N/A	0.123473
Rhola_00005380	cysteine desulfurase	F:molecular_function	AURMO_01092	#N/A	0.949877

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005390	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity; F:ion binding	AURMO_01091	#N/A	0.041145
Rhola_00005400	DNA ligase (NAD+)	F:DNA binding; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ligase activity; F:ion binding	AURMO_01090	D	3.38E-13
Rhola_00005410	DivIVA domain-containing protein	0	AURMO_00173	#N/A	0.218822
Rhola_00005420	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	P:translation; F:ligase activity; F:ion binding	#N/A	#N/A	0.349648
Rhola_00005430	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A	C:intracellular; P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; C:protein-containing complex; F:ion binding	AURMO_01087	#N/A	0.780473
Rhola_00005440	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	P:translation; F:ligase activity; F:ion binding	AURMO_01086	D	0.005351
Rhola_00005460	oligoribonuclease	F:nuclease activity; C:cytoplasm	AURMO_01076	#N/A	0.046048
Rhola_00005470	hydrophobic/amphiphilic exporter-1, HAE1 family	C:cellular_component; F:transmembrane transporter activity	AURMO_01636	G	2.80E-21
Rhola_00005480	tellurite resistance protein TerC	C:cellular_component	AURMO_00575	B	7.11E-12
Rhola_00005490	Uncharacterized membrane protein	C:cellular_component	#N/A	D	0.0008

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005510	hypothetical protein	F:isomerase activity	#N/A	#N/A	0.130825
Rhola_00005520	Short-chain dehydrogenase	F:oxidoreductase activity	AURMO_01236	B	0.00059
Rhola_00005530	argininosuccinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding	AURMO_01537	#N/A	0.483624
Rhola_00005540	glutathione peroxidase	P:response to stress; F:oxidoreductase activity	AURMO_00512	G	2.03E-23
Rhola_00005550	Uncharacterized protein, UPF0303 family	0	#N/A	E	1.85E-05
Rhola_00005560	DNA-binding transcriptional regulator, Lrp family	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	J	5.37E-08
Rhola_00005570	alanine dehydrogenase	P:cellular amino acid metabolic process; P:catabolic process; F:oxidoreductase activity	AURMO_01143	B	0.000305
Rhola_00005580	agmatine deiminase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process	AURMO_01484	D	4.05E-11
Rhola_00005590	N-carbamoylputrescine amidase	P:biological_process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	D	1.61E-09

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005600	Glutamate or tyrosine decarboxylase	F:lyase activity; F:ion binding; P:small molecule metabolic process	AURMO_01483	D	1.19E-14
Rhola_00005610	hypothetical protein	C:cellular_component	#N/A	A	0.00315
Rhola_00005620	thioredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process; P:small molecule metabolic process	AURMO_00944	#N/A	0.086405
Rhola_00005630	peptide-methionine (S)-S-oxide reductase	P:cellular protein modification process; F:oxidoreductase activity	AURMO_01068	#N/A	0.974624
Rhola_00005640	single-strand DNA-binding protein	#N/A	#N/A	#N/A	0.140768
Rhola_00005650	ATP-binding cassette protein, ChvD family	P:translation; F:ATPase activity; F:ion binding	AURMO_01065	#N/A	0.474279
Rhola_00005660	glutamate-1-semialdehyde 2,1-aminomutase	F:isomerase activity; F:ion binding	#N/A	A	1.19E-08
Rhola_00005670	acyl-CoA thioesterase-2	F:molecular_function; P:sulfur compound metabolic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01062	D	1.63E-06
Rhola_00005680	hypothetical protein	0	#N/A	D	4.74E-07
Rhola_00005690	hemoglobin	F:molecular_function	AURMO_01060	#N/A	0.050229
Rhola_00005700	small conductance mechanosensitive channel	C:cellular_component; P:transmembrane transport	AURMO_01059	#N/A	0.174861

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005710	aminopeptidase N	F:peptidase activity; F:ion binding	AURMO_01058	C	2.42E-05
Rhola_00005720	monovalent cation H+ antiporter-2, CPA2 family	C:cellular_component; F:transmembrane transporter activity	AURMO_00601	#N/A	0.15347
Rhola_00005730	ribose 5-phosphate isomerase B	P:carbohydrate metabolic process; F:isomerase activity	AURMO_01057	B	2.36E-06
Rhola_00005740	endonuclease-8	F:DNA binding; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds; F:lyase activity; F:ion binding	AURMO_01056	#N/A	0.134233
Rhola_00005770	trigger factor	C:cytoplasm; P:protein folding; P:cellular protein modification process; P:cell cycle; P:protein transport; F:isomerase activity; P:cell division	AURMO_01047	J	0.00339
Rhola_00005780	ATP-dependent Clp protease, protease subunit	C:cytoplasm; F:peptidase activity	AURMO_01037	G	2.51E-11
Rhola_00005790	ATP-dependent Clp protease, protease subunit	C:cytoplasm; F:peptidase activity	AURMO_01036	G	5.88E-15
Rhola_00005800	ATP-dependent Clp protease ATP-binding subunit ClpX	P:protein folding; F:peptidase activity; F:ion binding; F:unfolded protein binding	AURMO_01034	#N/A	0.021432

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005810	benzoate membrane transport protein	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.018474
Rhola_00005820	valyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00939	B	8.54E-17
Rhola_00005830	Isoleucyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00938	B	0.002327
Rhola_00005840	dihydrofolate synthase / folylpolyglutamate synthase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00937	E	0.009712
Rhola_00005850	Protein of unknown function (DUF4233)	C:cellular_component	#N/A	B	0.000148

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005860	nucleoside diphosphate kinase	P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00935	B	0.014826
Rhola_00005870	Uncharacterized membrane protein	C:cellular_component	AURMO_00933	#N/A	0.047967
Rhola_00005880	ribonuclease E	F:RNA binding; F:nuclease activity	AURMO_00932	G	7.94E-07
Rhola_00005890	large subunit ribosomal protein L21	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00931	#N/A	0.0494
Rhola_00005900	large subunit ribosomal protein L27	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00930	#N/A	0.144119
Rhola_00005910	GTP-binding protein	F:GTPase activity; C:cytoplasm; P:ribosome biogenesis; F:ion binding	AURMO_00929	G	2.85E-06
Rhola_00005920	glutamate 5-kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	AURMO_00928	G	7.30E-06
Rhola_00005930	glutamate-5-semialdehyde dehydrogenase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00927	#N/A	0.05955
Rhola_00005940	hypothetical protein	C:cellular_component	#N/A	#N/A	0.517767

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00005950	nicotinate-nucleotide adenylyltransferase	P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00925	J	2.66E-05
Rhola_00005960	hypothetical protein	C:cellular_component	#N/A	B	1.60E-08
Rhola_00005970	ribosome-associated protein	C:cytoplasm; P:translation; P:cellular component assembly; P:ribosome biogenesis	AURMO_00923	#N/A	0.651962
Rhola_00005990	hypothetical protein	0	#N/A	#N/A	0.085378
Rhola_00006000	deoxyribose-phosphate aldolase	C:cytoplasm; P:carbohydrate metabolic process; P:biosynthetic process; F:lyase activity; P:nucleobase-containing compound catabolic process; P:small molecule metabolic process	#N/A	B	0.000239
Rhola_00006010	phospholipase/carboxylesterase	F:molecular_function	#N/A	#N/A	0.042088
Rhola_00006020	Uncharacterized membrane protein, YccA/Bax inhibitor family	#N/A	#N/A	H	1.48E-05
Rhola_00006030	Putative SOS response-associated peptidase YedK	F:peptidase activity	AURMO_01241	I	5.34E-05
Rhola_00006040	membrane protein DedA, SNARE-associated domain	C:cellular_component	AURMO_00631	I	0.001505

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006050	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase	F:lyase activity	#N/A	H	2.23E-09
Rhola_00006060	para-aminobenzoate synthetase	P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00633	#N/A	0.424655
Rhola_00006070	leucyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00634	#N/A	0.022303
Rhola_00006080	competence protein ComEA	F:DNA binding; C:cellular_component; P:DNA metabolic process; P:response to stress	AURMO_00911	#N/A	0.0567
Rhola_00006090	competence protein ComEC	C:cellular_component; P:biological_process	AURMO_00910	M	0.000488
Rhola_00006100	DNA polymerase III, delta subunit	F:DNA binding; C:intracellular; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex	AURMO_00909	D	0.010784
Rhola_00006110	MFS transporter, CP family, cyanate transporter	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.183403

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006120	small subunit ribosomal protein S20	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	#N/A	G	0.001264
Rhola_00006130	GTP-binding protein LepA	F:GTPase activity; C:plasma membrane; F:translation factor activity, RNA binding; F:ion binding	AURMO_00907	#N/A	0.094203
Rhola_00006140	oxygen-independent coproporphyrinogen-3 oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_00905	I	0.0007
Rhola_00006150	hypothetical protein	C:cellular_component	#N/A	D	0.007072
Rhola_00006160	heat-inducible transcription repressor HrcA	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00904	G	0.008704
Rhola_00006170	molecular chaperone DnaJ	C:cytoplasm; P:protein folding; P:response to stress; P:biosynthetic process; F:ion binding; F:unfolded protein binding	AURMO_00903	#N/A	0.01806

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006180	16S rRNA (uracil1498-N3)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00902	G	0.000466
Rhola_00006190	histidine triad (HIT) family protein	F:molecular_function	#N/A	#N/A	0.059398
Rhola_00006200	phosphate starvation-inducible protein PhoH	F:ion binding	AURMO_00900	#N/A	0.760075
Rhola_00006210	probable rRNA maturation factor	F:nuclease activity; C:cytoplasm; F:peptidase activity; P:ribosome biogenesis; F:ion binding	AURMO_00899	K	0.000591
Rhola_00006220	Hemolysins and related proteins containing CBS domains	#N/A	#N/A	#N/A	0.281802
Rhola_00006230	GTP-binding protein Era	0	AURMO_00897	A	3.33E-07
Rhola_00006240	2-isopropylmalate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_00896	#N/A	0.48093
Rhola_00006250	DNA replication and repair protein RecO	P:DNA metabolic process; P:response to stress	AURMO_00687	#N/A	0.450372
Rhola_00006260	undecaprenyl diphosphate synthase	F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	AURMO_00688	D	1.55E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006270	glycyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01740	#N/A	0.624406
Rhola_00006280	putative TIM-barrel protein, nifR3 family	P:tRNA metabolic process; F:oxidoreductase activity; F:ion binding	AURMO_00691	D	3.10E-08
Rhola_00006290	dGTPase	F:molecular_function	AURMO_00692	A	9.05E-07
Rhola_00006300	DNA primase	F:DNA binding; C:chromosome; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex; F:ion binding	AURMO_00693	A	1.02E-09
Rhola_00006310	Phosphoglycerate dehydrogenase	F:molecular_function; P:biological_process	AURMO_00694	C	7.85E-15
Rhola_00006330	Signal transduction histidine kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity	#N/A	E	0.00008
Rhola_00006340	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	J	0.002452

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006350	Predicted branched-chain amino acid permease (azaleucine resistance)	C:cellular_component	AURMO_00696	#N/A	0.519103
Rhola_00006360	Branched-chain amino acid transport protein (AzlD)	C:cellular_component	#N/A	#N/A	0.347713
Rhola_00006370	peptide deformylase	P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	AURMO_00698	#N/A	0.526357
Rhola_00006380	Magnesium transporter NIPA	C:cellular_component; F:transmembrane transporter activity	AURMO_00699	#N/A	0.229493
Rhola_00006390	Glycosyltransferase involved in cell wall bisynthesis	F:molecular_function	AURMO_00700	B	1.43E-06
Rhola_00006410	hypothetical protein	#N/A	#N/A	#N/A	0.232458
Rhola_00006420	polar amino acid transport system permease protein	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	#N/A	0.312286
Rhola_00006430	polar amino acid transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.692188
Rhola_00006440	polar amino acid transport system substrate-binding protein	0	#N/A	#N/A	0.546465
Rhola_00006450	Predicted acetyltransferase, GNAT superfamily	F:N-acetyltransferase activity; F:transferase activity	#N/A	#N/A	0.78288

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006460	O-succinylbenzoate synthase	P:biosynthetic process; F:lyase activity; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	#N/A	0.638688
Rhola_00006470	thymidine kinase	P:DNA metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	AURMO_00306	A	0.002595
Rhola_00006480	3-oxoacyl-[acyl-carrier-protein] synthase II	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; P:small molecule metabolic process	AURMO_00720	#N/A	0.740714
Rhola_00006490	acyl carrier protein	F:molecular_function; C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; P:small molecule metabolic process	AURMO_00721	#N/A	0.02354
Rhola_00006500	3-oxoacyl-[acyl-carrier-protein] synthase-3	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; P:small molecule metabolic process	AURMO_00722	E	1.69E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006510	[acyl-carrier-protein] S-malonyltransferase	F:transferase activity, transferring acyl groups	AURMO_00723	C	4.64E-18
Rhola_00006520	PucR C-terminal helix-turn-helix domain-containing protein	0	AURMO_00724	B	6.91E-16
Rhola_00006530	pyruvate dehydrogenase E1 component	F:oxidoreductase activity; F:ion binding	AURMO_00725	B	0.000102
Rhola_00006540	Peroxiredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process	AURMO_00726	G	6.58E-23
Rhola_00006560	Purine-cytosine permease	C:cellular_component; F:transmembrane transporter activity	#N/A	A	5.02E-10
Rhola_00006570	dinuclear metal center protein, YbgI/SA1388 family	0	AURMO_00729	A	0.001751
Rhola_00006580	hypothetical protein	0	#N/A	C	0.001667
Rhola_00006590	probable phosphoglycerate mutase	F:nuclease activity; F:isomerase activity	AURMO_00731	A	1.19E-14
Rhola_00006610	polyphosphate glucokinase	C:cellular_component; F:kinase activity	AURMO_00732	B	5.17E-08
Rhola_00006620	methionyl aminopeptidase	P:cellular protein modification process; F:peptidase activity; F:ion binding	AURMO_00733	#N/A	0.220294
Rhola_00006630	hypothetical protein	F:peptidase activity	#N/A	#N/A	0.207235

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006640	ketopantoate hydroxymethyltransferase	C:cytoplasm; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00736	A	1.85E-07
Rhola_00006650	Enamine deaminase RidA, house cleaning of reactive enamine intermediates, YjgF/YER057c/UK114 family	0	#N/A	#N/A	0.186088
Rhola_00006660	NAD+ synthase (glutamine-hydrolysing)	C:cytoplasm; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00737	D	0.000222
Rhola_00006670	glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity	AURMO_00738	#N/A	0.772195
Rhola_00006680	glutamate-ammonia-ligase adenylyltransferase	P:biological_process; F:nucleotidyltransferase activity; F:ion binding	AURMO_00739	#N/A	0.062967

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006690	glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding	AURMO_00740	J	8.29E-11
Rhola_00006700	RDD family protein	C:cellular_component	#N/A	B	4.20E-07
Rhola_00006710	protein of unknown function (DUF4191)	C:cellular_component	AURMO_00742	J	0.000815
Rhola_00006720	lipoic acid synthetase	C:cytoplasm; P:cellular protein modification process; P:lipid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process; P:protein maturation	AURMO_00743	G	5.95E-21
Rhola_00006730	lipoyl(octanoyl) transferase	C:cytoplasm; P:cellular protein modification process; F:transferase activity, transferring acyl groups; F:ligase activity; P:protein maturation	AURMO_00744	G	4.40E-23
Rhola_00006740	hypothetical protein	#N/A	#N/A	#N/A	0.054991
Rhola_00006750	2-oxoglutarate dehydrogenase E2 component	F:transferase activity, transferring acyl groups	AURMO_00746	A	0.000366

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006760	dihydrolipoamide dehydrogenase	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process; F:ion binding	AURMO_00361	#N/A	0.421813
Rhola_00006770	leucyl aminopeptidase	C:cytoplasm; F:peptidase activity; F:ion binding	AURMO_00748	B	3.71E-22
Rhola_00006780	PAC2 family protein	0	AURMO_00749	B	0.000539
Rhola_00006790	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	C:membrane; C:integral component of membrane	#N/A	D	0.001083
Rhola_00006800	Predicted arabinose efflux permease, MFS family	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.193756
Rhola_00006810	RNA polymerase primary sigma factor	F:DNA binding; F:DNA-binding transcription factor activity; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00750	G	1.03E-09
Rhola_00006820	UDP-N-acetylmuramoylalanine-D-glutamate ligase	P:biosynthetic process; F:ligase activity; F:ion binding	#N/A	J	3.18E-05
Rhola_00006830	hypothetical protein	F:molecular_function; P:cellular amino acid metabolic process	#N/A	#N/A	0.07367
Rhola_00006840	hypothetical protein	0	#N/A	G	5.25E-11

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006850	DNA gyrase subunit B	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	AURMO_00753	L	4.36E-08
Rhola_00006860	DNA gyrase subunit A	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	AURMO_00754	#N/A	0.084521
Rhola_00006870	Uncharacterized proteins of the AP superfamily	F:molecular_function	AURMO_00755	A	0.012269
Rhola_00006880	Protein of unknown function (DUF3071)	0	AURMO_00756	#N/A	0.138294
Rhola_00006890	protein of unknown function (DUF4193)	0	#N/A	K	5.43E-05
Rhola_00006900	Protein of unknown function (DUF3093)	#N/A	#N/A	B	0.000533
Rhola_00006910	dUTP pyrophosphatase	P:biosynthetic process; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00759	#N/A	0.433111
Rhola_00006920	Protein of unknown function (DUF3710)	0	AURMO_00760	#N/A	0.064399
Rhola_00006930	Protein of unknown function (DUF3159)	C:cellular_component	AURMO_00761	C	0.000952
Rhola_00006940	aconitate hydratase	F:lyase activity	AURMO_00762	A	4.77E-10

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00006950	1-deoxy-D-xylulose-5-phosphate synthase	P:lipid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00763	G	2.45E-24
Rhola_00006960	ribonuclease D	F:nuclease activity	AURMO_00766	#N/A	0.111584
Rhola_00006970	Protein of unknown function (DUF3000)	0	AURMO_00767	#N/A	0.710574
Rhola_00006980	Pyrimidine reductase, riboflavin biosynthesis	F:5-amino-6-(5-phosphoribosylamino)uracil reductase activity; P:riboflavin biosynthetic process; P:oxidation-reduction process	#N/A	J	7.68E-07
Rhola_00006990	cysteine desulfuration protein SufE	0	AURMO_00769	I	0.000722
Rhola_00007000	thiosulfate/3-mercaptopyruvate sulfurtransferase	F:molecular_function	AURMO_00770	I	5.11E-06
Rhola_00007010	cell division protein ZapE	F:ion binding	AURMO_00771	#N/A	0.016726
Rhola_00007020	ammonium transporter, Amt family	C:cellular_component; F:transmembrane transporter activity	AURMO_00772	J	0.00116
Rhola_00007030	ammonium transporter, Amt family	C:cellular_component; F:transmembrane transporter activity	AURMO_00773	B	0.000294
Rhola_00007070	malate dehydrogenase (quinone)	P:generation of precursor metabolites and energy; F:oxidoreductase activity	AURMO_00302	B	7.65E-06

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007080	Predicted Fe2+/Mn2+ transporter, VIT1/CCC1 family	#N/A	#N/A	C	0.002439
Rhola_00007090	threonyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00777	#N/A	0.58906
Rhola_00007100	Diadenosine tetraphosphate (Ap4A) hydrolase	F:molecular_function	AURMO_00778	A	2.19E-07
Rhola_00007110	pyridoxal 5'-phosphate synthase pdxS subunit	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00779	#N/A	0.195028
Rhola_00007120	5'-phosphate synthase pdxT subunit	P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00780	#N/A	0.465745

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007130	DNA-binding regulatory protein, YebC/PmpR family	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00781	#N/A	0.319594
Rhola_00007140	Holliday junction endonuclease RuvC	F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding	AURMO_00782	#N/A	0.671876
Rhola_00007150	Holliday junction DNA helicase subunit RuvA	F:DNA binding; F:helicase activity; C:intracellular; P:DNA metabolic process; P:response to stress; C:protein-containing complex; F:ion binding; P:chromosome organization	AURMO_00783	E	0.000145
Rhola_00007160	Holliday junction DNA helicase subunit RuvB	F:DNA binding; F:helicase activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	AURMO_00784	#N/A	0.041451
Rhola_00007170	preprotein translocase subunit YajC	C:cellular_component	#N/A	#N/A	0.047755
Rhola_00007180	preprotein translocase subunit SecD	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	AURMO_00786	B	0.000141

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007190	preprotein translocase subunit SecF	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	AURMO_00787	B	8.63E-07
Rhola_00007200	GTP pyrophosphokinase	F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00788	H	0.006879
Rhola_00007210	protein of unknown function (DUF349)	0	AURMO_00790	B	0.004072
Rhola_00007220	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	C:cellular_component; P:cellular protein modification process; F:isomerase activity	AURMO_00791	#N/A	0.307307
Rhola_00007230	putative ATPase	F:DNA binding; F:helicase activity; P:biosynthetic process; F:ion binding	AURMO_00792	D	0.014922
Rhola_00007240	small subunit ribosomal protein S4	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00793	I	0.007824
Rhola_00007250	protein of unknown function (DUF948)	C:cellular_component	#N/A	I	0.004421
Rhola_00007260	hypothetical protein	#N/A	#N/A	#N/A	0.098714
Rhola_00007270	alanyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00795	#N/A	0.07496

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007280	putative holliday junction resolvase	F:nuclease activity; C:cytoplasm; P:ribosome biogenesis	AURMO_00796	#N/A	0.671964
Rhola_00007290	UPF0755 protein	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:lyase activity; P:cell wall organization or biogenesis	AURMO_00797	E	1.44E-05
Rhola_00007300	shikimate dehydrogenase	F:oxidoreductase activity	AURMO_00798	E	2.94E-08
Rhola_00007310	chorismate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	AURMO_00799	#N/A	0.792042
Rhola_00007320	shikimate kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	#N/A	E	0.000895
Rhola_00007330	3-dehydroquinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_00801	A	5.61E-05
Rhola_00007340	3-dehydroquinate dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	AURMO_00802	#N/A	0.541682

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007350	elongation factor P	C:cytoplasm; F:translation factor activity, RNA binding	AURMO_00803	#N/A	0.989041
Rhola_00007360	NusB antitermination factor	F:RNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00804	E	0.014828
Rhola_00007370	pyrimidine operon attenuation protein / uracil phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00805	B	0.002843
Rhola_00007380	aspartate carbamoyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00806	#N/A	0.031771
Rhola_00007390	dihydroorotase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00807	A	0.000815

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007400	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	A	1.92E-05
Rhola_00007410	carbamoyl-phosphate synthase small subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00809	A	8.37E-05
Rhola_00007420	carbamoyl-phosphate synthase large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00810	A	3.19E-09
Rhola_00007430	orotidine-5'-phosphate decarboxylase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00811	A	3.53E-09
Rhola_00007440	guanylate kinase	C:cytoplasm; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00812	C	0.000325

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007450	DNA-directed RNA polymerase subunit omega	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	#N/A	J	0.000245
Rhola_00007460	phosphopantothenoylcysteine decarboxylase / phosphopantothenate--cysteine ligase	P:catabolic process; P:biosynthetic process; F:lyase activity; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00814	J	3.47E-05
Rhola_00007470	replication restart DNA helicase PriA	F:DNA binding; F:helicase activity	AURMO_00816	D	1.05E-09
Rhola_00007480	methionyl-tRNA formyltransferase	F:molecular_function; P:tRNA metabolic process; P:translation; P:cellular protein modification process	AURMO_00817	#N/A	0.4013
Rhola_00007490	16S rRNA (cytosine967-C5)-methyltransferase	F:RNA binding; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00818	A	0.001134

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007500	ribulose-phosphate 3-epimerase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:isomerase activity; F:ion binding	AURMO_00819	#N/A	0.255656
Rhola_00007510	phosphoribosyl-ATP pyrophosphatase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.04117
Rhola_00007520	ATP phosphoribosyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00821	#N/A	0.998626
Rhola_00007530	cyclase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00822	#N/A	0.066551

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007540	phosphoribosyl-AMP cyclohydrolase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	K	0.000161
Rhola_00007550	anthranilate synthase component 1	P:biosynthetic process; F:lyase activity	AURMO_00824	A	1.32E-05
Rhola_00007560	Tryptophan-associated transmembrane protein (Trp_oprn_chp)	C:cellular_component	#N/A	C	0.002452
Rhola_00007570	hypothetical protein	C:cellular_component	#N/A	J	0.008704
Rhola_00007580	indole-3-glycerol phosphate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00827	B	0.003855
Rhola_00007590	tryptophan synthase beta chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00828	#N/A	0.444781

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007600	tryptophan synthase, alpha chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	AURMO_00829	#N/A	0.642275
Rhola_00007610	prolipoprotein diacylglyceryl transferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	AURMO_00830	A	5.54E-05
Rhola_00007620	glutamate synthase (NADPH/NADH) large chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00831	J	0.003744
Rhola_00007630	glutamate synthase (NADPH/NADH) small chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00832	#N/A	0.986301
Rhola_00007640	pyruvate kinase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00833	B	0.000634
Rhola_00007660	response regulator receiver and ANTAR domain protein	F:RNA binding; P:signal transduction	AURMO_00835	C	0.007215
Rhola_00007670	uncharacterized domain 1-containing protein	0	AURMO_00836	D	0.00611

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007680	DNA polymerase I	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity	AURMO_00837	E	2.85E-10
Rhola_00007690	small subunit ribosomal protein S1	F:molecular_function; C:ribosome	AURMO_00838	#N/A	0.053
Rhola_00007700	dephospho-CoA kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00839	B	3.09E-05
Rhola_00007710	Excinuclease ABC subunit B	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; C:protein-containing complex; F:ion binding	AURMO_00840	E	3.50E-06

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007720	excinuclease ABC subunit A	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; C:protein-containing complex; F:ion binding	AURMO_00841	#N/A	0.186299
Rhola_00007730	Excinuclease ABC subunit C	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; C:protein-containing complex	AURMO_00842	C	2.53E-06
Rhola_00007740	UPF0042 nucleotide-binding protein	F:kinase activity; F:ion binding	AURMO_00660	F	0.000251
Rhola_00007750	hypothetical protein	F:DNA binding; P:cell cycle; P:cell division	AURMO_00661	A	0.00274
Rhola_00007760	superoxide dismutase, Fe-Mn family	P:response to stress; F:oxidoreductase activity; F:ion binding	AURMO_00662	G	9.26E-08
Rhola_00007770	glyceraldehyde 3-phosphate dehydrogenase	P:carbohydrate metabolic process; F:oxidoreductase activity; P:small molecule metabolic process	AURMO_00663	J	4.73E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007780	phosphoglycerate kinase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00664	J	4.10E-07
Rhola_00007790	triosephosphate isomerase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00665	G	0.009303
Rhola_00007800	preprotein translocase subunit SecG	C:plasma membrane; P:protein transport; F:transmembrane transporter activity	#N/A	#N/A	0.922727
Rhola_00007810	RNA polymerase-binding protein	P:biosynthetic process; F:enzyme binding; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00667	#N/A	0.618879

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007820	6-phosphogluconolactonase	F:molecular_function; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy	AURMO_00670	J	0.003088
Rhola_00007830	glucose-6-phosphate dehydrogenase assembly protein OpcA	0	AURMO_00671	#N/A	0.070864
Rhola_00007840	glucose-6-phosphate 1-dehydrogenase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:small molecule metabolic process	AURMO_00672	J	0.005211
Rhola_00007850	glucose-6-phosphate isomerase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00673	L	0.002669
Rhola_00007860	transaldolase	F:molecular_function; C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy	AURMO_00674	L	1.32E-05
Rhola_00007870	transketolase	F:ion binding	AURMO_00675	J	1.09E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007880	protoheme IX farnesyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00676	B	0.006699
Rhola_00007890	deoxyribodipyrimidine photo-lyase	P:cellular protein modification process; F:lyase activity	AURMO_01673	G	4.37E-17
Rhola_00007900	cytochrome c oxidase assembly protein subunit 15	C:plasma membrane; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_00677	G	5.27E-20
Rhola_00007910	Fe-S cluster assembly protein SufB	P:sulfur compound metabolic process; P:biosynthetic process; P:cellular component assembly; P:cofactor metabolic process	AURMO_00678	G	1.45E-23
Rhola_00007920	Fe-S cluster assembly protein SufD	P:sulfur compound metabolic process; P:biosynthetic process; P:cellular component assembly; P:cofactor metabolic process	AURMO_00679	G	3.96E-25

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00007930	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin subunit	F:oxidoreductase activity	#N/A	G	4.01E-21
Rhola_00007940	Fe-S cluster assembly ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00681	G	2.25E-22
Rhola_00007950	Metal-sulfur cluster biosynthetic enzyme	0	AURMO_00682	G	1.83E-25
Rhola_00007960	biotin transport system substrate-specific component	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.29996
Rhola_00007970	ATPase components of ABC transporters with duplicated ATPase domains	F:ATPase activity; F:ion binding	AURMO_00685	J	0.001321
Rhola_00007980	Cytochrome oxidase assembly protein ShyY1	C:plasma membrane	AURMO_00895	G	1.78E-15
Rhola_00007990	Protein of unknown function (DUF3099)	C:cellular_component	#N/A	G	3.15E-22
Rhola_00008000	3-oxoacyl-[acyl-carrier-protein] reductase	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	AURMO_00893	D	1.85E-06
Rhola_00008010	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	F:oxidoreductase activity	AURMO_00844	A	0.001069
Rhola_00008020	phosphoserine phosphatase	F:phosphatase activity	AURMO_00892	#N/A	0.015975
Rhola_00008030	glucose-1-phosphate adenylyltransferase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:biosynthetic process; F:nucleotidyltransferase activity; F:ion binding	AURMO_00891	K	3.63E-08

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008040	starch synthase	P:carbohydrate metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	AURMO_00890	A	0.004606
Rhola_00008050	iron complex transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00889	B	0.002458
Rhola_00008060	large subunit ribosomal protein L31	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00888	#N/A	0.022033
Rhola_00008070	DNA polymerase-3 subunit epsilon	F:nuclease activity; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	AURMO_00887	#N/A	0.229944
Rhola_00008080	5,10-methylenetetrahydrofolate reductase (NAD(P))	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_01033	B	5.35E-08
Rhola_00008090	methionine synthase (B12-dependent)	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:methyltransferase activity; P:biosynthetic process; F:ion binding	AURMO_00100	B	0.000346

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008100	Pimeloyl-ACP methyl ester carboxylesterase	F:transferase activity, transferring acyl groups	AURMO_00886	B	1.27E-05
Rhola_00008110	Glycosyltransferase involved in cell wall bisynthesis	F:molecular_function	AURMO_00885	C	0.001265
Rhola_00008120	probable phosphoglycerate mutase	F:phosphatase activity	#N/A	#N/A	0.450372
Rhola_00008130	NAD-dependent protein deacetylase, SIR2 family	F:ion binding	AURMO_00884	#N/A	0.190238
Rhola_00008150	hypothetical protein	0	#N/A	#N/A	0.585789
Rhola_00008160	undecaprenyl-diphosphatase	P:cell morphogenesis; F:molecular_function; C:plasma membrane; P:biosynthetic process; P:cell wall organization or biogenesis	AURMO_00879	#N/A	0.58906
Rhola_00008170	Predicted ATP-dependent carboligase, ATP-grasp superfamily	F:ligase activity	AURMO_00878	#N/A	0.333495
Rhola_00008180	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	F:molecular_function	AURMO_00877	#N/A	0.032167
Rhola_00008190	tRNA (adenine57-N1/adenine58-N1)-methyltransferase	C:intracellular; P:tRNA metabolic process; F:methyltransferase activity; C:protein-containing complex	AURMO_00876	B	0.000634
Rhola_00008200	FKBP-type peptidyl-prolyl cis-trans isomerases 1	#N/A	#N/A	A	0.004606
Rhola_00008210	proteasome accessory factor B	#N/A	#N/A	A	1.37E-15
Rhola_00008220	proteasome accessory factor C	0	AURMO_00873	A	4.59E-14
Rhola_00008230	hypothetical protein	C:cellular_component	#N/A	C	0.002989

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008240	sec-independent protein translocase protein TatA	C:plasma membrane; P:protein transport; F:transmembrane transporter activity; C:protein-containing complex	#N/A	#N/A	0.289673
Rhola_00008250	sec-independent protein translocase protein TatC	C:plasma membrane; P:protein transport; F:transmembrane transporter activity; C:protein-containing complex	AURMO_00871	#N/A	0.148235
Rhola_00008260	ATP-dependent RNA helicase HelY	F:helicase activity; F:ion binding	AURMO_00870	#N/A	0.289743
Rhola_00008270	apolipoprotein N-acyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_00869	#N/A	0.016574
Rhola_00008280	RNA polymerase-binding protein	P:biosynthetic process; F:enzyme binding; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	G	2.01E-21
Rhola_00008290	glycerophosphoryl diester phosphodiesterase	F:molecular_function; P:lipid metabolic process	AURMO_00843	#N/A	0.311393
Rhola_00008300	Uncharacterized membrane protein YczE	C:cellular_component	AURMO_01605	#N/A	0.098795
Rhola_00008310	8-oxo-dGTP pyrophosphatase MutT, NUDIX family	F:molecular_function	#N/A	#N/A	0.0363

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008320	anthranilate phosphoribosyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00853	#N/A	0.401783
Rhola_00008330	cytochrome c oxidase subunit 3	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity	AURMO_00854	B	3.44E-07
Rhola_00008340	ubiquinol-cytochrome c reductase cytochrome c subunit	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:lyase activity; F:ion binding	AURMO_00855	#N/A	0.904315
Rhola_00008350	menaquinol-cytochrome c reductase iron-sulfur subunit precursor	C:cellular_component; F:oxidoreductase activity	AURMO_00856	#N/A	0.238668
Rhola_00008360	menaquinol-cytochrome c reductase cytochrome b subunit precursor	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity	AURMO_00857	#N/A	0.096519
Rhola_00008370	TipAS antibiotic-recognition domain-containing protein	0	#N/A	#N/A	0.204807

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008380	hypothetical protein	F:monooxygenase activity; P:oxidation-reduction process	#N/A	#N/A	0.33124
Rhola_00008390	Cytochrome c oxidase subunit IV	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity	#N/A	B	4.94E-06
Rhola_00008400	cytochrome c oxidase subunit 1	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity; F:ion binding	AURMO_00860	B	0.009904
Rhola_00008410	cytochrome c oxidase subunit 2	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity; F:ion binding	AURMO_00861	L	0.0008
Rhola_00008420	Iron-sulfur cluster assembly accessory protein	F:structural molecule activity; P:protein maturation	AURMO_00862	G	1.54E-15
Rhola_00008430	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase	F:molecular_function	AURMO_00863	D	1.27E-06
Rhola_00008440	Protein of unknown function (DUF3043)	C:cellular_component	AURMO_00864	#N/A	0.019029

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008450	dihydroorotate oxidase A	C:cytoplasm; C:plasma membrane; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00865	#N/A	0.9018
Rhola_00008460	transcriptional repressor NrdR	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00866	H	0.012468
Rhola_00008470	histidinol dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00867	#N/A	0.276804
Rhola_00008480	NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family	F:ion binding	#N/A	G	2.59E-15
Rhola_00008490	DNA polymerase-3 subunit alpha	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	AURMO_00868	#N/A	0.170403

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008500	ribosomal large subunit pseudouridine synthase D	F:RNA binding; F:isomerase activity; P:cellular nitrogen compound metabolic process	AURMO_00659	#N/A	0.056734
Rhola_00008510	signal peptidase II	#N/A	#N/A	#N/A	0.091763
Rhola_00008520	DivIVA domain-containing protein	C:cytoplasm; P:cell cycle; P:cell division	AURMO_00657	#N/A	0.914458
Rhola_00008530	YggT family protein	C:cellular_component	#N/A	B	1.08E-05
Rhola_00008540	cell division inhibitor SepF	P:reproduction; C:cytoplasm; P:cell cycle; P:cellular component assembly; P:cell division	#N/A	L	0.010636
Rhola_00008550	hypothetical protein	F:ion binding	AURMO_00654	J	3.37E-31
Rhola_00008560	cell division protein FtsZ	#N/A	#N/A	L	1.56E-24
Rhola_00008570	cell division protein FtsQ	C:plasma membrane; P:cell cycle; P:cell division	AURMO_00652	#N/A	0.107758
Rhola_00008580	UDP-N-acetylmuramate--L-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	AURMO_00651	C	3.65E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008590	UDP-N-acetylglucosamine-N-acetylmuramylpentapeptide N-acetylglucosamine transferase	P:cell morphogenesis; C:plasma membrane; P:carbohydrate metabolic process; P:lipid metabolic process; P:cell cycle; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cell division; P:cell wall organization or biogenesis	AURMO_00650	C	8.40E-07
Rhola_00008600	cell division protein FtsW	C:cellular_component; P:cell division	AURMO_00649	C	9.82E-05
Rhola_00008610	UDP-N-acetylmuramoylalanine--D-glutamate ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process; P:cell division; P:cell wall organization or biogenesis	AURMO_00648	C	0.003158

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008620	Phospho-N-acetylmuramoyl-pentapeptide-transferase	P:cell morphogenesis; F:molecular_function; C:plasma membrane; P:cell cycle; P:biosynthetic process; P:cell division; P:cell wall organization or biogenesis	AURMO_00647	#N/A	0.047961
Rhola_00008630	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	AURMO_00646	B	0.000216
Rhola_00008640	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	AURMO_00645	#N/A	0.027077
Rhola_00008650	cell division protein FtsI (penicillin-binding protein 3)	C:cellular_component; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:ion binding; P:cell division	AURMO_00644	#N/A	0.02411
Rhola_00008660	hypothetical protein	C:cellular_component	#N/A	#N/A	0.017088

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008670	16S rRNA (cytosine1402-N4)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00642	#N/A	0.366181
Rhola_00008680	MraZ protein	F:DNA binding; F:DNA-binding transcription factor activity; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:cell division	AURMO_00641	#N/A	0.068573
Rhola_00008690	Protein of unknown function (DUF3040)	C:cellular_component	#N/A	G	1.52E-14
Rhola_00008700	geranylgeranyl diphosphate synthase, type I	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_00638	#N/A	0.710574
Rhola_00008710	hypothetical protein	F:DNA binding	#N/A	B	0.004477
Rhola_00008720	Predicted glycosyl hydrolase	#N/A	#N/A	B	0.008272
Rhola_00008730	serine/threonine protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	AURMO_00635	#N/A	0.037637

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008740	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_00949	A	0.000493
Rhola_00008750	1-acyl-sn-glycerol-3-phosphate acyltransferase	F:transferase activity, transferring acyl groups	AURMO_00950	#N/A	0.078824
Rhola_00008760	glucokinase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00951	H	4.94E-06
Rhola_00008770	long-chain acyl-CoA synthetase	P:lipid metabolic process; F:ligase activity; P:small molecule metabolic process	AURMO_00952	A	3.12E-06
Rhola_00008780	peptide deformylase	P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	AURMO_00953	#N/A	0.091145
Rhola_00008790	MinD-like ATPase involved in chromosome partitioning or flagellar assembly	0	AURMO_00954	B	9.46E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008800	pyruvate carboxylase	P:carbohydrate metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding; P:small molecule metabolic process	AURMO_00955	J	0.004442
Rhola_00008810	Cellulose biosynthesis protein BcsQ	#N/A	#N/A	#N/A	0.710574
Rhola_00008820	MerR HTH family regulatory protein	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00957	#N/A	0.047967
Rhola_00008830	Predicted transcriptional regulators	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00958	B	0.002298
Rhola_00008840	FOG FHA domain	0	AURMO_00959	B	0.014088
Rhola_00008850	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	F:molecular_function; C:cellular_component; P:lipid metabolic process; P:biosynthetic process	#N/A	B	0.000169
Rhola_00008860	GTP-binding protein	P:ribosome biogenesis; F:ion binding	AURMO_00979	#N/A	0.24725
Rhola_00008870	cytidylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00980	#N/A	0.555726

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008880	prephenate dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00981	B	0.011885
Rhola_00008890	chorismate mutase	P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity	#N/A	#N/A	0.598621
Rhola_00008900	23S rRNA pseudouridine2605 synthase	F:RNA binding; F:isomerase activity; P:cellular nitrogen compound metabolic process	AURMO_00982	#N/A	0.12786
Rhola_00008910	segregation and condensation protein B	C:cytoplasm; P:cell cycle; P:chromosome segregation; P:cell division	AURMO_00983	#N/A	0.612841
Rhola_00008920	condensin subunit ScpA	C:cytoplasm; P:cell cycle; P:chromosome segregation; P:cell division	AURMO_00984	#N/A	0.476685
Rhola_00008930	chromosome partitioning protein	0	AURMO_00008	E	0.000251
Rhola_00008940	integrase/recombinase XerD	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:cell cycle; P:chromosome segregation; P:transposition; P:cell division	AURMO_00986	#N/A	0.116119
Rhola_00008950	ADP-ribose pyrophosphatase	F:molecular_function	AURMO_00987	B	0.000107

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00008960	CTP synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00988	B	4.09E-06
Rhola_00008970	DNA replication and repair protein RecN	P:DNA metabolic process; P:response to stress; F:ion binding	AURMO_00989	G	6.30E-11
Rhola_00008980	NAD+ kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00990	G	5.18E-21
Rhola_00008990	23S rRNA (cytidine1920-2'-O)/16S rRNA (cytidine1409-2'-O)-methyltransferase	F:RNA binding; P:biological_process; F:methyltransferase activity	AURMO_00991	#N/A	0.349002
Rhola_00009000	16S rRNA processing protein RimM	F:molecular_function; C:cytoplasm; C:ribosome; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00593	#N/A	0.056106
Rhola_00009010	hypothetical protein	F:RNA binding	#N/A	#N/A	0.01549
Rhola_00009020	small subunit ribosomal protein S16	#N/A	#N/A	I	0.006916

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009030	signal recognition particle subunit FFH/SRP54 (srp54)	F:RNA binding; F:GTPase activity; C:cytoplasm; P:protein targeting; C:protein-containing complex; F:ion binding	AURMO_00588	#N/A	0.102276
Rhola_00009040	fused signal recognition particle receptor	#N/A	#N/A	B	0.00026
Rhola_00009050	condensin subunit Smc	F:DNA binding; C:chromosome; C:cytoplasm; P:cell cycle; P:chromosome segregation; P:biosynthetic process; F:ion binding; P:chromosome organization	AURMO_01153	B	0.002429
Rhola_00009060	DNA-(apurinic or apyrimidinic site) lyase	F:DNA binding; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds; F:lyase activity; F:ion binding	AURMO_01158	N	0.014148
Rhola_00009070	ribonuclease-3	F:nuclease activity; C:cytoplasm; P:mRNA processing; P:tRNA metabolic process; F:rRNA binding; P:nucleobase-containing compound catabolic process; P:ribosome biogenesis; F:ion binding	AURMO_01159	#N/A	0.220635

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009080	large subunit ribosomal protein L32	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	#N/A	#N/A	0.03387
Rhola_00009090	uncharacterized protein	0	AURMO_01161	H	8.07E-06
Rhola_00009100	Phosphopantetheine adenylyltransferase	C:cytoplasm; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00586	H	0.000359
Rhola_00009110	ATP-dependent DNA helicase RecG	F:helicase activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	AURMO_00585	#N/A	0.119744
Rhola_00009120	16S rRNA (guanine966-N2)-methyltransferase	F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00584	#N/A	0.207404
Rhola_00009130	citrate synthase	C:cytoplasm; P:generation of precursor metabolites and energy; F:transferase activity, transferring acyl groups	AURMO_01207	B	0.000545

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009140	succinyldiaminopimelate aminotransferase apoenzyme	P:biosynthetic process; F:ion binding	AURMO_01208	J	1.90E-08
Rhola_00009150	NAD-dependent dihydropyrimidine dehydrogenase, PreA subunit	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	AURMO_01209	G	8.73E-06
Rhola_00009160	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase	F:molecular_function; C:cellular_component	#N/A	B	7.68E-16
Rhola_00009170	GTP-binding protein	F:GTPase activity; F:ion binding	AURMO_01212	G	0.00224
Rhola_00009180	hypothetical protein	C:cellular_component; F:peptidase activity; P:protein maturation	AURMO_01213	#N/A	0.030378
Rhola_00009190	hypothetical protein	#N/A	#N/A	#N/A	0.109141
Rhola_00009200	hypothetical protein	0	#N/A	K	0.002174
Rhola_00009210	energy-coupling factor transport system permease protein	C:cellular_component	#N/A	D	0.001571
Rhola_00009220	energy-coupling factor transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00103	#N/A	0.051317
Rhola_00009230	energy-coupling factor transport system substrate-specific component	C:cellular_component; F:transmembrane transporter activity	#N/A	F	0.008549
Rhola_00009240	DoxX-like family protein	#N/A	#N/A	L	0.001058
Rhola_00009250	hypothetical protein	0	#N/A	G	0.000555
Rhola_00009260	Uncharacterized membrane protein YeiH	C:cellular_component	#N/A	#N/A	0.780305
Rhola_00009270	Threonine/homoserine/homoserine lactone efflux protein	C:plasma membrane; P:transport	#N/A	#N/A	0.854988
Rhola_00009280	SsrA-binding protein	F:RNA binding; C:cytoplasm; P:translation	AURMO_00508	E	0.000263

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009300	cell division transport system permease protein	C:plasma membrane; P:cell cycle; P:cell division	AURMO_00507	#N/A	0.15722
Rhola_00009310	cell division transport system ATP-binding protein	C:plasma membrane; P:cell cycle; F:ATPase activity; F:ion binding; P:cell division	AURMO_00506	B	4.08E-05
Rhola_00009320	peptide chain release factor 2	C:cytoplasm; F:translation factor activity, RNA binding	AURMO_00560	B	8.68E-05
Rhola_00009330	Predicted arabinose efflux permease, MFS family	C:cellular_component; F:transmembrane transporter activity	AURMO_00559	E	0.010774
Rhola_00009340	hypothetical protein	C:cellular_component	#N/A	#N/A	0.082247
Rhola_00009350	hypothetical protein	C:cellular_component	#N/A	#N/A	0.47146
Rhola_00009360	hypothetical protein	#N/A	#N/A	#N/A	0.435947
Rhola_00009370	hypothetical protein	#N/A	#N/A	#N/A	0.14779
Rhola_00009380	tight adherence protein C	#N/A	#N/A	#N/A	0.052695
Rhola_00009390	type II secretion system protein F (GspF)	#N/A	#N/A	#N/A	0.02085
Rhola_00009400	pilus assembly protein CpaF	0	AURMO_00482	N	0.013995
Rhola_00009420	Sugar phosphate permease	C:cellular_component; P:transmembrane transport	AURMO_01325	#N/A	0.254824
Rhola_00009430	serine protease	F:peptidase activity	#N/A	H	3.04E-05
Rhola_00009440	phosphinothricin acetyltransferase	F:transferase activity, transferring acyl groups	AURMO_00415	#N/A	0.248231

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009450	Uracil-DNA glycosylase	C:cytoplasm; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds	AURMO_00414	#N/A	0.149954
Rhola_00009460	O-acetylhomoserine (thiol)-lyase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	AURMO_00411	H	0.008312
Rhola_00009470	homoserine O-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_00406	H	1.44E-10
Rhola_00009480	Protein of unknown function (DUF2029)	C:cellular_component	AURMO_00405	#N/A	0.021908
Rhola_00009490	Predicted arabinose efflux permease, MFS family	C:cellular_component	#N/A	#N/A	0.196537
Rhola_00009500	2,4-dienoyl-CoA reductase	F:oxidoreductase activity; F:ion binding	AURMO_01707	D	2.83E-05
Rhola_00009510	Hemolysin, contains CBS domains	C:cellular_component	AURMO_00403	C	0.006989
Rhola_00009520	Hemolysin, contains CBS domains	C:cellular_component; F:ion binding	AURMO_00402	A	4.26E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009530	2-oxoglutarate dehydrogenase E1 component	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transferase activity, transferring acyl groups; F:ion binding	AURMO_00429	A	9.34E-07
Rhola_00009540	GDSL-like Lipase/Acylhydrolase family protein	0	#N/A	A	1.15E-11
Rhola_00009550	mycothiol system anti-sigma-R factor	0	#N/A	G	7.85E-15
Rhola_00009560	RNA polymerase sigma-70 factor, ECF subfamily	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00426	G	3.43E-17
Rhola_00009570	3-phosphoshikimate 1-carboxyvinyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_00425	#N/A	0.584556
Rhola_00009580	ribosome biogenesis GTPase	F:GTPase activity; C:cytoplasm; F:rRNA binding; P:ribosome biogenesis; F:ion binding	AURMO_00424	#N/A	0.459926
Rhola_00009590	histidinol-phosphatase	P:lipid metabolic process; F:phosphatase activity	AURMO_00515	#N/A	0.758468

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009600	transcriptional regulator, GntR family	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.582891
Rhola_00009610	myo-inositol 2-dehydrogenase / D-chiro-inositol 1-dehydrogenase	P:carbohydrate metabolic process; P:catabolic process; F:oxidoreductase activity; P:small molecule metabolic process	#N/A	#N/A	0.91154
Rhola_00009620	inosose dehydratase	F:lyase activity; F:isomerase activity	#N/A	#N/A	0.742013
Rhola_00009630	transcriptional regulator, LacI family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.33124
Rhola_00009640	myo-inositol catabolism protein IolH	F:isomerase activity	#N/A	A	6.77E-11
Rhola_00009650	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase	P:carbohydrate metabolic process; P:catabolic process; F:ion binding; P:small molecule metabolic process	#N/A	A	0.002039
Rhola_00009660	5-deoxyglucuronate isomerase	P:carbohydrate metabolic process; P:catabolic process; F:isomerase activity; P:small molecule metabolic process	#N/A	#N/A	0.841598

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009670	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase	F:oxidoreductase activity	AURMO_01245	#N/A	0.903186
Rhola_00009680	hypothetical protein	F:lyase activity	#N/A	#N/A	0.896399
Rhola_00009690	5-dehydro-2-deoxygluconokinase	F:kinase activity	#N/A	#N/A	0.986301
Rhola_00009700	hypothetical protein	C:cellular_component	#N/A	#N/A	0.146603
Rhola_00009710	cysteine synthase A	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_00465	G	0.005211
Rhola_00009720	serine O-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	AURMO_00463	J	2.09E-11
Rhola_00009730	Protein of unknown function (DUF1761)	C:cellular_component	#N/A	#N/A	0.146488
Rhola_00009740	Fatty acid desaturase	C:cellular_component; P:lipid metabolic process; F:oxidoreductase activity	AURMO_00530	#N/A	0.037128
Rhola_00009750	Uncharacterized conserved protein YdhG, YjbR/CyaY-like superfamily, DUF1801 family	#N/A	#N/A	#N/A	0.047303
Rhola_00009760	hypothetical protein	C:cellular_component	#N/A	#N/A	0.472267

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009770	Uncharacterized conserved protein YndB, AHSA1/START domain	0	AURMO_01237	#N/A	0.550722
Rhola_00009780	hypothetical protein	F:ATPase activity; F:ion binding	AURMO_01242	#N/A	0.143286
Rhola_00009790	DNA polymerase-3 subunit epsilon	F:nuclease activity; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	D	0.000685
Rhola_00009800	DNA recombination protein RmuC	C:cellular_component	AURMO_01246	M	0.005844
Rhola_00009810	1-phosphofructokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding	AURMO_01550	G	0.001429
Rhola_00009820	fructose-1,6-bisphosphatase II	P:carbohydrate metabolic process; P:biosynthetic process; F:phosphatase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.51475
Rhola_00009830	fructose-bisphosphate aldolase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01249	L	0.000722
Rhola_00009840	hypothetical protein	0	#N/A	#N/A	0.076326

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009850	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	AURMO_01257	#N/A	0.302369
Rhola_00009860	Exodeoxyribonuclease VII large subunit	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; C:protein-containing complex; P:nucleobase-containing compound catabolic process	AURMO_01258	#N/A	0.612895
Rhola_00009870	Exodeoxyribonuclease VII small subunit	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; C:protein-containing complex; P:nucleobase-containing compound catabolic process	#N/A	#N/A	0.195028
Rhola_00009880	Protein of unknown function (DUF4245)	#N/A	#N/A	#N/A	0.378932
Rhola_00009890	carbonic anhydrase	P:biological_process; F:lyase activity; F:ion binding	AURMO_01261	#N/A	0.732767
Rhola_00009900	fumarase, class II	C:cytoplasm; P:generation of precursor metabolites and energy; F:lyase activity; C:protein-containing complex; P:small molecule metabolic process	AURMO_01262	#N/A	0.025091

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00009910	hypothetical protein	#N/A	#N/A	#N/A	0.202292
Rhola_00009920	leader peptidase (prepilin peptidase) / N-methyltransferase	#N/A	#N/A	H	1.08E-09
Rhola_00009930	Putative lumazine-binding	0	AURMO_01700	H	2.63E-09
Rhola_00009940	PhoH-like ATPase	F:ion binding	AURMO_01314	A	6.15E-06
Rhola_00009950	short-chain Z-isoprenyl diphosphate synthase	F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	AURMO_01315	E	3.13E-05
Rhola_00009960	hemolysin III	C:cellular_component	AURMO_01317	#N/A	0.018434
Rhola_00009970	hypothetical protein	C:cellular_component	#N/A	#N/A	0.085378
Rhola_00009980	protein of unknown function (DUF4307)	C:cellular_component	#N/A	#N/A	0.021908
Rhola_00009990	transcription elongation factor GreA	F:DNA binding; F:translation factor activity, RNA binding; F:enzyme binding	AURMO_01321	B	0.007387
Rhola_00010000	threonine dehydratase	P:cellular amino acid metabolic process; P:catabolic process; F:lyase activity; F:ion binding	AURMO_01322	#N/A	0.196583
Rhola_00010010	heat shock protein HtpX	C:plasma membrane; F:peptidase activity; F:ion binding	AURMO_01323	#N/A	0.030558
Rhola_00010020	LemA protein	C:cellular_component	AURMO_01324	I	0.002327
Rhola_00010040	NADH dehydrogenase	F:oxidoreductase activity	AURMO_01330	#N/A	0.021908
Rhola_00010050	type VII secretion-associated serine protease mycosin	C:cellular_component; F:peptidase activity	AURMO_01331	#N/A	0.142043
Rhola_00010060	hypothetical protein	0	AURMO_01332	#N/A	0.137709

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010070	Cell division protein FtsB	C:cellular_component	#N/A	B	1.33E-10
Rhola_00010080	enolase	C:extracellular region; C:cytosol; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:lyase activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01334	J	7.09E-06
Rhola_00010090	histidyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01335	#N/A	0.077399
Rhola_00010100	XTP/dITP diphosphohydrolase	P:biological_process; F:methyltransferase activity	AURMO_01336	#N/A	0.14184
Rhola_00010110	transcription-repair coupling factor	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ion binding; P:chromosome organization	AURMO_01341	#N/A	0.387106

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010120	peptidyl-tRNA hydrolase, PTH1 family	F:molecular_function; C:cytoplasm; P:translation	AURMO_01343	#N/A	0.176653
Rhola_00010130	large subunit ribosomal protein L25	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_01344	#N/A	0.063972
Rhola_00010140	basic amino acid/polyamine antiporter, APA family	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.058679
Rhola_00010150	ribose-phosphate pyrophosphokinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01350	#N/A	0.32219
Rhola_00010160	bifunctional UDP-N-acetylglucosamine pyrophosphorylase / Glucosamine-1-phosphate N-acetyltransferase	P:cell morphogenesis; C:cytoplasm; P:carbohydrate metabolic process; P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cell wall organization or biogenesis	AURMO_01351	#N/A	0.366181

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010180	ATPase components of ABC transporters with duplicated ATPase domains	F:ATPase activity; F:ion binding	AURMO_01359	#N/A	0.022236
Rhola_00010190	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	P:lipid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	AURMO_01360	C	0.000159
Rhola_00010200	hypothetical protein	F:ATP binding; P:terpenoid biosynthetic process; P:phosphorylation; F:4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase activity	#N/A	#N/A	0.060655
Rhola_00010210	16S rRNA (adenine1518-N6/adenine1519-N6)-dimethyltransferase	F:RNA binding; C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_01361	#N/A	0.14184
Rhola_00010220	TatD DNase family protein	F:nuclease activity; P:DNA metabolic process	AURMO_01362	E	0.013335
Rhola_00010230	methionyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_01363	B	0.01064

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010240	16S rRNA (cytidine1402-2'-O)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_01366	#N/A	0.258049
Rhola_00010250	Dolichyl-phosphate-mannose--protein O-mannosyl transferase	C:cellular_component; P:cellular protein modification process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	AURMO_01367	#N/A	0.03682
Rhola_00010260	hypothetical protein	0	#N/A	B	0.002252
Rhola_00010270	2,5-diketo-D-gluconate reductase A	F:oxidoreductase activity	AURMO_01133	G	5.50E-17
Rhola_00010280	hypothetical protein	F:molecular_function	AURMO_00603	G	8.11E-15
Rhola_00010290	Histone H1-like nucleoprotein HC2	F:DNA binding; P:chromosome organization	#N/A	A	0.000815
Rhola_00010300	hypothetical protein	C:cellular_component	#N/A	B	0.000108
Rhola_00010310	ribosomal-protein-alanine N-acetyltransferase	C:ribosome; F:transferase activity, transferring acyl groups; C:protein-containing complex	AURMO_01402	D	2.97E-11
Rhola_00010320	5-formyltetrahydrofolate cyclo-ligase	F:ligase activity; F:ion binding	AURMO_01403	A	0.009666
Rhola_00010330	Part of AAA domain-containing protein	0	AURMO_01405	#N/A	0.121249
Rhola_00010350	5-methylcytosine-specific restriction endonuclease McrA	F:nuclease activity	AURMO_01416	D	7.46E-05
Rhola_00010360	Cell wall-associated hydrolase, NlpC family	F:molecular_function; C:cellular_component	#N/A	#N/A	0.185867

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010370	phosphoserine aminotransferase apoenzyme	F:molecular_function; C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process	AURMO_01419	B	0.000555
Rhola_00010380	Protein of unknown function (DUF3027)	0	#N/A	J	0.007043
Rhola_00010390	cold-shock DNA-binding protein family	F:DNA binding; C:cytoplasm	AURMO_01421	J	0.008727
Rhola_00010400	hypothetical protein	C:cellular_component	#N/A	J	0.003971
Rhola_00010410	Helicase conserved C-terminal domain-containing protein	0	AURMO_01423	#N/A	0.796173
Rhola_00010420	DNA excision repair protein ERCC-3	F:DNA binding; F:helicase activity; F:ion binding; P:chromosome organization	AURMO_01424	J	0.011158
Rhola_00010430	two-component system, OmpR family, response regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01425	H	0.001161
Rhola_00010440	two-component system, OmpR family, sensor kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	AURMO_01426	#N/A	0.033307
Rhola_00010450	WXG100 family type VII secretion target	0	#N/A	#N/A	0.168041
Rhola_00010460	chaperonin GroEL	C:cytoplasm; P:protein folding; F:ion binding; F:unfolded protein binding	AURMO_01428	G	0.004336

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010470	cold shock protein (beta-ribbon, CspA family)	F:DNA binding; C:cytoplasm	#N/A	H	0.014929
Rhola_00010480	LytR cell envelope-related transcriptional attenuator	C:cellular_component	#N/A	#N/A	0.796825
Rhola_00010490	peptide-methionine (R)-S-oxide reductase	P:response to stress; F:oxidoreductase activity; F:ion binding	AURMO_00589	G	9.39E-18
Rhola_00010500	hypothetical protein	C:cellular_component	#N/A	G	3.18E-19
Rhola_00010520	Protein-disulfide isomerase	C:cellular_component; F:isomerase activity	#N/A	#N/A	0.45909
Rhola_00010530	carbohydrate ABC transporter ATP-binding protein, CUT1 family	P:transport; F:ATPase activity; F:ion binding	AURMO_00917	G	0.000733
Rhola_00010540	protein of unknown function (DUF4032)	F:kinase activity	AURMO_00918	#N/A	0.082029
Rhola_00010550	Protein of unknown function (DUF3117)	0	#N/A	#N/A	0.400862
Rhola_00010560	succinyldiaminopimelate desuccinylase	P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	AURMO_01201	#N/A	0.332786
Rhola_00010570	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; F:ion binding	AURMO_01202	#N/A	0.250088
Rhola_00010580	Bacterial RNA polymerase, alpha chain C terminal domain.	0	#N/A	#N/A	0.796987

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010590	thiamine-phosphate kinase	P:sulfur compound metabolic process; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00583	#N/A	0.366181
Rhola_00010600	Protein of unknown function (DUF3515)	0	AURMO_00582	D	1.56E-06
Rhola_00010610	D-alanine-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell wall organization or biogenesis	AURMO_00581	F	1.80E-06
Rhola_00010620	glycerol-3-phosphate dehydrogenase (NAD(P)+)	C:cytoplasm; P:carbohydrate metabolic process; P:lipid metabolic process; P:catabolic process; P:biosynthetic process; F:oxidoreductase activity; C:protein-containing complex	AURMO_00580	A	5.47E-07
Rhola_00010630	1-acyl-sn-glycerol-3-phosphate acyltransferase	C:cellular_component; F:transferase activity, transferring acyl groups	AURMO_00579	A	8.37E-05

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010640	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cell division; P:cell wall organization or biogenesis	AURMO_00578	#N/A	0.507876
Rhola_00010650	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	C:cytosol; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; C:protein-containing complex	AURMO_00577	J	0.004815
Rhola_00010660	3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_00576	#N/A	0.204079
Rhola_00010670	Predicted arabinose efflux permease, MFS family	C:cellular_component; P:transmembrane transport	AURMO_00495	#N/A	0.015547
Rhola_00010690	diacylglycerol kinase (ATP)	F:kinase activity	AURMO_00573	F	0.000124
Rhola_00010700	Cu2+-exporting ATPase	F:molecular_function; C:cellular_component	#N/A	B	5.73E-08
Rhola_00010710	L-ascorbate metabolism protein UlaG, beta-lactamase superfamily	F:molecular_function	#N/A	#N/A	0.730002
Rhola_00010720	hypothetical protein	C:cellular_component	#N/A	#N/A	0.32223

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010740	glutamyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00571	C	0.008475
Rhola_00010750	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	F:molecular_function	AURMO_01497	D	4.88E-15
Rhola_00010760	branched-chain amino acid aminotransferase	F:molecular_function; P:cellular amino acid metabolic process; P:biosynthetic process	AURMO_00570	D	2.06E-07
Rhola_00010770	3-isopropylmalate dehydrogenase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding	AURMO_00569	#N/A	0.323916
Rhola_00010780	Methyltransferase domain-containing protein	#N/A	#N/A	#N/A	0.248231
Rhola_00010790	Rhodanese-related sulfurtransferase	F:molecular_function	#N/A	#N/A	0.34807
Rhola_00010800	D-3-phosphoglycerate dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_00568	J	3.72E-09
Rhola_00010810	ketol-acid reductoisomerase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:isomerase activity; F:ion binding	AURMO_00565	#N/A	0.321505

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010820	acetolactate synthase, small subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:enzyme regulator activity	AURMO_00564	#N/A	0.121249
Rhola_00010830	acetolactate synthase, large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ion binding	AURMO_00563	#N/A	0.022074
Rhola_00010840	dihydroxy-acid dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	AURMO_00562	#N/A	0.283725
Rhola_00010850	hypothetical protein	#N/A	#N/A	G	8.77E-19
Rhola_00010860	Phytoene/squalene synthetase	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:small molecule metabolic process	AURMO_01714	#N/A	0.237055
Rhola_00010870	phytoene desaturase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity	AURMO_01713	G	1.37E-05
Rhola_00010880	lycopene cyclase domain-containing protein	C:cellular_component; F:isomerase activity	#N/A	G	2.74E-06
Rhola_00010890	lycopene cyclase domain-containing protein	C:cellular_component; F:isomerase activity	#N/A	G	0.004558

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010900	4-hydroxybenzoate polyprenyltransferase	C:cellular_component; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_01710	I	0.001731
Rhola_00010910	SprT-like family protein	#N/A	#N/A	D	0.011552
Rhola_00010920	nucleobase cation symporter-1, NCS1 family	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.099269
Rhola_00010930	cytosine deaminase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.157863
Rhola_00010940	8-oxo-dGTP diphosphatase	F:nucleotidyltransferase activity	AURMO_01223	J	2.80E-09
Rhola_00010950	quinolinate synthetase	C:cytoplasm; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01224	#N/A	0.24857

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00010960	L-aspartate oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01225	#N/A	0.383339
Rhola_00010970	nicotinate-nucleotide pyrophosphorylase [carboxylating]	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01226	#N/A	0.270287
Rhola_00010980	cysteine desulfurase	F:molecular_function	AURMO_01227	E	0.013023
Rhola_00010990	catechol 2,3-dioxygenase	F:oxidoreductase activity; F:lyase activity; F:ion binding	#N/A	G	1.04E-11
Rhola_00011000	deoxyribodipyrimidine photo-lyase	F:lyase activity	#N/A	G	2.57E-22
Rhola_00011010	hypothetical protein	#N/A	#N/A	G	5.23E-10
Rhola_00011030	peroxiredoxin Q/BCP	C:cell; F:oxidoreductase activity; P:homeostatic process	AURMO_00420	#N/A	0.026351
Rhola_00011040	hypothetical protein	C:cellular_component	#N/A	B	1.86E-13

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011050	WhiB family transcriptional regulator, redox-sensing transcriptional regulator	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	I	2.65E-10
Rhola_00011060	Two-component sensor histidine kinase, contains HisKA and HATPase domains	P:cellular protein modification process; F:kinase activity; F:ion binding	AURMO_00401	D	1.16E-06
Rhola_00011070	MinD-like ATPase involved in chromosome partitioning or flagellar assembly	#N/A	#N/A	D	0.000171
Rhola_00011080	SAF domain.	C:membrane; C:integral component of membrane	#N/A	N	0.000852
Rhola_00011090	hypothetical protein	0	#N/A	#N/A	0.016814
Rhola_00011100	hypothetical protein	0	#N/A	H	1.13E-11
Rhola_00011110	preprotein translocase subunit SecA	C:cytoplasm; C:plasma membrane; P:protein targeting; F:ion binding; P:transmembrane transport	AURMO_00390	#N/A	0.371749
Rhola_00011120	SSU ribosomal protein S30P /sigma 54 modulation protein	C:cytoplasm; P:translation	#N/A	H	1.18E-09
Rhola_00011130	comF family protein	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.100706
Rhola_00011140	Sporulation and spore germination	0	AURMO_00387	B	0.002403

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011150	two-component system, OmpR family, sensor histidine kinase MtrB	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	AURMO_00386	#N/A	0.039734
Rhola_00011160	two-component system, OmpR family, response regulator MtrA	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_00385	I	0.001058
Rhola_00011170	adenosylhomocysteinase	F:molecular_function; C:cytoplasm; P:small molecule metabolic process	AURMO_00384	G	4.64E-05
Rhola_00011180	phosphomannomutase	P:carbohydrate metabolic process; F:isomerase activity	AURMO_00383	J	5.99E-07
Rhola_00011190	homoserine dehydrogenase	0	#N/A	#N/A	0.54047
Rhola_00011200	hypothetical protein	0	AURMO_00380	G	0.014619
Rhola_00011210	Glycosyltransferase, GT2 family	F:molecular_function; C:cellular_component	AURMO_00379	N	2.03E-06
Rhola_00011220	transcription factor WhiB	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00378	I	0.002458

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011230	mannose-6-phosphate isomerase, type 1	P:carbohydrate metabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00377	#N/A	0.134233
Rhola_00011240	O-antigen ligase	C:cellular_component; F:ligase activity	AURMO_00375	#N/A	0.024314
Rhola_00011250	LysM domain-containing protein	0	AURMO_00443	H	2.47E-06
Rhola_00011260	hypothetical protein	0	#N/A	H	4.55E-09
Rhola_00011270	transcriptional attenuator, LytR family	C:cellular_component	AURMO_00373	#N/A	0.173225
Rhola_00011280	5-(carboxyamino)imidazole ribonucleotide mutase	P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00372	#N/A	0.100823
Rhola_00011290	5-(carboxyamino)imidazole ribonucleotide synthase	P:biosynthetic process; F:lyase activity; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00371	#N/A	0.76005
Rhola_00011300	PH domain-containing protein	C:cellular_component	#N/A	#N/A	0.698112

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011310	BirA family transcriptional regulator, biotin operon repressor / biotin-[acetyl-CoA-carboxylase] ligase	P:cellular protein modification process; F:ligase activity	AURMO_00367	H	2.82E-06
Rhola_00011320	propionyl-CoA carboxylase beta chain	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:ligase activity; C:protein-containing complex; P:small molecule metabolic process	AURMO_00366	D	3.88E-07
Rhola_00011330	Acyl-CoA carboxylase epsilon subunit	0	#N/A	I	0.006299
Rhola_00011340	hypothetical protein	C:cellular_component	#N/A	#N/A	0.025839
Rhola_00011350	Signal transduction histidine kinase	C:cellular_component; F:kinase activity	#N/A	#N/A	0.034367
Rhola_00011360	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	D	0.000403
Rhola_00011370	tRNA/tmRNA/rRNA uracil-C5-methylase, TrmA/RlmC/RlmD family	F:methyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_00364	#N/A	0.514423
Rhola_00011380	septum formation protein	F:molecular_function; C:cytoplasm; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00363	H	0.000141
Rhola_00011390	acetyl-CoA/propionyl-CoA carboxylase, biotin carboxylase, biotin carboxyl carrier protein	F:ligase activity; F:ion binding	AURMO_00362	H	0.009931

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011400	dihydrolipoamide dehydrogenase	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process; F:ion binding	AURMO_00747	#N/A	0.679035
Rhola_00011410	purine-nucleoside phosphorylase	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01527	#N/A	0.573398
Rhola_00011420	phosphomannomutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	AURMO_01528	#N/A	0.770418
Rhola_00011430	PTS system IIB component, L-Asc family	F:transmembrane transporter activity	#N/A	#N/A	0.180685
Rhola_00011440	PTS system, ascorbate-specific IIA component	F:kinase activity	#N/A	A	0.000204
Rhola_00011450	adenosine deaminase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	AURMO_00359	C	8.95E-06
Rhola_00011460	thymidine phosphorylase	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01529	A	5.83E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011470	cytidine deaminase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01530	A	8.12E-09
Rhola_00011480	nucleoside ABC transporter membrane protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_01531	A	1.15E-05
Rhola_00011490	simple sugar transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_01532	A	4.51E-07
Rhola_00011500	simple sugar transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_01535	A	2.75E-05
Rhola_00011510	basic membrane protein A	C:plasma membrane	AURMO_01536	H	1.95E-11
Rhola_00011520	mannose-1-phosphate guanylyltransferase	P:carbohydrate metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	AURMO_00358	M	0.014634
Rhola_00011530	succinate dehydrogenase subunit C	C:intracellular; P:generation of precursor metabolites and energy; F:oxidoreductase activity; C:protein-containing complex; F:ion binding	AURMO_00357	C	0.005678

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011540	succinate dehydrogenase / fumarate reductase membrane anchor subunit	C:intracellular; P:generation of precursor metabolites and energy; F:oxidoreductase activity; C:protein-containing complex; F:ion binding	AURMO_00356	A	2.99E-10
Rhola_00011550	succinate dehydrogenase subunit A	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	AURMO_00355	K	0.001982
Rhola_00011560	succinate dehydrogenase / fumarate reductase iron-sulfur subunit	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	AURMO_00354	H	0.002437
Rhola_00011570	Ferredoxin subunit of nitrite reductase or a ring-hydroxylating dioxygenase	#N/A	#N/A	B	0.00099
Rhola_00011580	exodeoxyribonuclease-3	F:nuclease activity; P:DNA metabolic process; P:response to stress	AURMO_00344	C	0.002484
Rhola_00011590	tryptophanyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	AURMO_00343	E	0.003149

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011600	diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase	P:biosynthetic process; F:oxidoreductase activity; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00341	J	4.15E-05
Rhola_00011610	riboflavin synthase alpha chain	F:transferase activity, transferring alkyl or aryl (other than methyl) groups	AURMO_00340	J	0.002365
Rhola_00011620	3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00339	J	0.009496
Rhola_00011630	6,7-dimethyl-8-ribityllumazine synthase	P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00338	#N/A	0.063149

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011640	hypothetical protein	C:cellular_component	#N/A	#N/A	0.853803
Rhola_00011650	hypothetical protein	0	#N/A	#N/A	0.742429
Rhola_00011660	ATP-binding cassette, subfamily B	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	AURMO_00336	G	1.78E-15
Rhola_00011670	Protein of unknown function (DUF4242)	0	#N/A	I	9.59E-05
Rhola_00011680	Acyl-CoA dehydrogenase	#N/A	#N/A	H	2.15E-08
Rhola_00011690	nitrate/nitrite transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	#N/A	0.160855
Rhola_00011700	NitT/TauT family transport system substrate-binding protein	0	#N/A	#N/A	0.352535
Rhola_00011710	NitT/TauT family transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	#N/A	0.037208
Rhola_00011720	Kynureninase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_01622	D	0.000359

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011730	tryptophan 2,3-dioxygenase	P:cellular amino acid metabolic process; P:catabolic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_01620	D	2.24E-08
Rhola_00011740	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	AURMO_01463	G	7.51E-25
Rhola_00011750	glycine hydroxymethyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	AURMO_01464	G	3.16E-24
Rhola_00011760	hypothetical protein	#N/A	#N/A	B	0.001267

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011770	formyltetrahydrofolate deformylase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01465	#N/A	0.136318
Rhola_00011780	Glycine rich protein	C:cellular_component	#N/A	N	3.68E-06
Rhola_00011790	isocitrate dehydrogenase (NADP)	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.307379
Rhola_00011800	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01508	#N/A	0.01507
Rhola_00011810	phosphoribosylglycinamide formyltransferase-1	F:molecular_function; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01510	#N/A	0.080542
Rhola_00011820	hypothetical protein	C:cellular_component	AURMO_01512	F	0.006366
Rhola_00011830	succinyl-CoA synthetase alpha subunit	P:generation of precursor metabolites and energy; F:ligase activity	AURMO_01515	B	2.72E-07

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011840	succinyl-CoA synthetase beta subunit	P:generation of precursor metabolites and energy; F:ligase activity; F:ion binding	AURMO_01516	B	0.004991
Rhola_00011850	DNA helicase-2 / ATP-dependent DNA helicase PcrA	F:DNA binding; F:helicase activity; C:cytoplasm; P:biosynthetic process; F:ion binding; P:chromosome organization	AURMO_01518	#N/A	0.104355
Rhola_00011860	glycerophosphoryl diester phosphodiesterase	F:molecular_function; P:lipid metabolic process	AURMO_01519	#N/A	0.357887
Rhola_00011870	GMP synthase (glutamine-hydrolysing)	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00242	#N/A	0.333875
Rhola_00011880	integral membrane protein	C:cellular_component	#N/A	#N/A	0.027974
Rhola_00011890	hypothetical protein	C:plasma membrane	#N/A	B	0.009303
Rhola_00011900	IMP dehydrogenase	F:oxidoreductase activity	AURMO_00246	#N/A	0.476649
Rhola_00011910	IMP dehydrogenase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00247	#N/A	0.836667

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00011920	branched-chain amino acid transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	AURMO_00248	A	9.59E-08
Rhola_00011930	amino acid/amide ABC transporter membrane protein 2, HAAT family	C:plasma membrane; F:transmembrane transporter activity	AURMO_00249	#N/A	0.069719
Rhola_00011940	branched-chain amino acid transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00250	A	0.000987
Rhola_00011950	branched-chain amino acid transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00251	A	0.012334
Rhola_00011960	amino acid/amide ABC transporter substrate-binding protein, HAAT family	P:amino acid transport	AURMO_00239	#N/A	0.052924
Rhola_00011970	chloramphenicol-sensitive protein RarD	C:plasma membrane	AURMO_00237	#N/A	0.049396
Rhola_00011980	chaperonin GroES	C:cytoplasm; P:protein folding; F:ion binding	AURMO_00235	G	0.001074
Rhola_00011990	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase	P:biological_process; F:methyltransferase activity	AURMO_00234	D	0.000334
Rhola_00012000	protein of unknown function (DUF4190)	C:cellular_component	#N/A	H	0.012468
Rhola_00012010	N6-L-threonylcarbamoyladenine synthase	#N/A	#N/A	A	6.77E-11
Rhola_00012020	tRNA threonylcarbamoyl adenosine modification protein YeaZ	#N/A	#N/A	C	0.012959
Rhola_00012030	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	P:tRNA metabolic process	AURMO_00227	A	0.000337
Rhola_00012040	alanine racemase	P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity; F:ion binding	AURMO_00226	A	0.000747

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012050	holo-[acyl-carrier protein] synthase	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.058833
Rhola_00012060	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	F:molecular_function; C:cytoplasm; P:carbohydrate metabolic process; P:biosynthetic process	AURMO_00224	B	1.83E-07
Rhola_00012070	pantothenate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00223	#N/A	0.419506
Rhola_00012080	Bacteriorhodopsin	C:cellular_component; F:transmembrane transporter activity	#N/A	I	3.05E-32
Rhola_00012090	phosphoglucosamine mutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	AURMO_00222	#N/A	0.023484
Rhola_00012100	small subunit ribosomal protein S9	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00221	I	0.005098

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012110	LSU ribosomal protein L13P	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00220	G	0.003763
Rhola_00012120	tRNA pseudouridine38-40 synthase	F:RNA binding; P:tRNA metabolic process; F:isomerase activity	AURMO_00217	#N/A	0.105865
Rhola_00012130	large subunit ribosomal protein L17	F:structural constituent of ribosome; C:ribosome; P:translation	AURMO_00216	I	0.002195
Rhola_00012140	DNA-directed RNA polymerase subunit alpha	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_00215	I	0.012959
Rhola_00012150	small subunit ribosomal protein S11	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00214	I	0.007148
Rhola_00012160	small subunit ribosomal protein S13	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00213	G	0.001264
Rhola_00012170	LSU ribosomal protein L36P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	#N/A	0.091066
Rhola_00012180	bacterial translation initiation factor 1 (bIF-1)	C:cytoplasm; F:translation factor activity, RNA binding; F:rRNA binding	AURMO_00211	I	0.004716

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012190	methionyl aminopeptidase	P:cellular protein modification process; F:peptidase activity; F:ion binding	AURMO_00209	#N/A	0.238668
Rhola_00012200	adenylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_00208	J	0.010052
Rhola_00012210	protein translocase subunit secY/sec61 alpha	C:plasma membrane; P:protein targeting; P:transmembrane transport	AURMO_00207	G	0.007725
Rhola_00012220	LSU ribosomal protein L15P	#N/A	#N/A	I	0.003811
Rhola_00012230	large subunit ribosomal protein L30	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	#N/A	#N/A	0.027109
Rhola_00012240	small subunit ribosomal protein S5	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00204	#N/A	0.033812
Rhola_00012250	large subunit ribosomal protein L18	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00203	#N/A	0.072536

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012260	large subunit ribosomal protein L6	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00202	#N/A	0.12059
Rhola_00012270	small subunit ribosomal protein S8	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00201	#N/A	0.070432
Rhola_00012280	large subunit ribosomal protein L5	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00200	G	0.005851
Rhola_00012290	large subunit ribosomal protein L24	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00199	I	0.008727
Rhola_00012300	LSU ribosomal protein L14P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00198	#N/A	0.021883
Rhola_00012310	small subunit ribosomal protein S17	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00197	#N/A	0.019086
Rhola_00012320	large subunit ribosomal protein L29	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	I	0.005832

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012330	LSU ribosomal protein L16P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00195	I	0.007748
Rhola_00012340	small subunit ribosomal protein S3	F:mRNA binding; F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00194	I	0.0051
Rhola_00012350	large subunit ribosomal protein L22	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00193	#N/A	0.023961
Rhola_00012360	small subunit ribosomal protein S19	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00192	#N/A	0.032821
Rhola_00012370	large subunit ribosomal protein L2	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00191	#N/A	0.020588
Rhola_00012380	large subunit ribosomal protein L23	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00190	#N/A	0.053597

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012390	large subunit ribosomal protein L4	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00189	#N/A	0.032228
Rhola_00012400	large subunit ribosomal protein L3	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00188	I	0.013716
Rhola_00012410	small subunit ribosomal protein S10	#N/A	#N/A	#N/A	0.017334
Rhola_00012420	hypothetical protein	0	AURMO_00141	G	2.68E-09
Rhola_00012430	hypothetical protein	0	#N/A	D	0.000842
Rhola_00012440	asparaginase	0	AURMO_00489	#N/A	0.222433
Rhola_00012450	elongation factor Tu	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	AURMO_00183	#N/A	0.015516
Rhola_00012460	elongation factor G	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	AURMO_00182	I	0.008277
Rhola_00012470	small subunit ribosomal protein S7	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00181	I	0.000352

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012480	SSU ribosomal protein S12P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	AURMO_00180	I	0.00288
Rhola_00012490	DNA-directed RNA polymerase subunit beta'	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding	AURMO_00178	G	1.02E-07
Rhola_00012500	DNA-directed RNA polymerase subunit beta	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_00177	G	3.44E-07
Rhola_00012510	hypothetical protein	0	#N/A	#N/A	0.868849
Rhola_00012520	hypothetical protein	0	#N/A	#N/A	0.861649
Rhola_00012530	hypothetical protein	#N/A	#N/A	#N/A	0.219788
Rhola_00012550	cation diffusion facilitator family transporter	C:cellular_component; F:transmembrane transporter activity	AURMO_01670	#N/A	0.130934
Rhola_00012560	tRNA(adenine34) deaminase	P:tRNA metabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	AURMO_01671	#N/A	0.025601

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012570	uracil phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01523	#N/A	0.185537
Rhola_00012580	hypothetical protein	#N/A	#N/A	#N/A	0.024314
Rhola_00012590	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01672	G	0.005891
Rhola_00012600	AAA domain-containing protein	#N/A	#N/A	I	0.000239
Rhola_00012610	membrane-associated protein	C:cellular_component	AURMO_01164	G	1.41E-25
Rhola_00012620	Nitroreductase	F:oxidoreductase activity	AURMO_01693	G	3.16E-24
Rhola_00012630	hypothetical protein	0	#N/A	H	2.22E-05
Rhola_00012640	Signal transduction histidine kinase	C:membrane; C:integral component of membrane; F:kinase activity; P:phosphorylation	#N/A	M	0.00624
Rhola_00012650	Signal transduction histidine kinase	C:cellular_component; F:kinase activity	#N/A	#N/A	0.031771
Rhola_00012660	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.534089

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012670	NRAMP (natural resistance-associated macrophage protein) metal ion transporters	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.831282
Rhola_00012680	hypothetical protein	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process	AURMO_01744	#N/A	0.861649
Rhola_00012690	NYN domain-containing protein	0	#N/A	#N/A	0.198226
Rhola_00012700	Leucine rich repeat-containing protein	0	#N/A	A	0.010536
Rhola_00012710	hypothetical protein	#N/A	#N/A	C	0.005844
Rhola_00012720	hypothetical protein	0	#N/A	#N/A	0.992064
Rhola_00012730	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	H	0.000129
Rhola_00012740	hypothetical protein	0	#N/A	H	0.014088
Rhola_00012750	RNA polymerase sigma-70 factor, ECF subfamily	F:DNA binding; F:DNA-binding transcription factor activity; C:cellular_component; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.056106
Rhola_00012760	Abi-like protein.	0	#N/A	N	0.005987
Rhola_00012770	hypothetical protein	0	AURMO_00689	G	1.59E-27
Rhola_00012780	hypothetical protein	0	#N/A	M	0.007795

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012790	hypothetical protein	C:cellular_component; F:ion binding	#N/A	C	0.002439
Rhola_00012800	hypothetical protein	0	#N/A	#N/A	0.118894
Rhola_00012810	Protein of unknown function (DUF3048)	#N/A	#N/A	K	0.000253
Rhola_00012820	Subtilisin-like serine proteases	F:peptidase activity	#N/A	H	1.58E-06
Rhola_00012830	UDP-glucose 4-epimerase	P:carbohydrate metabolic process; F:isomerase activity; P:small molecule metabolic process	AURMO_00423	#N/A	0.834143
Rhola_00012840	Choline kinase	F:kinase activity	AURMO_01172	E	0.012134
Rhola_00012850	CDP-glycerol glycerophosphotransferase	F:molecular_function; C:cellular_component	#N/A	#N/A	0.362526
Rhola_00012860	Glycosyltransferase, catalytic subunit of cellulose synthase and poly-beta-1,6-N-acetylglucosamine synthase	F:molecular_function; C:cellular_component	AURMO_00542	#N/A	0.037208
Rhola_00012870	teichoic acid transport system ATP-binding protein	F:ATPase activity; F:ion binding	AURMO_00447	B	0.001476
Rhola_00012880	teichoic acid transport system permease protein	C:plasma membrane; C:protein-containing complex; P:transmembrane transport	#N/A	#N/A	0.403817
Rhola_00012890	PTS system, fructose-specific IIC component	#N/A	#N/A	A	3.70E-16
Rhola_00012900	PTS system, fructose-specific, IIB component	#N/A	#N/A	A	0.001184
Rhola_00012910	PTS system, fructose-specific IIA component	C:cellular_component; F:kinase activity; F:transmembrane transporter activity	AURMO_00349	A	0.007824
Rhola_00012920	phosphocarrier protein	F:molecular_function; C:cytoplasm; P:transport	#N/A	#N/A	0.024926

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00012930	phosphotransferase system, enzyme I, PtsI	P:transport; F:kinase activity	AURMO_00353	G	0.004823
Rhola_00012940	L-lactate dehydrogenase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	G	0.006421
Rhola_00012950	Lipopolysaccharide biosynthesis protein, LPS glycosyltransferase	F:transferase activity, transferring glycosyl groups	#N/A	D	2.05E-05
Rhola_00012960	UTP--glucose-1-phosphate uridylyltransferase	P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01614	#N/A	0.028034
Rhola_00012970	CDP-glycerol glycerophosphotransferase	F:molecular_function	#N/A	#N/A	0.076776
Rhola_00012980	Permease of the drug/metabolite transporter (DMT) superfamily	C:cellular_component	#N/A	#N/A	0.677997
Rhola_00012990	FAR-17a/AIG1-like protein.	C:cellular_component	AURMO_00097	D	6.53E-07
Rhola_00013000	probable oxidoreductase, LLM family	F:oxidoreductase activity	AURMO_00916	G	1.02E-17

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Rhola_00013010	23S rRNA (adenine2503-C2)-methyltransferase	C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity; F:rRNA binding; P:ribosome biogenesis; F:ion binding	AURMO_01406	#N/A	0.015934
Rhola_00013020	sucrose phosphorylase	P:carbohydrate metabolic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on glycosyl bonds	#N/A	M	0.001974
Rhola_00013030	deoxyribodipyrimidine photolyase-related protein	F:lyase activity	AURMO_00962	#N/A	0.147143
Rhola_00013040	sortase A	#N/A	#N/A	H	0.007618
Rhola_00013050	Putative Ig domain-containing protein	C:cellular_component	#N/A	A	0.00002
Rhola_00013060	hypothetical protein	0	#N/A	H	3.28E-05
Rhola_00013070	DNA polymerase III, alpha subunit	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	H	4.57E-06
Rhola_00013080	Threonine/homoserine/homoserine lactone efflux protein	C:plasma membrane; P:transport	#N/A	#N/A	0.525521

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013090	Pyridoxamine 5'-phosphate oxidase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_01386	#N/A	0.043556
Rhola_00013100	raffinose/stachyose/melibiose transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	#N/A	0.337016
Rhola_00013110	raffinose/stachyose/melibiose transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	#N/A	0.492881
Rhola_00013120	raffinose/stachyose/melibiose transport system substrate-binding protein	#N/A	#N/A	C	2.63E-08
Rhola_00013130	hypothetical protein	C:cellular_component	#N/A	D	3.73E-14
Rhola_00013150	hypothetical protein (DUF2200)	#N/A	#N/A	#N/A	0.016212
Rhola_00013160	dipeptidase E	F:peptidase activity	#N/A	#N/A	0.541925
Rhola_00013170	hypothetical protein	#N/A	#N/A	#N/A	0.634976
Rhola_00013180	3-hydroxyacyl-CoA dehydrogenase	P:lipid metabolic process; P:catabolic process; F:oxidoreductase activity; P:small molecule metabolic process	AURMO_00764	A	0.000271
Rhola_00013190	acetyl-CoA acyltransferase	F:transferase activity, transferring acyl groups	AURMO_00765	A	0.004217

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013200	Acyl-coenzyme A oxidase	C:peroxisome; P:lipid metabolic process; P:catabolic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	AURMO_00094	A	0.012959
Rhola_00013210	Enoyl-CoA hydratase/carnithine racemase	F:lyase activity	AURMO_00407	G	2.13E-05
Rhola_00013240	hypothetical protein	0	#N/A	M	0.00677
Rhola_00013250	hypothetical protein	0	#N/A	#N/A	0.20206
Rhola_00013260	two component transcriptional regulator, LuxR family	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01452	#N/A	0.655728
Rhola_00013270	Signal transduction histidine kinase	C:cellular_component; F:kinase activity	#N/A	#N/A	0.592746
Rhola_00013280	hypothetical protein	0	#N/A	#N/A	0.073105
Rhola_00013290	CubicO group peptidase, beta-lactamase class C family	F:hydrolase activity	#N/A	#N/A	0.051104
Rhola_00013300	simple sugar transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.148444
Rhola_00013310	simple sugar transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	D	0.000187
Rhola_00013320	simple sugar transport system substrate-binding protein	P:transport	#N/A	#N/A	0.061358
Rhola_00013330	Sugar phosphate isomerase/epimerase	F:isomerase activity	#N/A	D	0.013171

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013340	Predicted dehydrogenase	F:oxidoreductase activity	#N/A	M	0.003767
Rhola_00013350	transcriptional regulator, LacI family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.322828
Rhola_00013360	fructose-1,6-bisphosphatase II	P:carbohydrate metabolic process; P:biosynthetic process; F:phosphatase activity; F:ion binding; P:small molecule metabolic process	AURMO_01248	A	2.74E-06
Rhola_00013370	EamA-like transporter family protein	C:cellular_component	#N/A	#N/A	0.550722
Rhola_00013380	hydroxypyruvate isomerase	F:isomerase activity	#N/A	#N/A	0.196499
Rhola_00013390	dTDP-4-dehydrorhamnose reductase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.196079
Rhola_00013400	myo-inositol 2-dehydrogenase / D-chiro-inositol 1-dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.242816
Rhola_00013410	inosose dehydratase	F:lyase activity; F:isomerase activity	#N/A	#N/A	0.541925
Rhola_00013420	Predicted dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.994548

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013430	transcriptional regulator, LacI family	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	H	9.29E-06
Rhola_00013440	simple sugar transport system substrate-binding protein	P:transport	#N/A	#N/A	0.874011
Rhola_00013450	simple sugar transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.721957
Rhola_00013460	simple sugar transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.307379
Rhola_00013470	Ribosomal protein S18 acetylase RimI	F:transferase activity, transferring acyl groups	#N/A	D	0.005192
Rhola_00013480	Adenylosuccinate synthetase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01631	I	0.002681
Rhola_00013490	tRNA G18 (ribose-2'-O)-methylase SpoU	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_01633	#N/A	0.118554

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013500	Na+/H+ antiporter, NhaA family	C:plasma membrane; F:transmembrane transporter activity; P:homeostatic process	AURMO_01340	E	5.06E-05
Rhola_00013510	NagD protein	F:molecular_function	#N/A	#N/A	0.077297
Rhola_00013520	Predicted arabinose efflux permease, MFS family	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.333495
Rhola_00013530	orotate phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	AURMO_01634	#N/A	0.359591
Rhola_00013540	exodeoxyribonuclease-3	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress	AURMO_01686	E	0.006366
Rhola_00013550	3-methyladenine DNA glycosylase AlkD	0	AURMO_00540	#N/A	0.807486
Rhola_00013560	Trk K+ transport system, NAD-binding component	C:cellular_component; F:transmembrane transporter activity	#N/A	A	1.86E-10
Rhola_00013570	ATP-dependent Clp protease ATP-binding subunit ClpB	F:peptidase activity; F:ion binding	AURMO_01698	#N/A	0.074672
Rhola_00013580	MerR family transcriptional regulator, heat shock protein HspR	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01702	#N/A	0.090318

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013590	molecular chaperone DnaJ	P:protein folding; F:unfolded protein binding	AURMO_01703	#N/A	0.107001
Rhola_00013600	molecular chaperone GrpE	#N/A	#N/A	#N/A	0.078892
Rhola_00013610	molecular chaperone DnaK	P:protein folding; F:ion binding; F:unfolded protein binding	AURMO_01705	#N/A	0.118894
Rhola_00013620	MFS transporter, UMF1 family	C:cellular_component	AURMO_01706	D	0.000197
Rhola_00013630	dye decolorizing peroxidase	F:oxidoreductase activity	AURMO_00328	B	0.001013
Rhola_00013640	hypothetical protein	#N/A	#N/A	B	0.001715
Rhola_00013650	dCTP deaminase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_01719	#N/A	0.982714
Rhola_00013660	Protein of unknown function (DUF2834)	C:cellular_component	AURMO_00169	#N/A	0.023318
Rhola_00013670	Cytochrome P450	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.045216
Rhola_00013680	PIF1-like helicase	F:helicase activity; P:DNA metabolic process; P:response to stress; P:homeostatic process; P:chromosome organization	AURMO_01721	#N/A	0.121719
Rhola_00013690	putative copper resistance protein D	C:cellular_component; P:transport	AURMO_01723	#N/A	0.366181
Rhola_00013700	Protein-S-isoprenylcysteine O-methyltransferase Ste14	C:cellular_component	#N/A	#N/A	0.042942
Rhola_00013710	DNA-binding protein HU-beta	F:DNA binding	#N/A	K	8.88E-09

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013720	small subunit ribosomal protein S14	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_01725	G	0.010185
Rhola_00013730	large subunit ribosomal protein L33	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	G	0.003734
Rhola_00013740	large subunit ribosomal protein L28	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	I	3.29E-05
Rhola_00013750	Fur family transcriptional regulator, ferric uptake regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	AURMO_01729	I	0.000514
Rhola_00013760	zinc/manganese transport system permease protein	F:helicase activity; C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	M	2.66E-09
Rhola_00013770	zinc/manganese transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	H	1.96E-07
Rhola_00013780	zinc/manganese transport system substrate-binding protein	P:transport; F:ion binding	#N/A	I	4.06E-07
Rhola_00013790	Predicted transcriptional regulator with C-terminal CBS domains	#N/A	#N/A	#N/A	0.71574
Rhola_00013800	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	F:transferase activity, transferring acyl groups	AURMO_00029	B	0.003493

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013810	pyruvate dehydrogenase E1 component beta subunit	F:oxidoreductase activity	AURMO_00028	B	0.002575
Rhola_00013820	pyruvate dehydrogenase E1 component alpha subunit	F:oxidoreductase activity	AURMO_00027	E	1.51E-05
Rhola_00013830	putative membrane protein	C:cellular_component	#N/A	#N/A	0.047312
Rhola_00013840	Alpha/beta hydrolase family protein	C:membrane; C:integral component of membrane; F:hydrolase activity, acting on ester bonds	#N/A	N	2.44E-05
Rhola_00013850	adenylosuccinate lyase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	AURMO_00023	E	0.001854
Rhola_00013860	hypothetical protein	C:cellular_component	#N/A	#N/A	0.329234
Rhola_00013870	hypothetical protein	C:cellular_component	#N/A	A	1.46E-13
Rhola_00013880	replicative DNA helicase	F:DNA binding; F:helicase activity; C:chromosome; P:DNA metabolic process; P:biosynthetic process; C:protein-containing complex; F:ion binding; P:chromosome organization	AURMO_00020	D	7.51E-25
Rhola_00013890	large subunit ribosomal protein L9	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00019	I	0.000899

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00013900	small subunit ribosomal protein S18	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	#N/A	#N/A	0.042634
Rhola_00013910	single-strand binding protein	F:DNA binding; P:biosynthetic process	AURMO_00017	I	0.005373
Rhola_00013920	SSU ribosomal protein S6P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	AURMO_00016	#N/A	0.071419
Rhola_00013930	poly(A) polymerase	F:RNA binding; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	AURMO_00015	E	0.013171
Rhola_00013940	ADP-ribose pyrophosphatase	F:molecular_function	#N/A	#N/A	0.248231
Rhola_00013950	hypothetical protein	C:cellular_component	#N/A	#N/A	0.056561
Rhola_00013960	putative peptidoglycan lipid II flippase	C:cellular_component	AURMO_00309	#N/A	0.188842
Rhola_00013970	thioredoxin reductase (NADPH)	C:cytoplasm; P:response to stress; F:oxidoreductase activity	AURMO_00013	G	1.67E-17
Rhola_00013980	thioredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process; P:small molecule metabolic process	AURMO_00012	G	8.72E-24
Rhola_00013990	DNA-binding transcriptional regulator, MocR family, contains an aminotransferase domain	F:DNA binding; P:biosynthetic process; F:ion binding	AURMO_00011	#N/A	0.028034

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00014000	D-alanine-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell wall organization or biogenesis	AURMO_00010	G	0.000216
Rhola_00014010	methionine adenosyltransferase	C:cytoplasm; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	AURMO_00815	J	3.44E-07
Rhola_00014020	chromosome partitioning protein, ParB family	F:DNA binding	AURMO_00009	#N/A	0.104182
Rhola_00014030	chromosome partitioning protein	0	AURMO_00985	I	0.00211
Rhola_00014040	16S rRNA (guanine527-N7)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	AURMO_00007	G	4.97E-08
Rhola_00014050	spoIIIJ-associated protein	F:DNA binding	AURMO_00006	I	1.48E-06
Rhola_00014060	YidC/Oxa1 family membrane protein insertase	F:molecular_function; C:cellular_component; P:biological_process	AURMO_00005	I	3.36E-09

Locus tag	Annotation	GO-slim term(s)	Best hit in *A. photophilum*	Expression group	BH adjusted p-value of Likelihood Ratio Test
Rhola_00014070	ribonuclease P protein component	F:RNA binding; F:nuclease activity; P:tRNA metabolic process	#N/A	G	0.001074
Rhola_00014080	LSU ribosomal protein L34P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	#N/A	0.024314

Table A.9 Expression data and groups for each *A. photophilum* gene. For each gene in *Aurantimicrobium photophilum*: Locus tag, annotation, GO-slim term(s) assigned (#N/A indicates that no GO-slim term was assigned to this gene), homolog in *R. lacicola* (#N/A indicates that no homolog exists in that genome), expression group (#N/A indicates that the gene did not group with any other genes), and Benjamini and Hochberg-adjusted p-value indicating probability of belonging to that expression group.

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00001	chromosomal replication initiator protein	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:ion binding	Rhola_00000010	F	7.41E-07
AURMO_00002	LSU ribosomal protein L34P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	1.95E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00003	ribonuclease P protein component	F:RNA binding; F:nuclease activity; P:tRNA metabolic process	#N/A	E	8.51E-06
AURMO_00004	hypothetical protein	C:plasma membrane	#N/A	#N/A	0.55329061
AURMO_00005	YidC/Oxa1 family membrane protein insertase	F:molecular_function; C:cellular_component; P:biological_process	Rhola_00014060	#N/A	0.050205737
AURMO_00006	spoIIIJ-associated protein	F:DNA binding	Rhola_00014050	E	5.22E-05
AURMO_00007	16S rRNA m(7)G-527 methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00014040	#N/A	0.031989928
AURMO_00008	chromosome partitioning protein	#N/A	Rhola_00008930	#N/A	0.210716891
AURMO_00009	ParB family chromosome partitioning protein	F:DNA binding	Rhola_00014020	#N/A	0.645527781
AURMO_00010	D-alanine-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell wall organization or biogenesis	Rhola_00014000	#N/A	0.263346389
AURMO_00011	DNA-binding transcriptional MocR family regulator	P:biosynthetic process; F:ion binding	Rhola_00013990	E	6.15E-03
AURMO_00012	thioredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process; P:small molecule metabolic process	Rhola_00013980	H	1.60E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00013	thioredoxin reductase (NADPH)	C:cytoplasm; P:response to stress; F:oxidoreductase activity	Rhola_00013970	E	6.91E-08
AURMO_00014	hypothetical protein	C:cellular_component	#N/A	#N/A	0.109259946
AURMO_00015	poly(A) polymerase	F:RNA binding; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00013930	#N/A	0.305697249
AURMO_00016	SSU ribosomal protein S6P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00013920	E	4.27E-11
AURMO_00017	single-strand binding protein	F:DNA binding; P:biosynthetic process	Rhola_00013910	E	2.05E-18
AURMO_00018	SSU ribosomal protein S18P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	#N/A	E	1.25E-10
AURMO_00019	LSU ribosomal protein L9P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00013890	E	1.03E-09

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00020	replicative DNA helicase	F:DNA binding; F:helicase activity; C:chromosome; P:DNA metabolic process; P:biosynthetic process; C:protein-containing complex; F:ion binding; P:chromosome organization	Rhola_00013880	#N/A	0.212942342
AURMO_00021	hypothetical protein	C:cellular_component	#N/A	#N/A	0.281679713
AURMO_00022	hypothetical protein	C:cellular_component	#N/A	#N/A	0.420772413
AURMO_00023	adenylosuccinate lyase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00013850	#N/A	0.029334215
AURMO_00024	hypothetical protein	#N/A	#N/A	#N/A	0.23655123
AURMO_00025	alpha/beta hydrolase family protein	F:molecular_function; C:cellular_component	#N/A	#N/A	0.734510716
AURMO_00026	putative membrane protein	C:cellular_component	#N/A	#N/A	0.09125006
AURMO_00027	pyruvate dehydrogenase E1 component alpha subunit	F:oxidoreductase activity	Rhola_00013820	#N/A	0.349041578
AURMO_00028	pyruvate dehydrogenase E1 component beta subunit	F:oxidoreductase activity	Rhola_00013810	#N/A	0.560024379
AURMO_00029	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	F:transferase activity, transferring acyl groups	Rhola_00013800	#N/A	0.028225357
AURMO_00030	Fic family protein	F:nucleotidyltransferase activity; F:ion binding	#N/A	N	6.80E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00031	threonine/homoserine/homoserine lactone efflux protein	C:plasma membrane; P:transport	#N/A	A	0.000147976
AURMO_00032	phytoene dehydrogenase-like protein	#N/A	#N/A	#N/A	0.289862978
AURMO_00033	AsnC family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	A	0.003044754
AURMO_00034	3-oxoacid CoA-transferase subunit A	F:molecular_function	#N/A	A	0.007533181
AURMO_00035	3-oxoacid CoA-transferase subunit B	F:molecular_function	#N/A	#N/A	0.381213292
AURMO_00036	acetyl-CoA C-acetyltransferase	F:transferase activity, transferring acyl groups	#N/A	#N/A	0.01900408
AURMO_00037	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.893029896
AURMO_00038	4-cresol dehydrogenase (hydroxylating)	F:oxidoreductase activity; F:ion binding	#N/A	A	1.09E-07
AURMO_00039	hypothetical protein	#N/A	#N/A	#N/A	0.928080166
AURMO_00040	alpha/beta hydrolase family protein DUF1100	F:molecular_function	#N/A	A	2.50E-05
AURMO_00041	3alpha(or 20beta)-hydroxysteroid dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.048043973
AURMO_00042	lactoylglutathione lyase/glyoxylase I family protein	F:molecular_function	#N/A	#N/A	0.032150358
AURMO_00043	DNA-binding transcriptional repressor PuuR	F:DNA binding	#N/A	A	4.27E-08
AURMO_00044	2-polyprenyl-6-methoxyphenol hydroxylase-like FAD-dependent oxidoreductase	F:oxidoreductase activity; F:ion binding	#N/A	A	2.58E-11

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00045	DNA-binding transcriptional LysR family regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.022904599
AURMO_00046	DHA1 family bicyclomycin/chloramphenicol resistance-like MFS transporter	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.34305357
AURMO_00047	catechol-2,3-dioxygenase	F:oxidoreductase activity; F:lyase activity	#N/A	M	1.22E-05
AURMO_00048	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.027985627
AURMO_00049	FAD/FMN-containing dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	A	0.000462223
AURMO_00050	ribose 5-phosphate isomerase B	P:carbohydrate metabolic process; F:isomerase activity	#N/A	#N/A	0.038524304
AURMO_00051	NADPH:quinone reductase-like Zn-dependent oxidoreductase	F:oxidoreductase activity	#N/A	#N/A	0.039839662
AURMO_00052	monosaccharide ABC transporter substrate-binding protein (CUT2 family)	P:carbohydrate transport	#N/A	A	2.21E-08
AURMO_00053	monosaccharide ABC transporter ATP-binding protein (CUT2 family)	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	A	0.000145914
AURMO_00054	monosaccharide ABC transporter membrane protein (CUT2 family)	C:plasma membrane; F:transmembrane transporter activity	#N/A	A	1.01E-09

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00055	quinol monooxygenase YgiN	F:oxidoreductase activity	#N/A	A	5.47E-05
AURMO_00056	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase in catechol pathway	F:lyase activity	#N/A	A	3.36E-07
AURMO_00057	succinate-semialdehyde dehydrogenase/glutarate-semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	A	0.007397082
AURMO_00058	DNA-binding transcriptional LysR family regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	A	0.00481434
AURMO_00059	kynurenine formamidase	P:cellular amino acid metabolic process; P:catabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.028131536
AURMO_00060	uncharacterized protein (TIGR02246 family)	F:dioxygenase activity; P:oxidation-reduction process	#N/A	A	6.25E-06
AURMO_00061	UDP-N-acetylmuramyl tripeptide synthase	P:biosynthetic process; F:ligase activity; F:ion binding	#N/A	B	5.15E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00062	hypothetical protein	F:molecular_function; P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	#N/A	J	4.77E-05
AURMO_00063	POT family proton-dependent oligopeptide transporter	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.035699824
AURMO_00064	alpha-beta hydrolase superfamily lysophospholipase	F:molecular_function	Rhola_00000540	#N/A	0.031285236
AURMO_00065	predicted GNAT family acetyltransferase	F:transferase activity	#N/A	#N/A	0.046930838
AURMO_00066	site-specific DNA-methyltransferase (adenine-specific)	F:DNA binding; P:DNA metabolic process; F:methyltransferase activity	Rhola_00000600	#N/A	0.237497839
AURMO_00067	hypothetical protein	F:molecular_function	#N/A	#N/A	0.698865809
AURMO_00068	hypothetical protein	#N/A	#N/A	M	5.07E-06
AURMO_00069	hypothetical protein	#N/A	#N/A	#N/A	0.180609355
AURMO_00070	hypothetical protein	#N/A	#N/A	M	8.16E-10
AURMO_00071	hypothetical protein	#N/A	#N/A	A	3.14E-03
AURMO_00072	hypothetical protein	#N/A	#N/A	A	6.46E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00073	ABC-type bacteriocin/lantibiotic exporter with double-glycine peptidase domain	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.174753703
AURMO_00074	NHLM bacteriocin system ABC transporter peptidase/ATP-binding protein	C:cellular_component; F:peptidase activity; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.179386861
AURMO_00075	HlyD family secretion protein	C:cellular_component	#N/A	#N/A	0.356903397
AURMO_00076	galactosyltransferase-like protein	F:transferase activity, transferring glycosyl groups	#N/A	A	4.44E-05
AURMO_00077	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.036921269
AURMO_00078	glycosyltransferase involved in cell wall biosynthesis	F:transferase activity	#N/A	#N/A	0.709153805
AURMO_00079	Anp1 protein	#N/A	#N/A	#N/A	0.991785716
AURMO_00080	hypothetical protein	#N/A	#N/A	#N/A	0.422314008
AURMO_00081	EmrB/QacA subfamily drug resistance transporter	C:plasma membrane; F:transmembrane transporter activity	Rhola_00000630	J	5.75E-07
AURMO_00082	HxlR family transcriptional regulator	#N/A	#N/A	#N/A	0.038752588
AURMO_00083	D-alanyl-D-alanine carboxypeptidase	F:peptidase activity	RHOLA_RS00320	#N/A	0.246579414
AURMO_00084	phosphoglucomutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	Rhola_00000650	N	2.76E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00085	prephenate dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:isomerase activity	Rhola_00000660	E	3.12E-03
AURMO_00086	seryl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00000700	J	3.24E-04
AURMO_00087	Cof subfamily protein (haloacid dehalogenase superfamily)/HAD superfamily hydrolase (TIGR01484 family)	F:phosphatase activity	Rhola_00000710	C	3.14E-03
AURMO_00089	LytR family transcriptional attenuator	C:cellular_component	Rhola_00000730	#N/A	0.030110049
AURMO_00091	hypothetical protein	#N/A	#N/A	#N/A	0.058681455
AURMO_00092	superfamily II DNA/RNA helicase	F:helicase activity; F:ion binding	RHOLA_RS01230	F	1.52E-04
AURMO_00093	uncharacterized membrane protein	C:cellular_component	#N/A	#N/A	0.054114902
AURMO_00094	acyl-coenzyme A oxidase	C:peroxisome; P:lipid metabolic process; P:catabolic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	Rhola_00013200	A	1.58E-19
AURMO_00095	EmrB/QacA subfamily drug resistance transporter	C:plasma membrane; F:transmembrane transporter activity	Rhola_00001510	#N/A	0.147204272

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00096	hypothetical protein	C:cellular_component	#N/A	A	1.76E-07
AURMO_00097	FAR-17a/AIG1-like protein	C:cellular_component	Rhola_00012990	A	3.33E-08
AURMO_00098	polyphosphate kinase 2	F:kinase activity	#N/A	#N/A	0.551112592
AURMO_00099	carboxymethylenebutenolidase	F:molecular_function	Rhola_00000940	#N/A	0.025551605
AURMO_00100	methionine synthase (B12-dependent)	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:methyltransferase activity; P:biosynthetic process; F:ion binding	Rhola_00008090	J	3.02E-08
AURMO_00101	predicted nucleotidyltransferase	F:DNA binding	#N/A	#N/A	0.271526664
AURMO_00102	energy-coupling factor transport system substrate-specific component	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.149123465
AURMO_00103	energy-coupling factor transport system ATP-binding protein	C:cellular_component; F:ATPase activity; F:ion binding	Rhola_00009220	#N/A	0.045510887
AURMO_00104	hypothetical protein	#N/A	#N/A	#N/A	0.805098292
AURMO_00105	hypothetical protein	C:cellular_component	#N/A	A	7.31E-08
AURMO_00106	hypothetical protein	#N/A	#N/A	#N/A	0.16149879
AURMO_00107	TetR family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.14373288

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00108	glutamate-1-semialdehyde 2,1-aminomutase	C:cytoplasm; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00002860	L	3.96E-08
AURMO_00109	porphobilinogen synthase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00002870	L	6.51E-07
AURMO_00110	uroporphyrinogen-III synthase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	L	4.00E-07
AURMO_00111	hydroxymethylbilane synthase	P:cellular protein modification process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00002880	L	9.93E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00112	glutamyl-tRNA reductase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00002890	L	0.00207936
AURMO_00113	uroporphyrinogen decarboxylase	C:cytoplasm; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00002900	#N/A	0.019740799
AURMO_00114	oxygen-dependent protoporphyrinogen oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00002910	L	6.12E-04
AURMO_00115	chlorite dismutase	F:oxidoreductase activity	Rhola_00002920	D	1.81E-12
AURMO_00116	ferrochelatase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00002930	D	3.36E-14

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00120	murein DD-endopeptidase MepM/ murein hydrolase activator NlpD	F:molecular_function; C:cellular_component	#N/A	#N/A	0.283620566
AURMO_00121	transposase-like protein	F:DNA binding	#N/A	#N/A	0.87624894
AURMO_00122	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.967984115
AURMO_00123	inorganic pyrophosphatase	C:cytoplasm; P:biological_process; F:ion binding	Rhola_00001580	#N/A	0.087885784
AURMO_00124	tRNA(Ile)-lysidine synthase	C:cytoplasm; P:tRNA metabolic process; F:ligase activity; F:ion binding	Rhola_00001590	#N/A	0.754672296
AURMO_00125	hypoxanthine phosphoribosyltransferase	C:cytoplasm; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00001600	#N/A	0.956525791
AURMO_00126	membrane protease FtsH catalytic subunit	C:plasma membrane; F:peptidase activity; P:catabolic process; F:ATPase activity; F:ion binding; P:cell division	Rhola_00001610	F	1.76E-12

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AURMO_00127	GTP cyclohydrolase I	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00001620	I	2.55E-05
AURMO_00128	dihydropteroate synthase	P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00001630	F	4.07E-03
AURMO_00129	dihydroneopterin aldolase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	#N/A	0.44606545

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00130	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00001650	#N/A	0.41303101
AURMO_00131	uncharacterized protein DUF3180	C:cellular_component	#N/A	#N/A	0.222143364
AURMO_00132	predicted short-subunit dehydrogenase-like oxidoreductase (DUF2520 family)	#N/A	Rhola_00001670	#N/A	0.09272871
AURMO_00133	pantothenate synthetase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00001680	#N/A	0.57661957
AURMO_00134	lysyl-tRNA synthetase class II	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00001690	E	2.94E-07
AURMO_00135	hypothetical protein	C:cellular_component	#N/A	#N/A	0.045766101
AURMO_00136	cardiolipin synthetase 2	F:molecular_function; C:plasma membrane; P:lipid metabolic process; P:biosynthetic process	#N/A	#N/A	0.479526895

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00137	maltooligosyl trehalose hydrolase	F:oxidoreductase activity	#N/A	#N/A	0.480734767
AURMO_00138	Cys-tRNA(Pro) deacylase	P:tRNA metabolic process; P:translation; F:lyase activity; F:ligase activity	#N/A	F	7.38E-05
AURMO_00139	TfoX/Sxy family transcriptional regulator of competence genes	#N/A	#N/A	H	2.37E-07
AURMO_00140	AhpD family alkylhydroperoxidase	F:oxidoreductase activity	#N/A	H	7.47E-07
AURMO_00141	hypothetical protein	F:oxidoreductase activity	Rhola_00012420	E	3.61E-09
AURMO_00142	ATP-dependent Clp protease ATP-binding subunit ClpC	F:peptidase activity; F:ion binding	Rhola_00001760	I	7.07E-26
AURMO_00143	N-acetylglutamate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00001770	#N/A	0.108837415
AURMO_00144	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	B	1.05E-03
AURMO_00145	GAF domain-containing protein	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	M	5.56E-26
AURMO_00146	aldehyde dehydrogenase	F:oxidoreductase activity	#N/A	A	1.42E-39
AURMO_00147	hypothetical protein	#N/A	#N/A	M	9.13E-34
AURMO_00148	Fic/DOC family protein	F:nucleotidyltransferase activity	#N/A	#N/A	0.926639807
AURMO_00149	hypothetical protein	#N/A	#N/A	#N/A	0.374342464

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AURMO_00150	DNA repair protein RadA/Sms	F:DNA binding; P:DNA metabolic process; P:response to stress; F:peptidase activity; F:ATPase activity; F:ion binding	Rhola_00001850	#N/A	0.092959955
AURMO_00152	LuxR family two component transcriptional regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.967984115
AURMO_00153	signal transduction histidine kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity	#N/A	#N/A	0.986137292
AURMO_00154	putative ABC transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	#N/A	0.936004247
AURMO_00155	putative ABC transport system permease protein	C:plasma membrane	#N/A	#N/A	0.867265656
AURMO_00156	uncharacterized repeat protein (TIGR02543 family)	C:cellular_component	#N/A	#N/A	0.063307351
AURMO_00157	signal transduction histidine kinase	C:cellular_component	#N/A	A	9.09E-03
AURMO_00158	LuxR family two component transcriptional regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.833875249
AURMO_00159	hypothetical protein	#N/A	#N/A	#N/A	0.234700272

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00160	DNA-binding NarL/FixJ family response regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	M	1.67E-05
AURMO_00161	signal transduction histidine kinase	C:cellular_component	#N/A	A	9.96E-07
AURMO_00162	uncharacterized protein DUF285	C:cellular_component; F:peptidase activity	#N/A	#N/A	0.53812721
AURMO_00163	hypothetical protein	#N/A	#N/A	#N/A	0.858516133
AURMO_00164	hypothetical protein	#N/A	#N/A	#N/A	0.997701299
AURMO_00165	AbrB family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.032551175
AURMO_00166	ATP-dependent RNA helicase CsdA	F:RNA binding; F:helicase activity; C:cytoplasm; P:response to stress; P:ribonucleoprotein complex assembly; P:nucleobase-containing compound catabolic process; P:ribosome biogenesis; F:ion binding	#N/A	#N/A	0.052108089
AURMO_00167	hypothetical protein	#N/A	#N/A	#N/A	0.617842985
AURMO_00168	hypothetical protein	F:DNA binding; F:DNA-binding transcription factor activity; P:regulation of transcription, DNA-templated	#N/A	#N/A	0.841481376
AURMO_00169	uncharacterized protein DUF2834	F:molecular_function; C:cellular_component	Rhola_00013660	#N/A	0.054031633

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00170	hypothetical protein	#N/A	#N/A	#N/A	0.335875546
AURMO_00171	ADP-ribose pyrophosphatase YjhB (NUDIX family)	P:biological_process; F:methyltransferase activity	#N/A	#N/A	0.59423606
AURMO_00172	hypothetical protein	#N/A	#N/A	#N/A	0.02895216
AURMO_00173	hypothetical protein	#N/A	Rhola_00005410	#N/A	0.177329631
AURMO_00174	hypothetical protein	C:cellular_component	#N/A	#N/A	0.83988302
AURMO_00175	SprT-like family protein	#N/A	RHOLA_RS05420	#N/A	0.108608694
AURMO_00176	hypothetical protein	F:transferase activity, transferring alkyl or aryl (other than methyl) groups	#N/A	#N/A	0.241008752
AURMO_00177	DNA-directed RNA polymerase subunit beta	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00012500	E	1.03E-11
AURMO_00178	DNA-directed RNA polymerase subunit beta'	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00012490	E	2.34E-30
AURMO_00179	hypothetical protein	C:cellular_component	#N/A	D	4.25E-07
AURMO_00180	SSU ribosomal protein S12P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012480	E	2.67E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00181	SSU ribosomal protein S7P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012470	E	2.40E-13
AURMO_00182	translation elongation factor 2 (EF-2/EF-G)	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	Rhola_00012460	E	1.85E-10
AURMO_00183	translation elongation factor 1A (EF-1A/EF-Tu)	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	Rhola_00012450	E	2.61E-04
AURMO_00184	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.04062281
AURMO_00185	cytochrome b561-like protein	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity	#N/A	#N/A	0.031586381
AURMO_00186	SulP family sulfate permease	C:cellular_component; F:transmembrane transporter activity	Rhola_00004690	A	5.56E-07
AURMO_00187	SSU ribosomal protein S10P	F:RNA binding; F:structural constituent of ribosome; C:ribosome; P:translation	RHOLA_RS06170	E	4.02E-05
AURMO_00188	LSU ribosomal protein L3P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012400	E	5.91E-16

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00189	LSU ribosomal protein L4P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012390	E	8.72E-15
AURMO_00190	LSU ribosomal protein L23P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012380	E	1.97E-17
AURMO_00191	LSU ribosomal protein L2P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012370	E	2.45E-18
AURMO_00192	SSU ribosomal protein S19P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012360	E	1.61E-13
AURMO_00193	large subunit ribosomal protein L22	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012350	E	1.72E-14
AURMO_00194	SSU ribosomal protein S3P	F:mRNA binding; F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012340	E	4.66E-17

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00195	LSU ribosomal protein L16P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012330	E	2.00E-16
AURMO_00196	LSU ribosomal protein L29P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	4.84E-16
AURMO_00197	small subunit ribosomal protein S17	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012310	E	2.28E-15
AURMO_00198	LSU ribosomal protein L14P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012300	E	3.32E-11
AURMO_00199	LSU ribosomal protein L24P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012290	E	2.71E-13
AURMO_00200	large subunit ribosomal protein L5	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012280	E	1.74E-13
AURMO_00201	SSU ribosomal protein S8P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012270	E	1.78E-17

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00202	large subunit ribosomal protein L6	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012260	E	2.95E-18
AURMO_00203	LSU ribosomal protein L18P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012250	E	5.19E-22
AURMO_00204	SSU ribosomal protein S5P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00012240	E	1.61E-13
AURMO_00205	LSU ribosomal protein L30P	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	#N/A	E	2.49E-14
AURMO_00206	LSU ribosomal protein L15P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	RHOLA_RS06075	E	3.17E-16
AURMO_00207	protein translocase subunit secY/sec61 alpha	C:plasma membrane; P:protein targeting; P:transmembrane transport	Rhola_00012210	E	2.07E-20

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00208	adenylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00012200	#N/A	0.430217224
AURMO_00209	methionyl aminopeptidase	P:cellular protein modification process; F:peptidase activity; F:ion binding	Rhola_00012190	#N/A	0.458625597
AURMO_00210	alpha-tubulin suppressor-like RCC1 family protein	C:cellular_component	#N/A	#N/A	0.911251539
AURMO_00211	translation initiation factor 1 (bIF-1)	C:cytoplasm; F:translation factor activity, RNA binding; F:rRNA binding	Rhola_00012180	F	5.54E-03
AURMO_00212	LSU ribosomal protein L36P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	F	8.00E-04
AURMO_00213	SSU ribosomal protein S13P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012160	E	1.78E-08
AURMO_00214	SSU ribosomal protein S11P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00012150	E	0.0007393

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00215	DNA-directed RNA polymerase subunit alpha	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00012140	E	7.52E-03
AURMO_00216	large subunit ribosomal protein L17	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00012130	E	6.27E-05
AURMO_00217	tRNA pseudouridine(38-40) synthase	F:RNA binding; P:tRNA metabolic process; F:isomerase activity	Rhola_00012120	#N/A	0.387644053
AURMO_00218	serine/threonine-protein kinase HipA	F:kinase activity	Rhola_00000050	#N/A	0.079249661
AURMO_00219	helix-turn-helix protein	F:DNA binding	#N/A	#N/A	0.830194273
AURMO_00220	LSU ribosomal protein L13P	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00012110	E	7.46E-11
AURMO_00221	small subunit ribosomal protein S9	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00012100	E	4.43E-10
AURMO_00222	phosphoglucosamine mutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	Rhola_00012090	E	1.06E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00223	pantothenate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00012070	#N/A	0.735227849
AURMO_00224	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	F:molecular_function; C:cytoplasm; P:carbohydrate metabolic process; P:cellular amino acid metabolic process; P:biosynthetic process	Rhola_00012060	#N/A	0.644488058
AURMO_00225	holo-[acyl-carrier protein] synthase	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.295554173
AURMO_00226	alanine racemase	P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity; F:ion binding	Rhola_00012040	L	1.17E-02
AURMO_00227	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	F:molecular_function; P:tRNA metabolic process	Rhola_00012030	A	0.000813456
AURMO_00228	tRNA threonylcarbamoyl adenosine modification protein YeaZ	P:tRNA metabolic process	#N/A	#N/A	0.020302511

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00229	ribosomal-protein-alanine N-acetyltransferase	P:cellular protein modification process; F:peptidase activity; F:transferase activity, transferring acyl groups; P:protein maturation	#N/A	#N/A	0.414639606
AURMO_00230	N6-L-threonylcarbamoyladenine synthase	C:cytoplasm; P:tRNA metabolic process; F:peptidase activity; F:transferase activity, transferring acyl groups; F:ion binding	RHOLA_RS05970	#N/A	0.040361381
AURMO_00231	uncharacterized protein DUF4190	C:cellular_component	#N/A	#N/A	0.432488662
AURMO_00232	4-aminobutyrate aminotransferase-like enzyme	F:lyase activity; F:ion binding	#N/A	#N/A	0.050584084
AURMO_00233	uncharacterized protein DUF4190	C:cellular_component	#N/A	#N/A	0.454624279
AURMO_00234	hypothetical protein	P:biological_process; F:methyltransferase activity	Rhola_00011990	#N/A	0.681464964
AURMO_00235	chaperonin GroES	C:cytoplasm; P:protein folding; F:ion binding	Rhola_00011980	G	9.38E-07
AURMO_00236	hypothetical protein	#N/A	#N/A	M	2.29E-18
AURMO_00237	chloramphenicol-sensitive protein RarD	C:plasma membrane	Rhola_00011970	#N/A	0.194328952
AURMO_00238	substrate-binding family protein	#N/A	#N/A	#N/A	0.155733141
AURMO_00239	amino acid/amide ABC transporter substrate-binding protein (HAAT family)	P:transport	Rhola_00011960	A	1.39E-04
AURMO_00240	hypothetical protein	#N/A	#N/A	N	8.04E-04
AURMO_00241	helix-turn-helix protein	F:DNA binding	#N/A	A	4.88E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00242	GMP synthase (glutamine-hydrolysing)	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00011870	#N/A	0.30328556
AURMO_00243	integral membrane protein	C:cellular_component	#N/A	#N/A	0.732910379
AURMO_00244	cytochrome oxidase assembly protein ShyY1	C:plasma membrane	#N/A	#N/A	0.117547245
AURMO_00245	glycerol-3-phosphate dehydrogenase	C:cytoplasm; F:oxidoreductase activity; C:protein-containing complex	#N/A	#N/A	0.377186994
AURMO_00246	IMP dehydrogenase	F:oxidoreductase activity	Rhola_00011900	#N/A	0.263346389
AURMO_00247	IMP dehydrogenase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011910	E	3.72E-03
AURMO_00248	amino acid/amide ABC transporter membrane protein 1 (HAAT family)	C:plasma membrane; F:transmembrane transporter activity	Rhola_00011920	A	1.05E-09
AURMO_00249	amino acid/amide ABC transporter membrane protein 2 (HAAT family)	C:plasma membrane; F:transmembrane transporter activity	Rhola_00011930	A	1.13E-13
AURMO_00250	amino acid/amide ABC transporter ATP-binding protein 1 (HAAT family)	F:ATPase activity; F:ion binding	Rhola_00011940	A	4.22E-10

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00251	amino acid/amide ABC transporter ATP-binding protein 2 (HAAT family)	F:ATPase activity; F:ion binding	Rhola_00011950	#N/A	0.030388568
AURMO_00252	excisionase family DNA binding protein	#N/A	#N/A	#N/A	0.038406002
AURMO_00253	hypothetical protein	#N/A	#N/A	K	0.011329946
AURMO_00254	hypothetical protein	#N/A	#N/A	M	2.63E-03
AURMO_00255	hypothetical protein	#N/A	#N/A	#N/A	0.136126007
AURMO_00256	NTP pyrophosphatase (non-canonical NTP hydrolase)	P:biosynthetic process; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.695669951
AURMO_00257	hypothetical protein	#N/A	#N/A	#N/A	0.446264722
AURMO_00258	restriction endonuclease BglII	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding	#N/A	A	3.19E-05
AURMO_00259	DNA (cytosine-5)-methyltransferase 1	P:DNA metabolic process; F:methyltransferase activity	#N/A	B	4.58E-05
AURMO_00260	hypothetical protein	#N/A	#N/A	N	4.84E-03
AURMO_00261	hypothetical protein	#N/A	#N/A	A	3.79E-07
AURMO_00262	PhoH-like protein	F:ion binding	#N/A	A	6.34E-12
AURMO_00263	helicase-like protein	F:helicase activity	#N/A	A	1.97E-17
AURMO_00264	uncharacterized protein DUF1998	#N/A	#N/A	A	1.44E-20
AURMO_00265	hypothetical protein	#N/A	#N/A	#N/A	0.068535434

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00266	hypothetical protein	C:cellular_component	#N/A	A	5.47E-15
AURMO_00267	hypothetical protein	C:cellular_component	#N/A	A	1.29E-17
AURMO_00268	EndoU nuclease-like protein	#N/A	#N/A	#N/A	0.796343999
AURMO_00269	hypothetical protein	#N/A	#N/A	N	1.72E-08
AURMO_00270	hypothetical protein	#N/A	#N/A	H	1.46E-03
AURMO_00271	hypothetical protein	#N/A	#N/A	M	1.16E-06
AURMO_00272	hypothetical protein	#N/A	#N/A	N	1.78E-06
AURMO_00273	EndoU nuclease-like protein	#N/A	#N/A	#N/A	0.40531797
AURMO_00274	hypothetical protein	#N/A	#N/A	M	2.03E-11
AURMO_00275	hypothetical protein	#N/A	#N/A	N	9.38E-03
AURMO_00276	hypothetical protein	#N/A	#N/A	N	8.35E-05
AURMO_00277	hypothetical protein	C:cellular_component	#N/A	A	1.50E-28
AURMO_00278	hypothetical protein	C:cellular_component	#N/A	#N/A	0.465013714
AURMO_00279	EndoU nuclease-like protein	#N/A	#N/A	G	1.49E-02
AURMO_00280	hypothetical protein	#N/A	#N/A	N	1.15E-06
AURMO_00281	hypothetical protein	C:cellular_component	#N/A	#N/A	0.97022812
AURMO_00282	hypothetical protein	#N/A	Rhola_00002720	#N/A	0.967984115
AURMO_00283	catalase-peroxidase	P:response to stress; P:catabolic process; F:oxidoreductase activity; F:ion binding; P:cofactor metabolic process	Rhola_00002730	#N/A	0.183677072
AURMO_00284	hypothetical protein	#N/A	#N/A	#N/A	0.956525791
AURMO_00285	hypothetical protein	#N/A	#N/A	#N/A	0.392325979

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00286	predicted nucleic acid-binding protein	F:nuclease activity; F:ion binding	#N/A	#N/A	0.304901727
AURMO_00287	hypothetical protein	#N/A	#N/A	#N/A	0.914067278
AURMO_00288	hypothetical protein	F:oxidoreductase activity; F:lyase activity	Rhola_00002770	N	3.03E-12
AURMO_00289	hypothetical protein	#N/A	#N/A	M	5.87E-05
AURMO_00290	FtsP/CotA-like multicopper oxidase with cupredoxin domain	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.563786809
AURMO_00291	Cu2+-exporting ATPase	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.180304391
AURMO_00292	hypothetical protein	#N/A	Rhola_00002980	#N/A	0.915625627
AURMO_00293	hypothetical protein	#N/A	#N/A	J	9.65E-08
AURMO_00295	nucleotidyltransferase AbiEii toxin of type IV toxin-antitoxin system	F:transferase activity	#N/A	#N/A	0.026633978
AURMO_00296	putative AbiEi antitoxin of type IV toxin-antitoxin system	#N/A	#N/A	#N/A	0.265546754
AURMO_00297	DNA polymerase-3 subunit gamma/tau	F:DNA binding; C:intracellular; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex; F:ion binding	Rhola_00003110	#N/A	0.895492107

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00298	DNA replication and repair protein RecR	F:DNA binding; P:DNA metabolic process; P:response to stress; F:ion binding	Rhola_00003120	#N/A	0.166795961
AURMO_00299	acetylornithine deacetylase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	A	6.92E-07
AURMO_00300	aspartate kinase	P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	Rhola_00003130	J	1.47E-02
AURMO_00301	aspartate-semialdehyde dehydrogenase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00003140	L	6.62E-04
AURMO_00302	malate dehydrogenase (quinone)	P:generation of precursor metabolites and energy; F:oxidoreductase activity	Rhola_00007070	#N/A	0.826424833
AURMO_00303	signal transduction histidine kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity	#N/A	#N/A	0.97022812
AURMO_00304	hypothetical protein	C:cellular_component	#N/A	#N/A	0.182392574

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00305	LuxR family two component transcriptional regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.822610267
AURMO_00306	thymidine kinase	C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	Rhola_00006470	B	1.04E-02
AURMO_00307	UDPglucose 6-dehydrogenase	P:carbohydrate metabolic process; P:biosynthetic process; F:oxidoreductase activity	#N/A	J	2.39E-03
AURMO_00308	polysaccharide deacetylase	P:carbohydrate metabolic process; P:catabolic process; F:hydrolase activity, acting on glycosyl bonds; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cell wall organization or biogenesis	#N/A	#N/A	0.922516408
AURMO_00309	putative peptidoglycan lipid II flippase	C:cellular_component	Rhola_00013960	#N/A	0.977181019

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00310	lipid II:glycine glycyltransferase (peptidoglycan interpeptide bridge formation enzyme)	P:biosynthetic process; F:transferase activity, transferring acyl groups; P:cell wall organization or biogenesis	#N/A	#N/A	0.636414656
AURMO_00311	predicted MPP superfamily phosphohydrolase	F:molecular_function; C:cellular_component	Rhola_00003160	E	1.29E-02
AURMO_00312	membrane peptidoglycan carboxypeptidase	F:ion binding	Rhola_00003170	E	2.05E-03
AURMO_00313	hypothetical protein	#N/A	#N/A	#N/A	0.087896298
AURMO_00314	enamine deaminase RidA (YjgF/YER057c/UK114 family)	#N/A	Rhola_00003190	#N/A	0.829060089
AURMO_00315	acetyl-coenzyme A synthetase	P:sulfur compound metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00003200	#N/A	0.033165869
AURMO_00316	pilus assembly protein CpaF	F:helicase activity	Rhola_00003210	#N/A	0.186342979
AURMO_00317	tight adherence protein B	C:cellular_component	#N/A	#N/A	0.304499939
AURMO_00318	uncharacterized protein DUF4244	C:cellular_component	#N/A	#N/A	0.533424802
AURMO_00319	hypothetical protein	C:cellular_component	#N/A	#N/A	0.838685339
AURMO_00320	secretion/DNA translocation related TadE-like protein	C:cellular_component	#N/A	#N/A	0.808928595

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00321	DNA topoisomerase I	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ion binding; P:chromosome organization	Rhola_00003260	K	9.20E-09
AURMO_00322	thymidylate kinase	P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00003270	#N/A	0.083963504
AURMO_00323	DNA polymerase-3 subunit delta'	P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00003280	#N/A	0.931998052
AURMO_00324	alpha/beta hydrolase family protein	F:molecular_function	Rhola_00003290	#N/A	0.110889217
AURMO_00325	peptidase M48-like protein	C:cellular_component; F:peptidase activity	#N/A	#N/A	0.858910695
AURMO_00326	predicted transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.020839609
AURMO_00327	hypothetical protein	#N/A	#N/A	#N/A	0.533424802
AURMO_00328	dye decolorizing peroxidase	C:cellular_component; F:oxidoreductase activity	Rhola_00013630	#N/A	0.716373431
AURMO_00329	hypothetical protein	C:cellular_component; P:transport; F:ion binding	#N/A	#N/A	0.024211029

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00331	transposase InsO family protein	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.44742204
AURMO_00332	RND superfamily putative drug exporter	C:cellular_component	Rhola_00002240	#N/A	0.553629646
AURMO_00333	succinate semialdehyde dehydrogenase	F:oxidoreductase activity	Rhola_00003450	#N/A	0.0457806
AURMO_00334	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	A	0.013940876
AURMO_00335	hypothetical protein	F:DNA binding	#N/A	#N/A	0.826240777
AURMO_00336	ATP-binding cassette subfamily B protein	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00011660	M	0.009478671
AURMO_00337	hypothetical protein	C:cellular_component	#N/A	G	4.93E-03
AURMO_00338	6,7-dimethyl-8-ribityllumazine synthase	P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011630	J	2.19E-20

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00339	3,4-dihydroxy 2-butanone 4-phosphate synthase/GTP cyclohydrolase II	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011620	J	2.58E-12
AURMO_00340	riboflavin synthase alpha chain	F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00011610	E	1.50E-08
AURMO_00341	diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase	P:biosynthetic process; F:oxidoreductase activity; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011600	E	3.71E-07
AURMO_00342	hypothetical protein	#N/A	#N/A	#N/A	0.545554952
AURMO_00343	tryptophanyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00011590	#N/A	0.530326372

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00344	exodeoxyribonuclease-3	F:nuclease activity; P:DNA metabolic process; P:response to stress	Rhola_00011580	#N/A	0.649167811
AURMO_00345	membrane protein	C:plasma membrane	#N/A	#N/A	0.080996256
AURMO_00346	phosphocarrier protein HPr	F:molecular_function; C:cytoplasm; P:transport	#N/A	A	3.84E-06
AURMO_00347	PTS system fructose-specific IIC component	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.035279789
AURMO_00348	PTS system IIB component (Fru family)	C:plasma membrane; F:transmembrane transporter activity	#N/A	A	0.000670932
AURMO_00349	PTS system fructose-specific IIA component	C:cellular_component; F:kinase activity; F:transmembrane transporter activity	Rhola_00012910	A	6.17E-03
AURMO_00350	1-phosphofructokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding	#N/A	A	7.44E-03
AURMO_00351	DeoR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.294758484
AURMO_00352	hypothetical protein	#N/A	#N/A	#N/A	0.600492909
AURMO_00353	phosphoenolpyruvate--protein phosphotransferase	C:cytoplasm; P:transport; F:kinase activity; F:ion binding	Rhola_00012930	#N/A	0.319423505

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00354	succinate dehydrogenase / fumarate reductase iron-sulfur subunit	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	Rhola_00011560	#N/A	0.902812277
AURMO_00355	succinate dehydrogenase subunit A	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	Rhola_00011550	#N/A	0.681427778
AURMO_00356	succinate dehydrogenase / fumarate reductase membrane anchor subunit	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity	Rhola_00011540	#N/A	0.048457719
AURMO_00357	succinate dehydrogenase subunit C	C:intracellular; P:generation of precursor metabolites and energy; F:oxidoreductase activity; C:protein-containing complex; F:ion binding	Rhola_00011530	#N/A	0.465515986
AURMO_00358	mannose-1-phosphate guanylyltransferase	P:carbohydrate metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00011520	#N/A	0.256363959
AURMO_00359	adenosine deaminase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	Rhola_00011450	E	2.84E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00360	purine-nucleoside phosphorylase	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	M	8.24E-04
AURMO_00361	dihydrolipoamide dehydrogenase	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process; F:ion binding	Rhola_00006760	#N/A	0.99111841
AURMO_00362	acetyl/propionyl-CoA carboxylase alpha subunit	F:ligase activity; F:ion binding	Rhola_00011390	#N/A	0.035312828
AURMO_00363	septum formation protein	F:molecular_function; C:cytoplasm; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011380	A	8.47E-05
AURMO_00364	tRNA/tmRNA/rRNA uracil-C5-methylase (TrmA/RlmC/RlmD family)	F:methyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00011370	J	1.22E-06
AURMO_00365	hypothetical protein	#N/A	#N/A	A	3.36E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00366	propionyl-CoA carboxylase beta chain	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:ligase activity; C:protein-containing complex; P:small molecule metabolic process	Rhola_00011320	A	2.10E-07
AURMO_00367	BirA family biotin operon repressor/biotin-[acetyl-CoA-carboxylase] ligase	P:cellular protein modification process; F:ligase activity	Rhola_00011310	#N/A	0.663824323
AURMO_00368	membrane protein YdbS with pleckstrin-like domain	C:cellular_component	#N/A	E	3.31E-11
AURMO_00369	dolichol-phosphate mannosyltransferase	P:biological_process; F:transferase activity, transferring glycosyl groups	Rhola_00001450	#N/A	0.015959285
AURMO_00370	putative flippase GtrA	C:cellular_component; P:carbohydrate metabolic process; P:biosynthetic process	#N/A	#N/A	0.563786809
AURMO_00371	5-(carboxyamino)imidazole ribonucleotide synthase	P:biosynthetic process; F:lyase activity; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011290	#N/A	0.480123934

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00372	5-(carboxyamino)imidazole ribonucleotide mutase	P:biosynthetic process; F:lyase activity; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011280	#N/A	0.732896355
AURMO_00373	LytR family transcriptional attenuator	C:cellular_component	Rhola_00011270	B	1.33E-03
AURMO_00374	O-antigen ligase	C:cellular_component; F:ligase activity	#N/A	#N/A	0.584154647
AURMO_00375	O-antigen ligase-like membrane protein	C:cellular_component; F:ligase activity	Rhola_00011240	#N/A	0.102724242
AURMO_00376	glutaryl-CoA dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	M	9.94E-09
AURMO_00377	mannose-6-phosphate isomerase type 1	P:carbohydrate metabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011230	#N/A	0.572361337
AURMO_00378	transcription factor WhiB	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00011220	#N/A	0.245904242
AURMO_00379	GT2 family glycosyltransferase	F:molecular_function; C:cellular_component	Rhola_00011210	E	5.28E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00380	hypothetical protein	C:cellular_component	Rhola_00011200	L	1.87E-04
AURMO_00381	hypothetical protein	#N/A	#N/A	#N/A	0.918759528
AURMO_00382	uncharacterized protein DUF3499	#N/A	#N/A	#N/A	0.931422612
AURMO_00383	phosphomannomutase	P:carbohydrate metabolic process; F:isomerase activity	Rhola_00011180	#N/A	0.518828056
AURMO_00384	adenosylhomocysteinase	F:molecular_function; C:cytoplasm; P:small molecule metabolic process	Rhola_00011170	J	6.38E-04
AURMO_00385	two-component system response regulator MtrA	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00011160	A	3.62E-09
AURMO_00386	two-component system sensor histidine kinase MtrB	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	Rhola_00011150	#N/A	0.384319055
AURMO_00387	sporulation and spore germination protein	#N/A	Rhola_00011140	#N/A	0.04091932
AURMO_00388	ComF family protein	P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.526520578
AURMO_00389	ribosomal subunit interface protein	P:biological_process	#N/A	M	3.36E-14

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00390	protein translocase subunit secA	C:cytoplasm; C:plasma membrane; P:protein targeting; F:ion binding; P:transmembrane transport	Rhola_00011110	E	9.98E-09
AURMO_00391	hypothetical protein	F:helicase activity; C:cellular_component	#N/A	#N/A	0.019627381
AURMO_00392	hypothetical protein	#N/A	#N/A	#N/A	0.043711352
AURMO_00393	hypothetical protein	#N/A	#N/A	#N/A	0.631103614
AURMO_00394	hypothetical protein	#N/A	Rhola_00001200	N	0.005723369
AURMO_00395	nucleotidyltransferase-like protein	F:transferase activity	Rhola_00001210	#N/A	0.723339954
AURMO_00396	excisionase family DNA binding protein	F:DNA binding	#N/A	#N/A	0.798258678
AURMO_00397	hypothetical protein	C:cellular_component	#N/A	#N/A	0.967984115
AURMO_00398	MinD-like ATPase involved in chromosome partitioning or flagellar assembly	F:molecular_function	RHOLA_RS05495	#N/A	0.926639807
AURMO_00399	NYN domain-containing protein	F:oxidoreductase activity	#N/A	M	2.94E-07
AURMO_00400	acetyl esterase/lipase	F:molecular_function; C:cellular_component	#N/A	#N/A	0.564734158
AURMO_00401	two-component sensor histidine kinase	P:cellular protein modification process; F:kinase activity; F:ion binding	Rhola_00011060	#N/A	0.698865809
AURMO_00402	CBS domain containing-hemolysin-like protein	C:cellular_component; F:ion binding	Rhola_00009520	#N/A	0.820458814
AURMO_00403	CBS domain containing-hemolysin-like protein	C:cellular_component	Rhola_00009510	M	1.18E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00404	hydroxyethylthiazole kinase-like uncharacterized protein yjeF	F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	A	8.41E-03
AURMO_00405	uncharacterized protein DUF2029	C:cellular_component; F:transferase activity, transferring glycosyl groups	Rhola_00009480	#N/A	0.596996402
AURMO_00406	homoserine O-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00009470	#N/A	0.019938447
AURMO_00407	enoyl-CoA hydratase/carnithine racemase	F:lyase activity	Rhola_00013210	#N/A	0.735265375
AURMO_00408	mRNA-degrading endonuclease toxin of MazEF toxin-antitoxin module	F:DNA binding	#N/A	#N/A	0.424520572
AURMO_00409	hypothetical protein	#N/A	#N/A	#N/A	0.290038672
AURMO_00410	uncharacterized protein DUF3467	#N/A	#N/A	#N/A	0.265832749

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00411	O-acetylhomoserine sulfhydrylase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:lyase activity; F:ion binding	Rhola_00009460	#N/A	0.876354823
AURMO_00412	fucose 4-O-acetylase-like acetyltransferase	C:cellular_component; F:transferase activity, transferring acyl groups	#N/A	E	7.83E-03
AURMO_00413	voltage-gated potassium channel	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	#N/A	0.10987933
AURMO_00414	uracil-DNA glycosylase	C:cytoplasm; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds	Rhola_00009450	#N/A	0.248814986
AURMO_00415	phosphinothricin acetyltransferase	F:transferase activity, transferring acyl groups	Rhola_00009440	#N/A	0.089536421
AURMO_00416	transcription factor WhiB	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	I	3.04E-03
AURMO_00417	hypothetical protein	C:cellular_component	#N/A	#N/A	0.285858133

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00418	hypothetical protein	#N/A	#N/A	#N/A	0.197888171
AURMO_00419	DNA-binding XRE family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.156413503
AURMO_00420	peroxiredoxin Q/BCP	C:cell; F:oxidoreductase activity; P:homeostatic process	Rhola_00011030	A	5.69E-03
AURMO_00421	dTDP-glucose 4,6-dehydratase	F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00000200	#N/A	0.833031622
AURMO_00422	dTDP-4-dehydrorhamnose 3,5-epimerase	P:biosynthetic process; F:oxidoreductase activity; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.790244989
AURMO_00423	UDP-glucose 4-epimerase	P:carbohydrate metabolic process; F:isomerase activity; P:small molecule metabolic process	Rhola_00012830	D	3.04E-03
AURMO_00424	ribosome biogenesis GTPase	F:GTPase activity; C:cytoplasm; F:rRNA binding; P:ribosome biogenesis; F:ion binding	Rhola_00009580	A	1.33E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00425	3-phosphoshikimate 1-carboxyvinyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00009570	#N/A	0.297020873
AURMO_00426	RNA polymerase sigma-70 factor (ECF subfamily)	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00009560	H	2.63E-05
AURMO_00427	mycothiol system anti-sigma-R factor	#N/A	#N/A	G	6.46E-05
AURMO_00428	IS30 family transposase	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.0457806
AURMO_00429	2-oxoglutarate dehydrogenase E1 component	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transferase activity, transferring acyl groups; F:ion binding	Rhola_00009530	#N/A	0.581153417
AURMO_00430	peptidoglycan/LPS O-acetylase OafA/YrhL	C:cellular_component; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.539063398
AURMO_00431	predicted membrane protein DUF2142	C:cellular_component	#N/A	#N/A	0.6645213

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00432	glycosyl transferase family 2	P:biological_process; F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.400636514
AURMO_00433	hypothetical protein	C:cellular_component	#N/A	#N/A	0.347248729
AURMO_00434	ABC-type bacteriocin/lantibiotic exporter with double-glycine peptidase domain	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	A	1.68E-07
AURMO_00435	glycosyltransferase involved in cell wall biosynthesis	F:transferase activity	#N/A	A	5.24E-07
AURMO_00436	hypothetical protein	F:molecular_function	#N/A	#N/A	0.129294874
AURMO_00437	glycosyltransferase involved in cell wall biosynthesis	F:molecular_function	#N/A	D	1.42E-02
AURMO_00438	hypothetical protein	F:transferase activity	#N/A	D	9.01E-06
AURMO_00439	glycosyl transferase family 2	F:molecular_function	#N/A	D	3.71E-03
AURMO_00440	predicted dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.02915728
AURMO_00441	dTDP-4-amino-4,6-dideoxygalactose transaminase	F:molecular_function	#N/A	#N/A	0.079601106
AURMO_00442	succinyltransferase-like protein	F:transferase activity, transferring acyl groups	#N/A	#N/A	0.085298982
AURMO_00443	VCBS repeat protein	#N/A	Rhola_00011250	#N/A	0.016173583
AURMO_00444	hypothetical protein	F:ATP binding	#N/A	A	0.000266593

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00445	glucose-1-phosphate thymidylyltransferase	P:carbohydrate metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; F:ion binding	Rhola_00000190	#N/A	0.587597832
AURMO_00446	ABC-2 type transport system permease protein	C:plasma membrane; C:protein-containing complex; P:transmembrane transport	#N/A	#N/A	0.846744661
AURMO_00447	ABC-type polysaccharide/polyol phosphate transport system ATPase subunit	F:ATPase activity; F:ion binding	Rhola_00012870	#N/A	0.408245323
AURMO_00448	glycosyl transferase family 1	F:molecular_function	#N/A	#N/A	0.030886082
AURMO_00449	transposase	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.728370432
AURMO_00450	hypothetical protein	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.070121723
AURMO_00452	arginyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00004090	#N/A	0.07589715
AURMO_00453	diaminopimelate decarboxylase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00004100	E	3.63E-08

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00454	homoserine dehydrogenase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00004110	E	6.18E-12
AURMO_00455	threonine synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00004120	J	4.17E-08
AURMO_00456	homoserine kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	Rhola_00004130	J	6.46E-05
AURMO_00457	N-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase	F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.124558862
AURMO_00458	transcription termination factor Rho	F:RNA binding; F:helicase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00004140	E	3.99E-11
AURMO_00459	peptide chain release factor 1 (bRF-1)	C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00004150	E	1.94E-09
AURMO_00460	dTDP-4-amino-4,6-dideoxygalactose transaminase	F:molecular_function	#N/A	E	2.52E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00461	glycosyltransferase involved in cell wall biosynthesis	F:transferase activity	#N/A	B	7.30E-03
AURMO_00462	rhamnosyltransferase	F:molecular_function	#N/A	#N/A	0.753659071
AURMO_00463	serine O-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00009720	#N/A	0.032551175
AURMO_00464	AAA ATPase-like protein	F:ATP binding	#N/A	M	0.002780292
AURMO_00465	cysteine synthase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00009710	F	2.30E-05
AURMO_00466	release factor glutamine methyltransferase	P:cellular protein modification process; F:methyltransferase activity	Rhola_00004160	#N/A	0.396898608
AURMO_00467	glycosyl transferase family 2	F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.959508134
AURMO_00468	translation factor SUA5	F:RNA binding; F:nucleotidyltransferase activity	Rhola_00004170	#N/A	0.640810338

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00469	UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase	C:cellular_component; F:transferase activity, transferring glycosyl groups	Rhola_00004180	#N/A	0.640810338
AURMO_00470	hypothetical protein	C:cellular_component	#N/A	#N/A	0.048829714
AURMO_00471	Fic family protein	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.058772951
AURMO_00472	ATP synthase F0 subcomplex A subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00004200	#N/A	0.178082394

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00473	ATP synthase F0 subcomplex C subunit	C:intracellular; C:plasma membrane; F:lipid binding; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.075517275
AURMO_00474	ATP synthase F0 subcomplex B subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00004220	#N/A	0.174357752
AURMO_00475	ATP synthase F1 subcomplex delta subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00004230	#N/A	0.033371325

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00476	ATP synthase F1 subcomplex alpha subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00004240	#N/A	0.631103614
AURMO_00477	ATP synthase F1 subcomplex gamma subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00004250	#N/A	0.0212102
AURMO_00478	F-type H+-transporting ATPase subunit beta	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00004260	#N/A	0.596996402

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00479	ATP synthase F1 subcomplex epsilon subunit	C:intracellular; C:plasma membrane; P:biosynthetic process; F:transmembrane transporter activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.59867004
AURMO_00480	hypothetical protein	#N/A	#N/A	N	0.007527422
AURMO_00481	transcriptional regulator with XRE-family HTH domain	F:DNA binding	#N/A	#N/A	0.590401938
AURMO_00482	pilus assembly protein CpaF	#N/A	Rhola_00009400	#N/A	0.108456758
AURMO_00483	tight adherence protein B	C:cellular_component	#N/A	#N/A	0.033013375
AURMO_00484	tight adherence protein C	C:cellular_component	#N/A	#N/A	0.932180881
AURMO_00485	hypothetical protein	C:cellular_component	#N/A	#N/A	0.833031622
AURMO_00486	TadE-like protein	C:cellular_component	#N/A	#N/A	0.805098292
AURMO_00487	hypothetical protein	C:cellular_component	#N/A	#N/A	0.802054975
AURMO_00488	putative Flp pilus-assembly TadE/G-like protein	C:cellular_component	#N/A	#N/A	0.977181019
AURMO_00489	asparaginase	#N/A	Rhola_00012440	#N/A	0.660949447
AURMO_00490	4-aminobutyrate aminotransferase/(S)-3-amino-2-methylpropionate transaminase	P:cellular amino acid metabolic process; F:ion binding	Rhola_00004410	#N/A	0.873456224

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00491	1-deoxy-D-xylulose 5-phosphate reductoisomerase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:isomerase activity; F:ion binding; P:small molecule metabolic process	Rhola_00004420	#N/A	0.918006862
AURMO_00492	RIP metalloprotease RseP	C:cellular_component; F:peptidase activity; F:ion binding	Rhola_00004430	N	2.05E-03
AURMO_00493	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	Rhola_00004440	#N/A	0.880092845
AURMO_00494	hypothetical protein	#N/A	#N/A	#N/A	0.674342193
AURMO_00495	predicted MFS family arabinose efflux permease	C:cellular_component; P:transmembrane transport	Rhola_00010670	#N/A	0.776082335
AURMO_00496	prolyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00004450	J	9.41E-04
AURMO_00497	NusA antitermination factor	F:DNA-binding transcription factor activity; C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00004460	#N/A	0.463864418
AURMO_00498	hypothetical protein	F:DNA binding	#N/A	E	4.40E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00499	translation initiation factor 2 (bIF-2)	F:GTPase activity; C:cytoplasm; F:translation factor activity, RNA binding; F:ion binding	Rhola_00004480	E	7.74E-10
AURMO_00500	ribosome-binding factor A	C:cytoplasm; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00004490	E	2.03E-09
AURMO_00501	2TM domain-containing protein	C:cellular_component	#N/A	A	4.85E-24
AURMO_00502	A/G-specific DNA-adenine glycosylase	F:DNA binding; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds	#N/A	#N/A	0.198847077
AURMO_00503	putative membrane protein	C:cellular_component	#N/A	A	1.47E-12
AURMO_00504	VIT1/CCC1 family predicted Fe2+/Mn2+ transporter	C:cell; F:transmembrane transporter activity; P:homeostatic process	Rhola_00002410	#N/A	0.1646175
AURMO_00505	hypothetical protein	C:cellular_component	#N/A	#N/A	0.172666372
AURMO_00506	cell division transport system ATP-binding protein	C:plasma membrane; P:cell cycle; F:ATPase activity; F:ion binding; P:cell division	Rhola_00009310	B	5.15E-22
AURMO_00507	cell division transport system permease protein	C:plasma membrane; P:cell cycle; P:cell division	Rhola_00009300	B	5.12E-08
AURMO_00508	SsrA-binding protein	F:RNA binding; C:cytoplasm; P:translation	Rhola_00009280	E	0.002364707
AURMO_00510	uncharacterized 5xTM membrane YitT family protein	C:cellular_component	#N/A	#N/A	0.379494379

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00511	hypothetical protein	#N/A	#N/A	#N/A	0.100036733
AURMO_00512	glutathione peroxidase	P:response to stress; F:oxidoreductase activity	Rhola_00005540	H	7.19E-08
AURMO_00513	flavin reductase (DIM6/NTAB) family NADH-FMN oxidoreductase RutF	F:oxidoreductase activity; F:ion binding	#N/A	E	5.05E-09
AURMO_00514	uncharacterized protein (DUF2236 family)	#N/A	Rhola_00003330	H	2.09E-08
AURMO_00515	histidinol-phosphate phosphatase	P:lipid metabolic process; F:phosphatase activity	Rhola_00009590	#N/A	0.829110959
AURMO_00517	metallo-beta-lactamase family protein	F:oxidoreductase activity	Rhola_00003400	A	3.10E-04
AURMO_00518	SdpI/YhfL family protein	C:cellular_component	#N/A	#N/A	0.812280115
AURMO_00519	formiminoglutamase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	Rhola_00000270	#N/A	0.477742178
AURMO_00520	imidazolonepropionase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00000290	H	4.10E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00521	urocanate hydratase	F:DNA binding; C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00000300	E	5.85E-04
AURMO_00522	histidine ammonia-lyase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00000280	E	3.38E-10
AURMO_00523	IclR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00000310	#N/A	0.090634353
AURMO_00524	small multidrug resistance pump	C:plasma membrane	#N/A	A	0.008253423
AURMO_00525	hypothetical protein	#N/A	#N/A	M	2.17E-03
AURMO_00527	uncharacterized protein YbjT (DUF2867 family)	C:cellular_component; F:isomerase activity	Rhola_00003570	M	1.05E-10
AURMO_00528	hypothetical protein	C:cellular_component	#N/A	#N/A	0.557557231
AURMO_00529	Cu+-exporting ATPase	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	#N/A	H	2.56E-12

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00530	fatty acid desaturase	C:cellular_component; P:lipid metabolic process; F:oxidoreductase activity	Rhola_00009740	I	0.000609033
AURMO_00531	hypothetical protein	C:cellular_component	#N/A	H	1.76E-03
AURMO_00532	helicase-like protein	F:helicase activity; F:ion binding	#N/A	E	3.46E-06
AURMO_00533	ZIP family zinc transporter	C:cellular_component	#N/A	#N/A	0.317385662
AURMO_00534	pimeloyl-ACP methyl ester carboxylesterase	F:molecular_function	#N/A	A	9.98E-03
AURMO_00535	PiT family inorganic phosphate transporter	C:cellular_component; F:transmembrane transporter activity	Rhola_00003470	#N/A	0.424520572
AURMO_00536	hypothetical protein	C:cellular_component	#N/A	#N/A	0.571018831
AURMO_00537	AGZA family xanthine/uracil permease-like MFS transporter	C:cellular_component; F:transmembrane transporter activity	#N/A	A	1.09E-07
AURMO_00538	hypothetical protein	#N/A	#N/A	#N/A	0.6645213
AURMO_00539	hypothetical protein	#N/A	#N/A	#N/A	0.329863491
AURMO_00540	3-methyladenine DNA glycosylase AlkD	#N/A	Rhola_00013550	#N/A	0.089009586
AURMO_00541	putative serine protease PepD	C:cellular_component; F:peptidase activity	Rhola_00004010	E	1.30E-02
AURMO_00542	cellulose synthase/poly-beta-1,6-N-acetylglucosamine synthase-like glycosyltransferase	C:cellular_component; F:transferase activity, transferring glycosyl groups	Rhola_00012860	#N/A	0.66687305
AURMO_00543	phosphatidylglycerophosphate synthase	F:molecular_function; C:cellular_component; P:lipid metabolic process; P:biosynthetic process	#N/A	#N/A	0.865720333

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AURMO_00544	GT2 family glycosyltransferase	F:molecular_function	#N/A	#N/A	0.495725019
AURMO_00545	hypothetical protein	F:molecular_function; C:cellular_component	#N/A	#N/A	0.525836106
AURMO_00546	superfamily I DNA/RNA helicase	F:DNA binding; F:helicase activity; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	Rhola_00003900	A	8.19E-05
AURMO_00547	DNA helicase-2/ATP-dependent DNA helicase PcrA	F:DNA binding; F:helicase activity; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	Rhola_00003910	#N/A	0.240634526
AURMO_00548	aminoglycoside phosphotransferase (APT) family kinase protein	F:kinase activity; P:phosphorylation; F:transferase activity	Rhola_00003920	C	1.50E-04
AURMO_00549	NAD+ diphosphatase	F:molecular_function	Rhola_00003930	#N/A	0.377186994
AURMO_00550	Rep family ATP-dependent DNA helicase	F:DNA binding; F:helicase activity; F:ion binding; P:chromosome organization	Rhola_00003940	#N/A	0.070036792
AURMO_00551	hypothetical protein	#N/A	#N/A	I	4.62E-04
AURMO_00552	putative hydrolase	F:molecular_function	Rhola_00003960	G	1.03E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00553	PDZ domain-containing protein	C:cellular_component; F:peptidase activity; P:catabolic process; F:ATPase activity; F:ion binding	Rhola_00003970	F	1.45E-05
AURMO_00554	hypothetical protein	C:plasma membrane	Rhola_00003980	F	1.07E-02
AURMO_00555	cytochrome bd-I ubiquinol oxidase subunit 1 apoprotein	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; C:protein-containing complex; F:ion binding	#N/A	A	1.03E-02
AURMO_00556	cytochrome bd-I ubiquinol oxidase subunit 2 apoprotein	C:cellular_component; F:oxidoreductase activity	#N/A	A	9.20E-03
AURMO_00557	ATP-binding cassette subfamily C protein CydD	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	A	1.01E-11
AURMO_00558	ATP-binding cassette subfamily C protein CydC	C:cell; F:ATPase activity; F:transmembrane transporter activity; P:homeostatic process; F:ion binding	#N/A	N	3.61E-09
AURMO_00559	predicted MFS family arabinose efflux permease	C:cellular_component; P:transmembrane transport	Rhola_00009330	#N/A	0.345389988
AURMO_00560	peptide chain release factor 2 (bRF-2)	C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00009320	#N/A	0.625336783
AURMO_00561	sugar phosphate isomerase/epimerase	F:isomerase activity	#N/A	E	1.05E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00562	dihydroxy-acid dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00010840	L	1.31E-07
AURMO_00563	acetolactate synthase large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ion binding	Rhola_00010830	J	7.58E-07
AURMO_00564	acetolactate synthase small subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:enzyme regulator activity	Rhola_00010820	L	7.39E-03
AURMO_00565	ketol-acid reductoisomerase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:isomerase activity; F:ion binding	Rhola_00010810	#N/A	0.037430384
AURMO_00566	hypothetical protein	C:cellular_component	#N/A	#N/A	0.259082162
AURMO_00567	hypothetical protein	C:cellular_component	#N/A	#N/A	0.168345635
AURMO_00568	D-3-phosphoglycerate dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00010800	F	1.44E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00569	3-isopropylmalate dehydrogenase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding	Rhola_00010770	#N/A	0.021892663
AURMO_00570	branched chain amino acid aminotransferase	F:molecular_function; P:cellular amino acid metabolic process; P:biosynthetic process	Rhola_00010760	#N/A	0.808708603
AURMO_00571	glutamyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00010740	#N/A	0.015671789
AURMO_00573	diacylglycerol kinase	F:kinase activity	Rhola_00010690	#N/A	0.78018472
AURMO_00575	tellurite resistance protein TerC	C:cellular_component	Rhola_00005480	#N/A	0.279304305
AURMO_00576	3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00010660	#N/A	0.020894685
AURMO_00577	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	C:cytosol; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:isomerase activity; C:protein-containing complex	Rhola_00010650	L	4.25E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00578	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cell division; P:cell wall organization or biogenesis	Rhola_00010640	#N/A	0.194328952
AURMO_00579	1-acyl-sn-glycerol-3-phosphate acyltransferase	C:cellular_component; F:transferase activity, transferring acyl groups	Rhola_00010630	L	0.001013764
AURMO_00580	glycerol-3-phosphate dehydrogenase (NAD(P)+)	C:cytoplasm; P:carbohydrate metabolic process; P:lipid metabolic process; P:catabolic process; P:biosynthetic process; F:oxidoreductase activity; C:protein-containing complex	Rhola_00010620	#N/A	0.78000227
AURMO_00581	D-alanine-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell wall organization or biogenesis	Rhola_00010610	A	4.70E-03
AURMO_00582	uncharacterized protein DUF3515	#N/A	Rhola_00010600	#N/A	0.702679137

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00583	thiamine-phosphate kinase	P:sulfur compound metabolic process; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00010590	#N/A	0.801568489
AURMO_00584	16S rRNA (guanine966-N2)-methyltransferase	F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00009120	#N/A	0.480123934
AURMO_00585	ATP-dependent DNA helicase RecG	F:helicase activity; F:ion binding; P:chromosome organization	Rhola_00009110	#N/A	0.373142551
AURMO_00586	phosphopantetheine adenylyltransferase	C:cytoplasm; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00009100	#N/A	0.234700272

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00587	signal recognition particle-docking protein FtsY	F:GTPase activity; C:cytoplasm; C:plasma membrane; P:protein targeting; F:ion binding	RHOLA_RS04500	#N/A	0.36149836
AURMO_00588	signal recognition particle subunit FFH/SRP54 (srp54)	F:RNA binding; F:GTPase activity; C:cytoplasm; P:protein targeting; C:protein-containing complex; F:ion binding	Rhola_00009030	#N/A	0.040585214
AURMO_00589	peptide-methionine (R)-S-oxide reductase	P:response to stress; F:oxidoreductase activity; F:ion binding	Rhola_00010490	A	0.005750169
AURMO_00590	2-phosphosulfolactate phosphatase	F:phosphatase activity; F:ion binding	#N/A	#N/A	0.504522078
AURMO_00591	SSU ribosomal protein S16P	F:structural constituent of ribosome; C:ribosome; P:translation	RHOLA_RS04490	E	2.55E-05
AURMO_00592	hypothetical protein	F:RNA binding	#N/A	E	4.33E-04
AURMO_00593	16S rRNA processing protein RimM	F:molecular_function; C:cytoplasm; C:ribosome; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00009000	E	1.09E-05
AURMO_00594	tRNA (guanine37-N(1)-) methyltransferase	C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity	Rhola_00005110	#N/A	0.523963699

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00595	large subunit ribosomal protein L19	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00005120	E	4.95E-09
AURMO_00596	signal peptidase I	C:cellular_component; F:peptidase activity	Rhola_00005130	E	0.006065571
AURMO_00597	RNase HII	F:RNA binding; F:nuclease activity; C:cytoplasm; F:ion binding	Rhola_00005140	#N/A	0.038235922
AURMO_00598	uncharacterized protein DUF2469	#N/A	Rhola_00005150	#N/A	0.086014493
AURMO_00599	DNA processing protein	P:biological_process	Rhola_00005180	#N/A	0.232113672
AURMO_00600	integrase/recombinase XerC	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:cell cycle; P:chromosome segregation; P:transposition; P:cell division	Rhola_00005190	#N/A	0.532109523
AURMO_00601	potassium/proton antiporter membrane subunit (CPA2 family)	C:cellular_component; F:transmembrane transporter activity	Rhola_00005720	A	0.010550822
AURMO_00602	potassium/proton antiporter regulatory subunit (CPA2 family)	F:transmembrane transporter activity	#N/A	#N/A	0.03194424
AURMO_00603	hypothetical protein	F:molecular_function	Rhola_00010280	E	2.38E-09
AURMO_00604	uncharacterized protein DUF4395	C:cellular_component	#N/A	I	2.93E-04
AURMO_00605	thioredoxin	C:cell; F:isomerase activity; P:homeostatic process	#N/A	I	1.24E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00606	thymidylate synthase (FAD)	F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00004680	C	7.14E-05
AURMO_00607	4-hydroxy-tetrahydrodipicolinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	Rhola_00004700	J	3.34E-03
AURMO_00608	ribonuclease J	F:RNA binding; F:nuclease activity; C:cytoplasm; P:ribosome biogenesis; F:ion binding	Rhola_00004710	K	5.95E-03
AURMO_00609	LacI family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	N	0.001524113
AURMO_00610	raffinose/stachyose/melibiose transport system substrate-binding protein	#N/A	#N/A	A	1.05E-06
AURMO_00611	raffinose/stachyose/melibiose transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	A	3.71E-07
AURMO_00612	raffinose/stachyose/melibiose transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	A	1.86E-05
AURMO_00613	alpha-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	Rhola_00002670	A	2.80E-08

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00614	S-DNA-T family DNA segregation ATPase FtsK/SpoIIIE	F:DNA binding; C:plasma membrane; P:cell cycle; P:chromosome segregation; F:ion binding; P:cell division	Rhola_00004720	#N/A	0.131418028
AURMO_00615	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	F:molecular_function; C:cellular_component; P:lipid metabolic process; P:biosynthetic process	Rhola_00004730	#N/A	0.689934133
AURMO_00616	competence/damage-inducible protein cinA	#N/A	Rhola_00004740	A	3.36E-03
AURMO_00617	helix-turn-helix protein	F:DNA binding	Rhola_00004750	H	1.24E-02
AURMO_00618	hypothetical protein	#N/A	#N/A	E	0.002616559
AURMO_00619	recombination protein RecA	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; F:ion binding	Rhola_00004770	#N/A	0.1530005
AURMO_00620	regulatory protein	C:cytoplasm; P:DNA metabolic process; P:response to stress	#N/A	#N/A	0.834216596
AURMO_00621	hypothetical protein	C:cellular_component	#N/A	#N/A	0.155733141
AURMO_00622	tRNA-i(6)A37 thiotransferase enzyme MiaB	C:cytoplasm; P:tRNA metabolic process; F:ion binding	Rhola_00004790	E	7.30E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00623	tRNA dimethylallyltransferase	P:tRNA metabolic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	Rhola_00004800	#N/A	0.97022812
AURMO_00624	diaminopimelate epimerase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity	Rhola_00004810	#N/A	0.715521086
AURMO_00625	hypothetical protein	#N/A	#N/A	#N/A	0.086014493
AURMO_00626	16S rRNA m(2)G 1207 methyltransferase	F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00004820	E	2.55E-07
AURMO_00627	hypothetical protein	C:cellular_component	#N/A	E	3.58E-07
AURMO_00628	hypothetical protein	#N/A	#N/A	#N/A	0.477742178
AURMO_00629	GTP-binding protein HflX	F:GTPase activity; C:cytoplasm; F:ion binding	Rhola_00004830	#N/A	0.728646908
AURMO_00630	phosphatidate phosphatase APP1	#N/A	#N/A	#N/A	0.355730473
AURMO_00631	membrane protein DedA with SNARE-associated domain	C:cellular_component	Rhola_00006040	#N/A	0.265546754
AURMO_00632	branched-subunit amino acid aminotransferase/4-amino-4-deoxychorismate lyase	F:lyase activity	#N/A	#N/A	0.997971106

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00633	anthranilate synthase component 1	F:molecular_function; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00006060	#N/A	0.067306826
AURMO_00634	leucyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00006070	J	1.57E-03
AURMO_00635	serine/threonine-protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	Rhola_00008730	#N/A	0.411037437
AURMO_00636	LysM repeat protein	F:lyase activity	#N/A	#N/A	0.632769568
AURMO_00637	hypothetical protein	F:DNA binding	#N/A	#N/A	0.454774772
AURMO_00638	geranylgeranyl diphosphate synthase type I	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00008700	#N/A	0.214705952
AURMO_00639	hypothetical protein	C:cellular_component	#N/A	G	2.92E-03
AURMO_00640	hypothetical protein	#N/A	#N/A	#N/A	0.576345792

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00641	division/cell wall cluster transcriptional repressor MraZ	F:DNA binding; F:DNA-binding transcription factor activity; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:cell division	Rhola_00008680	#N/A	0.311476687
AURMO_00642	16S rRNA (cytosine1402-N4)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00008670	#N/A	0.850075769
AURMO_00643	hypothetical protein	C:cellular_component; P:cell division	#N/A	#N/A	0.911251539
AURMO_00644	cell division protein FtsI (penicillin-binding protein 3)	C:cellular_component; F:transferase activity, transferring glycosyl groups; F:ion binding	Rhola_00008650	#N/A	0.867265656
AURMO_00645	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process; P:cell division; P:cell wall organization or biogenesis	Rhola_00008640	#N/A	0.695669951

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00646	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	Rhola_00008630	#N/A	0.425560799
AURMO_00647	phospho-N-acetylmuramoyl-pentapeptide-transferase	P:cell morphogenesis; F:molecular_function; C:plasma membrane; P:cell cycle; P:biosynthetic process; P:cell division; P:cell wall organization or biogenesis	Rhola_00008620	#N/A	0.176649288
AURMO_00648	UDP-N-acetylmuramoylalanine--D-glutamate ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process; P:cell division; P:cell wall organization or biogenesis	Rhola_00008610	#N/A	0.522407641
AURMO_00649	cell division-specific peptidoglycan biosynthesis regulator FtsW	C:cellular_component; P:cell division	Rhola_00008600	B	1.04E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00650	UDP-N-acetylglucosamine-N-acetylmuramylpentapeptide N-acetylglucosamine transferase	P:cell morphogenesis; C:plasma membrane; P:carbohydrate metabolic process; P:lipid metabolic process; P:cell cycle; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cell division; P:cell wall organization or biogenesis	Rhola_00008590	#N/A	0.070036792
AURMO_00651	UDP-N-acetylmuramate--L-alanine ligase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:ligase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	Rhola_00008580	E	0.001948065
AURMO_00652	cell division protein FtsQ	C:ribosome; C:plasma membrane; P:cell cycle; P:cell division	Rhola_00008570	J	1.09E-10
AURMO_00653	cell division protein FtsZ	P:reproduction; F:GTPase activity; C:cytoplasm; P:cell cycle; F:ion binding; P:cell division; P:protein-containing complex assembly	#N/A	A	0.010889071
AURMO_00654	hypothetical protein	F:ion binding	Rhola_00008550	J	1.17E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00655	cell division inhibitor SepF	P:reproduction; C:cytoplasm; P:cell cycle; P:cellular component assembly; P:cell division	#N/A	J	9.81E-09
AURMO_00656	YggT family protein	C:cellular_component	#N/A	B	6.97E-10
AURMO_00657	DivIVA domain-containing protein	C:cytoplasm; P:cell cycle; P:cell division	Rhola_00008520	#N/A	0.084258703
AURMO_00658	signal peptidase II	C:plasma membrane; F:peptidase activity	#N/A	#N/A	0.752787973
AURMO_00659	RluA family pseudouridine synthase	F:RNA binding; F:isomerase activity; P:cellular nitrogen compound metabolic process	Rhola_00008500	#N/A	0.39608037
AURMO_00660	UPF0042 nucleotide-binding protein	F:ion binding	Rhola_00007740	#N/A	0.689934133
AURMO_00661	hypothetical protein	F:DNA binding; P:cell cycle; P:cell division	Rhola_00007750	#N/A	0.280275177
AURMO_00662	Fe-Mn family superoxide dismutase	P:response to stress; F:oxidoreductase activity; F:ion binding	Rhola_00007760	H	1.91E-03
AURMO_00663	glyceraldehyde 3-phosphate dehydrogenase	P:carbohydrate metabolic process; F:oxidoreductase activity; P:small molecule metabolic process	Rhola_00007770	#N/A	0.059435201

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00664	phosphoglycerate kinase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00007780	E	1.20E-07
AURMO_00665	triosephosphate isomerase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00007790	#N/A	0.443717008
AURMO_00666	preprotein translocase subunit SecG	C:plasma membrane; P:protein transport; F:transmembrane transporter activity	#N/A	#N/A	0.407032397
AURMO_00667	RNA polymerase binding protein RbpA	P:biosynthetic process; F:enzyme binding; P:cellular nitrogen compound metabolic process	Rhola_00007810	#N/A	0.156949319

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00668	sugar-phosphatase	F:phosphatase activity	Rhola_00002450	#N/A	0.122800732
AURMO_00669	transposase IS481 family protein	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.832853708
AURMO_00670	6-phosphogluconolactonase	F:molecular_function; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy	Rhola_00007820	E	3.94E-06
AURMO_00671	glucose-6-phosphate dehydrogenase assembly protein OpcA	#N/A	Rhola_00007830	E	1.53E-05
AURMO_00672	glucose-6-phosphate 1-dehydrogenase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:small molecule metabolic process	Rhola_00007840	E	2.24E-07
AURMO_00673	glucose-6-phosphate isomerase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00007850	E	2.67E-09

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00674	transaldolase	F:molecular_function; C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy	Rhola_00007860	E	8.56E-04
AURMO_00675	transketolase	F:ion binding	Rhola_00007870	#N/A	0.683892528
AURMO_00676	protoheme IX farnesyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00007880	#N/A	0.869042311
AURMO_00677	cytochrome c oxidase assembly protein subunit 15	C:plasma membrane; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00007900	#N/A	0.979986456
AURMO_00678	iron-regulated ABC transporter membrane component SufB	P:sulfur compound metabolic process; P:biosynthetic process; P:cellular component assembly; P:cofactor metabolic process	Rhola_00007910	I	3.19E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00679	iron-regulated ABC transporter permease protein SufD	P:sulfur compound metabolic process; P:biosynthetic process; P:cellular component assembly; P:cofactor metabolic process	Rhola_00007920	F	1.48E-08
AURMO_00680	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin subunit	F:oxidoreductase activity	#N/A	F	0.00072179
AURMO_00681	Fe-S cluster assembly ATP-binding protein	F:ATPase activity; F:ion binding	Rhola_00007940	F	8.26E-10
AURMO_00682	metal-sulfur cluster biosynthetic enzyme	#N/A	Rhola_00007950	I	7.30E-04
AURMO_00683	cystathionine gamma-lyase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:lyase activity; F:ion binding	#N/A	#N/A	0.161104523
AURMO_00684	biotin transport system substrate-specific component	C:plasma membrane; F:transmembrane transporter activity	#N/A	A	7.30E-04
AURMO_00685	ATPase subunit of ABC transporter with duplicated ATPase domains	F:ATPase activity; F:ion binding	Rhola_00007970	E	5.86E-04
AURMO_00686	uncharacterized membrane protein YeiH	C:cellular_component	#N/A	#N/A	0.864632929
AURMO_00687	DNA replication and repair protein RecO	P:DNA metabolic process; P:response to stress	Rhola_00006250	#N/A	0.0298243

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AURMO_00688	undecaprenyl diphosphate synthase	F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	Rhola_00006260	#N/A	0.069908404
AURMO_00689	hypothetical protein	#N/A	Rhola_00012770	H	2.55E-08
AURMO_00690	predicted DsbA family dithiol-disulfide isomerase	F:oxidoreductase activity	#N/A	H	6.64E-09
AURMO_00691	nifR3 family TIM-barrel protein	P:tRNA metabolic process; F:oxidoreductase activity; F:ion binding	Rhola_00006280	H	2.89E-03
AURMO_00692	dGTPase	F:molecular_function	Rhola_00006290	#N/A	0.303155225
AURMO_00693	DNA primase	F:DNA binding; C:chromosome; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex; F:ion binding	Rhola_00006300	#N/A	0.581680355
AURMO_00694	phosphoglycerate dehydrogenase-like enzyme	F:kinase activity; F:oxidoreductase activity	Rhola_00006310	A	4.38E-06
AURMO_00696	predicted branched-subunit amino acid permease	C:cellular_component	Rhola_00006350	#N/A	0.747267583
AURMO_00697	branched-subunit amino acid transport protein AzlD	C:cellular_component	#N/A	#N/A	0.265546754
AURMO_00698	peptide deformylase	P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	Rhola_00006370	J	1.94E-05

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AURMO_00699	magnesium transporter NIPA	C:cellular_component; F:transmembrane transporter activity	Rhola_00006380	#N/A	0.136194715
AURMO_00700	glycosyltransferase involved in cell wall biosynthesis	F:transferase activity, transferring glycosyl groups	Rhola_00006390	B	4.89E-03
AURMO_00702	hypothetical protein	#N/A	#N/A	M	1.96E-18
AURMO_00703	hypothetical protein	#N/A	#N/A	#N/A	0.469760235
AURMO_00704	bifunctional DNA primase/polymerase-like protein	F:hydrolase activity, acting on acid anhydrides	#N/A	#N/A	0.332596264
AURMO_00705	P4 family phage/plasmid primase-like protien	#N/A	#N/A	#N/A	0.66256211
AURMO_00706	hypothetical protein	#N/A	#N/A	#N/A	0.930480076
AURMO_00707	hypothetical protein	C:cellular_component	#N/A	#N/A	0.060777496
AURMO_00708	hypothetical protein	C:cellular_component	#N/A	#N/A	0.023942643
AURMO_00709	hypothetical protein	C:cellular_component	#N/A	#N/A	0.168775238
AURMO_00710	uncharacterized protein DUF4352	C:cellular_component	#N/A	#N/A	0.052078818
AURMO_00711	DNA invertase Pin-like site-specific DNA recombinase	F:DNA binding; P:DNA metabolic process	#N/A	A	1.19E-24
AURMO_00712	reverse transcriptase (RNA-dependent DNA polymerase)	P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	A	8.50E-04
AURMO_00713	site-specific recombinase XerD	F:DNA binding; P:DNA metabolic process	#N/A	#N/A	0.016881151
AURMO_00714	chitinase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	#N/A	#N/A	0.699021055

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00715	hypothetical protein	#N/A	#N/A	B	6.42E-08
AURMO_00716	PadR family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.918046685
AURMO_00717	uncharacterized protein DUF3145	#N/A	#N/A	#N/A	0.036568848
AURMO_00718	hypothetical protein	F:DNA binding	#N/A	#N/A	0.702317596
AURMO_00719	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.703391792
AURMO_00720	3-oxoacyl-[acyl-carrier-protein] synthase II	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; P:small molecule metabolic process	Rhola_00006480	#N/A	0.483077161
AURMO_00721	acyl carrier protein	F:molecular_function; C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; P:small molecule metabolic process	Rhola_00006490	#N/A	0.034803029
AURMO_00722	3-oxoacyl-[acyl-carrier-protein] synthase-3	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; P:small molecule metabolic process	Rhola_00006500	#N/A	0.031285236
AURMO_00723	[acyl-carrier-protein] S-malonyltransferase	F:transferase activity, transferring acyl groups	Rhola_00006510	D	1.05E-02
AURMO_00724	PucR-like helix-turn-helix protein	F:DNA binding	Rhola_00006520	J	6.19E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00725	pyruvate dehydrogenase E1 component	F:oxidoreductase activity; F:ion binding	Rhola_00006530	#N/A	0.039006303
AURMO_00726	peroxiredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process	Rhola_00006540	#N/A	0.134821515
AURMO_00728	hypothetical protein	F:aminoacyl-tRNA ligase activity	#N/A	J	0.010968604
AURMO_00729	dinuclear metal center YbgI/SA1388 family protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	Rhola_00006570	#N/A	0.967984115
AURMO_00730	hypothetical protein	#N/A	#N/A	#N/A	0.162128136
AURMO_00731	ribonuclease HI	F:nuclease activity; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00006590	#N/A	0.091781396
AURMO_00732	polyphosphate glucokinase	F:kinase activity	Rhola_00006610	#N/A	0.088498941
AURMO_00733	methionine aminopeptidase type I	P:cellular protein modification process; F:peptidase activity; F:ion binding	Rhola_00006620	E	6.16E-03
AURMO_00734	hypothetical protein	F:peptidoglycan binding	#N/A	#N/A	0.114455947
AURMO_00735	transposase IS481 family protein	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.49445086

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00736	ketopantoate hydroxymethyltransferase	C:cytoplasm; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00006640	#N/A	0.682230621
AURMO_00737	NAD+ synthase (glutamine-hydrolysing)	C:cytoplasm; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00006660	#N/A	0.060327599
AURMO_00738	L-glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity	Rhola_00006670	#N/A	0.699021055
AURMO_00739	glutamate-ammonia-ligase adenylyltransferase	P:biological_process; F:nucleotidyltransferase activity; F:ligase activity; F:ion binding	Rhola_00006680	#N/A	0.199098041

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00740	glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding	Rhola_00006690	#N/A	0.050205737
AURMO_00741	RDD family protein	C:cellular_component	#N/A	#N/A	0.419223336
AURMO_00742	uncharacterized protein DUF4191	C:cellular_component	Rhola_00006710	L	9.05E-04
AURMO_00743	lipoic acid synthetase	C:cytoplasm; P:cellular protein modification process; P:lipid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process; P:protein maturation	Rhola_00006720	H	1.61E-05
AURMO_00744	lipoyl(octanoyl) transferase	C:cytoplasm; P:cellular protein modification process; F:transferase activity, transferring acyl groups; F:ligase activity; P:protein maturation	Rhola_00006730	#N/A	0.173432712
AURMO_00745	hypothetical protein	C:cellular_component	#N/A	#N/A	0.747267583
AURMO_00746	2-oxoglutarate dehydrogenase E2 component	F:transferase activity, transferring acyl groups	Rhola_00006750	K	1.47E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00747	dihydrolipoamide dehydrogenase	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process; F:ion binding	Rhola_00011400	#N/A	0.098401056
AURMO_00748	leucyl aminopeptidase	C:cytoplasm; F:peptidase activity; F:ion binding	Rhola_00006770	D	2.08E-04
AURMO_00749	predicted ATP-grasp superfamily ATP-dependent carboligase	F:ligase activity	Rhola_00006780	J	1.30E-03
AURMO_00750	RNA polymerase primary sigma factor	F:DNA binding; F:DNA-binding transcription factor activity; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00006810	J	5.05E-07
AURMO_00751	IS30 family transposase	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	N	2.57E-08
AURMO_00752	hypothetical protein	#N/A	#N/A	F	3.02E-03
AURMO_00753	DNA topoisomerase IV subunit B	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	Rhola_00006850	B	8.66E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00754	DNA gyrase subunit A	F:DNA binding; P:DNA metabolic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	Rhola_00006860	J	2.82E-19
AURMO_00755	type I phosphodiesterase/nucleotide pyrophosphatase	F:molecular_function	Rhola_00006870	#N/A	0.944461977
AURMO_00756	hypothetical protein	F:DNA binding	Rhola_00006880	#N/A	0.046796974
AURMO_00757	uncharacterized protein DUF4193	#N/A	#N/A	D	2.13E-04
AURMO_00758	hypothetical protein	C:cellular_component	#N/A	#N/A	0.76307711
AURMO_00759	dUTP pyrophosphatase	P:biosynthetic process; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00006910	#N/A	0.398166563
AURMO_00760	uncharacterized protein DUF3710	#N/A	Rhola_00006920	#N/A	0.06309107
AURMO_00761	uncharacterized protein DUF3159	C:cellular_component	Rhola_00006930	#N/A	0.051814918
AURMO_00762	aconitase	F:lyase activity	Rhola_00006940	#N/A	0.034471915
AURMO_00763	1-deoxy-D-xylulose-5-phosphate synthase	P:lipid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00006950	G	2.80E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00764	3-hydroxyacyl-CoA dehydrogenase	P:lipid metabolic process; P:catabolic process; F:oxidoreductase activity; P:small molecule metabolic process	Rhola_00013180	A	4.85E-24
AURMO_00765	acetyl-CoA acyltransferase	F:transferase activity, transferring acyl groups	Rhola_00013190	A	3.11E-11
AURMO_00766	ribonuclease D	F:nuclease activity	Rhola_00006960	B	2.67E-04
AURMO_00767	hypothetical protein	#N/A	Rhola_00006970	#N/A	0.240784129
AURMO_00768	hypothetical protein	P:biological_process	#N/A	#N/A	0.218887987
AURMO_00769	cysteine desulfuration protein SufE	#N/A	Rhola_00006990	#N/A	0.190775793
AURMO_00770	thiosulfate/3-mercaptopyruvate sulfurtransferase	F:molecular_function	Rhola_00007000	F	1.72E-03
AURMO_00771	cell division protein ZapE	F:ion binding; P:cell division	Rhola_00007010	#N/A	0.016889499
AURMO_00772	ammonium transporter	C:cellular_component; F:transmembrane transporter activity	Rhola_00007020	F	1.65E-03
AURMO_00773	ammonium transporter	C:cellular_component; F:transmembrane transporter activity	Rhola_00007030	#N/A	0.147864245
AURMO_00777	threonyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00007090	#N/A	0.902403803
AURMO_00778	ATP adenylyltransferase	F:nucleotidyltransferase activity	Rhola_00007100	#N/A	0.136194715

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00779	pyridoxal phosphate synthase yaaD subunit	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00007110	F	1.49E-05
AURMO_00780	pyridoxal phosphate synthase yaaE subunit	P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00007120	E	5.13E-08
AURMO_00781	YebC/PmpR family DNA-binding regulatory protein	F:DNA binding; C:cytoplasm; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00007130	#N/A	0.129294874
AURMO_00782	Holliday junction endonuclease RuvC	F:nuclease activity; P:DNA metabolic process; P:response to stress; F:ion binding	Rhola_00007140	#N/A	0.03447279

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00783	Holliday junction DNA helicase subunit RuvA	F:DNA binding; F:helicase activity; C:intracellular; P:DNA metabolic process; P:response to stress; C:protein-containing complex; F:ion binding; P:chromosome organization	Rhola_00007150	#N/A	0.030023892
AURMO_00784	Holliday junction DNA helicase subunit RuvB	F:DNA binding; F:helicase activity; P:DNA metabolic process; P:response to stress; F:ion binding; P:chromosome organization	Rhola_00007160	J	7.65E-03
AURMO_00785	preprotein translocase subunit YajC	C:cellular_component	#N/A	#N/A	0.826424833
AURMO_00786	preprotein translocase subunit SecD	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	Rhola_00007180	#N/A	0.415815058
AURMO_00787	protein translocase subunit secF	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	Rhola_00007190	L	0.000329471
AURMO_00788	GTP pyrophosphokinase	F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00007200	#N/A	0.030023892

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00789	hypothetical protein	F:methyltransferase activity; F:transferase activity; P:methylation	#N/A	#N/A	0.470483834
AURMO_00790	uncharacterized protein DUF349	#N/A	Rhola_00007210	#N/A	0.614644005
AURMO_00791	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	C:cellular_component; P:cellular protein modification process; F:isomerase activity	Rhola_00007220	C	6.85E-03
AURMO_00792	recombination protein MgsA	F:DNA binding; P:biosynthetic process; F:ion binding	Rhola_00007230	#N/A	0.190775793
AURMO_00793	small subunit ribosomal protein S4	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00007240	E	1.79E-07
AURMO_00794	hypothetical protein	#N/A	#N/A	#N/A	0.671106945
AURMO_00795	alanyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00007270	#N/A	0.032150358
AURMO_00796	putative Holliday junction resolvase	F:helicase activity; F:nuclease activity; C:cytoplasm; P:ribosome biogenesis	Rhola_00007280	#N/A	0.041980662

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00797	UPF0755 protein	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:lyase activity; P:cell wall organization or biogenesis	Rhola_00007290	C	3.70E-03
AURMO_00798	shikimate dehydrogenase	F:oxidoreductase activity	Rhola_00007300	#N/A	0.194328952
AURMO_00799	chorismate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	Rhola_00007310	J	1.11E-03
AURMO_00800	shikimate kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	#N/A	#N/A	0.038406002
AURMO_00801	3-dehydroquinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00007330	#N/A	0.079801697
AURMO_00802	3-dehydroquinate dehydratase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	Rhola_00007340	#N/A	0.505322383
AURMO_00803	translation elongation factor P (EF-P)	C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00007350	E	2.08E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00804	NusB antitermination factor	F:RNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00007360	E	1.82E-06
AURMO_00805	pyrimidine operon attenuation protein/uracil phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00007370	#N/A	0.956525791
AURMO_00806	aspartate carbamoyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00007380	#N/A	0.756803416
AURMO_00807	dihydroorotase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00007390	#N/A	0.6645213
AURMO_00808	hypothetical protein	C:cellular_component	#N/A	#N/A	0.221605317

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00809	carbamoyl-phosphate synthase small subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00007410	#N/A	0.438681575
AURMO_00810	carbamoyl-phosphate synthase large subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00007420	#N/A	0.291066529
AURMO_00811	orotidine-5'-phosphate decarboxylase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00007430	#N/A	0.199021133
AURMO_00812	guanylate kinase	C:cytoplasm; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00007440	#N/A	0.12638458

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00813	DNA-directed RNA polymerase subunit omega	F:DNA binding; P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.632769568
AURMO_00814	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	P:catabolic process; P:biosynthetic process; F:lyase activity; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00007460	#N/A	0.964002533
AURMO_00815	methionine adenosyltransferase	C:cytoplasm; P:sulfur compound metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00014010	E	9.60E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00816	replication restart DNA helicase PriA	F:DNA binding; F:helicase activity; C:chromosome; P:DNA metabolic process; P:biosynthetic process; C:protein-containing complex; F:ion binding; P:chromosome organization	Rhola_00007470	#N/A	0.017074453
AURMO_00817	methionyl-tRNA formyltransferase	F:molecular_function; P:tRNA metabolic process; P:translation; P:cellular protein modification process	Rhola_00007480	E	5.50E-03
AURMO_00818	16S rRNA (cytosine967-C5)-methyltransferase	F:RNA binding; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00007490	#N/A	0.068535434
AURMO_00819	ribulose-phosphate 3-epimerase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:isomerase activity; F:ion binding	Rhola_00007500	#N/A	0.975238742
AURMO_00820	phosphoribosyl-ATP pyrophosphatase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.036535497

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00821	ATP phosphoribosyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00007520	#N/A	0.096863738
AURMO_00822	cyclase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00007530	#N/A	0.030841885
AURMO_00823	phosphoribosyl-AMP cyclohydrolase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.562611459

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AURMO_00824	anthranilate synthase component I	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00007550	#N/A	0.049352727
AURMO_00825	uncharacterized membrane protein (TIGR02234 family)	C:cellular_component	#N/A	L	1.39E-03
AURMO_00826	hypothetical protein	C:cellular_component	#N/A	#N/A	0.775663919
AURMO_00827	indole-3-glycerol phosphate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00007580	#N/A	0.658926674
AURMO_00828	tryptophan synthase beta chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00007590	A	1.19E-09
AURMO_00829	tryptophan synthase alpha chain	P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00007600	A	1.39E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00830	prolipoprotein diacylglyceryl transferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:transmembrane transporter activity	Rhola_00007610	#N/A	0.059989236
AURMO_00831	glutamate synthase domain-containing protein 2	#N/A	Rhola_00007620	J	0.006935314
AURMO_00832	glutamate synthase (NADH) small subunit	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00007630	J	8.07E-14
AURMO_00833	pyruvate kinase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00007640	#N/A	0.117852164
AURMO_00835	response regulator receiver and ANTAR domain protein	F:RNA binding; P:signal transduction	Rhola_00007660	M	8.66E-05
AURMO_00836	uncharacterized protein (TIGR00369 family)	F:molecular_function	Rhola_00007670	#N/A	0.600242939

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AURMO_00837	DNA polymerase I	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00007680	#N/A	0.747267583
AURMO_00838	SSU ribosomal protein S1P	F:molecular_function; C:ribosome	Rhola_00007690	E	2.07E-07
AURMO_00839	dephospho-CoA kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00007700	M	1.63E-15
AURMO_00840	excinuclease ABC subunit B	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; C:protein-containing complex; F:ion binding	Rhola_00007710	#N/A	0.236483404

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AURMO_00841	excinuclease ABC subunit A	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; F:ATPase activity; C:protein-containing complex; F:ion binding	Rhola_00007720	A	0.006306272
AURMO_00842	excinuclease ABC subunit C	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:response to stress; C:protein-containing complex	Rhola_00007730	#N/A	0.695669951
AURMO_00843	glycerophosphoryl diester phosphodiesterase	F:molecular_function; P:lipid metabolic process	Rhola_00008290	#N/A	0.258035491
AURMO_00844	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity	Rhola_00008010	#N/A	0.458608338
AURMO_00845	8-oxo-dGTP pyrophosphatase MutT (NUDIX family)	F:molecular_function	#N/A	#N/A	0.577215972
AURMO_00846	uncharacterized membrane protein HdeD (DUF308 family)	C:cellular_component	#N/A	D	3.21E-04
AURMO_00847	glycine/D-amino acid oxidase-like deaminating enzyme	F:oxidoreductase activity	#N/A	N	1.63E-06
AURMO_00848	hypothetical protein	F:oxidoreductase activity	#N/A	#N/A	0.322310494
AURMO_00849	EamA-like transporter family protein	C:cellular_component	#N/A	#N/A	0.821299476
AURMO_00850	fucose permease	C:cellular_component; F:transmembrane transporter activity	Rhola_00003100	#N/A	0.240784129

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AURMO_00851	cyanate permease	C:cellular_component; P:transmembrane transport	#N/A	A	7.38E-05
AURMO_00852	glycerol kinase	P:carbohydrate metabolic process; P:catabolic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	#N/A	A	5.20E-12
AURMO_00853	anthranilate phosphoribosyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00008320	#N/A	0.62043839
AURMO_00854	cytochrome c oxidase subunit 3	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity	Rhola_00008330	#N/A	0.676774189
AURMO_00855	menaquinol-cytochrome c reductase cytochrome c1 subunit precursor	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:lyase activity; F:ion binding	Rhola_00008340	#N/A	0.497188103
AURMO_00856	menaquinol-cytochrome c reductase iron-sulfur subunit precursor	C:cellular_component; F:oxidoreductase activity	Rhola_00008350	#N/A	0.127655519

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AURMO_00857	menaquinol-cytochrome c reductase cytochrome b subunit precursor	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity	Rhola_00008360	A	3.71E-04
AURMO_00858	hypothetical protein	#N/A	#N/A	#N/A	0.332033201
AURMO_00859	cytochrome c oxidase subunit IV	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity	#N/A	#N/A	0.174809914
AURMO_00860	cytochrome c oxidase subunit 1	C:plasma membrane; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00008400	#N/A	0.021326735
AURMO_00861	cytochrome c oxidase subunit 2	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00008410	#N/A	0.694119818
AURMO_00862	iron-sulfur cluster assembly accessory protein	F:structural molecule activity; P:protein maturation	Rhola_00008420	#N/A	0.124144345

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AURMO_00863	acetylornithine deacetylase/succinyl-diaminopimelate desuccinylase-like protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	Rhola_00008430	D	5.27E-04
AURMO_00864	hypothetical protein	C:cellular_component	Rhola_00008440	#N/A	0.57661957
AURMO_00865	dihydroorotate oxidase A	C:cytoplasm; C:plasma membrane; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00008450	A	2.94E-07
AURMO_00866	transcriptional repressor NrdR	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00008460	#N/A	0.022484036
AURMO_00867	histidinol dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00008470	#N/A	0.477742178
AURMO_00868	DNA polymerase-3 subunit alpha	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00008490	#N/A	0.038676838

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AURMO_00869	apolipoprotein N-acyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00008270	#N/A	0.036669999
AURMO_00870	ATP-dependent RNA helicase HelY	F:helicase activity; F:ion binding	Rhola_00008260	A	2.19E-03
AURMO_00871	sec-independent protein translocase protein TatC	C:plasma membrane; P:protein transport; F:transmembrane transporter activity; C:protein-containing complex	Rhola_00008250	#N/A	0.177027334
AURMO_00872	sec-independent protein translocase protein TatA	C:plasma membrane; P:protein transport; F:transmembrane transporter activity; C:protein-containing complex	#N/A	#N/A	0.761051361
AURMO_00873	proteasome accessory factor C	C:proteasome complex; F:DNA binding	Rhola_00008220	#N/A	0.042398617
AURMO_00874	proteasome accessory factor B	C:proteasome complex	RHOLA_RS04085	E	1.60E-09
AURMO_00875	peptidylprolyl isomerase	P:cellular protein modification process; F:isomerase activity	RHOLA_RS04080	E	1.80E-14
AURMO_00876	tRNA (adenine57-N1/adenine58-N1)-methyltransferase	C:intracellular; P:tRNA metabolic process; F:methyltransferase activity; C:protein-containing complex	Rhola_00008190	E	5.38E-03

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AURMO_00877	HAD superfamily hydrolase (TIGR01509 family)	F:molecular_function	Rhola_00008180	#N/A	0.025599409
AURMO_00878	PAC2 family protein	F:ligase activity	Rhola_00008170	#N/A	0.903185444
AURMO_00879	undecaprenyl-diphosphatase	P:cell morphogenesis; F:molecular_function; C:plasma membrane; P:biosynthetic process; P:cell wall organization or biogenesis	Rhola_00008160	D	8.31E-06
AURMO_00881	hypothetical protein	#N/A	#N/A	C	3.59E-04
AURMO_00882	superfamily II DNA or RNA helicase	F:DNA binding; F:helicase activity; F:ion binding	#N/A	#N/A	0.026031909
AURMO_00883	tRNA G18 (ribose-2'-O)-methylase SpoU	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.613154702
AURMO_00884	NAD-dependent SIR2 family protein deacetylase	F:ion binding	Rhola_00008130	#N/A	0.486648274
AURMO_00885	glycosyltransferase involved in cell wall biosynthesis	F:transferase activity, transferring glycosyl groups	Rhola_00008110	#N/A	0.497690956
AURMO_00886	pimeloyl-ACP methyl ester carboxylesterase	F:molecular_function	Rhola_00008100	#N/A	0.122152538
AURMO_00887	DNA polymerase-3 subunit epsilon	F:nuclease activity; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	Rhola_00008070	C	1.45E-07

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AURMO_00888	LSU ribosomal protein L31P	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00008060	E	8.19E-05
AURMO_00889	iron complex transport system ATP-binding protein	F:ATPase activity; F:ion binding	Rhola_00008050	B	5.50E-03
AURMO_00890	glycogen synthase (ADP-glucose)	P:carbohydrate metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	Rhola_00008040	#N/A	0.324738536
AURMO_00891	glucose-1-phosphate adenylyltransferase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:biosynthetic process; F:nucleotidyltransferase activity; F:ion binding	Rhola_00008030	A	1.07E-06
AURMO_00892	phosphoserine phosphatase	F:phosphatase activity	Rhola_00008020	#N/A	0.076027171
AURMO_00893	3-oxoacyl-[acyl-carrier-protein] reductase	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	Rhola_00008000	#N/A	0.039839662
AURMO_00894	hypothetical protein	C:cellular_component	#N/A	N	1.30E-12
AURMO_00895	cytochrome oxidase assembly protein ShyY1	C:plasma membrane	Rhola_00007980	M	0.0028354
AURMO_00896	2-isopropylmalate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00006240	E	3.53E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00897	GTP-binding protein Era	F:GTPase activity; C:cytoplasm; C:plasma membrane; F:rRNA binding; P:ribosome biogenesis; F:ion binding	Rhola_00006230	A	1.32E-13
AURMO_00898	CBS domain containing-hemolysin-like protein	C:cellular_component; F:ion binding	RHOLA_RS03090	#N/A	0.020540962
AURMO_00899	probable rRNA maturation factor	F:nuclease activity; C:cytoplasm; F:peptidase activity; P:ribosome biogenesis; F:ion binding	Rhola_00006210	A	3.27E-05
AURMO_00900	phosphate starvation-inducible protein PhoH	F:ion binding	Rhola_00006200	A	1.49E-03
AURMO_00901	histidine triad (HIT) family protein	F:molecular_function	#N/A	#N/A	0.450428286
AURMO_00902	16S rRNA (uracil1498-N3)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00006180	F	1.34E-03
AURMO_00903	molecular chaperone DnaJ	C:cytoplasm; P:protein folding; P:response to stress; P:biosynthetic process; F:ion binding; F:unfolded protein binding	Rhola_00006170	E	4.47E-06
AURMO_00904	heat-inducible transcription repressor HrcA	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00006160	H	1.46E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00905	oxygen-independent coproporphyrinogen-3 oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00006140	B	2.21E-05
AURMO_00906	uncharacterized protein (UPF0548 family)	#N/A	#N/A	J	1.19E-06
AURMO_00907	GTP-binding protein LepA	F:GTPase activity; C:plasma membrane; F:translation factor activity, RNA binding; F:ion binding	Rhola_00006130	#N/A	0.025653733
AURMO_00908	SSU ribosomal protein S20P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	#N/A	#N/A	0.042317349
AURMO_00909	DNA polymerase III delta subunit	F:DNA binding; C:intracellular; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex	Rhola_00006100	#N/A	0.190318714
AURMO_00910	competence protein ComEC	C:cellular_component	Rhola_00006090	#N/A	0.794784648
AURMO_00911	competence protein ComEA	F:DNA binding; C:cellular_component; P:DNA metabolic process; P:response to stress	Rhola_00006080	#N/A	0.643272335

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AURMO_00912	aromatic acid exporter family member 1	C:cellular_component	#N/A	A	1.65E-08
AURMO_00913	beta-N-acetylhexosaminidase	C:cellular_component; P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	#N/A	H	1.48E-02
AURMO_00914	DNA-binding FrmR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	G	4.55E-03
AURMO_00915	NADPH-dependent 2,4-dienoyl-CoA reductase/sulfur reductase-like enzyme	C:cell; F:oxidoreductase activity; P:homeostatic process; F:ion binding	Rhola_00001300	F	9.32E-06
AURMO_00916	probable LLM family oxidoreductase	F:oxidoreductase activity	Rhola_00013000	E	3.20E-07
AURMO_00917	carbohydrate ABC transporter ATP-binding protein (CUT1 family)	F:ATPase activity; F:ion binding	Rhola_00010530	M	1.64E-03
AURMO_00918	lipopolysaccharide kinase (Kdo/WaaP) family protein	F:kinase activity	Rhola_00010540	#N/A	0.02824381
AURMO_00919	NADPH:quinone reductase-like Zn-dependent oxidoreductase	F:oxidoreductase activity	#N/A	M	7.06E-10
AURMO_00920	alkylphosphonate utilization operon protein PhnA	F:molecular_function	#N/A	#N/A	0.069054775
AURMO_00921	ribose 5-phosphate isomerase B	P:carbohydrate metabolic process; F:isomerase activity	#N/A	N	1.09E-10
AURMO_00923	ribosome-associated protein	C:cytoplasm; P:translation; P:cellular component assembly; P:ribosome biogenesis	Rhola_00005970	#N/A	0.822920274

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AURMO_00924	hypothetical protein	C:cellular_component	#N/A	#N/A	0.427575986
AURMO_00925	nicotinate-nucleotide adenylyltransferase	P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00005950	#N/A	0.252708793
AURMO_00926	hypothetical protein	C:cellular_component	#N/A	#N/A	0.900020608
AURMO_00927	glutamate-5-semialdehyde dehydrogenase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00005930	#N/A	0.291705001
AURMO_00928	glutamate 5-kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	Rhola_00005920	E	1.41E-06
AURMO_00929	GTP-binding protein	F:GTPase activity; C:cytoplasm; P:ribosome biogenesis; F:ion binding	Rhola_00005910	E	7.19E-08
AURMO_00930	LSU ribosomal protein L27P	F:structural constituent of ribosome; C:ribosome; P:translation	Rhola_00005900	F	5.16E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00931	LSU ribosomal protein L21P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00005890	E	8.46E-07
AURMO_00932	ribonuclease E	F:RNA binding; F:nuclease activity	Rhola_00005880	E	7.63E-11
AURMO_00933	uncharacterized membrane protein	C:cellular_component	Rhola_00005870	#N/A	0.091397619
AURMO_00934	DHA2 family lincomycin resistance protein-like MFS transporter	C:plasma membrane; F:transmembrane transporter activity	#N/A	E	1.09E-04
AURMO_00935	nucleoside diphosphate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00005860	#N/A	0.607155305
AURMO_00936	uncharacterized protein DUF4233	C:cellular_component	#N/A	#N/A	0.033692668
AURMO_00937	dihydrofolate synthase/folylpolyglutamate synthase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00005840	#N/A	0.033710653

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AURMO_00938	isoleucyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00005830	#N/A	0.165187284
AURMO_00939	valyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00005820	#N/A	0.058581653
AURMO_00940	hypothetical protein	#N/A	#N/A	A	6.92E-07
AURMO_00941	TM2 domain-containing protein	C:cellular_component	#N/A	#N/A	0.043560927
AURMO_00942	transposase-like protein	F:DNA binding	#N/A	A	4.27E-08
AURMO_00943	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	M	5.56E-05
AURMO_00944	thioredoxin	C:cell; F:oxidoreductase activity; P:homeostatic process; P:small molecule metabolic process	Rhola_00005620	#N/A	0.085450833
AURMO_00945	protein-S-isoprenylcysteine O-methyltransferase Ste14	C:cellular_component; P:biological_process; F:methyltransferase activity	#N/A	D	1.48E-03
AURMO_00946	uncharacterized protein DUF4395	C:cellular_component	#N/A	N	0.005750169

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AURMO_00947	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.037430384
AURMO_00948	putrescine:proton symporter (AAT family)	C:cellular_component; F:transmembrane transporter activity	#N/A	A	1.64E-08
AURMO_00949	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00008740	#N/A	0.625120991
AURMO_00950	1-acyl-sn-glycerol-3-phosphate acyltransferase	P:biological_process; F:methyltransferase activity; F:transferase activity, transferring acyl groups	Rhola_00008750	#N/A	0.622192941
AURMO_00951	glucokinase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00008760	#N/A	0.134534249
AURMO_00952	long-chain acyl-CoA synthetase	P:lipid metabolic process; F:ligase activity; P:small molecule metabolic process	Rhola_00008770	M	7.98E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00953	peptide deformylase	P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	Rhola_00008780	#N/A	0.298351218
AURMO_00954	MinD-like ATPase involved in chromosome partitioning or flagellar assembly	#N/A	Rhola_00008790	#N/A	0.197776973
AURMO_00955	pyruvate carboxylase	P:carbohydrate metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding; P:small molecule metabolic process	Rhola_00008800	L	4.27E-04
AURMO_00956	cellulose biosynthesis protein BcsQ	#N/A	RHOLA_RS04385	#N/A	0.39608037
AURMO_00957	MerR-like DNA binding protein	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00008820	#N/A	0.112943589
AURMO_00958	MerR-like DNA binding protein	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00008830	#N/A	0.36028565
AURMO_00959	type III secretion system (T3SS) inner membrane Yop/YscD-like protein	#N/A	Rhola_00008840	H	3.94E-07
AURMO_00960	superfamily II DNA/RNA helicase	F:helicase activity; F:ion binding	#N/A	E	8.66E-06
AURMO_00961	LPXTG-motif cell wall-anchored protein	C:cellular_component	#N/A	A	3.60E-05
AURMO_00962	deoxyribodipyrimidine photolyase-related protein	F:lyase activity	Rhola_00013030	N	0.005932481

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00963	DME family drug/metabolite transporter	C:cellular_component	#N/A	M	6.23E-09
AURMO_00964	glyceraldehyde 3-phosphate dehydrogenase	P:carbohydrate metabolic process; F:oxidoreductase activity; P:small molecule metabolic process	#N/A	#N/A	0.018771093
AURMO_00965	3-oxoacyl-[acyl-carrier protein] reductase	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.044408519
AURMO_00966	drug/metabolite transporter (DMT)-like permease	C:cellular_component	Rhola_00002610	#N/A	0.658926674
AURMO_00967	hypothetical protein	#N/A	#N/A	A	1.09E-08
AURMO_00968	threonine/homoserine/homoserine lactone efflux protein	C:plasma membrane; P:transport	#N/A	#N/A	0.048357186
AURMO_00969	uncharacterized protein (UPF0303 family)	#N/A	#N/A	#N/A	0.003441197
AURMO_00970	enamine deaminase RidA (YjgF/YER057c/UK114 family)	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	J	1.16E-06
AURMO_00971	carbonic anhydrase	F:lyase activity; F:ion binding	#N/A	E	5.58E-08
AURMO_00972	MFS transporter	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.122152538
AURMO_00973	hypothetical protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.092335665
AURMO_00974	hypothetical protein	#N/A	#N/A	#N/A	0.039180954
AURMO_00975	transmembrane secretion effector	C:cellular_component	#N/A	#N/A	0.363519685

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00977	uncharacterized membrane protein	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.365987002
AURMO_00978	ADP-ribose pyrophosphatase YjhB (NUDIX family)	F:molecular_function	#N/A	A	1.60E-06
AURMO_00979	GTP-binding protein	P:ribosome biogenesis; F:ion binding	Rhola_00008860	E	7.64E-08
AURMO_00980	cytidylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00008870	#N/A	0.330397272
AURMO_00981	prephenate dehydrogenase	P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00008880	#N/A	0.499702654
AURMO_00982	ribosomal large subunit pseudouridine synthase B	F:RNA binding; F:kinase activity; F:isomerase activity; P:cellular nitrogen compound metabolic process	Rhola_00008900	#N/A	0.794426437
AURMO_00983	segregation and condensation protein B	C:cytoplasm; P:cell cycle; P:chromosome segregation; P:cell division	Rhola_00008910	#N/A	0.088918106
AURMO_00984	condensin subunit ScpA	C:cytoplasm; P:cell cycle; P:chromosome segregation; P:cell division	Rhola_00008920	#N/A	0.743326214
AURMO_00985	chromosome partitioning protein	#N/A	Rhola_00014030	#N/A	0.362765835

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_00986	integrase/recombinase XerD	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:cell cycle; P:chromosome segregation; P:transposition; P:cell division	Rhola_00008940	#N/A	0.108456758
AURMO_00987	ADP-ribose pyrophosphatase	F:molecular_function	Rhola_00008950	D	7.05E-05
AURMO_00988	CTP synthase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00008960	C	4.88E-06
AURMO_00989	DNA replication and repair protein RecN	P:DNA metabolic process; P:response to stress; F:ion binding	Rhola_00008970	#N/A	0.0892986
AURMO_00990	NAD+ kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00008980	#N/A	0.931498526

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AURMO_00991	23S rRNA (cytidine1920-2'-O)/16S rRNA (cytidine1409-2'-O)-methyltransferase	F:RNA binding; P:biological_process; F:methyltransferase activity	Rhola_00008990	#N/A	0.347765786
AURMO_00992	hypothetical protein	#N/A	#N/A	#N/A	0.791258735
AURMO_00993	citrate synthase/2-methylcitrate synthase	C:cytoplasm; P:generation of precursor metabolites and energy; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.475169817
AURMO_00994	methylisocitrate lyase	P:lipid metabolic process; P:catabolic process; F:lyase activity; P:small molecule metabolic process	#N/A	#N/A	0.925180385
AURMO_00995	2-methylcitrate dehydratase	F:lyase activity	#N/A	#N/A	0.909727655
AURMO_00996	GntR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.565554043
AURMO_00997	propionyl-CoA synthetase	F:ligase activity	#N/A	A	1.52E-03
AURMO_00998	uncharacterized membrane protein (DUF485 family)	C:cellular_component	#N/A	A	6.87E-16
AURMO_00999	cation/acetate symporter	C:cellular_component; F:transmembrane transporter activity	Rhola_00003310	A	5.79E-10

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01000	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.87624894
AURMO_01001	hypothetical protein	F:DNA binding	#N/A	#N/A	0.967984115
AURMO_01002	HAD superfamily hydrolase (TIGR01450 family)	F:molecular_function	Rhola_00005090	E	2.51E-04
AURMO_01003	hypothetical protein	#N/A	Rhola_00005070	E	4.12E-07
AURMO_01007	tyrosyl-tRNA synthetase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00005030	L	3.24E-03
AURMO_01008	argininosuccinate lyase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity	Rhola_00005020	J	1.00E-05
AURMO_01009	ornithine carbamoyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; F:ion binding	Rhola_00005010	#N/A	0.167745419
AURMO_01010	N-acetylglutamate kinase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding	Rhola_00005000	#N/A	0.524718858

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AURMO_01011	glutamate N-acetyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups	Rhola_00004990	#N/A	0.469760235
AURMO_01012	N-acetyl-gamma-glutamyl-phosphate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00004980	#N/A	0.113872932
AURMO_01013	hypothetical protein	#N/A	#N/A	#N/A	0.112826139
AURMO_01014	phenylalanyl-tRNA synthetase beta subunit	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00004970	J	3.52E-11
AURMO_01015	phenylalanyl-tRNA synthetase alpha subunit	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00004960	J	3.48E-05
AURMO_01016	mRNA interferase MazF	F:DNA binding; F:nuclease activity	#N/A	#N/A	0.020540962
AURMO_01017	hypothetical protein	#N/A	#N/A	#N/A	0.080421934

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AURMO_01018	TrmH family RNA methyltransferase	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00004950	E	1.26E-11
AURMO_01019	LSU ribosomal protein L20P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; P:ribonucleoprotein complex assembly; P:ribosome biogenesis	Rhola_00004940	E	1.09E-08
AURMO_01020	large subunit ribosomal protein L35	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	6.41E-09
AURMO_01021	translation initiation factor IF-3	C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00004920	E	6.75E-10
AURMO_01022	hypothetical protein	F:isomerase activity	#N/A	J	0.0009718
AURMO_01023	TetR family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.069054775
AURMO_01024	RND superfamily putative drug exporter	C:cellular_component	Rhola_00002680	E	5.94E-04
AURMO_01025	YhgE/Pip-like protein	C:cellular_component	#N/A	E	8.66E-05
AURMO_01026	type III secretion system (T3SS) SseB-like protein	#N/A	Rhola_00004900	#N/A	0.838685339

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01027	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process	Rhola_00004890	#N/A	0.199098041
AURMO_01028	glutamine amidotransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00004880	#N/A	0.355730473
AURMO_01029	imidazoleglycerol-phosphate dehydratase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process	Rhola_00004870	J	2.23E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01030	histidinol phosphate aminotransferase	P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00004860	#N/A	0.138645647
AURMO_01031	hypothetical protein	C:cellular_component; P:cell division	#N/A	M	2.00E-16
AURMO_01032	SOS-response transcriptional repressor LexA	F:DNA binding; P:DNA metabolic process; P:response to stress; F:peptidase activity; P:biosynthetic process	Rhola_00004840	A	3.99E-05
AURMO_01033	5,10-methylenetetrahydrofolate reductase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00008080	#N/A	0.231811976
AURMO_01034	ATP-dependent Clp protease ATP-binding subunit ClpX	P:protein folding; F:peptidase activity; F:ion binding; F:unfolded protein binding	Rhola_00005800	J	2.50E-27
AURMO_01035	hypothetical protein	#N/A	#N/A	#N/A	0.115095908
AURMO_01036	ATP-dependent Clp protease protease subunit	C:cytoplasm; F:peptidase activity	Rhola_00005790	E	1.06E-22
AURMO_01037	ATP-dependent Clp protease protease subunit	C:cytoplasm; F:peptidase activity	Rhola_00005780	F	1.33E-21

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01038	hypothetical protein	#N/A	#N/A	#N/A	0.211757724
AURMO_01039	L-lysine exporter family protein LysE/ArgO	C:plasma membrane; P:transport	Rhola_00000240	#N/A	0.622192941
AURMO_01040	alkylmercury lyase-like protein	P:catabolic process; F:lyase activity	#N/A	A	9.17E-07
AURMO_01041	IS30 family transposase	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	M	2.69E-12
AURMO_01042	hypothetical protein	C:cellular_component	#N/A	#N/A	0.313082031
AURMO_01043	hypothetical protein	C:cellular_component	#N/A	#N/A	0.026633978
AURMO_01044	LuxR family two component transcriptional regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00000920	#N/A	0.743469263
AURMO_01045	signal transduction histidine kinase	C:cellular_component; F:kinase activity	Rhola_00000910	#N/A	0.967984115
AURMO_01046	gamma-glutamylcyclotransferase (GGCT)/AIG2-like uncharacterized protein YtfP	F:transferase activity	#N/A	#N/A	0.53812721
AURMO_01047	trigger factor	C:cytoplasm; P:protein folding; P:cellular protein modification process; P:cell cycle; P:protein transport; F:isomerase activity; P:cell division	Rhola_00005770	J	4.14E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01050	SOS response UmuD protein	F:DNA binding; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	M	4.00E-07
AURMO_01051	DNA polymerase V	F:DNA binding; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	M	4.99E-09
AURMO_01052	hypothetical protein	C:cellular_component	#N/A	A	4.03E-03
AURMO_01053	raffinose/stachyose/melibiose transport system permease protein	C:plasma membrane; P:transmembrane transport	#N/A	#N/A	0.824797388
AURMO_01054	carbohydrate ABC transporter membrane protein 1 (CUT1 family)	C:plasma membrane; P:transmembrane transport	#N/A	#N/A	0.666331053
AURMO_01055	hypothetical protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.485636574
AURMO_01056	endonuclease-8/formamidopyrimidine-DNA glycosylase	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds; F:lyase activity; F:ion binding	Rhola_00005740	#N/A	0.575365295
AURMO_01057	ribose 5-phosphate isomerase B	P:carbohydrate metabolic process; F:isomerase activity	Rhola_00005730	#N/A	0.632769568

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01058	aminopeptidase N	F:peptidase activity; F:ion binding	Rhola_00005710	#N/A	0.131605503
AURMO_01059	small conductance mechanosensitive channel	C:cellular_component; P:transmembrane transport	Rhola_00005700	#N/A	0.300395424
AURMO_01060	hemoglobin	F:molecular_function; P:transport	Rhola_00005690	#N/A	0.732910379
AURMO_01061	hypothetical protein	#N/A	#N/A	#N/A	0.305231286
AURMO_01062	acyl-CoA thioesterase-2	F:molecular_function; P:sulfur compound metabolic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00005670	#N/A	0.060327599
AURMO_01063	nitrite reductase/ring-hydroxylating ferredoxin subunit	F:oxidoreductase activity	#N/A	#N/A	0.04972186
AURMO_01064	acyl-CoA thioester hydrolase	F:hydrolase activity	#N/A	#N/A	0.030079994
AURMO_01065	ATP-binding cassette ChvD family protein	P:translation; F:ATPase activity; F:ion binding	Rhola_00005650	J	1.98E-05
AURMO_01066	hypothetical protein	#N/A	#N/A	#N/A	0.087896298
AURMO_01067	single-strand DNA-binding protein	F:DNA binding; P:biosynthetic process	RHOLA_RS02800	E	4.94E-10
AURMO_01068	peptide-methionine (S)-S-oxide reductase	P:cellular protein modification process; F:oxidoreductase activity	Rhola_00005630	#N/A	0.06483585

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01069	secretory lipase	F:molecular_function; P:lipid metabolic process; P:catabolic process	#N/A	M	1.70E-04
AURMO_01070	threonine/homoserine efflux transporter RhtA	C:cellular_component	#N/A	#N/A	0.023876614
AURMO_01071	hypothetical protein	#N/A	#N/A	#N/A	0.687275664
AURMO_01073	succinate-semialdehyde dehydrogenase/glutarate-semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.038549786
AURMO_01074	putative transposase	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	A	5.36E-03
AURMO_01075	helix-turn-helix protein	F:DNA binding	#N/A	A	1.64E-04
AURMO_01076	oligoribonuclease	F:nuclease activity; C:cytoplasm	Rhola_00005460	#N/A	0.325248832
AURMO_01078	hypothetical protein	C:cellular_component	#N/A	#N/A	0.700042423
AURMO_01079	hypothetical protein	#N/A	#N/A	#N/A	0.251302196
AURMO_01080	hypothetical protein	F:kinase activity	#N/A	A	8.99E-03
AURMO_01081	energy-coupling factor transport system permease protein	C:cellular_component	#N/A	#N/A	0.892633772
AURMO_01082	energy-coupling factor transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	#N/A	0.100546586
AURMO_01083	energy-coupling factor transport system substrate-specific component	C:cellular_component	#N/A	F	3.52E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01084	DNA polymerase-4	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:nucleotidyltransferase activity; F:ion binding	#N/A	#N/A	0.114930251
AURMO_01085	hypothetical protein	C:cellular_component	#N/A	#N/A	0.555742441
AURMO_01086	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	P:translation; F:ligase activity; F:ion binding	Rhola_00005440	J	4.88E-04
AURMO_01087	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A	C:intracellular; P:translation; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; C:protein-containing complex; F:ion binding	Rhola_00005430	L	4.05E-06
AURMO_01088	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	P:translation; F:ligase activity; F:ion binding	#N/A	E	4.32E-05
AURMO_01089	DNA polymerase-3 subunit epsilon	F:DNA binding; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity	#N/A	A	7.58E-07
AURMO_01090	DNA ligase (NAD+)	P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ligase activity; F:ion binding	Rhola_00005400	#N/A	0.046277032

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01091	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	F:RNA binding; C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity; F:ion binding	Rhola_00005390	#N/A	0.015688992
AURMO_01092	cysteine desulfurase	F:molecular_function	Rhola_00005380	#N/A	0.021046148
AURMO_01093	glycogen operon protein	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:hydrolase activity, acting on glycosyl bonds	Rhola_00005370	E	2.73E-07
AURMO_01094	starch synthase (maltosyl-transferring)	P:carbohydrate metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on glycosyl bonds	Rhola_00005360	A	4.80E-11
AURMO_01095	1,4-alpha-glucan branching enzyme	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; F:hydrolase activity, acting on glycosyl bonds; F:ion binding	Rhola_00005350	A	1.05E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01096	putative thioredoxin	C:cell; P:homeostatic process	Rhola_00005340	#N/A	0.808928595
AURMO_01097	hypothetical protein	C:cellular_component	Rhola_00005330	#N/A	0.764598792
AURMO_01098	DivIVA protein	#N/A	#N/A	#N/A	0.674342193
AURMO_01099	predicted PurR-regulated permease PerM	C:cellular_component	Rhola_00005310	A	0.000566322
AURMO_01100	hypothetical protein	F:molecular_function	Rhola_00005300	#N/A	0.135370031
AURMO_01101	hypothetical protein	#N/A	#N/A	#N/A	0.086836014
AURMO_01102	hypothetical protein	C:cellular_component	Rhola_00005280	#N/A	0.518504102
AURMO_01103	DivIVA domain-containing protein	#N/A	#N/A	#N/A	0.154229124
AURMO_01104	phosphatidate cytidylyltransferase	C:cellular_component; F:nucleotidyltransferase activity	Rhola_00005250	#N/A	0.035042004
AURMO_01105	ribosome recycling factor	C:cytoplasm; P:translation	Rhola_00005240	#N/A	0.674342193
AURMO_01106	uridylate kinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00005230	#N/A	0.930480076
AURMO_01107	translation elongation factor Ts (EF-Ts)	C:cytoplasm; F:translation factor activity, RNA binding	Rhola_00005220	E	1.08E-06
AURMO_01108	small subunit ribosomal protein S2	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	Rhola_00005210	E	2.36E-08
AURMO_01109	hypothetical protein	#N/A	#N/A	#N/A	0.957289003

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01110	MFS transporter	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.313082031
AURMO_01111	peptidase M23-like protein	F:molecular_function	#N/A	#N/A	0.738977401
AURMO_01112	hypothetical protein	C:cellular_component	#N/A	#N/A	0.609278857
AURMO_01113	dihydrodipicolinate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00004640	#N/A	0.463864418
AURMO_01114	probable phosphoglycerate mutase	#N/A	#N/A	#N/A	0.051743804
AURMO_01115	predicted Zn-dependent peptidase	F:peptidase activity; F:ion binding	Rhola_00004630	#N/A	0.017159964
AURMO_01116	aryl-alcohol dehydrogenase-like predicted oxidoreductase	F:oxidoreductase activity	#N/A	#N/A	0.407032397
AURMO_01117	polyribonucleotide nucleotidyltransferase	F:RNA binding; C:cytoplasm; F:nucleotidyltransferase activity; P:nucleobase-containing compound catabolic process; F:ion binding	Rhola_00004620	E	8.74E-11
AURMO_01118	small subunit ribosomal protein S15	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00004610	E	4.96E-07
AURMO_01119	uncharacterized membrane protein YhaH (DUF805 family)	C:cellular_component	#N/A	A	1.28E-33
AURMO_01120	uncharacterized membrane protein YhaH (DUF805 family)	C:cellular_component	#N/A	#N/A	0.024478194

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01121	uncharacterized membrane protein YhaH (DUF805 family)	C:cellular_component	#N/A	#N/A	0.272088299
AURMO_01122	hypothetical protein	#N/A	#N/A	#N/A	0.749286079
AURMO_01123	phospholipase/carboxylesterase	F:molecular_function	#N/A	#N/A	0.488566387
AURMO_01124	peptidylprolyl isomerase	P:cellular protein modification process; F:isomerase activity	#N/A	#N/A	0.120617458
AURMO_01125	ethanolamine:proton symporter (EAT family)	C:cellular_component; F:transmembrane transporter activity	#N/A	A	4.91E-09
AURMO_01126	hypothetical protein	#N/A	#N/A	#N/A	0.644611722
AURMO_01127	glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity	#N/A	M	3.91E-04
AURMO_01128	putative glutamine amidotransferase	P:cellular amino acid metabolic process; F:transferase activity, transferring glycosyl groups	#N/A	A	9.87E-06
AURMO_01129	betaine-aldehyde dehydrogenase	F:oxidoreductase activity	#N/A	A	3.98E-06
AURMO_01130	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity	#N/A	A	6.57E-05
AURMO_01131	GntR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	A	3.27E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01132	amino acid exporter (AAE family)	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.162738057
AURMO_01133	diketogulonate reductase-like aldo/keto reductase	F:oxidoreductase activity	Rhola_00010270	#N/A	0.32049157
AURMO_01134	adenine phosphoribosyltransferase	C:cytoplasm; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	#N/A	#N/A	0.632958265
AURMO_01135	aspartate ammonia-lyase	P:generation of precursor metabolites and energy; F:lyase activity	Rhola_00000890	#N/A	0.078290071
AURMO_01136	aldehyde dehydrogenase (NAD+)	F:oxidoreductase activity	#N/A	A	4.23E-17
AURMO_01137	predicted amidohydrolase	P:biological_process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.720782163

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01138	riboflavin kinase/FMN adenylyltransferase	P:biosynthetic process; F:kinase activity; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00004580	#N/A	0.040361381
AURMO_01139	hypothetical protein	C:cellular_component	#N/A	#N/A	0.864932764
AURMO_01140	hypothetical protein	C:cellular_component	#N/A	#N/A	0.022439427
AURMO_01141	tRNA pseudouridine synthase B	F:RNA binding; P:tRNA metabolic process; F:isomerase activity	Rhola_00004500	#N/A	0.08243687
AURMO_01143	L-alanine dehydrogenase	P:cellular amino acid metabolic process; P:catabolic process; F:oxidoreductase activity; F:ion binding	Rhola_00005570	#N/A	0.14251149
AURMO_01144	FtsK/SpoIIIE family protein	F:DNA binding; F:ion binding	#N/A	#N/A	0.470370894
AURMO_01145	FHA domain-containing protein	#N/A	#N/A	#N/A	0.019475805
AURMO_01146	transglutaminase superfamily protein	C:cellular_component	#N/A	#N/A	0.093279116
AURMO_01147	uncharacterized protein (DUF58 family)	C:cellular_component	#N/A	#N/A	0.410850658
AURMO_01148	MoxR-like ATPase	F:ATPase activity; F:ion binding	#N/A	#N/A	0.024028372
AURMO_01149	hypothetical protein	C:cellular_component	#N/A	#N/A	0.038759799

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01150	serine/threonine protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	#N/A	#N/A	0.079249661
AURMO_01151	protein phosphatase	P:cellular protein modification process; F:phosphatase activity	#N/A	#N/A	0.061623183
AURMO_01152	FHA domain-containing protein	#N/A	#N/A	#N/A	0.609401435
AURMO_01153	condensin subunit Smc	F:DNA binding; C:chromosome; C:cytoplasm; P:cell cycle; P:chromosome segregation; P:biosynthetic process; F:ion binding; P:chromosome organization	Rhola_00009050	#N/A	0.056232777
AURMO_01154	IclR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.131605503
AURMO_01155	D-serine deaminase-like pyridoxal phosphate-dependent protein	F:lyase activity	#N/A	M	6.72E-03
AURMO_01156	mRNA-degrading endonuclease RelE of RelBE toxin-antitoxin system	F:molecular_function	#N/A	M	3.99E-09
AURMO_01157	prevent-host-death family protein	#N/A	#N/A	A	2.70E-26

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01158	DNA-(apurinic or apyrimidinic site) lyase	F:DNA binding; P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds; F:lyase activity; F:ion binding	Rhola_00009060	#N/A	0.032763203
AURMO_01159	ribonuclease-3	F:nuclease activity; C:cytoplasm; P:mRNA processing; P:tRNA metabolic process; F:rRNA binding; P:nucleobase-containing compound catabolic process; P:ribosome biogenesis; F:ion binding	Rhola_00009070	E	3.14E-03
AURMO_01160	LSU ribosomal protein L32P	F:structural constituent of ribosome; C:ribosome; P:translation; C:protein-containing complex	#N/A	E	1.43E-02
AURMO_01161	uncharacterized protein	#N/A	Rhola_00009090	#N/A	0.798390758
AURMO_01162	peptidoglycan/LPS O-acetylase OafA/YrhL	C:cellular_component; F:transferase activity, transferring acyl groups	#N/A	A	4.71E-03
AURMO_01164	membrane-associated protein	C:cellular_component	Rhola_00012610	#N/A	0.086041344
AURMO_01165	membrane-associated protein	C:cellular_component	Rhola_00004060	#N/A	0.568384045
AURMO_01166	PhzF family phenazine biosynthesis protein	P:biosynthetic process; F:isomerase activity	#N/A	#N/A	0.224517138
AURMO_01167	cyclic-di-GMP-binding biofilm dispersal mediator protein	F:oxidoreductase activity	Rhola_00003520	M	1.82E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01168	XTP/dITP diphosphohydrolase	P:biosynthetic process; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00004050	A	6.98E-05
AURMO_01169	RNAse PH	F:RNA binding; F:nuclease activity; P:tRNA metabolic process; F:nucleotidyltransferase activity; P:nucleobase-containing compound catabolic process; P:ribosome biogenesis	Rhola_00004040	A	6.53E-07
AURMO_01170	glutamate racemase	P:cell morphogenesis; P:biosynthetic process; F:isomerase activity; P:cell wall organization or biogenesis	Rhola_00004030	#N/A	0.261158215
AURMO_01171	hypothetical protein	#N/A	#N/A	#N/A	0.045030181
AURMO_01172	choline kinase	F:kinase activity; F:transferase activity, transferring acyl groups; F:nucleotidyltransferase activity	Rhola_00012840	#N/A	0.038343324
AURMO_01173	ABC-2 type transport system permease protein	C:plasma membrane; C:protein-containing complex; P:transmembrane transport	#N/A	#N/A	0.069620564

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01174	ABC-2 type transport system ATP-binding protein	F:ATPase activity; F:ion binding	Rhola_00000160	#N/A	0.407032397
AURMO_01175	glutaryl-CoA dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	A	1.48E-04
AURMO_01176	crotonobetainyl-CoA:carnitine CoA-transferase CaiB-like acyl-CoA transferase	F:molecular_function	#N/A	#N/A	0.466319205
AURMO_01177	D-amino-acid:oxygen oxidoreductase (deaminating)	P:cellular amino acid metabolic process; F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.133876193
AURMO_01178	uncharacterized protein DUF3107	F:ATP binding	#N/A	F	1.49E-07
AURMO_01179	tRNA-(MS[2]IO[6]A)-hydroxylase MiaE-like protein	#N/A	Rhola_00003870	#N/A	0.249475419
AURMO_01180	superfamily II DNA/RNA helicase	F:helicase activity; F:ion binding	Rhola_00003860	F	1.60E-05
AURMO_01181	Sap-like sulfolipid-1-addressing protein	C:cellular_component	#N/A	N	0.00061239
AURMO_01182	heme-degrading monooxygenase HmoA	F:oxidoreductase activity	#N/A	#N/A	0.04707888
AURMO_01183	hypothetical protein	F:molecular_function	Rhola_00003840	#N/A	0.03761882
AURMO_01184	Xaa-Pro aminopeptidase	F:peptidase activity; F:ion binding	Rhola_00003830	#N/A	0.259082162
AURMO_01185	uncharacterized membrane protein	C:cellular_component	#N/A	#N/A	0.023878103
AURMO_01186	DNA-binding transcriptional LysR family regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.454899483

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01187	L-proline dehydrogenase	F:DNA-binding transcription factor activity; P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process	#N/A	M	4.48E-10
AURMO_01188	CBS domain protein	C:cellular_component; F:transmembrane transporter activity	Rhola_00003810	#N/A	0.391506021
AURMO_01189	uncharacterized membrane protein	C:cellular_component	Rhola_00003800	#N/A	0.123401621
AURMO_01190	ATP-binding protein involved in chromosome partitioning	F:ATPase activity; F:ion binding	Rhola_00003790	#N/A	0.59423606
AURMO_01191	betaine-aldehyde dehydrogenase	F:oxidoreductase activity	Rhola_00004350	M	0.000616385
AURMO_01192	AsnC family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00004340	#N/A	0.216241749
AURMO_01193	hypothetical protein	F:ion binding	Rhola_00004330	#N/A	0.05162773
AURMO_01194	methylated-DNA-[protein]-cysteine S-methyltransferase	C:cytoplasm; P:DNA metabolic process; P:response to stress; F:methyltransferase activity	#N/A	#N/A	0.093279116

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01195	DNA-3-methyladenine glycosylase I	P:DNA metabolic process; P:response to stress; F:hydrolase activity, acting on glycosyl bonds	Rhola_00004310	#N/A	0.162572091
AURMO_01196	helix-turn-helix protein	F:DNA binding	#N/A	M	4.27E-08
AURMO_01197	sec-independent protein translocase protein TatB	C:cellular_component; P:protein transport	#N/A	#N/A	0.977181019
AURMO_01198	predicted O-methyltransferase YrrM	P:biological_process; F:methyltransferase activity	#N/A	C	5.72E-03
AURMO_01199	uncharacterized protein DUF3117	#N/A	#N/A	#N/A	0.612762463
AURMO_01200	hypothetical protein	C:cellular_component; P:cellular protein modification process; P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.430217224
AURMO_01201	succinyldiaminopimelate desuccinylase	P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	Rhola_00010560	#N/A	0.015691331

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01202	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; F:ion binding	Rhola_00010570	#N/A	0.385401793
AURMO_01203	CshA-type fibril repeat protein	C:cellular_component	#N/A	#N/A	0.115412956
AURMO_01204	hypothetical protein	F:DNA binding	#N/A	N	4.99E-07
AURMO_01205	alcohol dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.056816201
AURMO_01206	hypothetical protein	C:cellular_component	#N/A	J	4.44E-07
AURMO_01207	citrate synthase	C:cytoplasm; P:generation of precursor metabolites and energy; F:transferase activity, transferring acyl groups	Rhola_00009130	#N/A	0.953381152
AURMO_01208	succinyldiaminopimelate aminotransferase	P:biosynthetic process; F:ion binding	Rhola_00009140	#N/A	0.072971722
AURMO_01209	NAD-dependent dihydropyrimidine dehydrogenase PreA subunit	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	Rhola_00009150	#N/A	0.253701109
AURMO_01210	hypothetical protein	C:cellular_component	#N/A	N	0.002321717
AURMO_01211	high-affinity iron transporter	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	#N/A	0.122408637

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01212	GTP-binding protein TypA/BipA	F:GTPase activity; F:translation factor activity, RNA binding; F:ion binding	Rhola_00009170	E	2.13E-04
AURMO_01213	hypothetical protein	C:cellular_component; F:peptidase activity; P:protein maturation	Rhola_00009180	#N/A	0.996011608
AURMO_01214	hypothetical protein	#N/A	#N/A	#N/A	0.718668512
AURMO_01215	TetR family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.018793658
AURMO_01216	nicotinamidase-related amidase	F:molecular_function	#N/A	N	1.44E-16
AURMO_01217	hypothetical protein	F:DNA binding	#N/A	#N/A	0.188859239
AURMO_01218	uncharacterized protein with HEPN domain	F:transferase activity	#N/A	#N/A	0.40531797
AURMO_01219	glycine dehydrogenase (decarboxylating)	P:cellular amino acid metabolic process; P:catabolic process; F:oxidoreductase activity	#N/A	#N/A	0.079249661
AURMO_01220	glycine cleavage system H protein	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; C:protein-containing complex	#N/A	M	1.48E-08
AURMO_01221	aminomethyltransferase	P:cellular amino acid metabolic process; F:methyltransferase activity; P:catabolic process	#N/A	M	1.34E-07
AURMO_01222	amino acid/polyamine/organocation transporter (APC superfamily)	C:cellular_component; F:transmembrane transporter activity	#N/A	A	1.70E-19

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01223	8-oxo-dGTP diphosphatase	F:nucleotidyltransferase activity	Rhola_00010940	#N/A	0.222143364
AURMO_01224	quinolinate synthetase	C:cytoplasm; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00010950	#N/A	0.13241193
AURMO_01225	L-aspartate oxidase	C:cytoplasm; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00010960	#N/A	0.384041036

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01226	nicotinate-nucleotide pyrophosphorylase [carboxylating]	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00010970	G	7.84E-04
AURMO_01227	cysteine desulfurase	F:molecular_function	Rhola_00010980	#N/A	0.095654374
AURMO_01228	polyketide cyclase/dehydrase/lipid transport protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.831800484
AURMO_01229	SOUL heme-binding protein	F:ion binding	Rhola_00001900	#N/A	0.285858133
AURMO_01230	putative MATE family efflux protein	C:cellular_component; F:transmembrane transporter activity	#N/A	E	4.20E-03
AURMO_01231	uncharacterized protein YdhG (YjbR/CyaY superfamily)	#N/A	#N/A	A	8.24E-12
AURMO_01232	uncharacterized protein DUF4287	#N/A	#N/A	M	0.013471927
AURMO_01233	transposase-like protein	F:DNA binding	#N/A	#N/A	0.71464768
AURMO_01234	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.556948977
AURMO_01235	hypothetical protein	C:cellular_component	#N/A	A	1.32E-05
AURMO_01236	short-subunit dehydrogenase	F:oxidoreductase activity	Rhola_00005520	A	0.000549864
AURMO_01237	uncharacterized protein YndB with AHSA1/START domain	#N/A	Rhola_00009770	#N/A	0.044506246
AURMO_01238	hypothetical protein	F:oxidoreductase activity	#N/A	#N/A	0.022053622

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01239	uncharacterized membrane protein YjjP (DUF1212 family)	C:cellular_component	#N/A	#N/A	0.871228382
AURMO_01240	addiction module HigA family antidote	F:DNA binding	#N/A	#N/A	0.122152538
AURMO_01241	putative SOS response-associated peptidase YedK	F:peptidase activity	Rhola_00006030	#N/A	0.313231044
AURMO_01242	hypothetical protein	F:ATPase activity; F:ion binding	Rhola_00009780	J	6.75E-05
AURMO_01243	hypothetical protein	C:cellular_component	#N/A	#N/A	0.407032397
AURMO_01244	hypothetical protein	C:cellular_component	#N/A	#N/A	0.258425377
AURMO_01245	malonate-semialdehyde dehydrogenase (acetylating)/methylmalonate-semialdehyde dehydrogenase	F:oxidoreductase activity	Rhola_00009670	N	1.34E-05
AURMO_01246	DNA recombination protein RmuC	C:cellular_component	Rhola_00009800	A	1.11E-15
AURMO_01247	CP family cyanate transporter-like MFS transporter	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.80027144
AURMO_01248	fructose-1,6-bisphosphatase II	P:carbohydrate metabolic process; P:biosynthetic process; F:phosphatase activity; F:ion binding; P:small molecule metabolic process	Rhola_00013360	#N/A	0.124152246

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01249	fructose-bisphosphate aldolase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:lyase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00009830	#N/A	0.763735273
AURMO_01250	hypothetical protein	C:cellular_component	#N/A	#N/A	0.213724197
AURMO_01251	L-iditol 2-dehydrogenase	#N/A	Rhola_00001840	#N/A	0.225782498
AURMO_01252	mannitol 2-dehydrogenase	#N/A	Rhola_00001830	#N/A	0.077080228
AURMO_01253	carbohydrate ABC transporter membrane protein 2 (CUT1 family)	C:plasma membrane; P:transmembrane transport	Rhola_00001820	A	2.40E-10
AURMO_01254	sorbitol/mannitol transport system permease protein	C:plasma membrane; P:transmembrane transport	Rhola_00001810	A	2.06E-07
AURMO_01255	sorbitol/mannitol transport system substrate-binding protein	P:transport	Rhola_00001800	A	2.71E-13
AURMO_01256	AraC-like DNA-binding protein	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00001790	A	6.34E-21

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01257	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	Rhola_00009850	#N/A	0.021903157
AURMO_01258	exodeoxyribonuclease VII large subunit	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; C:protein-containing complex; P:nucleobase-containing compound catabolic process	Rhola_00009860	#N/A	0.76286743
AURMO_01259	exodeoxyribonuclease VII small subunit	F:nuclease activity; C:cytoplasm; P:DNA metabolic process; C:protein-containing complex; P:nucleobase-containing compound catabolic process	#N/A	#N/A	0.892598933
AURMO_01260	uncharacterized protein DUF4245	F:molecular_function; C:cellular_component	#N/A	#N/A	0.967984115
AURMO_01261	carbonic anhydrase	P:biological_process; F:lyase activity; F:ion binding	Rhola_00009890	D	6.57E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01262	fumarase class II	C:cytoplasm; P:generation of precursor metabolites and energy; F:lyase activity; C:protein-containing complex; P:small molecule metabolic process	Rhola_00009900	A	1.58E-06
AURMO_01263	aryl-alcohol dehydrogenase-like predicted oxidoreductase	F:oxidoreductase activity	#N/A	A	3.77E-04
AURMO_01264	hypothetical protein	F:oxidoreductase activity	#N/A	A	5.42E-06
AURMO_01265	putative transposase	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	M	2.70E-11
AURMO_01266	transposase-like protein	F:DNA binding	#N/A	#N/A	0.950920826
AURMO_01267	4-carboxy-2-hydroxymuconate semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.024068673
AURMO_01268	protocatechuate 4,5-dioxygenase beta subunit	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.028225357
AURMO_01269	protocatechuate 4,5-dioxygenase alpha subunit	F:oxidoreductase activity	#N/A	#N/A	0.023515891
AURMO_01270	2-pyrone-4,6-dicarboxylate hydrolase	F:molecular_function	#N/A	A	0.002521826
AURMO_01271	4-oxalomesaconate hydratase	P:catabolic process; F:lyase activity; P:secondary metabolic process; F:ion binding	#N/A	#N/A	0.04246996
AURMO_01272	4-oxalomesaconate tautomerase	F:isomerase activity	#N/A	#N/A	0.027493547
AURMO_01273	4-hydroxy-4-methyl-2-oxoglutarate aldolase	P:biological_process; F:methyltransferase activity; F:lyase activity	#N/A	#N/A	0.26693172

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01274	IclR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.732910379
AURMO_01275	uncharacterized protein with HEPN domain	#N/A	#N/A	#N/A	0.7132795
AURMO_01276	hypothetical protein	F:nucleotidyltransferase activity	#N/A	#N/A	0.407757374
AURMO_01277	IclR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	M	0.000421159
AURMO_01278	p-hydroxybenzoate 3-monooxygenase	F:oxidoreductase activity; F:ion binding	#N/A	M	2.78E-03
AURMO_01279	benzaldehyde dehydrogenase (NAD+)	F:oxidoreductase activity	#N/A	A	0.004225355
AURMO_01280	PadR family transcriptional regulator	F:DNA binding	#N/A	#N/A	0.386120575
AURMO_01281	vanillate demethylase subunit A	F:methyltransferase activity; F:oxidoreductase activity	#N/A	A	6.04E-04
AURMO_01282	vanillate demethylase subunit B	C:cellular_component; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	#N/A	A	1.09E-02

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01283	MarR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	A	0.002653436
AURMO_01284	acyl-CoA reductase-like NAD-dependent aldehyde dehydrogenase	F:oxidoreductase activity	#N/A	A	0.000514966
AURMO_01285	transketolase subunit A	F:molecular_function	#N/A	#N/A	0.035850013
AURMO_01286	transketolase	F:molecular_function	#N/A	#N/A	0.061505089
AURMO_01287	(R,R)-butanediol dehydrogenase/meso-butanediol dehydrogenase/diacetyl reductase/L-iditol 2-dehydrogenase	F:oxidoreductase activity; F:ion binding	#N/A	A	7.30E-03
AURMO_01288	ribose ABC transporter ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	A	1.66E-05
AURMO_01289	ribose transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	A	3.22E-11
AURMO_01290	monosaccharide ABC transporter substrate-binding protein (CUT2 family)	#N/A	#N/A	A	7.83E-21
AURMO_01291	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity	#N/A	A	1.30E-03
AURMO_01292	D-tagatose 3-epimerase	F:isomerase activity	#N/A	M	8.01E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01293	6-phosphofructokinase	C:cytoplasm; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.78947641
AURMO_01294	muconolactone D-isomerase	P:catabolic process; F:isomerase activity	#N/A	#N/A	0.109259946
AURMO_01295	protocatechuate 4,5-dioxygenase alpha subunit	F:oxidoreductase activity	#N/A	#N/A	0.332033201
AURMO_01296	protocatechuate 4,5-dioxygenase beta subunit	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.105318443
AURMO_01297	alpha/beta hydrolase family protein	F:transferase activity, transferring acyl groups	#N/A	A	2.07E-04
AURMO_01298	aldehyde dehydrogenase (NAD+)	F:oxidoreductase activity	#N/A	#N/A	0.026633978
AURMO_01299	HD domain-containing protein	F:hydrolase activity	#N/A	#N/A	0.033165869
AURMO_01300	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin reductase subunit	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.892214269
AURMO_01301	2Fe-2S ferredoxin	P:generation of precursor metabolites and energy; F:oxidoreductase activity	#N/A	#N/A	0.801568489
AURMO_01302	NAD(P)-dependent dehydrogenase (short-subunit alcohol dehydrogenase family)	F:oxidoreductase activity	#N/A	#N/A	0.161475125
AURMO_01303	metal dependent phosphohydrolase	F:molecular_function	#N/A	#N/A	0.13478261
AURMO_01304	pyruvate,water dikinase	F:kinase activity	#N/A	A	3.14E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01305	pyruvate,water dikinase	F:kinase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.108837415
AURMO_01306	hypothetical protein	F:oxidoreductase activity; F:ion binding	#N/A	N	0.001341699
AURMO_01307	IclR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.761024366
AURMO_01308	transporter family-2 protein	C:cellular_component	#N/A	#N/A	0.188970578
AURMO_01309	hypothetical protein	C:cellular_component	#N/A	#N/A	0.131568643
AURMO_01310	hypothetical protein	C:cellular_component	#N/A	#N/A	0.171087469
AURMO_01311	citrate lyase subunit beta/citryl-CoA lyase	F:lyase activity; F:ion binding	Rhola_00000740	B	4.45E-04
AURMO_01312	3-oxoadipate enol-lactonase	F:molecular_function	#N/A	N	3.99E-03
AURMO_01313	leader peptidase (prepilin peptidase)/N-methyltransferase	C:cellular_component; F:peptidase activity	#N/A	M	7.15E-17
AURMO_01314	PhoH-like ATPase	F:ion binding	Rhola_00009940	A	8.09E-16
AURMO_01315	short-chain Z-isoprenyl diphosphate synthase	F:transferase activity, transferring alkyl or aryl (other than methyl) groups; F:ion binding	Rhola_00009950	#N/A	0.629687059
AURMO_01316	Fic family protein	F:nucleotidyltransferase activity	#N/A	#N/A	0.587029738
AURMO_01317	channel protein (hemolysin III family)	C:cellular_component	Rhola_00009960	#N/A	0.911208765
AURMO_01318	TipAS antibiotic-recognition protein	#N/A	#N/A	L	0.006266236
AURMO_01319	hypothetical protein	C:cellular_component	#N/A	#N/A	0.214705952

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AURMO_01320	uncharacterized protein DUF4307	C:cellular_component	#N/A	#N/A	0.78505275
AURMO_01321	transcription elongation factor GreA	F:DNA binding; F:translation factor activity, RNA binding; F:enzyme binding	Rhola_00009990	#N/A	0.057042836
AURMO_01322	threonine dehydratase	P:cellular amino acid metabolic process; P:catabolic process; F:lyase activity; F:ion binding	Rhola_00010000	#N/A	0.880000999
AURMO_01323	heat shock protein	C:plasma membrane; F:peptidase activity; F:ion binding	Rhola_00010010	#N/A	0.034759283
AURMO_01324	LemA protein	C:cellular_component	Rhola_00010020	#N/A	0.223354938
AURMO_01325	nitrate/nitrite transporter NarK	C:cellular_component; P:transmembrane transport	Rhola_00009420	I	1.46E-03
AURMO_01326	amylosucrase	P:carbohydrate metabolic process; F:transferase activity, transferring glycosyl groups	#N/A	N	1.26E-02
AURMO_01327	prevent-host-death family protein	#N/A	#N/A	#N/A	0.436821682
AURMO_01328	mRNA-degrading endonuclease RelE of RelBE toxin-antitoxin system	F:molecular_function	#N/A	#N/A	0.533424802
AURMO_01330	NADH dehydrogenase FAD-containing subunit	F:oxidoreductase activity	Rhola_00010040	E	5.03E-04
AURMO_01331	subtilase family protein	C:cellular_component; F:peptidase activity	Rhola_00010050	#N/A	0.492118113
AURMO_01332	hypothetical protein	#N/A	Rhola_00010060	#N/A	0.240081374
AURMO_01333	cell division protein FtsB	C:cellular_component	#N/A	B	2.70E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01334	enolase	C:extracellular region; C:cytosol; P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; F:lyase activity; C:protein-containing complex; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00010080	L	0.01103842
AURMO_01335	histidyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00010090	#N/A	0.876840248
AURMO_01336	XTP/dITP diphosphohydrolase	F:molecular_function	Rhola_00010100	#N/A	0.023874419
AURMO_01337	hypothetical protein	C:cellular_component	#N/A	#N/A	0.024068537
AURMO_01338	phosphoenolpyruvate carboxykinase (GTP)	C:cytoplasm; P:carbohydrate metabolic process; P:biosynthetic process; F:kinase activity; F:lyase activity; F:ion binding; P:small molecule metabolic process	Rhola_00001340	#N/A	0.2887926
AURMO_01339	predicted transcriptional regulator	F:DNA binding	#N/A	M	1.15E-03

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01340	sodium/proton antiporter (NhaA family)	C:plasma membrane; F:transmembrane transporter activity; P:homeostatic process	Rhola_00013500	#N/A	0.01516352
AURMO_01341	transcription-repair coupling factor	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ion binding; P:chromosome organization	Rhola_00010110	E	4.54E-09
AURMO_01342	hypothetical protein	#N/A	#N/A	#N/A	0.278595949
AURMO_01343	PTH1 family peptidyl-tRNA hydrolase	F:molecular_function; C:cytoplasm; P:translation	Rhola_00010120	J	2.96E-13
AURMO_01344	large subunit ribosomal protein L25	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00010130	E	3.85E-08
AURMO_01345	6-phosphogluconate dehydrogenase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:small molecule metabolic process	Rhola_00002630	J	5.93E-03
AURMO_01346	fructokinase	P:carbohydrate metabolic process; F:kinase activity	Rhola_00002430	#N/A	0.036074655
AURMO_01347	hypothetical protein	C:cellular_component	#N/A	#N/A	0.092071402
AURMO_01348	tRNA(fMet)-specific endonuclease VapC	F:nuclease activity	#N/A	#N/A	0.300395424

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01349	antitoxin VapB	F:DNA binding	#N/A	#N/A	0.952194709
AURMO_01350	ribose-phosphate pyrophosphokinase	C:cytoplasm; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00010150	A	0.000522567
AURMO_01351	UDP-N-acetylglucosamine pyrophosphorylase /glucosamine-1-phosphate N-acetyltransferase	P:cell morphogenesis; C:cytoplasm; P:carbohydrate metabolic process; P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring acyl groups; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cell wall organization or biogenesis	Rhola_00010160	#N/A	0.891889546
AURMO_01353	MarR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.952194709

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01354	hypothetical protein	C:cellular_component	#N/A	#N/A	0.049984421
AURMO_01355	AbrB family looped-hinge helix DNA binding protein	F:DNA binding	#N/A	#N/A	0.398179846
AURMO_01356	PIN domain nuclease of toxin-antitoxin system	F:molecular_function	#N/A	#N/A	0.698865809
AURMO_01357	hypothetical protein	#N/A	#N/A	M	1.36E-16
AURMO_01358	hypothetical protein	F:mRNA binding	#N/A	M	0.001051797
AURMO_01359	ATPase subunit of ABC transporter with duplicated ATPase domains	F:DNA binding; C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ATPase activity; F:ion binding	Rhola_00010180	#N/A	0.18523768
AURMO_01360	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	P:lipid metabolic process; P:biosynthetic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	Rhola_00010190	J	3.56E-04
AURMO_01361	dimethyladenosine transferase	F:RNA binding; C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis	Rhola_00010210	D	1.08E-03
AURMO_01362	TatD DNase family protein	F:nuclease activity; P:DNA metabolic process	Rhola_00010220	D	0.00899727

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01363	methionyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00010230	J	9.65E-06
AURMO_01364	hypothetical protein	#N/A	#N/A	#N/A	0.763735273
AURMO_01365	EndoU nuclease-like protein	#N/A	#N/A	#N/A	0.98117377
AURMO_01366	16S rRNA (cytidine1402-2'-O)-methyltransferase	C:cytoplasm; F:methyltransferase activity; P:cellular nitrogen compound metabolic process; P:ribosome biogenesis; F:ion binding	Rhola_00010240	#N/A	0.324987216
AURMO_01367	dolichyl-phosphate-mannose-protein mannosyltransferase	C:cellular_component; P:cellular protein modification process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups	Rhola_00010250	#N/A	0.049753286
AURMO_01368	L-serine dehydratase	P:carbohydrate metabolic process; P:biosynthetic process; F:lyase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.21457518

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01369	homocysteine S-methyltransferase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:methyltransferase activity; P:biosynthetic process; F:ion binding	#N/A	#N/A	0.850075769
AURMO_01370	hypothetical protein	C:cellular_component	#N/A	A	6.89E-04
AURMO_01371	uncharacterized protein (DUF305 family)	#N/A	#N/A	#N/A	0.035699824
AURMO_01372	hypothetical protein	#N/A	Rhola_00003050	E	1.64E-03
AURMO_01373	AhpD family alkylhydroperoxidase	C:cellular_component; F:oxidoreductase activity	#N/A	#N/A	0.024068537
AURMO_01374	DNA-binding FrmR family transcriptional regulator	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.346711749
AURMO_01375	Cu2+-exporting ATPase	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.037343607
AURMO_01376	3-phenylpropionate/trans-cinnamate dioxygenase ferredoxin reductase subunit	F:oxidoreductase activity	#N/A	#N/A	0.689934133
AURMO_01377	homocysteine S-methyltransferase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; F:methyltransferase activity; P:biosynthetic process; F:ion binding	#N/A	#N/A	0.285317767

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01378	predicted MFS family arabinose efflux permease	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.749546511
AURMO_01379	ATP-dependent helicase HrpA	F:helicase activity; F:ion binding	Rhola_00002700	#N/A	0.051931766
AURMO_01380	LPXTG-motif cell wall-anchored protein	C:extracellular region; C:cell wall; F:ion binding	#N/A	E	9.58E-36
AURMO_01381	ribonucleoside-diphosphate reductase beta chain	C:cellular_component; P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.55074868
AURMO_01382	hypothetical protein	#N/A	#N/A	#N/A	0.966935482
AURMO_01383	ribonucleoside-diphosphate reductase alpha chain	P:biosynthetic process; F:oxidoreductase activity; F:ion binding	Rhola_00001730	#N/A	0.391506021
AURMO_01384	predicted MFS family arabinose efflux permease	C:cellular_component; P:transmembrane transport	#N/A	#N/A	0.015563501
AURMO_01385	cystathionine beta-lyase	P:biosynthetic process; F:lyase activity; F:ion binding	Rhola_00003500	N	0.000408369

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01386	pyridoxamine 5'-phosphate oxidase	P:biosynthetic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00013090	M	5.04E-05
AURMO_01387	NADP-dependent 3-hydroxy acid dehydrogenase YdfG	F:oxidoreductase activity	#N/A	#N/A	0.018028202
AURMO_01388	phosphate ABC transporter ATP-binding protein (PhoT family)	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	#N/A	0.308628508
AURMO_01389	LPXTG-site transpeptidase (sortase) family protein	C:cellular_component	#N/A	#N/A	0.892633772
AURMO_01390	hypothetical protein	C:cellular_component	#N/A	#N/A	0.622192941
AURMO_01391	dihydroorotate dehydrogenase (fumarate)	C:cellular_component	#N/A	#N/A	0.199210792
AURMO_01392	hypothetical protein	#N/A	#N/A	#N/A	0.629995772
AURMO_01393	hypothetical protein	#N/A	#N/A	#N/A	0.80027144
AURMO_01394	hypothetical protein	#N/A	#N/A	#N/A	0.76307711
AURMO_01395	hypothetical protein	C:cellular_component	#N/A	#N/A	0.122152538
AURMO_01396	uncharacterized protein DUF4333	C:cellular_component	#N/A	#N/A	0.349167681

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01397	phosphate ABC transporter substrate-binding protein (PhoT family)	C:plasma membrane; C:protein-containing complex; F:ion binding; P:transmembrane transport	#N/A	M	1.33E-04
AURMO_01398	phosphate ABC transporter membrane protein 2 (PhoT family)	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.290751686
AURMO_01399	phosphate transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.158017528
AURMO_01400	serine/threonine-protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	#N/A	#N/A	0.265591794
AURMO_01401	hypothetical protein	C:cellular_component	#N/A	C	1.72E-04
AURMO_01402	ribosomal-protein-alanine N-acetyltransferase	F:transferase activity, transferring acyl groups	Rhola_00010310	#N/A	0.015791509
AURMO_01403	5-formyltetrahydrofolate cyclo-ligase	F:ligase activity; F:ion binding	Rhola_00010320	E	0.001574584
AURMO_01404	hypothetical protein	#N/A	#N/A	#N/A	0.787662797
AURMO_01405	hypothetical protein	#N/A	Rhola_00010330	B	7.51E-08
AURMO_01406	23S rRNA (adenine2503-C2)-methyltransferase	C:cytoplasm; P:tRNA metabolic process; F:methyltransferase activity; F:rRNA binding; P:ribosome biogenesis; F:ion binding	Rhola_00013010	#N/A	0.440159843
AURMO_01407	hypothetical protein	#N/A	#N/A	#N/A	0.055346032

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01408	hypothetical protein	#N/A	#N/A	H	1.07E-04
AURMO_01409	cobalt-zinc-cadmium efflux system protein	C:cellular_component; F:transmembrane transporter activity	#N/A	M	0.002841548
AURMO_01410	cation efflux family protein	C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.085392225
AURMO_01411	ArsR family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.204325208
AURMO_01412	hypothetical protein	#N/A	#N/A	#N/A	0.10992921
AURMO_01413	abortive infection Abi-like protein	#N/A	#N/A	#N/A	0.680300208
AURMO_01414	hypothetical protein	#N/A	#N/A	#N/A	0.338737373
AURMO_01416	HNH endonuclease	F:nuclease activity	Rhola_00010350	A	6.64E-09
AURMO_01417	cell wall-associated NlpC family hydrolase	C:membrane; C:integral component of membrane; F:hydrolase activity	#N/A	#N/A	0.191598294
AURMO_01418	DtxR family iron (metal) dependent repressor	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.99111841

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01419	phosphoserine aminotransferase	F:molecular_function; C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process	Rhola_00010370	#N/A	0.065384548
AURMO_01420	hypothetical protein	#N/A	#N/A	#N/A	0.028173848
AURMO_01421	putative cold-shock DNA-binding protein	F:DNA binding; C:cytoplasm	Rhola_00010390	E	5.17E-05
AURMO_01422	hypothetical protein	C:cellular_component	#N/A	#N/A	0.658461049
AURMO_01423	XPB/Ssl2-like helicase family protein	F:helicase activity	Rhola_00010410	#N/A	0.308084508
AURMO_01424	DNA excision repair protein ERCC-3	F:DNA binding; F:helicase activity; F:ion binding	Rhola_00010420	J	1.49E-05
AURMO_01425	two-component system OmpR family response regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00010430	F	1.63E-05
AURMO_01426	two-component system OmpR family sensor kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	Rhola_00010440	#N/A	0.168869146
AURMO_01427	WXG100 family type VII secretion target	#N/A	#N/A	#N/A	0.35622403
AURMO_01428	chaperonin GroEL	C:cytoplasm; P:protein folding; F:ion binding; F:unfolded protein binding	Rhola_00010460	G	3.72E-08
AURMO_01429	Putative lipoprotein YerB precursor	#N/A	RHOLA_RS06365	B	1.72E-04

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01430	putative cold-shock DNA-binding protein	F:DNA binding; C:cytoplasm	#N/A	#N/A	0.004894411
AURMO_01431	LytR cell envelope-related transcriptional attenuator	C:cellular_component	#N/A	#N/A	0.30328556
AURMO_01432	uncharacterized protein DUF3263	#N/A	#N/A	E	3.19E-05
AURMO_01434	thioredoxin-like protein	C:cellular_component	#N/A	#N/A	0.196222608
AURMO_01435	23S rRNA (guanosine2251-2'-O)-methyltransferase	F:RNA binding; F:methyltransferase activity; P:cellular nitrogen compound metabolic process	Rhola_00003750	#N/A	0.689197074
AURMO_01436	cysteinyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00003740	#N/A	0.960177397
AURMO_01437	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:kinase activity; F:nucleotidyltransferase activity; F:lyase activity; F:ion binding; P:small molecule metabolic process	Rhola_00003730	#N/A	0.516356899
AURMO_01438	CarD family transcriptional regulator	#N/A	Rhola_00003720	#N/A	0.122152538
AURMO_01439	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.755640367

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AURMO_01440	phosphoglycerate mutase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; P:catabolic process; P:biosynthetic process; F:isomerase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00003670	#N/A	0.10551511
AURMO_01441	hypothetical protein	F:molecular_function	Rhola_00003660	#N/A	0.455318687
AURMO_01442	hypothetical protein	P:biological_process; F:methyltransferase activity	Rhola_00003640	#N/A	0.043875816
AURMO_01443	hypothetical protein	C:membrane; C:integral component of membrane	#N/A	#N/A	0.833031622
AURMO_01444	DNA-binding response OmpR family regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00003600	#N/A	0.817346433
AURMO_01445	polyphosphate kinase	P:biosynthetic process; F:kinase activity; C:protein-containing complex; F:ion binding; P:small molecule metabolic process	Rhola_00003590	#N/A	0.036535497
AURMO_01446	8-oxo-dGTP diphosphatase	F:molecular_function	Rhola_00003580	#N/A	0.342396764

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01447	hypothetical protein	F:DNA-directed 5'-3' RNA polymerase activity; P:RNA biosynthetic process	#N/A	#N/A	0.493191765
AURMO_01448	hypothetical protein	C:cellular_component	#N/A	#N/A	0.44742204
AURMO_01449	disulfide bond formation protein DsbB	C:cellular_component; P:protein folding; F:oxidoreductase activity	#N/A	D	1.28E-03
AURMO_01450	hypothetical protein	C:cellular_component	#N/A	#N/A	0.98186731
AURMO_01451	uncharacterized repeat protein (TIGR02543 family)	C:cellular_component	#N/A	#N/A	0.6645213
AURMO_01452	DNA-binding NarL/FixJ family response regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00013260	#N/A	0.684159563
AURMO_01453	signal transduction histidine kinase	C:cellular_component	#N/A	#N/A	0.675766018
AURMO_01454	hypothetical protein	C:cellular_component	#N/A	#N/A	0.547094861
AURMO_01456	uncharacterized protein DUF998	C:cellular_component	Rhola_00003530	#N/A	0.063251272
AURMO_01457	hypothetical protein	F:oxidoreductase activity	#N/A	H	1.23E-08
AURMO_01458	hypothetical protein	#N/A	#N/A	#N/A	0.047744282
AURMO_01459	poly-gamma-glutamate synthesis protein (capsule biosynthesis protein)	#N/A	#N/A	#N/A	0.081158224
AURMO_01460	poly(glycerol-phosphate) alpha-glucosyltransferase	F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.712859518

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01461	carbonic anhydrase/acetyltransferase-like protein (isoleucine patch superfamily)	F:transferase activity, transferring acyl groups	#N/A	#N/A	0.086244883
AURMO_01462	transposase IS481 family protein	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.734260457
AURMO_01463	methylenetetrahydrofolate dehydrogenase (NADP+)/methenyltetrahydrofolate cyclohydrolase	P:cellular amino acid metabolic process; P:sulfur compound metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:cofactor metabolic process	Rhola_00011740	#N/A	0.280341605
AURMO_01464	serine hydroxymethyltransferase	C:cytoplasm; P:cellular amino acid metabolic process; F:methyltransferase activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00011750	#N/A	0.995052925

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01465	formyltetrahydrofolate deformylase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011770	J	4.14E-08
AURMO_01466	4,5-DOPA dioxygenase extradiol	F:oxidoreductase activity; F:ion binding	#N/A	H	2.32E-12
AURMO_01467	hypothetical protein	#N/A	#N/A	A	2.84E-18
AURMO_01468	hypothetical protein	#N/A	#N/A	D	4.69E-03
AURMO_01469	predicted ferric reductase	C:cellular_component; F:oxidoreductase activity	Rhola_00000530	E	6.03E-05
AURMO_01470	uncharacterized protein with FMN-binding domain	C:cellular_component; F:ion binding	#N/A	#N/A	0.324683546
AURMO_01471	thiamine biosynthesis lipoprotein	P:cellular protein modification process; F:ion binding	#N/A	#N/A	0.39608037
AURMO_01472	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase	C:plasma membrane; F:transmembrane transporter activity; F:ion binding	Rhola_00003390	N	6.91E-08
AURMO_01473	LSU ribosomal protein L1P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex	Rhola_00002380	E	3.52E-16

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01474	LSU ribosomal protein L11P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00002370	E	1.01E-07
AURMO_01475	transcription antitermination protein nusG	P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00002360	E	1.67E-05
AURMO_01476	preprotein translocase subunit SecE	C:plasma membrane; P:protein targeting; F:transmembrane transporter activity	#N/A	E	5.05E-04
AURMO_01478	aspartate aminotransferase	P:biosynthetic process; F:ion binding	Rhola_00002330	#N/A	0.180098869
AURMO_01479	hypothetical protein	#N/A	#N/A	#N/A	0.864932764
AURMO_01480	UDP-N-acetylmuramate dehydrogenase	P:cell morphogenesis; C:cytoplasm; P:cell cycle; P:biosynthetic process; F:oxidoreductase activity; F:ion binding; P:cell division; P:cell wall organization or biogenesis	Rhola_00002320	#N/A	0.76307711
AURMO_01481	acyl dehydratase	F:molecular_function	Rhola_00002310	#N/A	0.230421909
AURMO_01482	acyl dehydratase	#N/A	Rhola_00002300	#N/A	0.624335004
AURMO_01483	glutamate/tyrosine decarboxylase-like PLP-dependent enzyme	F:lyase activity; F:ion binding; P:small molecule metabolic process	Rhola_00005600	E	3.16E-04

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AURMO_01484	agmatine deiminase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process	Rhola_00005580	H	6.38E-03
AURMO_01485	hypothetical protein	C:cellular_component	#N/A	N	1.24E-02
AURMO_01486	TIR-like protein DUF1863	#N/A	#N/A	N	1.20E-06
AURMO_01487	lactococcin 972 family bacteriocin	#N/A	#N/A	M	2.51E-09
AURMO_01488	hypothetical protein	#N/A	#N/A	N	4.62E-07
AURMO_01489	hypothetical protein	#N/A	#N/A	M	3.32E-11
AURMO_01490	putative ABC transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	A	6.53E-11
AURMO_01491	hypothetical protein	C:cellular_component	#N/A	A	4.54E-22
AURMO_01492	uncharacterized protein DUF3800	#N/A	#N/A	M	7.47E-17
AURMO_01493	2Fe-2S ferredoxin	P:generation of precursor metabolites and energy; F:oxidoreductase activity	#N/A	#N/A	0.151160538
AURMO_01494	uncharacterized zinc-type alcohol dehydrogenase-like protein	F:oxidoreductase activity; F:ion binding	Rhola_00001530	#N/A	0.788054887
AURMO_01495	NADPH-dependent 2,4-dienoyl-CoA reductase/sulfur reductase-like enzyme	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.049753286
AURMO_01496	ferredoxin	P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.218109193

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AURMO_01497	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase/2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	F:isomerase activity	Rhola_00010750	#N/A	0.238645418
AURMO_01498	3,4-dihydroxyphenylacetate 2,3-dioxygenase	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.325385942
AURMO_01499	5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase	F:oxidoreductase activity	#N/A	#N/A	0.563609049
AURMO_01500	putative glutamine amidotransferase	P:cellular amino acid metabolic process; F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.26473055
AURMO_01501	DNA-binding MarR family transcriptional regulator	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.227345628
AURMO_01502	cytochrome P450	F:oxidoreductase activity; F:ion binding	#N/A	#N/A	0.749151265
AURMO_01503	GMP synthase (glutamine-hydrolysing)	F:molecular_function; P:cellular amino acid metabolic process	#N/A	#N/A	0.021613844
AURMO_01504	GMP synthase-like glutamine amidotransferase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.067418408

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01505	glutamine synthetase	P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity	#N/A	#N/A	0.124971677
AURMO_01506	diamine N-acetyltransferase	F:transferase activity, transferring acyl groups	#N/A	N	2.87E-12
AURMO_01507	dimethylargininase	C:cellular_component; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.548956716
AURMO_01508	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011800	J	2.51E-04
AURMO_01509	hypothetical protein	#N/A	#N/A	#N/A	0.428641611
AURMO_01510	formyl transferase-like protein	F:molecular_function; P:biosynthetic process; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011810	#N/A	0.30328556
AURMO_01511	hypothetical protein	C:cellular_component	#N/A	#N/A	0.80027144
AURMO_01512	hypothetical protein	C:cellular_component	Rhola_00011820	J	1.39E-06
AURMO_01513	hypothetical protein	#N/A	#N/A	J	7.17E-04
AURMO_01514	hypothetical protein	C:cellular_component	#N/A	#N/A	0.023874419

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01515	succinyl-CoA synthetase (ADP-forming) alpha subunit	P:generation of precursor metabolites and energy; F:ligase activity	Rhola_00011830	#N/A	0.023815385
AURMO_01516	succinyl-CoA synthetase (ADP-forming) beta subunit	P:generation of precursor metabolites and energy; F:ligase activity; F:ion binding	Rhola_00011840	#N/A	0.089331732
AURMO_01517	VIT1/CCC1 family predicted Fe2+/Mn2+ transporter	C:cell; F:transmembrane transporter activity; P:homeostatic process	#N/A	J	1.63E-03
AURMO_01518	DNA helicase-2/ATP-dependent DNA helicase PcrA	F:DNA binding; F:helicase activity; F:ion binding; P:chromosome organization	Rhola_00011850	G	1.46E-02
AURMO_01519	glycerophosphoryl diester phosphodiesterase	F:molecular_function; P:lipid metabolic process	Rhola_00011860	H	1.50E-03
AURMO_01520	uncharacterized YccA/Bax inhibitor family protein	C:cellular_component	#N/A	G	1.00E-02
AURMO_01521	pyridoxamine 5'-phosphate oxidase-like protein	F:molecular_function	#N/A	E	1.24E-02
AURMO_01522	DoxX-like protein	C:cellular_component	#N/A	#N/A	0.855791501
AURMO_01523	uracil phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00012570	#N/A	0.571018831
AURMO_01524	aldehyde dehydrogenase family protein	F:oxidoreductase activity	#N/A	#N/A	0.837463972

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AURMO_01525	aldehyde dehydrogenase (NAD+)	F:oxidoreductase activity	#N/A	#N/A	0.114147249
AURMO_01526	deoxyribose-phosphate aldolase	C:cytoplasm; P:biosynthetic process; F:lyase activity; P:nucleobase-containing compound catabolic process; P:small molecule metabolic process	#N/A	I	6.29E-04
AURMO_01527	purine-nucleoside phosphorylase	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011410	#N/A	0.07264424
AURMO_01528	phosphomannomutase	P:carbohydrate metabolic process; F:isomerase activity; F:ion binding	Rhola_00011420	#N/A	0.051743804
AURMO_01529	thymidine phosphorylase	F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00011460	E	2.64E-10

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01530	cytidine deaminase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:nucleobase-containing compound catabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00011470	E	7.73E-09
AURMO_01531	nucleoside ABC transporter membrane protein	C:plasma membrane; F:transmembrane transporter activity	Rhola_00011480	K	5.95E-06
AURMO_01532	nucleoside ABC transporter membrane protein	C:plasma membrane; F:transmembrane transporter activity	Rhola_00011490	#N/A	0.082504041
AURMO_01533	transposase-like protein	F:DNA binding	#N/A	#N/A	0.953381152
AURMO_01534	transposase InsO family protein	F:molecular_function; P:DNA metabolic process; P:transposition	#N/A	#N/A	0.391064474
AURMO_01535	nucleoside ABC transporter ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00011500	#N/A	0.015688992
AURMO_01536	nucleoside-binding protein	C:plasma membrane	Rhola_00011510	A	9.40E-19
AURMO_01537	argininosuccinate synthase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:ligase activity; F:ion binding	Rhola_00005530	#N/A	0.058838359
AURMO_01538	predicted dehydrogenase	F:oxidoreductase activity	Rhola_00000260	A	8.04E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01539	predicted NBD/HSP70 family sugar kinase	F:kinase activity; P:phosphorylation	Rhola_00002590	#N/A	0.80027144
AURMO_01540	xylose isomerase	C:cytoplasm; P:carbohydrate metabolic process; F:isomerase activity; F:ion binding; P:small molecule metabolic process	Rhola_00002580	#N/A	0.023874419
AURMO_01541	xylulokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding; P:small molecule metabolic process	Rhola_00002570	#N/A	0.05626032
AURMO_01542	monosaccharide ABC transporter substrate-binding protein (CUT2 family)	#N/A	Rhola_00002640	A	9.89E-09
AURMO_01543	D-xylose transport system ATP-binding protein	F:ATPase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00002650	A	4.42E-03
AURMO_01544	D-xylose transport system permease protein	C:plasma membrane; F:transmembrane transporter activity	Rhola_00002660	A	4.00E-03
AURMO_01545	aldose 1-epimerase	P:carbohydrate metabolic process; F:isomerase activity	#N/A	A	1.19E-02
AURMO_01546	saccharopine dehydrogenase-like NADP-dependent oxidoreductase	F:oxidoreductase activity; F:ion binding	Rhola_00002550	#N/A	0.0632602
AURMO_01547	manganese transport protein	C:plasma membrane; F:transmembrane transporter activity	Rhola_00001750	#N/A	0.041455421

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AURMO_01548	LSU ribosomal protein L12P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	2.24E-10
AURMO_01549	large subunit ribosomal protein L10	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding; C:protein-containing complex; P:ribosome biogenesis	Rhola_00002500	E	5.53E-11
AURMO_01550	1-phosphofructokinase	P:carbohydrate metabolic process; F:kinase activity; F:ion binding	Rhola_00009810	#N/A	0.191598294
AURMO_01551	two-component system OmpR family sensor kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	#N/A	E	8.95E-04
AURMO_01552	two-component system OmpR family response regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	F	2.52E-03
AURMO_01553	YqaJ-like recombinase protein	F:peptidase activity	#N/A	#N/A	0.795025831
AURMO_01554	RimJ/RimL family protein N-acetyltransferase	F:transferase activity, transferring acyl groups	#N/A	#N/A	0.161278679

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01555	histidinol-phosphate aminotransferase	P:cellular amino acid metabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding	#N/A	#N/A	0.060648267
AURMO_01556	acetoacetate decarboxylase	F:lyase activity	#N/A	#N/A	0.258601459
AURMO_01557	amino acid/polyamine/organocation transporter (APC superfamily)	C:cellular_component; F:isomerase activity; F:transmembrane transporter activity	#N/A	A	8.52E-08
AURMO_01558	homodimeric fumarase (class I)	P:generation of precursor metabolites and energy; F:lyase activity; F:ion binding	#N/A	#N/A	0.783768529
AURMO_01559	NADPH:quinone reductase-like Zn-dependent oxidoreductase	F:oxidoreductase activity	#N/A	#N/A	0.073890942
AURMO_01560	aromatic-L-amino-acid decarboxylase	F:lyase activity; F:ion binding; P:small molecule metabolic process	#N/A	H	1.22E-03
AURMO_01561	ATP-binding cassette subfamily B protein	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	H	5.75E-07
AURMO_01562	ATP-binding cassette subfamily B protein	C:cellular_component; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	#N/A	E	8.74E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01563	amidase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	A	1.84E-05
AURMO_01564	hypothetical protein	C:cellular_component	#N/A	M	9.70E-14
AURMO_01565	MarR family protein	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00002220	#N/A	0.373142551
AURMO_01566	tellurite resistance protein TerC	C:cellular_component	Rhola_00002210	#N/A	0.173445722
AURMO_01567	hypothetical protein	C:cellular_component	Rhola_00002200	#N/A	0.381955257
AURMO_01570	alpha-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	Rhola_00002260	D	0.009489001
AURMO_01571	peptidase M23-like protein	F:molecular_function; C:cellular_component	#N/A	H	0.002758923
AURMO_01572	myo-inositol-1(or 4)-monophosphatase	P:carbohydrate metabolic process; P:lipid metabolic process; P:catabolic process; F:phosphatase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.288981726
AURMO_01573	hypothetical protein	F:DNA binding; F:DNA-binding transcription factor activity; P:regulation of transcription, DNA-templated	#N/A	N	4.32E-05

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01574	HEPN domain-containing protein	#N/A	#N/A	A	7.83E-21
AURMO_01575	hypothetical protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	#N/A	#N/A	0.134719663
AURMO_01576	fusaric acid resistance family protein	C:cellular_component	#N/A	#N/A	0.474120544
AURMO_01577	isocitrate dehydrogenase	P:carbohydrate metabolic process; P:generation of precursor metabolites and energy; F:oxidoreductase activity; F:ion binding; P:small molecule metabolic process	#N/A	#N/A	0.074058781
AURMO_01578	hypothetical protein	F:DNA binding	#N/A	#N/A	0.15705651
AURMO_01579	uncharacterized repeat protein (TIGR02543 family)	C:cellular_component	#N/A	#N/A	0.345146599
AURMO_01581	hypothetical protein	#N/A	#N/A	#N/A	0.155025243
AURMO_01582	hypothetical protein	#N/A	Rhola_00002170	D	2.78E-05
AURMO_01583	uncharacterized membrane protein	C:cellular_component	#N/A	M	1.27E-03
AURMO_01584	DNA-binding Lrp family transcriptional regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.578317107
AURMO_01585	carboxylesterase type B	F:molecular_function	#N/A	A	2.59E-06
AURMO_01586	alpha-beta hydrolase superfamily lysophospholipase	F:molecular_function	#N/A	#N/A	0.019936623
AURMO_01587	death-on-curing protein	F:kinase activity	#N/A	#N/A	0.876840248

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01588	hypothetical protein	P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.477742178
AURMO_01589	taurine--2-oxoglutarate transaminase	F:ion binding	#N/A	A	5.50E-04
AURMO_01590	uncharacterized protein DUF1905	#N/A	#N/A	#N/A	0.885635654
AURMO_01591	IS30 family transposase	F:DNA binding; P:DNA metabolic process; P:transposition	#N/A	M	4.27E-11
AURMO_01592	phosphate ABC transporter ATP-binding protein (PhoT family)	C:plasma membrane; F:ATPase activity; F:transmembrane transporter activity; F:ion binding	Rhola_00004540	#N/A	0.193329996
AURMO_01593	phosphate ABC transporter membrane protein 2 (PhoT family)	C:plasma membrane; F:transmembrane transporter activity	RHOLA_RS02250	G	4.33E-04
AURMO_01594	phosphate ABC transporter membrane protein 1 (PhoT family)	C:plasma membrane; F:transmembrane transporter activity	Rhola_00004520	E	4.02E-05
AURMO_01595	phosphate ABC transporter substrate-binding protein (PhoT family)	C:plasma membrane; C:protein-containing complex; F:ion binding; P:transmembrane transport	#N/A	F	1.52E-03
AURMO_01596	PhoU-like phosphate uptake regulator	C:cell; C:cytoplasm; P:transport; P:homeostatic process	Rhola_00003680	#N/A	0.060777496

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AURMO_01597	two-component system sensor histidine kinase SenX3	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	Rhola_00003690	#N/A	0.107218821
AURMO_01598	two-component system response regulator RegX3	F:DNA binding; P:signal transduction; P:biosynthetic process; F:kinase activity; P:cellular nitrogen compound metabolic process	Rhola_00003700	#N/A	0.308321175
AURMO_01599	DNA-binding transcriptional ArsR family regulator	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	N	0.001022813
AURMO_01600	glycerol uptake facilitator-like aquaporin	C:cellular_component; F:transmembrane transporter activity	Rhola_00002740	#N/A	0.046551551
AURMO_01601	protein-tyrosine-phosphatase	F:oxidoreductase activity	Rhola_00001880	#N/A	0.479548453
AURMO_01602	ferredoxin--NADP+ reductase	F:oxidoreductase activity	Rhola_00001460	#N/A	0.922516408
AURMO_01603	phosphoribosylamine--glycine ligase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00001360	J	2.58E-11

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01604	phosphoribosylaminoimidazole-succinocarboxamide synthase	P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00001350	#N/A	0.034846165
AURMO_01605	hypothetical protein	C:cellular_component	Rhola_00008300	#N/A	0.029170457
AURMO_01606	hypothetical protein	#N/A	#N/A	#N/A	0.324683546
AURMO_01607	hypothetical protein	C:cellular_component	#N/A	#N/A	0.09158898
AURMO_01608	uncharacterized protein (DUF305 family)	#N/A	Rhola_00001370	#N/A	0.015866107
AURMO_01609	FtsP/CotA-like multicopper oxidase with cupredoxin domain	C:cellular_component; F:oxidoreductase activity; F:ion binding	Rhola_00003020	G	0.002802691
AURMO_01610	copper ion binding protein	P:transport; F:ion binding	#N/A	#N/A	0.530326372
AURMO_01611	lysophospholipase L1-like esterase	F:molecular_function	#N/A	#N/A	0.154959871
AURMO_01612	phosphatidylinositol alpha 1,6-mannosyltransferase	F:transferase activity, transferring glycosyl groups	#N/A	#N/A	0.34147591
AURMO_01613	membrane-associated protein	C:cellular_component	#N/A	#N/A	0.545089772
AURMO_01614	UDP-glucose pyrophosphorylase	P:biosynthetic process; F:nucleotidyltransferase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00012960	#N/A	0.903896586
AURMO_01615	hypothetical protein	#N/A	#N/A	A	1.09E-15
AURMO_01616	non-ribosomal peptide synthetase-like protein	C:cellular_component; F:ion binding	#N/A	#N/A	0.06163701

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01617	peptidase M1-like protein	F:peptidase activity; F:ion binding	#N/A	#N/A	0.051931766
AURMO_01618	phosphopantetheinyl transferase	F:ion binding	#N/A	#N/A	0.79908954
AURMO_01619	oligo-1,6-glucosidase	P:carbohydrate metabolic process; F:hydrolase activity, acting on glycosyl bonds	Rhola_00002250	#N/A	0.677964816
AURMO_01620	tryptophan 2,3-dioxygenase	P:cellular amino acid metabolic process; P:catabolic process; F:oxidoreductase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00011730	M	6.88E-06
AURMO_01621	hypothetical protein	F:hydrolase activity	#N/A	N	0.01485882
AURMO_01622	kynureninase	C:cytoplasm; P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; P:cellular nitrogen compound metabolic process; F:ion binding; P:cofactor metabolic process	Rhola_00011720	#N/A	0.031721026

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01623	phosphoribosylformylglycinamidine synthase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	#N/A	E	6.76E-17
AURMO_01624	phosphoribosylformylglycinamidine synthase subunit I	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00001240	#N/A	0.044394592
AURMO_01625	integral membrane protein	C:cellular_component	Rhola_00002690	#N/A	0.430005435
AURMO_01626	phosphoribosylformylglycinamidine synthase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00001230	#N/A	0.03680419
AURMO_01627	hypothetical protein	C:cellular_component	#N/A	#N/A	0.355730473
AURMO_01628	Htaa protein	#N/A	#N/A	#N/A	0.828653121
AURMO_01629	chorismate mutase	F:isomerase activity; P:small molecule metabolic process	#N/A	#N/A	0.969258343

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AURMO_01630	drug/metabolite transporter (DMT)-like permease	C:cellular_component	#N/A	#N/A	0.221605317
AURMO_01631	adenylosuccinate synthetase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00013480	E	1.00E-02
AURMO_01632	thiopurine S-methyltransferase	P:biological_process; F:methyltransferase activity	RHOLA_RS05360	A	0.000104325
AURMO_01633	tRNA G18 (ribose-2'-O)-methylase SpoU	F:RNA binding; P:tRNA metabolic process; F:methyltransferase activity	Rhola_00013490	#N/A	0.15969467
AURMO_01634	orotate phosphoribosyltransferase	P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00013530	#N/A	0.342065848
AURMO_01635	drug/metabolite transporter (DMT)-like permease	C:cellular_component	Rhola_00003560	#N/A	0.148219143
AURMO_01636	HAE1 family hydrophobic/amphiphilic exporter-1	C:cellular_component; F:transmembrane transporter activity	Rhola_00005470	I	2.01E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01637	amino acid/polyamine/organocation transporter (APC superfamily)	F:DNA binding; C:cellular_component; F:transmembrane transporter activity	#N/A	#N/A	0.504522078
AURMO_01638	fluoride ion exporter CrcB/FEX	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.117287814
AURMO_01639	camphor resistance protein CrcB	C:plasma membrane; F:transmembrane transporter activity	#N/A	#N/A	0.88610112
AURMO_01640	hypothetical protein	#N/A	#N/A	#N/A	0.557557231
AURMO_01641	hypothetical protein	C:plasma membrane	#N/A	#N/A	0.704391883
AURMO_01642	phosphoribosylformylglycinamidine cyclo-ligase	C:cytoplasm; P:biosynthetic process; F:ligase activity; P:cellular nitrogen compound metabolic process; F:ion binding; P:small molecule metabolic process	Rhola_00001410	#N/A	0.097591501
AURMO_01643	amidophosphoribosyltransferase	P:cellular amino acid metabolic process; P:biosynthetic process; F:transferase activity, transferring glycosyl groups; P:cellular nitrogen compound metabolic process; F:ion binding	Rhola_00001400	J	1.64E-03
AURMO_01644	hypothetical protein	C:cellular_component	#N/A	#N/A	0.590401938
AURMO_01645	hypothetical protein	#N/A	#N/A	#N/A	0.78000227

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01646	heptaprenyl diphosphate synthase	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00002150	#N/A	0.175125478
AURMO_01647	demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	F:methyltransferase activity; P:biosynthetic process; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00002140	#N/A	0.294696395
AURMO_01648	isochorismate synthase	P:biosynthetic process; F:isomerase activity	Rhola_00002120	#N/A	0.045822615
AURMO_01649	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	P:biosynthetic process; F:ion binding; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00002110	A	0.00061239
AURMO_01650	phospholipase D-like protein	C:cellular_component	#N/A	#N/A	0.698865809
AURMO_01651	uncharacterized protein DUF4229	C:cellular_component	#N/A	#N/A	0.760092087
AURMO_01652	1,4-dihydroxy-2-naphthoate prenyltransferase	C:plasma membrane; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00002080	#N/A	0.023325393
AURMO_01653	O-succinylbenzoic acid--CoA ligase	F:ligase activity	RHOLA_RS01020	#N/A	0.436058123

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AURMO_01654	1,4-dihydroxy-2-naphthoyl-CoA synthase	P:biosynthetic process; F:lyase activity; P:small molecule metabolic process; P:cofactor metabolic process	Rhola_00002060	#N/A	0.187211409
AURMO_01655	O-succinylbenzoate synthase	P:cellular amino acid metabolic process; P:catabolic process; P:biosynthetic process; F:lyase activity; F:isomerase activity; F:ion binding; P:cofactor metabolic process	Rhola_00002050	#N/A	0.970859665
AURMO_01656	cytochrome c-type biogenesis protein CcsB	F:molecular_function; C:cellular_component; P:protein-containing complex assembly	Rhola_00002040	#N/A	0.424113482
AURMO_01657	cytochrome c biogenesis protein	C:cellular_component	Rhola_00002030	#N/A	0.581680355
AURMO_01658	cytochrome c biogenesis protein CcdA	C:cellular_component; F:oxidoreductase activity; P:protein-containing complex assembly	Rhola_00002020	#N/A	0.422552827
AURMO_01659	thiol-disulfide isomerase/thioredoxin	C:cell; F:oxidoreductase activity; F:isomerase activity; P:homeostatic process	Rhola_00002010	#N/A	0.578883077
AURMO_01660	broad specificity phosphatase PhoE	#N/A	Rhola_00002000	#N/A	0.166921048

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AURMO_01661	aspartyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00001990	J	6.25E-03
AURMO_01662	glutaredoxin	C:cell; P:generation of precursor metabolites and energy; F:oxidoreductase activity; P:homeostatic process	#N/A	#N/A	0.245426302
AURMO_01663	putative oligomerization/nucleic acid binding protein	C:cellular_component	#N/A	E	1.51E-03
AURMO_01664	stress responsive alpha/beta barrel protein	#N/A	#N/A	#N/A	0.612762463
AURMO_01665	glutaredoxin-like protein DUF836	#N/A	#N/A	#N/A	0.023652475
AURMO_01666	regulatory ArsR family protein	F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.036010219
AURMO_01667	Trk-type K+ transport system membrane component	C:cellular_component; F:transmembrane transporter activity	Rhola_00003370	N	2.17E-03
AURMO_01668	trk system potassium uptake protein TrkA	F:transmembrane transporter activity	Rhola_00003380	#N/A	0.058167498

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01669	pyrroline-5-carboxylate reductase	C:cytoplasm; P:cellular amino acid metabolic process; P:biosynthetic process; F:oxidoreductase activity	Rhola_00001860	#N/A	0.475169817
AURMO_01670	cation diffusion facilitator family transporter	C:cellular_component; F:transmembrane transporter activity	Rhola_00012550	A	2.72E-05
AURMO_01671	tRNA(adenine34) deaminase	P:tRNA metabolic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:ion binding	Rhola_00012560	#N/A	0.354504062
AURMO_01672	transcriptional regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00012590	E	3.63E-07
AURMO_01673	deoxyribodipyrimidine photo-lyase type I	P:cellular protein modification process; F:lyase activity	Rhola_00007890	E	1.04E-02
AURMO_01674	rhodanese-related sulfurtransferase	C:cellular_component; F:nucleotidyltransferase activity	#N/A	H	1.47E-03
AURMO_01675	transglutaminase-like putative cysteine protease	P:proteolysis; F:peptidase activity	#N/A	#N/A	0.050202244
AURMO_01676	uncharacterized alpha-E superfamily protein	#N/A	#N/A	N	9.15E-03
AURMO_01677	uncharacterized circularly permuted ATP-grasp superfamily protein	#N/A	#N/A	M	0.000221209

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01678	hypothetical protein	#N/A	#N/A	#N/A	0.094020197
AURMO_01679	PadR family transcriptional regulator	#N/A	#N/A	M	3.26E-23
AURMO_01680	predicted unusual protein kinase regulating ubiquinone biosynthesis (AarF/ABC1/UbiB family)	C:cellular_component; F:kinase activity	Rhola_00002780	#N/A	0.049106929
AURMO_01681	predicted nuclease with RNAse H fold	F:molecular_function	#N/A	#N/A	0.151160538
AURMO_01682	GT2 family glycosyltransferase	F:molecular_function	#N/A	#N/A	0.14305914
AURMO_01683	hypothetical protein	F:oxidoreductase activity	#N/A	M	1.24E-02
AURMO_01685	transglutaminase superfamily protein	P:proteolysis; F:peptidase activity; P:regulation of apoptotic process	#N/A	#N/A	0.068278999
AURMO_01686	exodeoxyribonuclease-3	F:DNA binding; F:nuclease activity; P:DNA metabolic process; P:response to stress	Rhola_00013540	E	6.31E-04
AURMO_01687	hypothetical protein	C:cellular_component	#N/A	#N/A	0.640810338
AURMO_01688	hypothetical protein	#N/A	#N/A	#N/A	0.922516408
AURMO_01689	short-subunit dehydrogenase	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	#N/A	A	2.71E-08
AURMO_01690	hypothetical protein	#N/A	Rhola_00002810	G	1.54E-03
AURMO_01691	L-threonine aldolase	P:cellular amino acid metabolic process; F:lyase activity	Rhola_00002830	N	1.24E-05
AURMO_01692	hypothetical protein	#N/A	#N/A	#N/A	0.14373288
AURMO_01693	nitroreductase	F:oxidoreductase activity	Rhola_00012620	E	5.28E-05
AURMO_01694	HNH endonuclease	F:nuclease activity	#N/A	#N/A	0.960177397

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01695	adenine-specific methyltransferase EcoRI-like protein	P:biological_process; F:methyltransferase activity	#N/A	#N/A	0.98186731
AURMO_01696	helix-turn-helix protein	F:DNA binding	#N/A	#N/A	0.043983726
AURMO_01697	uncharacterized protein DUF3800	#N/A	#N/A	M	8.93E-27
AURMO_01698	ATP-dependent Clp protease ATP-binding subunit ClpB	F:peptidase activity; F:ion binding	Rhola_00013570	G	4.16E-15
AURMO_01699	16S rRNA (guanine1207-N2)-methyltransferase	F:DNA binding; C:cytoplasm; P:DNA metabolic process; F:methyltransferase activity; P:ribosome biogenesis	#N/A	#N/A	0.518504102
AURMO_01700	putative lumazine-binding protein	#N/A	Rhola_00009930	#N/A	0.058626881
AURMO_01701	hypothetical protein	C:cellular_component	#N/A	#N/A	0.021711595
AURMO_01702	MerR family transcriptional regulator/heat shock protein HspR	F:DNA binding; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00013580	G	2.59E-13
AURMO_01703	molecular chaperone DnaJ	F:DNA binding; P:protein folding; F:unfolded protein binding	Rhola_00013590	G	1.57E-13
AURMO_01704	molecular chaperone GrpE	C:cytoplasm; P:protein folding; F:enzyme regulator activity	#N/A	G	9.06E-08
AURMO_01705	molecular chaperone DnaK	P:protein folding; F:ion binding; F:unfolded protein binding	Rhola_00013610	G	1.02E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01706	UMF1 family MFS transporter	C:cellular_component	Rhola_00013620	A	2.94E-09
AURMO_01707	2,4-dienoyl-CoA reductase-like NADH-dependent reductase (Old Yellow Enzyme family)	F:oxidoreductase activity; F:ion binding	Rhola_00009500	#N/A	0.258425377
AURMO_01708	helix-turn-helix protein	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	M	1.31E-02
AURMO_01709	hypothetical protein	#N/A	#N/A	M	1.16E-02
AURMO_01710	4-hydroxybenzoate polyprenyltransferase	C:cellular_component; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	Rhola_00010900	#N/A	0.117547245
AURMO_01711	lycopene cyclase domain-containing protein	C:cellular_component; F:isomerase activity	#N/A	#N/A	0.685389937
AURMO_01712	lycopene cyclase domain-containing protein	C:cellular_component; F:isomerase activity	#N/A	#N/A	0.070036792
AURMO_01713	phytoene desaturase	P:lipid metabolic process; P:biosynthetic process; F:oxidoreductase activity; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:small molecule metabolic process	Rhola_00010870	N	0.001171113

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01714	phytoene/squalene synthetase	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups; P:small molecule metabolic process	Rhola_00010860	H	4.34E-03
AURMO_01715	geranylgeranyl diphosphate synthase type II	P:lipid metabolic process; P:biosynthetic process; F:transferase activity, transferring alkyl or aryl (other than methyl) groups	#N/A	G	8.15E-03
AURMO_01716	isopentenyl-diphosphate delta-isomerase	C:cytoplasm; P:lipid metabolic process; P:biosynthetic process; F:isomerase activity; F:ion binding	#N/A	#N/A	0.025187034
AURMO_01717	predicted nucleic acid-binding protein	F:nuclease activity; F:ion binding	#N/A	M	3.11E-03
AURMO_01718	prevent-host-death family protein	#N/A	#N/A	M	9.06E-14
AURMO_01719	dCTP deaminase	P:biosynthetic process; F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process	Rhola_00013650	#N/A	0.083963504
AURMO_01720	predicted DCC family thiol-disulfide oxidoreductase YuxK	#N/A	#N/A	#N/A	0.133952665

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01721	PIF1-like helicase	F:helicase activity; P:DNA metabolic process; P:response to stress; P:homeostatic process; P:chromosome organization	Rhola_00013680	E	7.95E-06
AURMO_01722	hypothetical protein	C:cellular_component	#N/A	#N/A	0.024765444
AURMO_01723	putative copper resistance protein D	C:cellular_component; P:transport	Rhola_00013690	B	4.20E-03
AURMO_01724	DNA-binding protein HU-beta	F:DNA binding; P:chromosome organization	#N/A	D	5.93E-03
AURMO_01725	SSU ribosomal protein S14P	F:structural constituent of ribosome; C:ribosome; P:translation; F:rRNA binding	Rhola_00013720	E	2.41E-08
AURMO_01726	LSU ribosomal protein L33P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	4.95E-09
AURMO_01727	LSU ribosomal protein L28P	F:structural constituent of ribosome; C:ribosome; P:translation	#N/A	E	7.84E-08
AURMO_01728	Fic/DOC family protein	#N/A	#N/A	N	9.05E-08
AURMO_01729	Fur family zinc uptake regulator	F:DNA binding; F:DNA-binding transcription factor activity; P:biosynthetic process; P:cellular nitrogen compound metabolic process	Rhola_00013750	M	1.46E-07

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01730	ABC-type Mn2+/Zn2+ transport system permease subunit	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	N	8.60E-06
AURMO_01731	ABC-type Mn2+/Zn2+ transport system permease subunit	C:plasma membrane; F:transmembrane transporter activity; C:protein-containing complex	#N/A	N	1.62E-10
AURMO_01732	manganese/iron transport system ATP-binding protein	F:ATPase activity; F:ion binding	#N/A	M	1.60E-05
AURMO_01733	zinc/manganese transport system substrate-binding protein/manganese/iron transport system substrate-binding protein	P:transport; P:cell adhesion; F:ion binding	#N/A	N	8.49E-06
AURMO_01734	UPF0176 protein	F:molecular_function	Rhola_00000470	#N/A	0.683892528
AURMO_01735	uroporphyrinogen-III synthase	P:biosynthetic process; F:lyase activity; P:cellular nitrogen compound metabolic process; P:small molecule metabolic process; P:cofactor metabolic process	#N/A	#N/A	0.224517138
AURMO_01736	uncharacterized protein DUF3618	C:cellular_component	#N/A	#N/A	0.710609812
AURMO_01737	putative superfamily III holin-X	C:cellular_component	#N/A	#N/A	0.954661206
AURMO_01738	hypothetical protein	#N/A	#N/A	#N/A	0.090475904

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01739	hypothetical protein	F:oxygen-dependent protoporphyrinogen oxidase activity; C:cytoplasm; P:porphyrin-containing compound biosynthetic process; P:protoporphyrinogen IX biosynthetic process; F:oxidoreductase activity; P:oxidation-reduction process	#N/A	#N/A	0.294696395
AURMO_01740	glycyl-tRNA synthetase	C:cytoplasm; P:tRNA metabolic process; P:translation; P:cellular amino acid metabolic process; F:ligase activity; F:ion binding	Rhola_00006270	J	7.05E-05
AURMO_01741	putative endopeptidase	F:peptidase activity	Rhola_00000480	E	1.24E-07
AURMO_01742	3-oxoacyl-[acyl-carrier protein] reductase	F:oxidoreductase activity; F:transferase activity, transferring acyl groups	#N/A	#N/A	0.166795961
AURMO_01743	phosphoglycolate phosphatase	F:phosphatase activity	#N/A	#N/A	0.177329631
AURMO_01744	hypothetical protein	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process	Rhola_00012680	#N/A	0.285858133
AURMO_01745	phosphoglycolate phosphatase	F:phosphatase activity	#N/A	J	7.38E-05
AURMO_01746	hypothetical protein	#N/A	#N/A	E	1.18E-03
AURMO_01747	hypothetical protein	#N/A	#N/A	A	2.26E-06

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01748	hypothetical protein	#N/A	#N/A	#N/A	0.026633978
AURMO_01749	hypothetical protein	#N/A	#N/A	#N/A	0.728838677
AURMO_01750	HNH endonuclease	F:nuclease activity	#N/A	#N/A	0.099862437
AURMO_01751	adenine-specific methyltransferase EcoRI-like protein	C:cytoplasm; C:plasma membrane; P:transport; F:methyltransferase activity; C:organelle	#N/A	#N/A	0.973137914
AURMO_01752	helix-turn-helix protein	F:DNA binding	#N/A	G	2.20E-06
AURMO_01753	EndoU nuclease-like protein	#N/A	#N/A	I	0.009201642
AURMO_01754	hypothetical protein	#N/A	#N/A	N	1.12E-05
AURMO_01756	ferredoxin-NADP reductase	C:cellular_component; P:generation of precursor metabolites and energy; F:methyltransferase activity; F:oxidoreductase activity; F:ion binding	#N/A	M	2.24E-03
AURMO_01757	thiamine biosynthesis lipoprotein	P:cellular protein modification process; F:ion binding	#N/A	#N/A	0.018948169
AURMO_01758	hypothetical protein	#N/A	#N/A	A	0.010968604
AURMO_01759	hypothetical protein	#N/A	#N/A	#N/A	0.018348976
AURMO_01760	DNA-binding response OmpR family regulator	F:DNA binding; P:signal transduction; P:biosynthetic process; P:cellular nitrogen compound metabolic process	#N/A	#N/A	0.863661551

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01761	signal transduction histidine kinase	C:cellular_component; P:cellular protein modification process; P:signal transduction; F:kinase activity; F:ion binding	#N/A	#N/A	0.25724282
AURMO_01762	type III secretion system (T3SS) inner membrane Yop/YscD-like protein	#N/A	Rhola_00000450	J	1.02E-02
AURMO_01763	pSer/pThr/pTyr-binding forkhead associated (FHA) protein	C:cellular_component	#N/A	#N/A	0.426934475
AURMO_01764	protein phosphatase	C:cellular_component; P:cellular protein modification process; F:phosphatase activity	Rhola_00000430	#N/A	0.070121723
AURMO_01765	cell elongation-specific peptidoglycan biosynthesis regulator RodA	C:cellular_component; P:cell division	Rhola_00000420	#N/A	0.761024366
AURMO_01766	cell elongation-specific peptidoglycan D,D-transpeptidase	F:ion binding	Rhola_00000410	#N/A	0.988899892
AURMO_01767	serine/threonine-protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	Rhola_00000400	#N/A	0.362765835
AURMO_01768	serine/threonine-protein kinase	C:cellular_component; P:cellular protein modification process; F:kinase activity; F:ion binding	Rhola_00000390	#N/A	0.135464204

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01769	para-aminobenzoate synthetase component 2	F:molecular_function; P:cellular amino acid metabolic process	Rhola_00000380	#N/A	0.395164726
AURMO_01770	hypothetical protein	C:cellular_component	#N/A	#N/A	0.755904708
AURMO_01771	sortase A	C:cellular_component	#N/A	#N/A	0.034694192
AURMO_01772	uncharacterized protein UPF0233	C:plasma membrane; P:cell cycle; P:cell division	#N/A	#N/A	0.115412956
AURMO_01773	membrane associated rhomboid family serine protease	C:cellular_component; F:peptidase activity	#N/A	I	0.000303975
AURMO_01774	peptidyl-prolyl cis-trans isomerase A (cyclophilin A)	P:protein folding; P:cellular protein modification process; F:isomerase activity	Rhola_00000330	E	0.001809486
AURMO_01775	hypothetical protein	C:cellular_component	#N/A	#N/A	0.027334521
AURMO_01776	hypothetical protein	F:peptidase activity	Rhola_00002800	#N/A	0.384740909
AURMO_01777	lipid II:glycine glycyltransferase (peptidoglycan interpeptide bridge formation enzyme)	P:biosynthetic process; F:transferase activity, transferring acyl groups; P:cell wall organization or biogenesis	#N/A	#N/A	0.261158215
AURMO_01778	uncharacterized protein with HEPN domain	#N/A	#N/A	#N/A	0.432730921
AURMO_01779	hypothetical protein	F:DNA binding; F:nucleotidyltransferase activity	#N/A	#N/A	0.266558231
AURMO_01780	bacteriocin resistance YdeI/OmpD-like protein	F:molecular_function; C:cellular_component; P:biological_process	#N/A	#N/A	0.640810338
AURMO_01781	hypothetical protein	F:ligase activity	#N/A	#N/A	0.986392974

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01782	fibronectin type III domain protein	C:cellular_component	#N/A	G	1.34E-02
AURMO_01783	hypothetical protein	C:cellular_component	#N/A	#N/A	0.391506021
AURMO_01784	hypothetical protein	F:DNA binding	#N/A	#N/A	0.194328952
AURMO_01787	transmembrane protein DUF3566	C:cellular_component	#N/A	#N/A	0.307249997
AURMO_01788	DNA gyrase subunit A	F:DNA binding; C:chromosome; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	Rhola_00000080	#N/A	0.090695298
AURMO_01789	DNA gyrase subunit B	F:DNA binding; C:chromosome; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:isomerase activity; F:ATPase activity; F:ion binding; P:chromosome organization	Rhola_00000070	#N/A	0.032551175
AURMO_01790	predicted nucleic acid-binding Zn ribbon protein	#N/A	Rhola_00000040	#N/A	0.689934133
AURMO_01791	DNA replication and repair protein RecF	F:DNA binding; C:cytoplasm; P:DNA metabolic process; P:response to stress; P:biosynthetic process; F:ion binding	Rhola_00000030	#N/A	0.091397619

Locus Tag	Annotation	GO-slim term(s)	Best hit in *R. lacicola*	Expression group	BH adjusted p-value of Likelihood Ratio Test
AURMO_01792	DNA polymerase-3 subunit beta	F:DNA binding; F:nuclease activity; C:cytoplasm; P:DNA metabolic process; P:biosynthetic process; F:nucleotidyltransferase activity; C:protein-containing complex	#N/A	#N/A	0.016071392

Table A.10 Enrichment of GO-slim terms in expression groups of *Rhodoluna lacicola*. Odds ratios were calculated as the ratio of the representation of a term in a group to its representation in the genome: (A/B)/(C/D). Ratio p-values were corrected using Benjamini-Hochberg procedure.

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
tRNA metabolic process	A-D	10	254	37	1186	1.261759	0.808081	0.31594
transmembrane transport	A-D	2	254	24	1186	0.389287	0.999339	0.957051
small molecule metabolic process	A-D	27	254	139	1186	0.907039	0.999339	0.703911
nucleobase-containing compound catabolic process	A-D	3	254	9	1186	1.555886	0.808081	0.359387
nucleic acid phosphodiester bond hydrolysis	A-D	1	254	2	1186	2.332902	0.827801	0.442229
lipid metabolic process	A-D	8	254	29	1186	1.287842	0.808081	0.328182
chromosome organization	A-D	5	254	18	1186	1.296775	0.808081	0.385826
cellular nitrogen compound metabolic process	A-D	32	254	196	1186	0.762461	0.999339	0.92705
cellular amino acid metabolic process	A-D	28	254	106	1186	1.233224	0.808081	0.203434
cell division	A-D	8	254	27	1186	1.383157	0.808081	0.272703
cell cycle	A-D	7	254	22	1186	1.485231	0.808081	0.245192
biosynthetic process	A-D	64	254	303	1186	0.98626	0.899818	0.562386
transport	A-D	1	254	20	1186	0.233607	0.999339	0.98273
translation	A-D	8	254	83	1186	0.450249	0.999339	0.9935
protein targeting	A-D	2	254	7	1186	1.333792	0.872706	0.490897
protein folding	A-D	1	254	9	1186	0.519003	0.999339	0.856415
chromosome segregation	A-D	1	254	6	1186	0.778341	0.999339	0.743374
cellular protein modification process	A-D	4	254	27	1186	0.691904	0.999339	0.820784
cell wall organization or biogenesis	A-D	4	254	14	1186	1.333794	0.808081	0.397746
signal transduction	A-D	2	254	17	1186	0.549519	0.999339	0.872642
response to stress	A-D	7	254	38	1186	0.860216	0.999339	0.702235

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
protein-containing complex assembly	A-D	1	254	2	1186	2.332902	0.827801	0.442229
biological_process	A-D	3	254	19	1186	0.737398	0.999339	0.771766
secondary metabolic process	A-D	1	254	1	1186	4.662124	0.808081	0.322505
cell morphogenesis	A-D	4	254	13	1186	1.436304	0.808081	0.35436
generation of precursor metabolites and energy	A-D	12	254	40	1186	1.400437	0.808081	0.201954
cofactor metabolic process	A-D	14	254	53	1186	1.233215	0.808081	0.294217
catabolic process	A-D	8	254	28	1186	1.333798	0.808081	0.300164
sulfur compound metabolic process	A-D	4	254	17	1186	1.098607	0.899818	0.522882
carbohydrate metabolic process	A-D	14	254	53	1186	1.233215	0.808081	0.294217
DNA metabolic process	A-D	16	254	57	1186	1.310425	0.808081	0.215595
tRNA metabolic process	G-J	4	265	37	1186	0.48403	0.999339	0.955098
transport	G-J	3	265	20	1186	0.671484	0.999339	0.818015
transmembrane transport	G-J	3	265	24	1186	0.559623	0.999339	0.893093
translation	G-J	23	265	83	1186	1.240009	0.808081	0.223627
sulfur compound metabolic process	G-J	11	265	17	1186	2.893075	0.660631	0.008258
small molecule metabolic process	G-J	36	265	139	1186	1.159046	0.808081	0.257992
signal transduction	G-J	4	265	17	1186	1.053022	0.899818	0.552524
ribosome biogenesis	G-J	4	265	20	1186	0.89516	0.999339	0.662893
response to stress	G-J	8	265	38	1186	0.942218	0.974663	0.621348
regulation of transcription, DNA-templated	G-J	1	265	1	1186	4.468946	0.808081	0.332728
protein-containing complex assembly	G-J	1	265	2	1186	2.236196	0.827801	0.454801
protein targeting	G-J	1	265	7	1186	0.639526	0.999339	0.801017
protein maturation	G-J	3	265	5	1186	2.682916	0.808081	0.167824
protein folding	G-J	3	265	9	1186	1.491362	0.808081	0.381649
lipid metabolic process	G-J	5	265	29	1186	0.771759	0.999339	0.768987

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
homeostatic process	G-J	4	265	17	1186	1.053022	0.899818	0.552524
generation of precursor metabolites and energy	G-J	11	265	40	1186	1.230574	0.808081	0.328285
DNA metabolic process	G-J	3	265	57	1186	0.235692	0.999339	0.999339
cofactor metabolic process	G-J	17	265	53	1186	1.435151	0.808081	0.13474
cellular protein modification process	G-J	8	265	27	1186	1.325791	0.808081	0.306213
cellular nitrogen compound metabolic process	G-J	57	265	196	1186	1.301327	0.808081	0.067075
cellular component assembly	G-J	2	265	4	1186	2.2362	0.808081	0.303474
cellular amino acid metabolic process	G-J	21	265	106	1186	0.886716	0.999339	0.722663
cell wall organization or biogenesis	G-J	1	265	14	1186	0.319845	0.999339	0.951161
cell morphogenesis	G-J	1	265	13	1186	0.34444	0.999339	0.940336
catabolic process	G-J	11	265	28	1186	1.75744	0.808081	0.08991
carbohydrate metabolic process	G-J	16	265	53	1186	1.350794	0.808081	0.189724
biosynthetic process	G-J	76	265	303	1186	1.122474	0.808081	0.233645
biological_process	G-J	5	265	19	1186	1.17758	0.827801	0.455291
nucleobase-containing compound catabolic process	G-J	1	265	9	1186	0.497469	0.999339	0.866898
riboflavin biosynthetic process	G-J	1	265	1	1186	4.468946	0.808081	0.332728
protein transport	G-J	1	265	4	1186	1.118808	0.978257	0.635867
oxidation-reduction process	G-J	1	265	3	1186	1.491359	0.899818	0.554473
chromosome organization	G-J	1	265	18	1186	0.248785	0.999339	0.978041
cell division	G-J	1	265	27	1186	0.16587	0.999339	0.996333
cell cycle	G-J	1	265	22	1186	0.20356	0.999339	0.990103
transport	M-N	3	32	20	1186	5.541817	0.808081	0.024727
transmembrane transport	M-N	3	32	24	1186	4.620813	0.808081	0.037505

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
small molecule metabolic process	M-N	1	32	139	1186	0.266795	0.999339	0.973641
signal transduction	M-N	1	32	17	1186	2.178175	0.808081	0.387706
response to stress	M-N	2	32	38	1186	1.949265	0.808081	0.294726
phosphorylation	M-N	1	32	2	1186	18.35462	0.808081	0.078972
homeostatic process	M-N	1	32	17	1186	2.178175	0.808081	0.387706
DNA metabolic process	M-N	3	32	57	1186	1.949311	0.808081	0.224017
chromosome organization	M-N	1	32	18	1186	2.057335	0.808081	0.404041
cellular nitrogen compound metabolic process	M-N	2	32	196	1186	0.378372	0.999339	0.962654
carbohydrate metabolic process	M-N	3	32	53	1186	2.096185	0.808081	0.196306
biosynthetic process	M-N	3	32	303	1186	0.367125	0.999339	0.982399
biological_process	M-N	2	32	19	1186	3.893254	0.808081	0.110928

Table A.11 Enrichment of GO-slim terms in expression groups of *Aurantimicrobium photophilum*. Odds ratios were calculated as the ratio of the representation of a term in a group to its representation in the genome: (A/B)/(C/D). Ratio p-values were corrected using Benjamini-Hochberg procedure.

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
tRNA metabolic process	A-D	2	206	40	1513	0.367377	0.999872	0.96768
transposition	A-D	2	206	21	1513	0.699617	0.999872	0.780842
transport	A-D	5	206	14	1513	2.621061	0.651168	0.070323
transmembrane transport	A-D	5	206	20	1513	1.835348	0.793284	0.176285
small molecule metabolic process	A-D	14	206	142	1513	0.724236	0.999872	0.897464
signal transduction	A-D	1	206	21	1513	0.349888	0.999872	0.939363
ribosome biogenesis	A-D	5	206	24	1513	1.529697	0.824808	0.267067

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
response to stress	A-D	5	206	40	1513	0.918111	0.992915	0.640936
reproduction	A-D	1	206	2	1513	3.668038	0.850637	0.319176
protein-containing complex assembly	A-D	1	206	3	1513	2.446431	0.892353	0.40097
protein folding	A-D	1	206	10	1513	0.734583	0.999872	0.75492
phosphorylation	A-D	1	206	2	1513	3.668038	0.850637	0.319176
oxidation-reduction process	A-D	1	206	2	1513	3.668038	0.850637	0.319176
nucleobase-containing compound catabolic process	A-D	2	206	11	1513	1.335142	0.946888	0.474772
lipid metabolic process	A-D	3	206	35	1513	0.629683	0.999872	0.848947
homeostatic process	A-D	1	206	17	1513	0.432191	0.999872	0.899345
generation of precursor metabolites and energy	A-D	6	206	48	1513	0.91811	0.992915	0.6416
DNA metabolic process	A-D	14	206	82	1513	1.253797	0.824808	0.266976
cofactor metabolic process	A-D	4	206	53	1513	0.554464	0.999872	0.920616
chromosome organization	A-D	3	206	16	1513	1.376835	0.892353	0.404864
cellular protein modification process	A-D	1	206	35	1513	0.209953	0.999872	0.98961
cellular nitrogen compound metabolic process	A-D	17	206	220	1513	0.567691	0.999872	0.991955
cellular amino acid metabolic process	A-D	4	206	123	1513	0.238964	0.999872	0.999872
cell wall organization or biogenesis	A-D	3	206	12	1513	1.83535	0.824808	0.267299
cell morphogenesis	A-D	2	206	13	1513	1.12984	0.963497	0.553119
cell division	A-D	4	206	27	1513	1.088073	0.946888	0.520796
cell cycle	A-D	3	206	23	1513	0.958019	0.992915	0.618931
catabolic process	A-D	4	206	39	1513	0.753408	0.999872	0.773334
carbohydrate transport	A-D	1	206	1	1513	7.330896	0.814148	0.226152
carbohydrate metabolic process	A-D	9	206	58	1513	1.139574	0.900376	0.416841
biosynthetic process	A-D	29	206	334	1513	0.637855	0.999872	0.990696

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
biological_process	A-D	4	206	21	1513	1.398674	0.850637	0.354734
tRNA metabolic process	E-I	8	243	40	1513	1.24509	0.850637	0.348514
transmembrane transport	E-I	4	243	20	1513	1.245093	0.914666	0.431926
translation	E-I	56	243	84	1513	4.146666	4.52E-11	4.18E-13
sulfur compound metabolic process	E-I	7	243	20	1513	2.177996	0.651168	0.072352
small molecule metabolic process	E-I	21	243	142	1513	0.920857	0.992915	0.669315
signal transduction	E-I	4	243	21	1513	1.185831	0.946888	0.464279
ribosome biogenesis	E-I	9	243	24	1513	2.33358	0.401776	0.033481
ribonucleoprotein complex assembly	E-I	1	243	2	1513	3.110285	0.850637	0.361265
response to stress	E-I	7	243	40	1513	1.089581	0.946888	0.483002
protein targeting	E-I	3	243	7	1513	2.666575	0.724655	0.152291
protein maturation	E-I	1	243	4	1513	1.556122	0.946888	0.526049
protein folding	E-I	7	243	10	1513	4.353157	0.101128	0.005618
nucleobase-containing compound catabolic process	E-I	4	243	11	1513	2.262756	0.724655	0.14529
mRNA processing	E-I	1	243	1	1513	6.21563	0.824808	0.258392
lipid metabolic process	E-I	6	243	35	1513	1.067349	0.946888	0.51154
homeostatic process	E-I	4	243	17	1513	1.464657	0.850637	0.332462
generation of precursor metabolites and energy	E-I	6	243	48	1513	0.778392	0.999872	0.774747
DNA metabolic process	E-I	4	243	82	1513	0.303853	0.999872	0.99831
cofactor metabolic process	E-I	9	243	53	1513	1.057281	0.946888	0.496996
chromosome organization	E-I	3	243	16	1513	1.16731	0.946888	0.502364
cellular protein modification process	E-I	7	243	35	1513	1.245091	0.850637	0.365065
cellular nitrogen compound metabolic process	E-I	36	243	220	1513	1.018847	0.946888	0.49296
cellular component assembly	E-I	2	243	4	1513	3.110294	0.814148	0.197887

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
cellular amino acid metabolic process	E-I	12	243	123	1513	0.607589	0.999872	0.965924
cell wall organization or biogenesis	E-I	1	243	12	1513	0.519014	0.999872	0.8558
cell morphogenesis	E-I	1	243	13	1513	0.479103	0.999872	0.875678
cell division	E-I	2	243	27	1513	0.461363	0.999872	0.924055
cell cycle	E-I	1	243	23	1513	0.270834	0.999872	0.971653
catabolic process	E-I	9	243	39	1513	1.436518	0.814148	0.218096
carbohydrate metabolic process	E-I	8	243	58	1513	0.858874	0.992915	0.709073
biosynthetic process	E-I	48	243	334	1513	0.89485	0.999872	0.768492
tRNA metabolic process	J-L	9	78	40	1513	4.357229	0.021127	0.000782
translation	J-L	14	78	84	1513	3.229379	0.020154	0.00056
sulfur compound metabolic process	J-L	2	78	20	1513	1.938697	0.850637	0.298614
small molecule metabolic process	J-L	11	78	142	1513	1.502204	0.724655	0.150146
ribosome biogenesis	J-L	1	78	24	1513	0.808318	0.992915	0.717105
response to stress	J-L	1	78	40	1513	0.485074	0.999872	0.872588
reproduction	J-L	1	78	2	1513	9.66225	0.724655	0.14152
protein transport	J-L	1	78	5	1513	3.873784	0.824808	0.262795
protein targeting	J-L	1	78	7	1513	2.768253	0.850637	0.333862
protein folding	J-L	2	78	10	1513	3.87383	0.724655	0.11743
lipid metabolic process	J-L	1	78	35	1513	0.554351	0.999872	0.836661
homeostatic process	J-L	1	78	17	1513	1.140926	0.992915	0.597942
generation of precursor metabolites and energy	J-L	2	78	48	1513	0.808314	0.992915	0.711924
DNA metabolic process	J-L	3	78	82	1513	0.709819	0.999872	0.791976
cofactor metabolic process	J-L	7	78	53	1513	2.559721	0.401776	0.03127
chromosome organization	J-L	3	78	16	1513	3.631774	0.651168	0.066438
cellular protein modification process	J-L	2	78	35	1513	1.108342	0.963497	0.551319
cellular nitrogen compound metabolic process	J-L	17	78	220	1513	1.498511	0.724655	0.098086

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
cellular component assembly	J-L	1	78	4	1513	4.840177	0.814148	0.224429
cellular amino acid metabolic process	J-L	26	78	123	1513	4.095057	8.71E-06	1.61E-07
cell division	J-L	3	78	27	1513	2.153833	0.804665	0.186265
cell cycle	J-L	3	78	23	1513	2.527876	0.724655	0.137779
catabolic process	J-L	1	78	39	1513	0.497509	0.999872	0.866106
carbohydrate metabolic process	J-L	4	78	58	1513	1.337481	0.850637	0.370185
biosynthetic process	J-L	32	78	334	1513	1.857663	0.092382	0.004277
transposition	M-N	5	86	21	1513	4.182115	0.196172	0.012715
transport	M-N	1	86	14	1513	1.256446	0.970417	0.566077
transmembrane transport	M-N	1	86	20	1513	0.879714	0.992915	0.68858
small molecule metabolic process	M-N	5	86	142	1513	0.619615	0.999872	0.8962
signal transduction	M-N	3	86	21	1513	2.511139	0.724655	0.140692
response to stress	M-N	2	86	40	1513	0.879712	0.992915	0.66992
regulation of transcription, DNA-templated	M-N	1	86	2	1513	8.767476	0.724655	0.154325
lipid metabolic process	M-N	3	86	35	1513	1.507506	0.850637	0.341639
homeostatic process	M-N	1	86	17	1513	1.034872	0.992915	0.632454
generation of precursor metabolites and energy	M-N	1	86	48	1513	0.36667	0.999872	0.93267
DNA metabolic process	M-N	7	86	82	1513	1.501407	0.814148	0.214667
cofactor metabolic process	M-N	2	86	53	1513	0.664001	0.999872	0.802742
cellular nitrogen compound metabolic process	M-N	12	86	220	1513	0.959635	0.992915	0.60006
cellular amino acid metabolic process	M-N	6	86	123	1513	0.858246	0.992915	0.69846
cell division	M-N	1	86	27	1513	0.651721	0.999872	0.788183
cell adhesion	M-N	1	86	1	1513	17.4956	0.724655	0.105761
catabolic process	M-N	5	86	39	1513	2.254039	0.724655	0.091997
carbohydrate metabolic process	M-N	3	86	58	1513	0.91003	0.992915	0.646474
biosynthetic process	M-N	15	86	334	1513	0.790198	0.999872	0.830581

GO-Slim Term	Gene Groups	GO-slim Term Count in Group (A)	Number of Genes in Group Assigned Any GO-slim Term (B)	Number of Genes with GO-slim term in Whole Genome (C)	Total Number of Genes Assigned GO-slim Terms (D)	Ratio	BH Corrected p-value	Ratio p-value
biological_process	M-N	1	86	21	1513	0.837843	0.992915	0.705294

Table A.12 Significantly enriched gene clusters among 27 *Microbacteriaceae* species from freshwater, soil, and marine environments. Gene cluster ID numbers, assigned COG functions, enrichment score, adjusted p-value, and percentage of a given environment that were calculated during construction of the pan-genome of 27 *Microbacteriaceae* species. A gene cluster was labeled enriched in an environment or environments if it had an enrichment score greater than 12 and an adjusted p-value (q-value) less than 0.05.

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00000867	Peroxiredoxin	18.98918997	0.027730034	freshwater, soil	0	0.9231	0.8571
GC_00000822	Uncharacterized conserved protein YabN, contains tetrapyrrole methylase and MazG-like pyrophosphatase domain	14.34995756	0.027730034	freshwater, soil	0.1429	0.9231	0.8571
GC_00000969	Glutaredoxin	14.07502265	0.027730034	freshwater, soil	0	0.8462	0.7143
GC_00000736	Forkhead associated (FHA) domain, binds pSer, pThr, pTyr	13.39580374	0.027730034	freshwater, soil	0.2857	0.9231	1
GC_00000887	UDP-N-acetylenolpyruvoylglucosamine reductase	12.75696552	0.037919393	freshwater, soil	0.1429	0.7692	1
GC_00002581	DNA-binding transcriptional regulator, Lrp family	17.5329091	0.027730034	marine	0.7143	0	0
GC_00002548	ABC-type transport system, periplasmic component	17.5329091	0.027730034	marine	0.7143	0	0
GC_00002503	NhaP-type Na+/H+ or K+/H+ antiporter	17.5329091	0.027730034	marine	0.7143	0	0
GC_00002483	Uncharacterized membrane protein YfcA	17.5329091	0.027730034	marine	0.7143	0	0
GC_00002468	ABC-type dipeptide/oligopeptide/nickel transport system, permease component	17.5329091	0.027730034	marine	0.7143	0	0
GC_00001406	ABC-type proline/glycine betaine transport system, permease component	16.9170857	0.027730034	marine	1	0.0769	0.2857
GC_00002371	ABC-type proline/glycine betaine transport system, periplasmic component	13.77514862	0.027730034	marine	0.7143	0	0.1429
GC_00003574	Uncharacterized protein involved in exopolysaccharide biosynthesis	13.41538756	0.027730034	marine	0.5714	0	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00003048	DNA-binding response regulator, OmpR family, contains REC and winged-helix (wHTH) domain	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003096	Arginase family enzyme	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003402	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003442	Uroporphyrinogen-III methylase (siroheme synthase)	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003134	Energy-coupling factor transporter transmembrane protein EcfT	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003568	Sugar or nucleoside kinase, ribokinase family	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003187	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003104	K+-sensing histidine kinase KdpD	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003087	#N/A	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003262	NADH pyrophosphatase NudC, Nudix superfamily	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003403	ABC-type dipeptide/oligopeptide/nickel transport system, permease component	13.41538756	0.027730034	marine	0.5714	0	0
GC_00003203	ABC-type antimicrobial peptide transport system, permease component	13.41538756	0.027730034	marine	0.5714	0	0
GC_00002379	Rubrerythrin	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002237	Cell division septum initiation DivIVA, interacts with FtsZ, MinD and other proteins	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002124	CDP-diglyceride synthetase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002332	Predicted arabinose efflux permease, MFS family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002329	Uncharacterized membrane protein YdbS, contains bPH2 (bacterial pleckstrin homology) domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002093	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002270	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002039	Uridine kinase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002412	Tetratricopeptide (TPR) repeat	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00001810	Thiamine monophosphate kinase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002306	Chromosome segregation ATPase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00001781	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002251	Beta-lactamase class A	13.39580374	0.027730034	marine	0.7143	0.0769	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00002040	Alkylhydroperoxidase family enzyme, contains CxxC motif	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002086	Membrane proteinase PrsW, cleaves anti-sigma factor RsiW, M82 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002409	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002026	Glutaredoxin	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002336	Signal transduction histidine kinase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002347	Multisubunit Na+/H+ antiporter, MnhB subunit	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002031	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002067	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002315	Anionic cell wall polymer biosynthesis enzyme, LytR-Cps2A-Psr (LCP) family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002216	Serine protease, subtilisin family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002194	3-methyladenine DNA glycosylase Mpg	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002403	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002140	Predicted acetyltransferase, GNAT superfamily	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002188	O6-methylguanine-DNA--protein-cysteine methyltransferase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002032	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002034	Serine/threonine protein kinase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00001947	Sec-independent protein secretion pathway component TatC	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002301	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002061	Pimeloyl-ACP methyl ester carboxylesterase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002263	Primosomal protein N' (replication factor Y) - superfamily II helicase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002383	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002143	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002369	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002367	Ribonuclease HII	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002109	DNA-binding response regulator, NarL/FixJ family, contains REC and HTH domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00001937	DNA-binding transcriptional regulator, AcrR family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002054	DNA-binding transcriptional regulator, LysR family	13.39580374	0.027730034	marine	0.7143	0.0769	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00002107	Peptidoglycan biosynthesis protein MviN/MurJ, putative lipid II flippase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002167	Predicted arabinose efflux permease, MFS family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002406	DNA-binding transcriptional regulator, MarR family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002282	Lysophospholipase, alpha-beta hydrolase superfamily	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002000	ABC-type transport system, periplasmic component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002020	Geranylgeranyl pyrophosphate synthase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002214	Serine/threonine protein phosphatase PrpC	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002284	Predicted endonuclease distantly related to archaeal Holliday junction resolvase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002091	Rhodanese-related sulfurtransferase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002366	Uncharacterized membrane protein YdbS, contains bPH2 (bacterial pleckstrin homology) domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002024	Predicted PurR-regulated permease PerM	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002090	Cytochrome oxidase assembly protein ShyY1	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002046	ABC-type dipeptide/oligopeptide/nickel transport system, permease component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002027	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002023	Ribosome-associated translation inhibitor RaiA	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002295	Cell division septum initiation DivIVA, interacts with FtsZ, MinD and other proteins	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002335	ABC-type oligopeptide transport system, ATPase component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002113	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002344	ABC-type dipeptide/oligopeptide/nickel transport system, permease component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002234	Phosphoglycolate phosphatase, HAD superfamily	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002014	Membrane associated serine protease, rhomboid family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002200	Diacylglycerol kinase family enzyme	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002302	Sortase (surface protein transpeptidase)	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002246	Bacterial cell division protein FtsW, lipid II flippase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002036	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00002262	Serine/threonine protein phosphatase PrpC	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002225	Uncharacterized conserved protein YvlB, contains DUF4097 and DUF4098 domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002230	NADPH-dependent ferric siderophore reductase, contains FAD-binding and SIP domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002215	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002130	Mannosyltransferase related to Gpi18	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002380	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002119	Inorganic triphosphatase YgiF, contains CYTH and CHAD domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002359	Predicted house-cleaning NTP pyrophosphatase, Maf/HAM1 superfamily	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002101	Uncharacterized protein	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002001	Cysteine sulfinate desulfinase/cysteine desulfurase or related enzyme	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002205	ABC-type dipeptide/oligopeptide/nickel transport system, ATPase component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002129	Glycosyltransferase, catalytic subunit of cellulose synthase and poly-beta-1,6-N-acetylglucosamine synthase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002229	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002065	Sensor histidine kinase YesM	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002177	Predicted DNA-binding transcriptional regulator YafY, contains an HTH and WYL domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002111	Predicted esterase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002345	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002172	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002280	LysM repeat	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002042	Uncharacterized membrane protein YvlD, DUF360 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002342	Predicted O-methyltransferase YrrM	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002180	Arginase family enzyme	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002038	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002338	Hydroxymethylpyrimidine pyrophosphatase and other HAD family phosphatases	13.39580374	0.027730034	marine	0.7143	0.0769	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00002070	Uncharacterized conserved protein YabN, contains tetrapyrrole methylase and MazG-like pyrophosphatase domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002035	Redox-sensitive bicupin YhaK, pirin superfamily	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002162	Predicted secreted protein containing a PDZ domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002300	Fermentation-respiration switch protein FrsA, has esterase activity, DUF1100 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002243	Predicted Rossmann fold nucleotide-binding protein DprA/Smf involved in DNA uptake	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002307	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002133	Uncharacterized protein, UPF0548 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002259	Septal ring factor EnvC, activator of murein hydrolases AmiA and AmiB	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002355	Cytoplasmic iron level regulating protein YaaA, DUF328/UPF0246 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002097	Protoporphyrinogen oxidase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002160	UDP-N-acetylenolpyruvoylglucosamine reductase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002258	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002128	Cell division protein DamX, binds to the septal ring, contains C-terminal SPOR domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002304	Cytochrome oxidase assembly protein ShyY1	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002047	Pimeloyl-ACP methyl ester carboxylesterase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002041	Broad specificity phosphatase PhoE	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002033	Nucleotide-binding universal stress protein, UspA family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002015	Porphobilinogen deaminase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002165	Predicted DNA-binding transcriptional regulator YafY, contains an HTH and WYL domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002400	Uncharacterized membrane protein YdcZ, DUF606 family	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002267	Predicted nucleic acid-binding protein, contains Zn-ribbon domain (includes truncated derivatives)	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002150	DnaJ-class molecular chaperone with C-terminal Zn finger domain	13.39580374	0.027730034	marine	0.7143	0.0769	0

Gene Cluster IDs	COG_FUNCTION	Enrichment score	Adjusted p-value (q-value)	Enriched environment	% of marine genomes	% of freshwater genomes	% of soil genomes
GC_00002185	Signal transduction histidine kinase	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002311	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002155	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002377	Uncharacterized conserved protein, DUF58 family, contains vWF domain	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002106	Cell division protein FtsI/penicillin-binding protein 2	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002394	Multisubunit Na+/H+ antiporter, MnhG subunit	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002382	Predicted oxidoreductase (related to aryl-alcohol dehydrogenase)	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002019	Forkhead associated (FHA) domain, binds pSer, pThr, pTyr	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002299	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002231	Glycosyltransferase involved in cell wall bisynthesis	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002249	ABC-type oligopeptide transport system, ATPase component	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002166	Methylase of polypeptide chain release factors	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002075	Hemolysin or related protein, contains CBS domains	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002222	Cell division protein FtsB	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002116	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002126	#N/A	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00002417	Multisubunit Na+/H+ antiporter, MnhE subunit	13.39580374	0.027730034	marine	0.7143	0.0769	0
GC_00001600	Uncharacterized conserved protein YbjT, contains NAD(P)-binding and DUF2867 domains	12.56024896	0.04130569	marine	0.8571	0.0769	0.2857
GC_00001584	F420-0:Gamma-glutamyl ligase (F420 biosynthesis)	12.56024896	0.04130569	marine	0.8571	0.0769	0.2857
GC_00003257	Protein-disulfide isomerase	13.41538756	0.027730034	soil	0	0	0.5714
GC_00003331	Uncharacterized membrane protein	13.41538756	0.027730034	soil	0	0	0.5714

Table A.13 Predicted COG Functions associated with freshwater, soil, and marine environments among 27 *Microbacteriaceae* species. Predicted COG functions, assigned gene cluster ids, enrichment score, adjusted p-value, and percentage of a given environment that were calculated during construction of the pan-genomes of 27 *Microbacteriaceae* species. A gene cluster was labeled associated with an environment or environments if the proportion of genomes in an environment was equal to 1 or the proportion was greater than three times that of other environments. Additionally, a COG function was only labeled as associated with an environment if present in three or more of the genomes for a given environment. COG Functions present in all of the 27 genomes are not reported here.

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
3-methyladenine DNA glycosylase AlkC	5.057005	0.802067	freshwater	GC_00009153, GC_00011002, GC_00021657, GC_00025120	0.3077	0	0
Acetyl-CoA carboxylase beta subunit	3.635541	0.802067	freshwater	GC_00006663, GC_00020391	0.2308	0	0
Alkylated DNA repair dioxygenase AlkB	3.635541	0.802067	freshwater	GC_00005439, GC_00018460	0.2308	0	0
Arginine/lysine/ornithine decarboxylase	3.281557	0.802067	freshwater	GC_00003602, GC_00004612, GC_00006344, GC_00008593, GC_00012885, GC_00014796, GC_00016443	0.4615	0.1429	0.1429
Asparagine synthetase B (glutamine-hydrolyzing)	3.281557	0.802067	freshwater	GC_00004903, GC_00006944, GC_00008268, GC_00011190, GC_00020841, GC_00029931	0.4615	0.1429	0.1429
Cell division protein FtsN	3.635541	0.802067	freshwater	GC_00005712, GC_00011089	0.2308	0	0
Cob(I)alamin adenosyltransferase	3.635541	0.802067	freshwater	GC_00007303, GC_00016384	0.2308	0	0
Dipeptidyl aminopeptidase/acylaminoacyl peptidase	4.746858	0.802067	freshwater	GC_00003677, GC_00003918, GC_00011656, GC_00017285, GC_00017587, GC_00020599, GC_00029460, GC_00030894	0.5385	0.1429	0.1429
Disulfide bond formation protein DsbB	3.635541	0.802067	freshwater	GC_00005060	0.2308	0	0
DNA gyrase inhibitor GyrI	3.281557	0.802067	freshwater	GC_00002727, GC_00011532, GC_00013062, GC_00022094	0.4615	0.1429	0.1429
Ferritin	3.635541	0.802067	freshwater	GC_00005106	0.2308	0	0

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
Fido, protein-threonine AMPylation domain	5.712409	0.802067	freshwater	GC_00005955, GC_00020774, GC_00023073, GC_00024837, GC_00025785, GC_00025802, GC_00030669	0.4615	0.1429	0
Flagellar biosynthesis chaperone FliJ	5.057005	0.802067	freshwater	GC_00005732, GC_00016483, GC_00025161	0.3077	0	0
mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system	4.746858	0.802067	freshwater	GC_00002073, GC_00006842, GC_00010092, GC_00015244, GC_00020507, GC_00023283	0.5385	0.1429	0.1429
Phage-related protein	3.635541	0.802067	freshwater	GC_00006205, GC_00027008	0.2308	0	0
Phosphohistidine swiveling domain of PEP-utilizing enzymes	3.635541	0.802067	freshwater	GC_00003684	0.2308	0	0
Polygalacturonase	3.635541	0.802067	freshwater	GC_00013373, GC_00014192, GC_00027028	0.2308	0	0
Predicted nuclease of the RNAse H fold, HicB family	7.394508	0.802067	freshwater	GC_00002656, GC_00005028, GC_00009044, GC_00023990	0.5385	0	0.1429
Predicted RNA-binding protein, contains PUA-like EVE domain	6.608067	0.802067	freshwater	GC_00003365, GC_00015151	0.3846	0	0
Ribulose kinase	3.635541	0.802067	freshwater	GC_00003993	0.2308	0	0
RNA processing exonuclease, beta-lactamase fold, Cft2 family	3.281557	0.802067	freshwater	GC_00002411, GC_00009994, GC_00019024	0.4615	0.1429	0.1429
Sporulation protein YlmC, PRC-barrel domain family	3.635541	0.802067	freshwater	GC_00006008, GC_00017066	0.2308	0	0
Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain	3.635541	0.802067	freshwater	GC_00004791	0.2308	0	0
Type V secretory pathway, adhesin AidA	3.635541	0.802067	freshwater	GC_00021593, GC_00022062, GC_00025656	0.2308	0	0
Uncharacterized conserved protein YtfP, gamma-glutamylcyclotransferase (GGCT)/AIG2-like family	3.635541	0.802067	freshwater	GC_00013885, GC_00026761, GC_00026977	0.2308	0	0
Uncharacterized Zn-finger protein, UBP-type	3.635541	0.802067	freshwater	GC_00003225, GC_00012664	0.2308	0	0
3-hydroxy-3-methylglutaryl CoA synthase	3.189963	0.802067	soil	GC_00009601, GC_00027840, GC_00031008	0.0769	0	0.2857

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
Adenine-specific DNA methylase	7.922091	0.802067	soil	GC_00005833, GC_00006878, GC_00007761, GC_00009917, GC_00011827, GC_00016058, GC_00017305, GC_00018438, GC_00020018, GC_00020363, GC_00025041, GC_00028200	0.1538	0.1429	0.7143
Glutathionyl-hydroquinone reductase	3.189963	0.802067	soil	GC_00004476	0.0769	0	0.2857
L-lactate permease	3.189963	0.802067	soil	GC_00012599, GC_00022229, GC_00026619	0.0769	0	0.2857
Membrane-bound metal-dependent hydrolase YbcI, DUF457 family	3.189963	0.802067	soil	GC_00012391, GC_00013831, GC_00022427	0.0769	0	0.2857
Metal-dependent hydrolase, beta-lactamase superfamily II	3.189963	0.802067	soil	GC_00007620, GC_00016168, GC_00018521	0.0769	0	0.2857
Mevalonate kinase	3.189963	0.802067	soil	GC_00020372, GC_00021423, GC_00024566, GC_00026222, GC_00026826	0.0769	0	0.2857
Mevalonate pyrophosphate decarboxylase	3.189963	0.802067	soil	GC_00012670, GC_00018647, GC_00026757	0.0769	0	0.2857
Phage head maturation protease	3.189963	0.802067	soil	GC_00014038, GC_00025834, GC_00027833	0.0769	0	0.2857
Phage portal protein BeeE	3.189963	0.802067	soil	GC_00023539, GC_00024978, GC_00027929	0.0769	0	0.2857
Predicted double-glycine peptidase	3.189963	0.802067	soil	GC_00016174, GC_00026502, GC_00029008	0.0769	0	0.2857
Predicted N-acetyltransferase YhbS	3.189963	0.802067	soil	GC_00008368, GC_00017789, GC_00018813	0.0769	0	0.2857
Secreted phosphatase, PhoX family	4.797985	0.802067	soil	GC_00002373, GC_00026817	0.1538	0.1429	0.5714
Uncharacterized conserved protein YdiU, UPF0061 family	6.103663	0.802067	soil	GC_00004872, GC_00028780	0.0769	0	0.4286
Uncharacterized membrane protein YqgA, affects biofilm formation	3.189963	0.802067	soil	GC_00004744	0.0769	0	0.2857
V8-like Glu-specific endopeptidase	7.290878	0.802067	soil	GC_00007075, GC_00007189, GC_00020806, GC_00025794	0.1538	0	0.5714
5-keto 4-deoxyuronate isomerase	3.189963	0.802067	marine	GC_00004771	0.0769	0.2857	0
6-pyruvoyl-tetrahydropterin synthase	3.189963	0.802067	marine	GC_00023151, GC_00023245, GC_00024193	0.0769	0.2857	0
ABC-type enterochelin transport system, ATPase component	10.29196	0.802067	marine	GC_00001896	0.0769	0.7143	0.1429

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
ABC-type enterochelin transport system, periplasmic component	10.29196	0.802067	marine	GC_00005027, GC_00007708, GC_00024844, GC_00025608	0.0769	0.7143	0.1429
ABC-type enterochelin transport system, permease component	10.29196	0.802067	marine	GC_00002349, GC_00003929, GC_00006285, GC_00010480, GC_00025117, GC_00028086	0.0769	0.7143	0.1429
Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase	10.29196	0.802067	marine	GC_00002383, GC_00012418, GC_00029576	0.0769	0.7143	0.1429
Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase	3.189963	0.802067	marine	GC_00002696	0.0769	0.2857	0
Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnG	3.189963	0.802067	marine	GC_00004136	0.0769	0.2857	0
Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnH	3.189963	0.802067	marine	GC_00004812	0.0769	0.2857	0
Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnI	3.189963	0.802067	marine	GC_00004864	0.0769	0.2857	0
Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnL	3.189963	0.802067	marine	GC_00003718	0.0769	0.2857	0
Anion-transporting ATPase, ArsA/GET3 family	3.189963	0.802067	marine	GC_00026716, GC_00027243, GC_00027364	0.0769	0.2857	0
CBS domain	7.290878	0.802067	marine	GC_00003020, GC_00018851, GC_00026661	0.1538	0.5714	0
DNA/RNA endonuclease G, NUC1	6.328871	0.802067	marine	GC_00002286, GC_00004843	0.2308	0.7143	0.1429
Ectoine hydroxylase-related dioxygenase, phytanoyl-CoA dioxygenase (PhyH) family	3.189963	0.802067	marine	GC_00009421, GC_00022865, GC_00027571	0.0769	0.2857	0
Glycine cleavage system regulatory protein	9.522379	0.802067	marine	GC_00002711	0.0769	0.5714	0
GTP-binding protein EngB required for normal cell division	9.643605	0.802067	marine	GC_00004260	0	0.4286	0
Ligand-binding SRPBCC domain	6.781414	0.802067	marine	GC_00005046, GC_00009344, GC_00020683, GC_00028081	0.0769	0.5714	0.1429
Lipoprotein-anchoring transpeptidase ErfK/SrfK	7.922091	0.802067	marine	GC_00004252, GC_00004587, GC_00006315, GC_00010170, GC_00022119, GC_00024015, GC_00030291	0.1538	0.7143	0.1429

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
NAD(P)H-nitrite reductase, large subunit	6.328871	0.802067	marine	GC_00001588, GC_00005184, GC_00006091, GC_00017474, GC_00023188	0.2308	0.7143	0.1429
Phosphoenolpyruvate carboxylase	4.797985	0.802067	marine	GC_00001765	0.1538	0.5714	0.1429
Predicted glycosyl transferase	3.189963	0.802067	marine	GC_00006295, GC_00010870	0.0769	0.2857	0
Predicted NAD/FAD-dependent oxidoreductase	6.103663	0.802067	marine	GC_00006074, GC_00021286, GC_00025753	0.0769	0.4286	0
Predicted RNA-binding protein YlxR, DUF448 family	9.643605	0.802067	marine	GC_00005523, GC_00015136	0	0.4286	0
Predicted transcriptional regulator, contains HTH domain	4.797985	0.802067	marine	GC_00013304, GC_00013317, GC_00019049, GC_00024433, GC_00027648, GC_00028624, GC_00030322	0.1538	0.5714	0.1429
Purine-nucleoside phosphorylase	3.189963	0.802067	marine	GC_00007140, GC_00017251	0.0769	0.2857	0
Ribose 1,5-bisphosphokinase PhnN	3.189963	0.802067	marine	GC_00006728, GC_00008755, GC_00012540, GC_00018205, GC_00019478	0.0769	0.2857	0
Sensor histidine kinase YesM	13.3958	0.644832	marine	GC_00002065	0.0769	0.7143	0
Transcriptional antiterminator	3.189963	0.802067	marine	GC_00005734, GC_00025940	0.0769	0.2857	0
tRNA G46 methylase TrmB	7.922091	0.802067	marine	GC_00001970, GC_00019223	0.1538	0.7143	0.1429
Type I site-specific restriction endonuclease, part of a restriction-modification system	3.189963	0.802067	marine	GC_00011066, GC_00014430, GC_00026796, GC_00029841	0.0769	0.2857	0
Uncharacterized conserved protein, contains NRDE domain	13.3958	0.644832	marine	GC_00005319, GC_00006726, GC_00006976	0.0769	0.7143	0
Uncharacterized conserved protein, DUF849 family	3.189963	0.802067	marine	GC_00017483, GC_00025200, GC_00031004	0.0769	0.2857	0
Uncharacterized membrane protein MutK, may be involved in DNA repair	6.328871	0.802067	marine	GC_00001558	0.2308	0.7143	0.1429
Uncharacterized protein YxjI	3.189963	0.802067	marine	GC_00020105, GC_00027686, GC_00028815	0.0769	0.2857	0
ADP-heptose:LPS heptosyltransferase	4.359993	0.802067	marine, soil	GC_00006544, GC_00007181, GC_00007793, GC_00010334, GC_00020977	0	0.2857	0.2857
ATP-dependent 26S proteasome regulatory subunit	3.856758	0.802067	marine, soil	GC_00005461, GC_00017913	0	0.2857	0.1429
Bacteriophytochrome (light-regulated signal transduction histidine kinase)	1.947775	0.967588	marine, soil	GC_00003135, GC_00011156, GC_00029470	0.0769	0.2857	0.2857

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
cAMP-binding domain of CRP or a regulatory subunit of cAMP-dependent protein kinases	3.476679	0.802067	marine, soil	GC_00006441, GC_00006573, GC_00009575, GC_00013706, GC_00014526, GC_00016287, GC_00016862, GC_00027032	0.0769	0.4286	0.2857
Cytosine/uracil/thiamine/allantoin permease	6.171846	0.802067	marine, soil	GC_00004716, GC_00010130, GC_00016121	0	0.4286	0.2857
DNA-binding response regulator, LytR/AlgR family	4.34161	0.802067	marine, soil	GC_00001897, GC_00014660	0.0769	0.4286	0.4286
Glutathionylspermidine synthase	3.856758	0.802067	marine, soil	GC_00008580, GC_00021954	0	0.2857	0.1429
GTPase, G3E family	3.476679	0.802067	marine, soil	GC_00005871, GC_00012167, GC_00017963, GC_00021903, GC_00027385	0.0769	0.2857	0.4286
Histidinol phosphatase or a related phosphatase	3.856758	0.802067	marine, soil	GC_00007262, GC_00027760	0	0.1429	0.2857
Hydroxyethylthiazole kinase, sugar kinase family	7.417734	0.802067	marine, soil	GC_00001569	0.0769	0.5714	0.5714
Murein tripeptide amidase MpaA	3.476679	0.802067	marine, soil	GC_00005690, GC_00015862, GC_00019972, GC_00023774, GC_00025929, GC_00026180	0.0769	0.2857	0.4286
Na+dependent transporter, SNF family	5.828346	0.802067	marine, soil	GC_00002005, GC_00005337	0.0769	0.5714	0.2857
NADH:ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na□ antiporter, MnhA subunit	3.856758	0.802067	marine, soil	GC_00025064, GC_00025199, GC_00028816	0	0.1429	0.2857
Phage-related tail protein	3.856758	0.802067	marine, soil	GC_00011942, GC_00015577, GC_00024763	0	0.1429	0.2857
Phosphoheptose isomerase	3.856758	0.802067	marine, soil	GC_00008920, GC_00027579	0	0.1429	0.2857
Predicted choloylglycine hydrolase	4.359993	0.802067	marine, soil	GC_00002236	0	0.2857	0.2857
Predicted glycoside hydrolase or deacetylase ChbG, UPF0249 family	3.856758	0.802067	marine, soil	GC_00006337, GC_00027467	0	0.2857	0.1429
Queuine/archaeosine tRNA-ribosyltransferase	3.856758	0.802067	marine, soil	GC_00007740, GC_00030427	0	0.1429	0.2857
Radical SAM superfamily enzyme, MoaA/NifB/PqqE/SkfB family	3.856758	0.802067	marine, soil	GC_00005682, GC_00014338, GC_00019757	0	0.2857	0.1429
S-ribosylhomocysteine lyase LuxS, autoinducer biosynthesis	5.828346	0.802067	marine, soil	GC_00002028, GC_00017484	0.0769	0.5714	0.2857
Secreted trypsin-like serine protease	3.856758	0.802067	marine, soil	GC_00007305, GC_00007306, GC_00014822, GC_00015953, GC_00016649	0	0.2857	0.1429
Sensor histidine kinase, LytS/YehU family	3.476679	0.802067	marine, soil	GC_00001888	0.0769	0.2857	0.4286

COG Function	Enrichment Score	Adjusted q-value	Associated Groups	Gene Cluster IDs	% of freshwater genomes	% of marine genomes	% of soil genomes
Toxin component of the Txe-Axe toxin-antitoxin module, Txe/YoeB family	6.171846	0.802067	marine, soil	GC_00002493	0	0.2857	0.4286
TRAP-type C4-dicarboxylate transport system, small permease component	1.947775	0.967588	marine, soil	GC_00011513, GC_00021314, GC_00021577, GC_00022256, GC_00026114, GC_00029417	0.0769	0.2857	0.2857
TRAP-type uncharacterized transport system, periplasmic component	7.16388	0.802067	marine, soil	GC_00004068, GC_00018113, GC_00025394, GC_00028965	0	0.4286	0.4286
Uncharacterized conserved protein YcbX, contains MOSC and Fe-S domains	6.129789	0.802067	marine, soil	GC_00006956, GC_00006957, GC_00007596, GC_00012235, GC_00030798	0.0769	0.5714	0.4286
Uncharacterized conserved protein YjdB, contains Ig-like domain	3.476679	0.802067	marine, soil	GC_00005422, GC_00006689, GC_00007110, GC_00022960, GC_00028898, GC_00030075	0.0769	0.2857	0.4286
Uncharacterized domain/protein associated with RNAses G and E	5.828346	0.802067	marine, soil	GC_00002808, GC_00018863, GC_00023116	0.0769	0.5714	0.2857
Uncharacterized inner membrane protein YnfA, drug/metabolite transporter superfamily	3.856758	0.802067	marine, soil	GC_00003711	0	0.2857	0.1429
Uncharacterized membrane protein YbhN, UPF0104 family	3.856758	0.802067	marine, soil	GC_00021890, GC_00025874, GC_00029972, GC_00030604	0	0.2857	0.1429
Uncharacterized membrane protein YdjX, TVP38/TMEM64 family, SNARE-associated domain	1.947775	0.967588	marine, soil	GC_00008938, GC_00009461, GC_00026566, GC_00029320	0.0769	0.2857	0.2857
Uncharacterized membrane protein YoaT, DUF817 family	6.171846	0.802067	marine, soil	GC_00002980, GC_00017042	0	0.2857	0.4286