Virulence determinants of Lactococcus garvieae, an important pathogen of trout

Rosemarie Billenness, BVMedSci (Hons) ID: 4309279

Thesis submitted to the
University of Nottingham
for the degree of
Master of Research

April 2018

Abstract

Lactococcus garvieae is a common pathogen in global aquaculture and has also been isolated as the causative agent of bovine mastitis and in gastrointestinal disorders in humans, where lactococcosis is considered an emerging disease. In aquaculture, the disease manifests with septicaemia, nervous and cutaneous pathology and death in multiple fish species. Outbreaks can cause up to 100% mortality in rainbow trout populations, and the subsequent impact on food production and potential contamination of food for human consumption make devising effective methods to diagnose and control the disease even more important for both human and animal health. Compounding this is the relative lack of knowledge on the virulence factors involved in *L. garvieae* pathogenesis, its ubiquitous nature in the aquaculture environment and the difficulties involved in differentiating the disease from streptococcal infections with similar clinical manifestations.

Pragmatic Insertion Mutant Mapping System (PIMMS) is a transposon insertion sequencing and mapping based strategy which enables identification and comparison of genes which are important for Gram-positive bacterial growth in different environmental conditions using the mutagen pGhost9:IS*S1*. PIMMS was successfully used to interrogate an *L. garvieae* 02106 bacterial mutant library to determine which genes were essential for bacterial replication in media and those essential for bacterial growth in fish serum. 398 genes were identified as essential for the growth of *L. garvieae* after screening in fish serum, the majority involved in bacterial metabolism. Various bioinformatic platforms were employed to further categorise these by functional group and to identify genes with potential involvement in virulence which could form useful vaccination candidates, diagnostic markers or therapeutic targets. Ultimately four genes

were identified: *divIB, spsB, ancA* and the hypothetical protein LAG_00167 which were extracellular or cell-wall associated, conserved amongst other *L. garvieae* bacterial strains and may provide targets for future targets for therapeutic intervention, prophylaxis or diagnostic test development. Additionally a number of essential metabolic pathways and additional genes of interest were also identified that may also provide alternate control and diagnostic strategies.

This study has identified a number of putative virulence factors for *L. garvieae* infections in the fish host, with the findings relevant to the aquaculture industry, veterinary intervention strategies for fish and cattle health and with potential human food safety implications, where protection of the consumer is paramount in reducing the risk of zoonotic disease.

Acknowledgements

I would like to firstly thank the University of Nottingham, School of Veterinary Medicine and Science for giving me the opportunity to undertake research within my veterinary degree, and providing both generous funding and excellent facilities to allow me to do so.

Special thanks go to my supervisors Dr Sharon Egan, for her constant and encouraging input and advice both inside and outside the lab, and Professor Jamie Leigh for his wealth of knowledge and for pushing my thoughts in new directions. For patiently answering countless queries on the vast, technical and novel area of bioinformatics including the use of much of the software involved in my work, I extend thanks to Dr Adam Blanchard and Mr Andrew Warry. I would also like to thank Dr Sabine Tötemeyer, Dr Tracey Coffey, Dr Julia Kydd and Miss Emma Drinkall for their positivity and chats over tea, and to the other post-graduate students for brightening many a computer-based day in the office.

On a personal level, I cannot express my gratitude enough for the unwavering presence of my family, at home or away. To Nan, I hope I made you so proud.

Table of Contents

Abstract i

Acknowledgements iii

Table of Contents iv

1.0 Introduction 1

1.1 The aquaculture industry 1

1.1.1 Common species in aquaculture 3

1.1.2 Trout farming in the UK 3

1.1.3 Important infectious diseases in trout production 6

1.1.4 The immune system of fish 8

1.1.5 Vaccination against bacterial disease in aquaculture 9

1.1.6 Use of antimicrobial drugs in aquaculture 11

1.2 *Lactococcus garvieae* 12

1.2.1 Lactococcosis 12

1.2.2 Diagnosis of *L. garvieae* infection 14

1.2.3 Current control strategies against *L. garvieae* 14

1.2.4 Virulence determinants of *Lactococcus garvieae* 17

1.2.4.1 Capsule 17

1.2.4.2 Toxin-associated proteins 18

1.2.4.3 Adhesion 18

1.3 Identifying bacterial virulence determinants and their functions 19

1.3.1 Essential genes 19

1.3.2 Transposon insertion sequencing 19

1.3.3 Pragmatic Insertional Mutation Mapping (PIMMS) 27

1.3.4 Predicting the function of bacterial genes 29

1.4 Summary 30

1.5 Aims and Objectives 32

2.0 Materials and Methods 33

2.1 Bacterial strains and growth 33

2.2 Extraction of chromosomal DNA from *L. garvieae* 33

2.3 Extraction of pGh9 plasmid from *S. uberis* 34

2.4 Quantification of DNA concentration 34

2.5 Separation of DNA by gel electrophoresis 35

2.6 Purification of reaction products 35

2.7 Amplification of regions of interest by PCR 35

2.8 Restriction endonuclease digestion of DNA 37

2.9 Inverse PCR analysis of pGh9:*ISS1* element flanking regions 37

2.10 Ligation of fragments post-digestion 37

2.11 De-salting of DNA prior to electroporation 38

2.12 Electroporation of *E. coli* 38

2.13 Bioinformatic analysis 38

3.0 Results 39

3.1 Analysis of pGh9 integration within *L. garvieae* individual mutants 39

3.2 PIMMS analysis of *L. garvieae* before and after growth in salmonid serum 43

3.3 Essential genes in the *L. garvieae* genome 47

3.4 Analysis of essential genes for *L. garvieae* growth in the input and output pools 49

3.5 Essential genes identified as unique to either input or output pools 53

3.6 Truncated sequences important for *L. garvieae* growth 57

3.7 Analysis of subcellular location of genes essential for growth in fish serum 60

3.8 Homology of the essential genes of *L. garvieae* 64

3.9 Involvement of essential genes in metabolic pathways 71

3.10 Further investigation of LAG_00167 and *ancA* 77

3.11 Development of site-directed mutagenesis for genes of interest 81

4.0 Discussion 85

4.1 PIMMS based analysis of genes essential for *L. garvieae* growth 85

4.2 Analysis of genes determined to be essential for *L. garvieae* survival... 88

4.3 Investigating *divIB, spsB, ancA,* and LAG_00167 as important genes in the virulence of *L. garvieae* 02106 in fish 98

4.4 Future work 104

4.5 Conclusion 106

References 109

Appendices 133

Appendix 1 133

Appendix 2 134

Appendix 3 173

1.0 Introduction

1.1 The aquaculture industry

With the prospect of feeding a global population of 8.5 billion people by 2030, the world's agricultural industry is under ever-increasing pressure to be more productive, resourceful and environmentally conscious. Only 30% of the world's surface has land coverage, and not all of this land is suitable or available for use in arable or pastoral farming (Melorose, Perroy and Careas, 2015). With an anticipated 100% increase in demand for food over the next decade, farming for aquatic sources of protein such as fish and aquatic molluscs could present a solution (Ma, Khan and Miyan K, 2011). These practices can utilise regions not suitable for other farming techniques and also offer other significant advantages over land-based pastoral farming (Troell *et al.*, 2014). Capture-based fishing remains unsustainable due to continued depletion of ocean fish stocks, but aquaculture in either caged marine environments or land-based establishments could pose a plausible solution for some of the problems facing food production in the coming decades (Melorose, Perroy and Careas, 2015). Compared to most domestic species, fish have a higher feed conversion rate and hence a reduced requirement for feed to achieve the same weight gain in a set time period (Besson *et al.*, 2014). For example, the average feed required for Norwegian Atlantic Salmon to gain 1 kg of bodyweight is around 1.15 kg of feed, but on average a pig or lamb would require 2.63 kg or 6.30 kg of feed for the same weight gain, respectively (Ytrestøyl, Aas and Åsgård, 2015).

Fish are relied upon as the primary source of dietary protein for over 1 billion people across the globe, with the majority consumed in developing countries (FAO, 2015). Their importance as part of the global diet is illustrated by the annual 3% increase in food fish intake per person per year in the last decade,

equating to the average person consuming around 10.4kg of food fish per year. From an economic perspective, the global catch has an estimated value of over US$160 billion, with freshwater fisheries increasing the overall value of the industry even further (FAO, 2015). Aquaculture can be undertaken in any water type, from freshwater through to seawater dependent on the species farmed and additional efficiency can be gained by using mixed fish populations or by co-culture with farmed domestic species or crops including rice and vegetables (Ma, Khan and Miyan K, 2011).

As of 2015, the Food and Agriculture Organisation of the United Nations (FAO) had 201 registered countries and territories producing food through aquaculture (FAO, 2015). The aquaculture industry represents an essential source of financial income and employment, particularly across Africa and Asia. These continents have experienced the greatest growth and activity in aquatic animal production, with African countries experiencing a 10% increase in aquaculture production in the last 7 years, whilst 90% of the world's aquaculture produce is currently from countries across Asia (FAO, 2015). Indeed, whilst capture-based systems have experienced just 1.2% annual growth since 1970, aquaculture has become the fastest-growing sector of the global food production industry, with annual growth averaging at 8.9% in the same period (Subasinghe, 2005). In the EU, it is the UK, France, Greece, Spain and Italy that generate most of the aquaculture production by value and volume. The UK generates over 22% of the value of EU aquaculture, and nearly 17% of its volume at 203,263 tonnes, the majority of which is through salmon and trout farming (European Commission, 2016).

1.1.1 Common species in aquaculture

Species cultivated in aquaculture facilities can be divided into four main groups: finfish, crustacea, molluscs and other aquatic animals such as sea urchins. The production of finfish dominates the industry on all continents (FAO, 2015).

In the EU, salmon, trout and seabream together contribute nearly 50% of the value of the industry (European Commission, 2016). In the UK aquaculture predominantly occurs in Scotland, where over 168,000 tonnes of finfish were produced in 2012 to a value of over £500 million. The dominant species farmed is Atlantic salmon, which contributes 80% of the volume and 89% of the value to UK aquaculture as a whole. Trout (rainbow, sea and brown) are also extensively farmed across the UK and are the third highest group of aquaculture species in terms of value and volume in the UK after salmon and mussel (European Commission, 2016). In England and Wales rainbow trout and sea or brown trout contribute over 8,300 tonnes of production every year, with emerging business being seen in farming tilapia and Atlantic char (Ellis et al., 2012). Water temperature is important for maximising production of different fish varieties, with waters less than 21°C supporting cold-water species such as trout and salmon compared to waters exceeding this temperature which are more suited to species such as tilapia, carp and bass (Balayut, 1989; FAO, 2015).

1.1.2 Trout farming in the UK

Trout belong to the Salmonidae family along with salmon and char. The most well-known trout species include brown and sea (variants of *Salmo trutta*), lake (*Salvelinus namaycush*), and rainbow (*Oncorhynchus mykiss*) varieties. Rainbow trout are native to lakes and rivers in the west of the USA and have become a popular sport and market fish after their introduction to a further 82 countries

worldwide, including the UK (Figure 1.1) (Halveson, 2011). Commercial strains of rainbow trout have been developed to offer different advantageous qualities, from improved hardiness and disease resistance, to improved growth rates in farm environments (Wong and Zohar, 2015). These advantages come about through polyploidy, which is the means by which most farmed trout are made reproductively sterile. Sterility ensures that more energy is retained for growth and not diverted towards gonadal development and prevents genetic contamination of native wild populations (Xu *et al.*, 2015). However, trout farming is not without its difficulties. The increased growth rates of polyploidy fish can contribute to musculoskeletal deformity, which can result from environmental factors (Amoroso *et al.*, 2016). Whilst rainbow trout are able to tolerate a wide array of environmental conditions (setting them apart from other trout species), four fundamental habitat factors are required for optimal growth of trout in any water body: cold water; clear water; clean water; and water with adequate dissolved oxygen (Woynarovich, Hoitsy and Moth-Poulsen, 2011). Stocking density has also been identified as a key factor in determining both welfare and productivity in commercial fish farms. In rainbow trout, a stocking density of over 30kg m^{-3} is suggested to lead to increased stress, reduced water oxygen levels and increased rates of fin erosion (North *et al.*, 2006). By fulfilling these requirements and optimising the use of autumn- or spring-spawning strains, there is maximal year-round production of the species in farms across the UK (Woynarovich, Hoitsy and Moth-Poulsen, 2011).

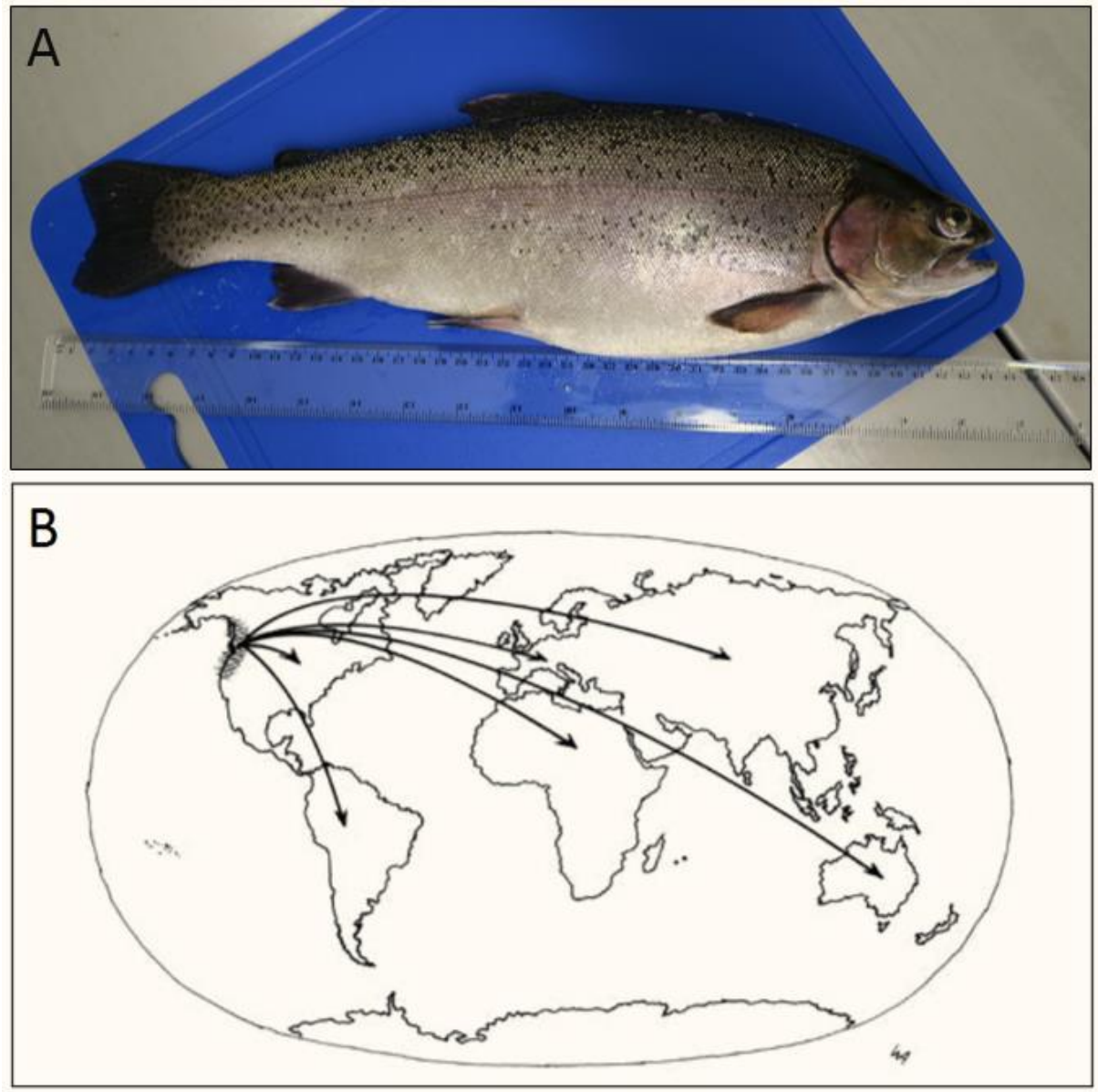


Figure 1.1 The rainbow trout and its global distribution.

A) The typical adult rainbow trout weighs 2-3kg and around 40cm in length. The species can be distinguished by their colourful markings, ranging from silver-green dorsally to pink along the lateral line and many irregular dark spots across the skin. The tail is almost square with a slight fork.

B) Trout originated from North America and have since been transported and farmed across the globe for food and sport. Whilst they inhabit colder upper sections of rivers and oceans they can also tolerate temperate climates in Australia and South Africa (Woynarovich, Hoitsy and Moth-Poulsen, 2011).

1.1.3 Important infectious diseases in trout production

As in other species, infectious diseases in fish can be viral, bacterial, fungal, parasitic, or protozoal. The diagnosis of infection mainly relies on observation of clinical signs within the fish population and subsequent detection of the causative agent with an antibody, PCR or genetic test. Other diagnostic techniques include histology, cell culture to identify viral infection and culture in bacteriological media to confirm bacterial infection (Noga, 2010). Systemic viral disease is common but is not treatable, and can only be prevented by careful management and immunisation protocols where available. Common viral infections of salmonids including rainbow trout are Infectious Pancreatic Necrosis (IPN), and Infectious Hemopoietic Necrosis (IHN), both of which are most serious in rainbow trout cultured in freshwater, with young salmonids also susceptible to Viral Hemorrhagic Septicaemia (VHS) (Noga, 2010). Vaccination can be carried out to control IPN using recombinant DNA technology, although this is not commonly performed in rainbow trout (Christie, 1997; Bostock *et al.*, 2010). Against IHN and VHS, DNA vaccines are efficacious, with more conventional killed or live vaccines being much less effective in the aquaculture environment (Anderson *et al.*, 1996; Kim *et al.*, 2000).

Aquatic bacteria pose a particular problem as they are frequently ubiquitous in the environment and are capable of surviving independent of a host. Hence re-infection after successful antibiotic usage is highly likely, making bacterial infection cost the aquaculture industry up to several billion dollars every year (Austin and Austin, 2012, Pridgeon, 2012). Many of these bacteria, such as *Aeromonas* spp., *Streptococcus* spp.*,* and *Lactococcus* spp. are opportunistic pathogens; where fish experiencing stressors such as limited resource availability or varying water temperature, show a dramatically increased risk of

infection (Austin and Austin, 2012). Of the Gram-negative bacterial infections in aquaculture, *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Chryseobacterium* sp., *Flavobacterium* spp., *Pseudomonas* and *Vibrio* spp affect trout. Infection with *Aeromonas salmonicida,* which classically causes furunculosis, is one of the most common and important diseases in salmonids, but rainbow trout demonstrate a greater degree of intrinsic resistance to this disease compared to Atlantic salmon and brown trout (Cipriano, Ford and Jones, 1994; Noga, 2010; Pridgeon, 2012; Yáñez, Houston and Newman, 2014).

Multiple Gram-positive cocci (GPC) are responsible for disease in freshwater and marine fish species. Seven GPC pathogenic to fish species such as trout include *Streptococcus iniae, S. parauberis, S. agalactiae, Lactococcus piscium, L. garvieae*, and *Vagococcus salmoninarum* (Pridgeon, 2012).

Streptococcal infections (including those caused by closely-related genera *Lactococcus, Vagococcus,* and *Enterococcus*) of rainbow trout manifest as fatal haemorrhagic septicaemia with lethargy, anorexia, dark skin pigmentation, erratic swimming and exophthalmos being common clinical signs. The bacterial species can be crudely differentiated using environmental temperature: *Vagococcus salmoninarum* and *L. piscium* generally cause disease at temperatures below 15°C, whereas *L. garvieae*, *S. iniae, S. agalactiae* and *S. parauberis* infections generally cause septicaemic disease in water temperatures above 15°C. Otherwise, distinguishing these bacteria as causative agents of disease is difficult without molecular testing. *S. iniae, S. parauberis,* and *L. garvieae* are also considered pathogens in marine aquaculture (Meyburgh *et al*., 2017). Streptococcal infections are further significant as zoonoses, with *S. agalactiae* and *S. iniae* posing particular risk of infection to human populations

from the aquaculture industry (Agnew *et al.*, 2007; Fulde *et al.*, 2013; Gibello *et al.*, 2016).

1.1.4 The immune system of fish

Teleost fish comprise over 90% of known fish species in the globe, however their immune system and response to infectious disease is not as well characterised as their mammalian counterparts. Compared to mammals, some differences stem from the organs involved in the immune response in fish. Both utilise the thymus, spleen and mucosa-associated lymphoid tissue (MALT), but in fish MALT also includes the gills. More notable differences include the complete lack of both bone marrow and lymph nodes in fish, which are key immunological components and organs in the mammalian body. Instead, the teleost kidney has a major lymphoid role and is structurally organised very differently in fish compared to the same organ in mammals. The teleost kidney is considered to have multiple compartments both anatomically and functionally. The most relevant division when considering the immune response is the 'head kidney' and 'tail kidney' denoting their relative locations in the retroperitoneal space. The head kidney has the major immunological role and lacks excretory tissue with the parenchyma spread across a system of sinusoids supported by the kidney stroma. Sinusoids are lined by endothelial cells and covered with phagocytic reticular cells, with the stroma playing a role in non-specific immunity and clearing cellular debris. The head kidney is also the major site of antibody production in the specific immune response, and macrophages associated with the sinusoids are able to maintain memory of specific antigens for months after exposure by infection or vaccination (reviewed by Press and Evensen, 1999). Given the ability to induce both antibody and cell mediated responses the use of

vaccination to protect fish populations from disease can and has been very effective for a number of infectious diseases important in aquaculture.

A typical immune response in fish initially involves the non-specific action of the skin, gills and gut (MALT), after which blood-borne pathogens or debris can be filtered out via the kidney and spleen whilst exposing populations of leukocytes to their associated antigens and inciting a specific immunoglobulin, or antibody, response. Differences also arise here, as the immunoglobulin (Ig) classes utilised by fish are not consistent with those in the mammalian immune system when challenged by pathogens. In mammals, five immunoglobulin types are described, but in fish only three have been identified: IgM, IgD, and IgT. IgM and IgD are ubiquitous in most classes of vertebrates, but IgT is specific to fish, and is found in most model teleost species including rainbow trout (Zhang *et al.*, 2010). Whereas IgM is regarded as being uniquely involved in both systemic and mucosal immune responses, IgT has been found to elicit a purely mucosal response with increased numbers of IgT+ B cells found in the gut of parasite-challenged fish, whereas the IgM response was confined to serum (Zhang *et al.*, 2010; reviewed by Mashoof and Criscitiello, 2016). These differences could be critical to designing effective prophylaxis against specific pathogens in fish.

1.1.5 Vaccination against bacterial disease in aquaculture

Most infectious disease control in aquaculture can be successfully managed or prevented with good husbandry, including regular checks of water quality, debris accumulation and stocking density, previously highlighted as important elements in successful rainbow trout farming (Austin and Austin, 2012). Genetically resistant stock can be utilised in areas where disease is enzootic, although this strategy is not yet widely implemented and specific prophylaxis may still be required against particular pathogens (Austin and Austin, 2012). Vaccination has

become commonplace in aquaculture units over the last 30 years in order to control various bacterial infections (Sommerset *et al.*, 2005; Pridgeon, 2012). These vaccines come in six general types: bacterins, containing killed bacteria such as the USA *Aeromonas salmonicida* vaccine; attenuated live bacterial vaccines such as those for *Edwardsiella*; toxoid vaccines containing inactive toxins instead of whole bacteria; subunit vaccines typically containing a protein subunit of bacteria and not whole organisms; conjugated vaccines where a bacterial protein is joined to other immune-stimulating proteins; and experimental DNA vaccines such as those containing DNA or recombinant vector vaccines (reviewed by Pridgeon, 2012). Bacterins and attenuated live bacterial vaccines are most commonly used in aquaculture, although attenuated, live vaccines usually stimulate a greater immunoglobulin response and are considered to confer a greater level and length of protection from disease than bacterin-based vaccines (Pridgeon, 2012). Those against edwardsiellosis, enteric redmouth disease (ERM), furunculosis, Hitra disease and vibriosis are all in commercial use. Vaccinations in aquaculture can be administered by individual injection, orally via food or by immersion bath techniques depending on the pathogen, vaccine formulations available and user preference (Defoirdt, Sorgeloos and Bossier, 2011; Austin and Austin, 2012). Individual injection can be preferred in select groups of important fish such as broodstock, however in-feed or immersion techniques are far less time-consuming and labour-intensive for protecting thousands of individual fish and may be preferable methods for all forms of mass drug administration.

1.1.6 Use of antimicrobial drugs in aquaculture

Control of bacterial infections can also be undertaken using antimicrobial based approaches, however long-term use and administration has implications for food safety and antimicrobial resistance. Many antimicrobial agents, including oxytetracycline, beta-lactams such as amoxicillin, and more recently florphenicol are being routinely used to combat many bacterial infections of fish (Michel, Kerouault and Martin, 2003). Unfortunately, the narrow spectrum of drugs used to treat bacterial infections in aquaculture include those that are also important for human medicine, with transfer of resistance to potential human pathogens presenting an additional risk to public health. Resistance determinants for tetracyclines, quinolones, and beta-lactams, all of which are vital in human medicine, have been found to be shared between aquatic bacteria, fish pathogens and human pathogens, where it has been indicated that resistance originated in the aquatic environment before spreading (Cabello *et al.*, 2013). 80% of antibiotic used in aquaculture facilities reach the environment in active form as a water contaminant (Cabello *et al.*, 2013), which can select for resistance elsewhere. Furthermore, antibiotic residues in water present a threat to food safety. To minimise this risk, specific withdrawal times for each drug must be adhered to in order to protect the consumer, however this can prolong the harvest of fish from the aquaculture system which has an economic impact (Romero, Feijoó and Navarrete, 2012). An additional compounding issue with antimicrobial use is that bacteria are often ubiquitous in the environment, so cessation of treatment with antimicrobials often leads to rapid re-infection. The combined impact of risk to food safety, environmental and human health is a motivation for greater research into vaccine development and alternative

methods of disease control (Defoirdt, Sorgeloos and Bossier, 2011; Wendlandt *et al.*, 2015).

1.2 *Lactococcus garvieae*

1.2.1 Lactococcosis

Lactococcus garvieae is a Gram-positive coccoid bacterium. It is a prominent pathogen in fish and an emerging pathogen in mastitis cases in the dairy industry, as well as being considered a potential zoonosis with increasing reports of infection in humans (Chan *et al.*, 2011; Gibello *et al.*, 2016; Meyburgh, Bragg and Boucher, 2017). Immunocompromised individuals and those with pre-existing gastrointestinal disease are particularly at risk after ingestion of raw fish, with recovery from the resulting gastrointestinal disease tending to be slow and reliant on the successful implementation of β-lactam based antibiotic protocols (Zuily, Mami and Meune, 2011; Rasmussen *et al.*, 2014). Rarely, infection has been found to cause infective endocarditis which can subsequently lead to intracranial haemorrhage and much increased risk of death (Zuily, Mami and Meune, 2011; Rasmussen *et al.*, 2014).

Studies have identified the bacterium in a number of other sources, namely milk and in cases of mastitis in cattle, as well as in soil and vegetable matter (Kawanishi *et al.*, 2007; Leigh *et al.*, 2010; Miyauchi *et al.*, 2012a; Moumene *et al.*, 2016; Altin, Nikerel and Şahin, 2017). Epidemiologically-related strains, for example those from different species in aquaculture and those from cow and buffalo samples, display close relation to each other within similar host species groups, but have been found to be relatively distinct between species (Vela *et al.*, 2000).

The disease in fish manifests in the form of a fatal hyperacute, haemorrhagic septicaemia, similar to infections caused by other Gram-positive cocci such as

Streptococcus and *Enterococcus* genera (Vendrell *et al.*, 2006; Austin and Austin, 2012). Other clinical signs include enteritis, exophthalmos, meningoencephalitis, subcutaneous haemorrhage, erratic swimming, congestion of many internal organs and ultimately death. The disease severely affects rainbow trout, where outbreaks have led to up to 98% mortality (Vendrell *et al.*, 2006; Meyburgh, Bragg and Boucher, 2017), whereas turbot and sea bass do not tend to develop as severe clinical signs (Vendrell *et al.*, 2006; Türe et al., 2014). However, when many different species of fish were infected with an *L. garvieae* strain from an English outbreak of lactococcosis in rainbow trout, bacteria could be isolated from internal organs of every species used, including Atlantic salmon, brown trout and even seven species of non-salmonid species, cyprinids. This suggests that these fish species, despite demonstrating variable susceptibility to disease, may still pose a threat to susceptible fish species as carriers of the bacterium (Verner-Jeffreys *et al.*, 2011). It has been shown that infection can be achieved experimentally through submersion in contaminated water (Avci *et al.*, 2014). Outbreaks have occurred on rainbow trout farms most commonly in Italy, and also in the United States, Australia, South Africa, Japan, Korea, Taiwan, Iran, Israel, Bulgaria, Greece, Spain, Portugal, and England (Meyburgh, Bragg and Boucher, 2017). *L. garvieae* is classed as a 'warm water pathogen', thriving at temperatures above 21˚C and the prospect of climate change with warmer water temperatures increases the risk of future outbreaks in fish populations worldwide.

With the potential severity of an outbreak, its importance as a zoonosis, and the potential for increased disease incidence in future, *L. garvieae* poses a significant economic and welfare threat to the aquaculture industry and potential risk to human health (Eldar and Ghittino, 1999; Vendrell *et al.*, 2006).

1.2.2 Diagnosis of *L. garvieae* infection

Clinical lactococcosis is difficult to distinguish from streptococcal infections in the field, due to the indistinguishable clinical signs demonstrated by fish infected with these closely-related species. Where biochemical tests exist to identify which species of Gram-positive coccus is the cause of infection, these typically only have poorly discriminatory power between bacterial species (Vendrell *et al.*, 2006). The issue is compounded by there being only relatively few examples of reference isolates from diseased fish in databases. Currently PCR assays are the most common method employed to specifically identify and differentiate *L. garvieae* from *L. lactis*, *Streptococcus* and *Aeromonas* spp, with previous success seen with those using the 16S-23S rRNA internal transcribed spacer (ITS) region, and the 16S rRNA genes pLG-1 and -2 using (Zlotkin *et al.*, 1998; Dang *et al.*, 2012). Using 16S rRNA gene sequencing and analysis of various biochemical tests has additionally made identification of different strains possible. Biochemical testing can include observing the ability of the microorganism to oxide or utilise compounds from different carbon sources, with this principle leading to the design of test kits which enable the user to perform these studies with relative ease. Such techniques have been used to differentiate isolates of bacterial species such as *L. garvieae* and *S. iniae*, showing significant improvement in this area for identifying Gram-positive cocci (Verner-Jeffreys *et al.*, 2011).

1.2.3 Current control strategies against *L. garvieae*

As for other bacterial infections, antibiotics have widely been used in the control of lactococcal infections in fish, and in any human infection with the bacterium (Kawanishi *et al.*, 2005; Zuily, Mami and Meune, 2011). These compounds are usually administered orally with feed. Whilst antibiotics such as oxytetracycline,

erythromycin, and amoxycillin are highly effective against *Lactococcus* in rainbow trout (Kawanishi *et al.*, 2005), infected fish tend to be anorexic and thus ingestion and treatment success are much reduced (Bercovier, Ghittino and Eldar, 1997).

The risk to future treatment success, as with all Gram positive infections, depends in part on preventing resistance to commonly-used antibiotics, particularly of the β-lactam class which are currently used in aquaculture units, but also form the current mainstay of treatment in humans (Wang *et al.*, 2007). The development of antimicrobial resistance in bacteria has become a global health concern and *L. garvieae* has not been exempt from this. Genes conferring resistance to tetracyclines, erythromycin, and lincomycin have all been confirmed in isolates of *L. garvieae*, and multiple resistance to more than one antimicrobial in a single isolate has also been identified (Kawanishi *et al.*, 2005; Maki *et al.*, 2008; Flórez *et al.*, 2012). In streptococcal pathogens of fish, resistance is mainly transferred via plasmid exchange, and R plasmids containing the resistance genes *ermB* and *tet*(S) from erythromycin-, lincomycin-, and oxytetracycline-resistant *L. garvieae* isolates have all been characterised (Meyburgh, Bragg and Boucher, 2017). As a result, there is a need for alternative chemotherapeutic and preventative drugs to combat outbreaks of *L. garvieae* in fish stocks.

One more recently explored option for management of lactococcosis is administration of endogenous probiotics with inhibitory activity against *L. garvieae*, which could offer a viable alternative to using chemical drugs against the disease. One study found that administration of specific gut-derived strains of *L. lactis* and *L. sakei* in feed significantly decreased mortality resulting from *L.*

garvieae infection, representing an additional non-antibiotic source of management against lactococcosis (Pérez-Sánchez *et al.*, 2011).

Whilst probiotics show promise for future control of lactococcosis in aquaculture, vaccination is currently considered the optimal control method against the disease. Commercial vaccines are available for most major diseases of fish (Sommerset *et al.*, 2005), with AMALIN™ Rensa being one available licensed vaccine for lactococcosis in yellowtail, amberjack and hiramasa. This is an inactivated vaccine for oral administration and has the benefit of zero withdrawal time in these species (MSD Animal Health, 2017). Experimental bivalent vaccines against *L. garvieae* and *A. hydrophila* have been shown to be effective; comparing intra-peritoneal vaccination with adjuvanted and aqueous preparations against a negative control in 635 rainbow trout which had been experimentally infected with *L. garvieae* TW446.B3, zero mortality was observed when challenged 30 days from vaccination. The non-vaccinated groups experienced 70% after challenge 30 days from vaccination. In terms of relative percentage survival rate (1 - (% mortality in vaccinated fish/% mortality in controls) x 100), the aqueous vaccine demonstrated 100% relative survival after the 30 day challenge, and the adjuvanted vaccine showed 95% relative survival (Bastardo *et al.*, 2012). Adjuvanted vaccines have been shown to offer protection for up to 8 months (Ravelo *et al.*, 2006). Multiple studies have shown subunit vaccines to elicit a greater degree of protection than whole bacterial vaccines in fish (Ra *et al.*, 2009; Zhou *et al.*, 2010), however there are few reports of their use against lactococcal species. A major limiting factor in vaccine development against *L. garvieae* is the lack of studies reporting the pathogenic mechanisms of the bacterium. However, advancements in genetic sequencing

offer potential for further developments in this field, and the knowledge of the major virulence factors in the species will broaden knowledge of this area.

1.2.4 Virulence determinants of *Lactococcus garvieae*

Factors which have already been identified as important for virulence of various strains of *L. garvieae* will be introduced below.

1.2.4.1 Capsule

Encapsulation has long been considered a virulence factor in many Gram-positive and Gram-negative bacterial species, as the capsule masks cell surface antigens from the immune system and prevents desiccation in the environment (Johnson, 1991; Musher, 1992). The capsule has been found to be a major immunogen and a target for antimicrobial drugs in many bacterial species, as shedding of the capsule on exposure to these compounds can be used as a technique to prevent destruction (Kietzman *et al.*, 2016).

A number of studies comparing pathogenic and non-pathogenic strains of *L. garvieae* from fish have shown that the presence of a capsule is crucial for virulence in fish (Morita *et al.*, 2011a; Ture and Altinok, 2016). Possession of a capsule gene cluster has since been found to be a vital virulence factor of the bacterium in fish (Kawanishi *et al.*, 2007; Miyauchi *et al.*, 2012b). Non-capsulated phenotypes also induced a reduced immune response in fish, based upon reduced levels of serum agglutinating antibody titres in fish challenged with the two phenotypes (Yoshida *et al.*, 1996; Kawanishi *et al.*, 2007; Morita *et al.*, 2011a; Miyauchi *et al.*, 2012b).

However, encapsulation is not the sole requirement for virulence in *L. garvieae,* as identified by Ture et *al.* (2012), where just one of 34 fish-virulent strains expressed the capsule gene cluster when analysed by multiplex PCR.

1.2.4.2 Toxin-associated proteins

Many Gram-positive cocci produce toxins which enable them to act as pathogens (Barnett *et al.*, 2015). Haemolytic toxins from *L. garvieae* have been found to be linked to virulence. The fish-virulent Lg2 strain expressed virulence genes for haemolysins 1, 2 and 3 (*hly*1, 2 and 3) involved in the breakdown of blood cells which elicits the typical symptoms of lactococcosis such as subcutaneous haemorrhage. Lg2 has also been studied for expressing the virulence gene *sodA,* encoding superoxide dismutase (*sodA*) involved in reducing oxidative damage and found to be important in bacterial virulence (Poyart *et al.*, 2001; Esteve-Gassent *et al.*, 2015; Ture and Altinok, 2016). Toxins generated by the bacteria can be lethal to white blood cells, as seen in a study on yellowtail (Kusuda R, 1988). The ADP-ribosyltransferase exotoxin, which transfers ADP-ribose to essential proteins in the host, has been found to contribute to virulence in multiple pathogens including *Corynebacterium diphtheria* (Holbourn *et al.*, 2006; Aguado-Urda *et al.*, 2012). This toxin has been found encoded on a plasmid in a clinical *L. garvieae* isolate providing transfer potential between bacterial populations by conjugation, although its experimental toxicity is yet to be determined (Aguado-Urda *et al.*, 2012).

1.2.4.3 Adhesion

Adhesins are cell-surface components that facilitate the binding of bacteria to host cell receptors. They are present in commensal bacteria but may also be a factor enabling pathogenic bacteria to bind and subsequently cause disease in host tissue (Kline *et al.*, 2009). *L. garvieae* has been found to demonstrate three protein sequences (PsaA, PavA, and enolase) with high similarity to adhesive virulence factors in other streptococcal species, as well as adhesin clusters 1 and 2 (*adh*CI and *adh*CII) and adhesin (*adh*) (Miyauchi *et al.*, 2012a; Ture and

Altinok, 2016). The other genes with potential involvement in adhesion include those coding for sortase-anchored proteins, which are covalently attached to peptidoglycan in the cell wall of Gram positive bacteria. These contribute to the assembly of pili to aid adhesion (Marraffini, DeDent and Schneewind, 2006). Sortase anchored proteins have been previously noted to be important for the establishment and persistence of disease, and as such are likely to be virulence factors (Egan *et al.*, 2010). Sortase enzymes cleave LPxTG (or similar) motifs in the sortase-anchored proteins, with these motifs found expressed in the *L. garvieae* genome and in over 100 surface proteins in most streptococcal species, suggesting that this method of anchoring is universal (Miyauchi *et al.*, 2012a). The expression of these structures on the cell surface could make them promising candidates for diagnosis and/or therapy.

1.3 Identifying bacterial virulence determinants and their functions

1.3.1 Essential genes

A gene is classed as essential if its absence results in an organism's complete inability to survive (Mushegian and Koonin, 1996). An essential genome contains a collection of genes that enable bacteria to survive in a given environment. When that environment can be linked to infection, for example the genes required for growth of a mastitis pathogen in milk, or a blood-borne pathogen in serum, it can allow genes related to pathogenesis to be identified (Gibson *et al.*, 2010).

1.3.2 Transposon insertion sequencing

An effective way to identify a large number of potentially essential genes involved in bacterial virulence is to use a combination of transposon-insertion mutant generation and high throughput sequencing (Chao *et al.*, 2016). This enables a phenotypic comparison between field strains of bacteria and knock-out

mutants, and hence can identify new gene functions. There are a number of different methods which use transposon insertion sequencing (TIS)-based techniques but essentially all have the same underlying approach (Chao *et al.*, 2016). Transposons are mobile genetic elements found in the genome of almost all organisms, which can move from one location in a genome to another, mediated by the action of an enzyme, transposase (Pray, 2008). In a TIS study, transposon mutagenesis is initially used to create a pool of mutants, each of which has a single disruptive lesion in their genome, ideally at random points throughout the chromosome to avoid transposon insertion bias. If the transposon inserts into and disrupts a sequence considered essential for bacterial growth and survival (those considered and termed 'essential' or housekeeping genes), then that bacterial mutant will be unable to proliferate and its absence (or low abundance) within the mutant pool is subsequently detected by extensive sequencing (Chao *et al.*, 2016). Ultimately, the bacterial mutants dominating the population will be those whose mutation gives them a distinct survival advantage in comparison to the others in the pool. Bioinformatic-based analysis of the resulting sequences can then be used to quantify and determine the chromosomal location of all insertions within the mutant pool when grown under different controlled conditions, with the prevalence of an insertion or insertions within a given sequence the fitness of each mutant in each environment. It is thus possible to recognise those genes which offer distinct advantages to the bacterium in specific environments (as outlined in Figure 1.2). With this information genes involved in colonisation and / or survival within a host environment (essential for virulence) can be identified and genomic datasets from different strains and species can be compared to also

identify ‘conditionally essential’ genes which are only involved in virulence in certain environmental conditions (Blanchard, 2015; Chao *et al.*, 2016).

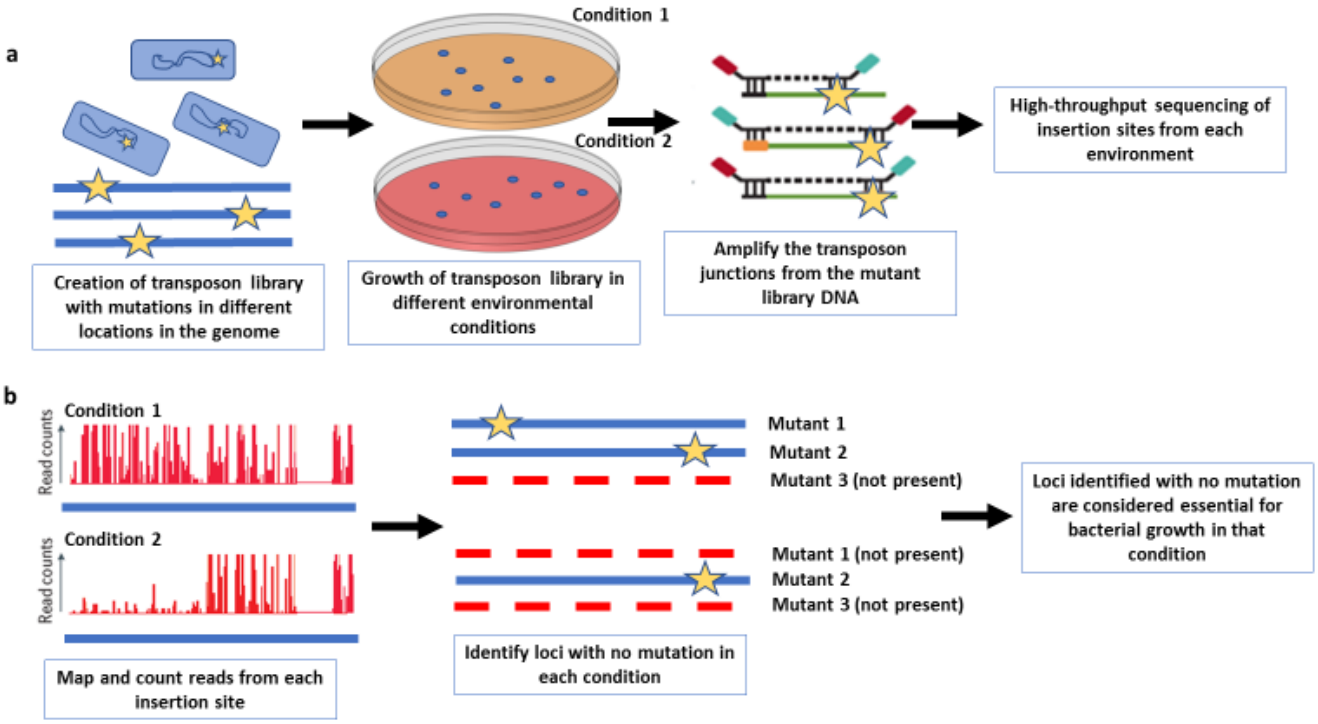


Figure 1.2 Flow diagram illustrating the transposon insertion sequencing (TIS) protocol.

a) The library of mutants containing multiple insertions in non-essential genes is generated, and grown under different conditions (condition 1 here is non-selective and condition 2 is selective). The viable mutants are subsequently recovered. The transposon junctions identified in the pools are attached to sequencing adaptors and then amplified by PCR before undergoing high-throughput sequencing.

b) The sequences identified are mapped to the genome, and analysed to identify the genomic loci which are significantly underrepresented in that growth condition.
These loci represent genes which are essential for that bacteria to survive in the particular growth condition, as their lack of presence in the resulting population indicates that mutation of that locus was detrimental to the growth of the host bacteria (Figure adapted from Chao *et al.*, 2016).

There are 4 TIS approaches that have been used frequently: transposon sequencing (Tn-seq); insertion sequencing (INSeq); high-throughput insertion tracking by deep sequencing (HITS); and transposon-directed insertion site sequencing (TraDIS) (van Opijnen and Camilli, 2013). In all, genomic DNA is purified from the pool of mutants and cleaved using specific endonucleases or by random shearing (Figure 1.3). Subsequently, one or more adaptors are attached to the DNA fragments in order to allow the amplification of those containing transposon sequences by PCR (Figure 1.3). The final step is to use massively parallel sequencing (MPS) on the amplified fragments to locate the transposon and determine the relative abundance of mutants which contain that transposon at that specific site (van Opijnen and Camilli, 2013; Figure 1.3). MPS allows for the simultaneous screening for mutations in multiple loci throughout the genome and has dramatically increased the throughput of sequencing techniques (Tucker, Marra and Friedman, 2009). The main difference between Tn-seq and INSeq is the use of a PAGE gel purification step after adaptor ligation and PCR in INSeq, whereas Tn-seq instead uses an agarose gel purification at the same point. In comparison, after shearing of the DNA in the HITS and TraDIS techniques, the DNA ends are repaired, and there is the addition of a poly(A) tail. After the PCR step, HITS involves the PCR products undergoing gel-based size selection and affinity purification before they are sequenced. However in TraDIS, sequencing is undertaken directly on the PCR products themselves rather than relying on sequencer to generate reads, by modifying the sequencing parameters to increase production of desired fragments (Langridge *et al.*, 2009; van Opijnen and Camilli, 2013). When combined with inverse PCR, MPS enables comprehensive identification of multiple mutated coding sequences in a relatively short space of time: 25 million bases of genetic code (the entire

genomic sequence of some organisms such as fungi) can be read within a four-hour period, making it a highly efficient technique for genomic analysis (Rogers and Venter, 2005).

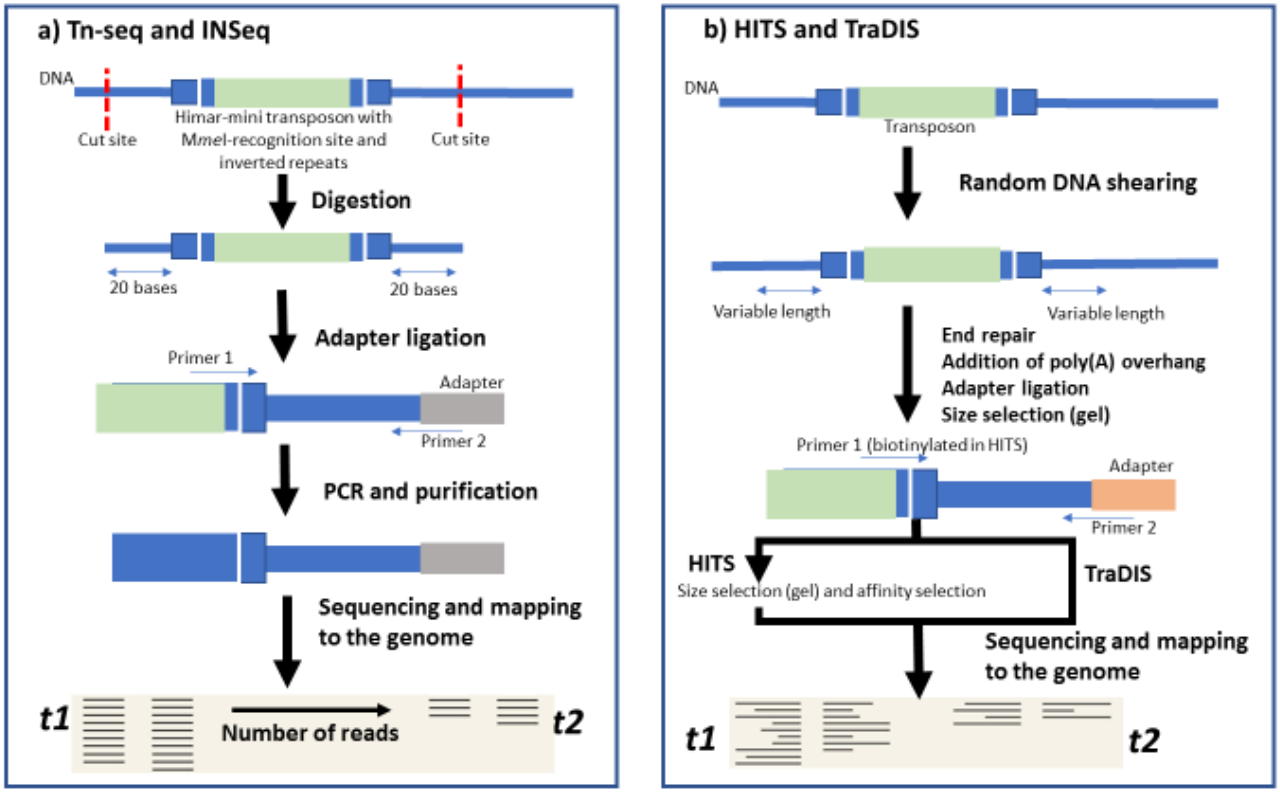


Figure 1.3 Outline of the four most commonly-used methods of massively parallel sequencing of transposon insertions.

Each begins with pooled genomic DNA from the pool of transposon insertion mutants, and ends with sequencing of both left and right transposon junctions. The amount of sequences (reads) from each junction may differ from the beginning of the experiment (*t1*) to the end (*t2*), after a selection process on the mutant library. In this case, fewer reads are identified between the start and end of the experiment, indicating that the particular insertion mutation involved decreases the fitness of that bacterial mutant. Adapted from van Opijnen and Camilli, 2013.

Every TIS technique has its limitations. For instance, Tn-Seq and INSeq are only useful for pathogens which are mutated via the mariner transposon system. The protocol is centred on the introduction of a *Mme*I endonuclease site into the insertion sequence, which allows for digestion of chromosomal DNA downstream to the transposon by 20 base pairs. Not only is the use of the mariner transposon system restricted due to pseudo-random insertion bias, but the recognition site is 4bp before the insertion terminal sequence ends, leaving potentially insufficient (16bp) chromosomal DNA to align to a reference genome without ambiguity (Lampe, 2010). In contrast, the advantageous feature of TraDIS to generate reads independent of a sequencer is also its biggest limitation. Because of this custom-sequencing protocol, core parameters of the sequencer must be modified to accommodate it, and custom primers are required which are both expensive and frequently wasted in optimisation. Typically the use of TraDIS requires direct access to a sequencing machine, as the necessary alterations to the settings are often not conducive to commercial sequencing services (Langridge *et al.*, 2009). Other limitations to TIS techniques include the random development of bottlenecks, both biological and technical, which mask changes in the population due to selection and can lead to spurious findings. A bottleneck describes the size of a population being reduced and hence its composition altered in a process of 'genetic drift'. In *in vivo* studies, biological bottlenecks may arise where many bacteria are killed or stochastically removed in the process of establishing an infection. Technical bottlenecks may occur throughout the TIS process as a result of sample handling or operator error (van Opijnen and Camilli, 2013). It is subsequently impossible to tell whether fluctuations in prevalence of certain genotypes is because of a lack of fitness or as a result of chance. Identifying bottlenecks relies on the recognition

of a loss of mutants with disrupted non-essential genes, which would be expected to be present at greater numbers in the recovered library (Van Opijnen and Camilli, 2012).

In a TIS experiment, numerous mutations are simultaneously analysed, meaning that the relative abundance of a mutation is given by the sequence read depth. This can then be directly associated to the frequency of a unique insertion within a population. A risk with this is that if the sequenced DNA bases are read incorrectly, sequence reads may align to alternative locations in the genome and hence produce false insertion points. Avoiding this requires the use of a prescribed cut-off for data analysis, for example where it has been found that identifying a single insertion ≥3 times this provides a very strong indication that it is not an artefact that has been amplified by chance (Klein *et al.*, 2012).

A final issue with these techniques is that a specific gene of interest must be identified based upon previous research on that gene or similar genes in other bacterial species, else the system risks becoming too subjective.

The combination of inverse PCR and MPS has led to the recent development of an additional TIS-based method, the Pragmatic Insertional Mutation Mapping System (PIMMS), which not only involves the identification of insertional mutation loci within individual mutant genomes, but also analyses those mutations within an entire population of mutant bacteria (Blanchard *et al.*, 2016).

1.3.3 Pragmatic Insertional Mutation Mapping (PIMMS)

PIMMS is a TIS-based protocol devised to enable detection of essential and conditionally essential genes. The protocol was first developed for use in *Streptococcus uberis* but can be used to detect such genes in other streptococci and related bacterial species (Blanchard, 2015; Blanchard *et al.*, 2016). The

technique relies upon the temperature-sensitive insertional mutagen pGhost9::IS*S1,* which has previously been found to integrate randomly across the *S. uberis* genome (Ward *et al.*, 2001) with the same mutagen having been found to successfully integrate randomly into the genomes of other *Streptococcus, Lactococcus* and *Enterococcus* species (Maguin and Ge, 1996; Spellerberg *et al.*, 1999; Baureder and Hederstedt, 2012). After integration of the plasmid, the PIMMS process uses inverse PCR to amplify re-circularised randomly generated acoustically sheared fragments of a specific size in order to amplify the sequences which flank the plasmid insertion sites (Blanchard, 2015). Inverse PCR has previously been used to determine individual mutations in species of bacteria such as *Pseudomonas abietaniphila* (Martin and Mohn, 1999)*, Helicobacter pylori* (Salama, Shepherd and Falkow, 2004) and *S. uberis* (Ward *et al.*, 2001) in other bacterial mutant libraries*.* The use of inverse PCR in combination with high-throughput technology to analyse different bacterial mutant populations simultaneously give PIMMS the distinct advantage over previously mentioned TIS methods (Blanchard *et al.*, 2016) as it is relatively simple and can use conventional library preparations of bacteria and sequencing protocols. In conjunction with a bespoke bioinformatic analysis program it has been shown to be able to identify and statistically determine the requirement for different sequences between two populations. Unlike in the mariner-based TIS protocols TN-Seq and INSeq, there is neither transposition bias to a particular insertion motif, nor an insertional bias towards specific DNA structures involved when using the pGhost9::IS*S1* plasmid (Lampe, 2010; Green *et al.*, 2012; Blanchard *et al.*, 2016).

The bioinformatic pipeline specifically identifies the ISS1 transposon within the plasmid and the bacterial genome junction to confirm the location within each

DNA sequence analysed. To be applicable to other bacterial species where alternate transposons are used for mutagenesis studies, the pipeline could be to be redeveloped to identify the alternate transposon:genome junction, although the application of appropriate bioinformatics software can allow extrapolation between species. Another potential disadvantage is that the rate of mapping of genome:transposon junctions is estimated at approximately 50%. This is the result of the primers used in the inverse PCR reactions amplifying either just the plasmid or the insertion sequence depending on their orientation, which means that 50% of the sequencing information is discarded during initial analysis. Given this, a high proportion of good quality sequence reads is essential to ensure a wide representation of genes deemed to be essential for proliferation in a given environment can be detected at a statistically meaningful level within the bacterial population.

1.3.4 Predicting the function of bacterial genes

Determining which genes are essential for bacterial virulence does not necessarily inform us of exactly how they evade the host immune system and contribute to disease. Much more information in this area can be divulged by evaluating essential genes in relation to the metabolic and biochemical pathways in which they play a role. A metabolic pathway is comprised of a series of metabolic reactions which lead from one to the next in a cascade, with the product of one reaction being critical for the success of the next (Karp, 2001). Databases of knowledge regarding metabolic pathways enable functional comparison and inference between species. The largest of these databases is the Kyoto Encyclopaedia of Genes and Genomes (KEGG), which contains genetic catalogues for all completely sequenced genomes and their annotated functions (Ogata *et al.*, 1999). KEGG thus enables the user to link genomic information to

higher order function. Utilising this information as well as literature databases and annotations from SwissProt (UniProt, 2013) and GenBank (Benson *et al.*, 2013), Rapid Annotation of microbial genomes using Subsystems Technology (RAST) can allow for a broader identification of gene function, with genes able to be categorised by their functionally-related proteins (Overbeek *et al.*, 2005). Targeting genes relating to specific essential functions, such as DNA metabolism and cell division, could become the basis for highly effective therapy development, and hence TIS based mutation mapping strategies could greatly enhance the treatment and identification of disease.

1.4 Summary

Lactococcus garvieae is responsible for disease in aquaculture systems across the globe, with potentially increasing economic consequences for the rapidly-growing industry of aquaculture. Its importance as a zoonotic disease with growing prevalence in humans also makes it important for food safety to be able to accurately control and diagnose *L. garvieae* infections. Antibiotic resistance is a severe handicap to the potential for treatment of lactococcosis in aquaculture systems, and hence alternatives are necessary for effective disease control. One aspect restricting the development of effective control measures against *L. garvieae* is the lack of knowledge regarding pathogenesis, virulence factors and their corresponding genes. A number of bacterial components, such as the capsule, have been identified as being related to virulence, and together these offer potential as bases for diagnostic test development and future therapies (Reviewed by Meyburgh, Bragg and Boucher, 2017). There are a number of methods available that may be used to identify genes directly involved in virulence of *L. garvieae*, including high throughput sequencing of bacterial mutant libraries that contain transposon elements within a single location. The

PIMMS protocol and bioinformatic pipeline simultaneously maps and quantifies mutations using the pGhost9:ISS1 transposon and in combination with protein annotation programmes can rapidly enhance functional gene characterisation. Their use can rapidly identify potentially important genes for both virulence and infection and streamline functional analysis of these genes and their products, to provide powerful data to improve fish health and welfare through targeted control strategies against *L. garvieae*.

1.5 Aims and Objectives

- To characterise genes determined as essential for both bacterial growth in general and for survival of *Lactococcus garvieae* in fish serum using PIMMS bioinformatics based comparative analysis.
- To use characterise the identified essential genes to determine potential functional roles of their encoded proteins and further understand their potential involvement in bacterial virulence.
- To identify genes which could be relevant future targets for the diagnosis of or vaccination against lactococcosis in aquaculture systems in rainbow trout

2.0 Materials and Methods

2.1 Bacterial strains and growth

Unless otherwise expressed, all reagents were obtained from Sigma-Aldrich. *L. garvieae* was routinely grown in BHI media at 37°C for 16 hours, with mutagenised bacterial strains containing the pGh9:IS*S1* plasmid routinely grown with the addition of 1ug/ml erythromycin (Ery). *L. garvieae* strains 00021, 02106, 03017, 03080 and 03084 were supplied by Dr D. Verner-Jeffreys from CEFAS. *Streptococcus uberis* strain 0140J containing the pGh9:IS*S1* plasmid, a mutagenised culture of *L. garvieae* strain 02106 generated using pGh9:IS*S1*, mutant pools and genomic sequence information were supplied by Dr Sharon Egan at the University of Nottingham. Five bacterial mutant pools of mutagenised strain 02106 were cultured as above. Bacteria were harvested from BHI-Ery plates using sterile saline (Sigma-Aldrich) and stored in 25% glycerol at -80°C. Each mutant pool was subsequently grown in salmon fish serum provided by Dr D. Verner-Jeffreys for 4.5 hours then cultured on BHI-Ery and harvested as above. DNA was extracted from mutant pools grown under media and fish serum conditions, acoustically sheared and prepared for inverse PCR as previously described (Blanchard 2016) and sent for sequencing analysis to Barts and the London Genome Centre (Queen Mary University of London).

2.2 Extraction of chromosomal DNA from *L. garvieae*

All centrifugation steps were performed at 13,000 x *g* for 5 min at room temperature in an MSE benchtop microfuge unless otherwise indicated. 3mL of culture containing approximately 1.6 x 10^9 CFU/ml was centrifuged and the resultant cell pellet resuspended in 0.5mL of Tris EDTA buffer (TE buffer; 10mM Tris-HCl, 5mM EDTA, pH 8 (Fisher)) and re- centrifuged as above. Cells were resuspended in cell wall disruption buffer (30 units/mL mutanolysin, 10 mg/mL

lysozyme in TE buffer) and incubated at 37°C for 30 minutes. Cell lysis was completed with the addition of 20µL of lysis buffer (20% SDS (w/v) (BDH Prolabo) in 50 mM Tris-HCl and 20m mM EDTA pH 7.8), and 150µg/ml Proteinase K, and incubated for 1 hour at 37°C. Protein was precipitated by the addition of saturated NaCl (approximately 6.0M) and centrifugation (17,000 x *g*,10 min). The supernatant was retained and centrifuged as above. An equal volume of Tris-equilibrated phenol:chloroform:isoamyl alcohol (25:24:1) was added to the retained supernatant and centrifuged (13, 000 *g*, 3 min) to separate phases. The upper aqueous phase was retained and the DNA precipitated by adding 2 volumes of ice-cold 100% ethanol and holding the samples on ice for 2 hours. The precipitated DNA was centrifuged and the resulting pellet washed with ice cold 70% ethanol. The pellet was thoroughly air-dried at room temperature before resuspension in 50 µL of TE buffer containing 20 µg/mL RNAase A and incubation for 30 minutes at 37°C. Samples were stored at -20°C until required or 4**°**C overnight.

2.3 Extraction of pGh9 plasmid from *S. uberis*

S. uberis strain 0140J containing the pGh9:IS*S1* plasmid was cultured overnight in BHI broth containing 1ug/ml erythromycin. 20 mL of culture was centrifuged at 17000*g*, washed with TE buffer, resuspended in cell wall disruption buffer as above and held at 37°C for 1 hour. After re-centrifugation, the plasmid was extracted using the commercially available QIAprep Miniprep kit (Qiagen).

2.4 Quantification of DNA concentration

DNA was quantified using Qubit working solution of a 1:200 dilution of Qubit dsDNA BR reagent A in Qubit dsDNA BR Buffer according to manufacturer's instructions and a 1:200 dilution of the DNA samples quantified using the Qubit 2.0 Fluorometer (Invitrogen).

2.5 Separation of DNA by gel electrophoresis

All DNA electrophoresis-based separation was performed using 1% agarose/TAE gels at 70-100V. DNA was diluted 5:1 with a loading buffer (0.025% bromophenol blue, 0.025% xylene cyanol, 40% sucrose) and Hyperladder 1kb (Bioline) was routinely used as a molecular weight marker. Gels were stained post-separation in ethidium bromide (0.5µg/ml) and visualised using a UV transilluminator (UVP).

2.6 Purification of reaction products

Products generated by PCR were purified according to the QIAquick PCR Purification Kit (Qiagen). Where reaction products were separated by gel electrophoresis, the desired DNA product was extracted and purified following the MinElute Gel extraction Kit (Qiagen) protocol. Plasmid DNA was purified using the QIAprep Miniprep Kit (Qiagen) according to manufacturer instructions.

2.7 Amplification of regions of interest by PCR

PCR reactions used approximately 250ng of *L. garvieae* DNA, 0.5µM forward and reverse primers (Outlined in table 2.1), 200µM of dNTPs (Thermo Scientific), 1X HF Phusion buffer (NEB) and 1U of Phusion DNA polymerase (NEB) in a BioER LifeEco thermal cycler. DNA was denatured at 98°C for 5 minutes, then amplified by holding at 98°C for 10 seconds, 60°C for 30 seconds, and 72°C for 1 minute. Amplification was repeated for 35 cycles, before extension at 72°C for 8 minutes. Optimal annealing temperature for each primer pair was calculated using an online Tm calculator (NEB) and ranged between 57-60 °C. 20% of the final product was analysed by gel electrophoresis and purified as above.

Table 2.1: Primers used in this study

Primer ID (forward/reverse)	Primer sequence (top: forward; bottom: reverse)	Target site	T_m (annealing temp, °C)	Product length (bp)
1090/1091	5'-TCTTGTAGAatTCGGTGCTGCT-3'[a] 5'-GAGGATCCTTGCTCAGACTCTTC-3'[b]	*divIB*	67	401
1104/1105	5'-TCCTTAggATCCAAGTATTGCG-'3[b] 5'-AGACCTCTTTGAAAAgCtTCAG-3'[c]		64	378
1096/1097	5'-CAAAGCgAATtCGTCAAAAC-3'[a] 5'-ACGCTTTACAACGTCTTTTGTT-3'[d′]	*spsB*	61	391
1098/1099	5'-TAGGGGATAtCCGTATTGTGTC-3'[d] 5'-CACAAT[1]ACCTTGCTGCTGTTTA-3'[c′]		64	390
1106/1107	5'-GCATGGTgaATTCGTAGAAATG-3'[a] 5'-TGCTCCCCATCCTTAAGTAAAT-3'[d″]	LAG_00167	65	742
1108/1109	5'-TTCAGATaTCGATAGGTTTTGCTC-3'[d] 5'-GCTTACCACGTAaAGCTTATTTCT-3'[c]		64	370
1112/1113	5'-GTTACAGaATtCATTGCAGCAGATATCA-3'[a] 5'-GTCTCAGTATCCTCTTGGATATCCT-3'[d]	LAG_00168	66	577
1116/1117	5'-TGGCCGgATaTCCTTAATCGT -3'[d] 5'-CTTCCACAGAAATAAGCTtTACGTG-3'[c]		65	338
064/082	5′-AGAACCGAAGAAtTcGAACGCTC-3′ 5′-CCAACAGCGACAATAATCACATC-3′	Insertion sequence S1	65	808

Superscript notation indicates restriction enzyme (RE) site incorporated into primer during design: [a]: EcoRI; [b]: BamHI; [c]:HindIII; [d]: EcoRV. Incorporated nucleotides are indicated in lowercase. All primers were from Sigma-Aldrich

[*]: primer sequence is downstream of the associated RE site.

[**]: Relevant RE site naturally present in primer sequence

2.8 Restriction endonuclease digestion of DNA

All restriction enzyme digests of DNA were performed using *Hin*dIII-HF, *Eco*RI-HF, *Eco*RV-HF, *BamH*I-HF and *Pvu*II-HF (NEB) in CutSmart buffer using between 50-100U of the enzyme relevant to the primers used (Table 2.1). Reactions were routinely incubated for 4-16 hours at 37°C in a total reaction volume of 30µl.

2.9 Inverse PCR analysis of pGh9:*ISS1* element flanking regions

5µg of genomic DNA from individual bacterial mutants (n=40) from *L. garvieae* strain 01206 was digested with 5 units of *Hin*dIII restriction enzyme as described with complete digestion confirmed by gel electrophoresis. The remaining digested DNA was heat-inactivated at 65°C for 20 minutes and approximately 1µg was ligated as above at 14°C for 16 hours. Approximately 200ng of this re-circularised genomic DNA was used as template for an inverse PCR amplification reaction using the pGh9 plasmid-specific primer pair P064 and P082 (Table 2.1) and conditions for Phusion polymerase amplification as previously described. DNA was denatured at 98°C for 5 minutes, then amplified by holding at 98°C for 10 seconds, 63°C for 30 seconds, and 72°C for 1 minute for 35 amplification cycles, before a final extension at 72°C for 8 minutes.

2.10 Ligation of fragments post-digestion

Ligation of digested *L. garvieae* DNA generated interrupted gene sequences for insertion into the pGh9 plasmid. Reactions utilised 500ng of digested DNA, 1x ligase buffer (NEB) and 400 NEB units T4 DNA ligase (NEB) at 4°C overnight. The product was separated by gel electrophoresis and purified as previously described. Ligation of these inserts into the pGh9 vector was performed at a 5:1 molar ratio of insert to plasmid, calculated using the online NEB Biocalculator (NEB).

2.11 De-salting of DNA prior to electroporation

Removal of salt from the ligation reaction products was achieved by performing dialysis in 1% agarose/0.1 M glucose solidified agar according to the protocol outlined by Atrazhev and Elliott (1996). Ligations were desalted on ice for 90 minutes and 5µl of the ligated plasmid used for subsequent electroporation.

2.12 Electroporation of *E. coli*

The desalted ligated reactions were electroporated into TOP10F' (Thermo) electrocompetent *E. coli* using Bio-Rad Gene Pulser to deliver 1.8kV, at 25µF capacitance, with the pulse controller set to 200Ω. Pre-warmed (28°C) SOC media free of antibiotic was added to the reaction mixture after electroporation, and the cell suspension incubated with shaking at 200rpm at 28°C for 1-2 hours. Dilutions of 10^0 and 10^{-10} of this suspension were then plated on LB agar containing 200 µg/mL erythromycin and incubated for 48 hours at 28°C.

2.13 Bioinformatic analysis

The *L. garvieae* 02106 genome was sequenced by MicrobesNG (University of Birmingham) and the trimmed FASTQ files used to assemble and annotate the bacterial genome using PROKKA (Seemann, 2014) and RAST (Overbeek *et al.*, 2014). Genome sequence data from 5 pools of *L. garvieae* 02106 mutants grown in BHI (input pools), and 5 pools grown in fish serum (output pools) were obtained from Barts and the London Genome centre. The resulting raw FASTQ sequence data was analysed by freely available software in a Linux system and each sequence read was assessed for sequence quality of >30 Phred score. The PIMMS bioinformatic pipeline (Blanchard 2015) was then used to process the sequence reads and map them to the *L. garvieae* 02106 genome. Data from this analysis and the *L. garvieae* 02106 nucleotide and protein sequence were provided by Dr Sharon Egan and Dr Adam Blanchard. Comparison files were

generated to identify changes between mutant populations in the input and output pools, with further analysis completed using BLAST (Altschul *et al.*, 1990), SignalP (Petersen *et al.*, 2011), PSORTb (Yu *et al.*, 2010), RAST (Aziz *et al.*, 2008), and KEGG (Ogata *et al.*, 1999). EdgeR statistical analysis (Robinson, McCarthy and Smyth, 2010) was performed by Dr Adam Blanchard and was sorted by false discovery rate (FDR) with a threshold value of <0.05 to consider a gene significantly differentially regulated in the output pool compared to the input pool.

3.0 Results

3.1 Analysis of pGh9 integration within *L. garvieae* individual mutants

Previously generated *L. garvieae* 02106 pGh9:ISS1 bacterial mutant pools consisted of 5 populations of approximately 20,000 bacteria and were designated mutant pools 1-5 (MP1-5). Bacteria were harvested directly after overnight growth at 37°C from BHI solid media in the presence of 1µg/ml erythromycin (BHI/Ery). Bacterial colonies were harvested directly from plates using sterile saline and stored in 25% glycerol at -80°C until used. This population is referred to as the input pool in the subsequent analysis sections. For analysis of the effect of bacterial growth in fish serum, each of these mutant pools were re-grown in salmon serum for 4 hours at 37°C and then grown on BHI/Ery solid agar and harvested as above. This population is referred to as the output pool in the subsequent analysis sections.

MP2 was selected to determine the random nature of insertion. This was achieved using 40 colonies obtained from input (20 colonies) and output (20 colonies) populations (before and after growth in fish serum, respectively).

The difference in the chromosomal restriction fragment sizes containing insertion was estimated by inverse PCR of HindIII digested (Figure 3.1) using re-

circularised chromosomal DNA and amplification using outward reading ISS1 specific primers (P064 and P082; Table 2.1). The differences observed in amplified product sizes detected (Figure 3.2) indicated that insertion of the plasmid had occurred in a variety of different locations within the individual *L. garvieae* mutated bacterial strains analyised.

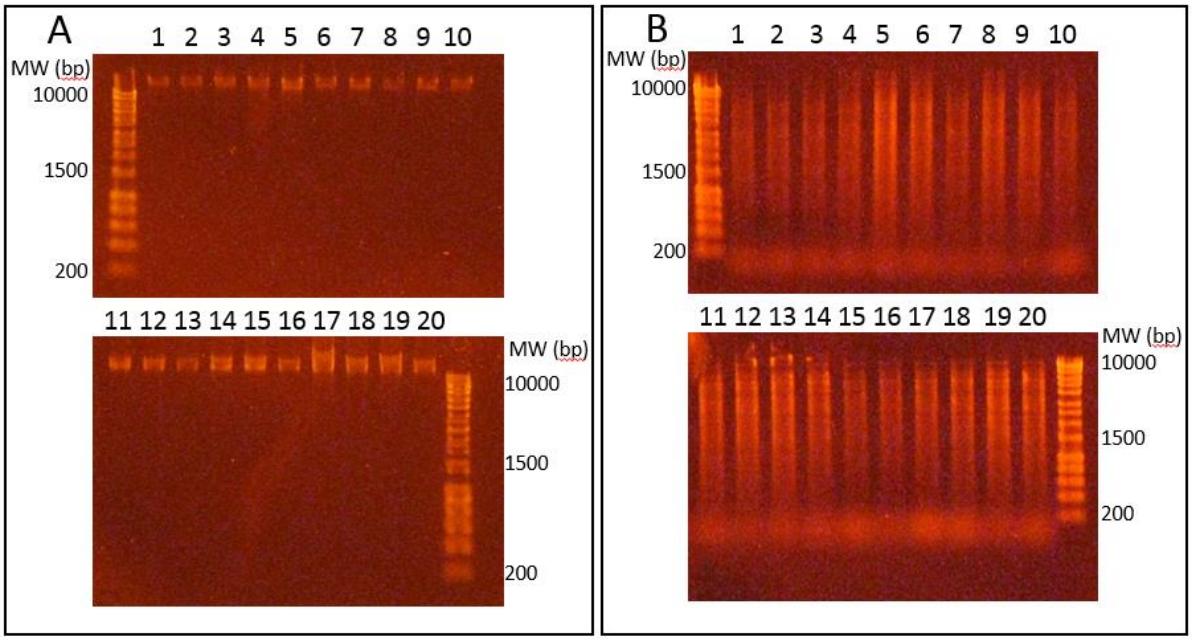
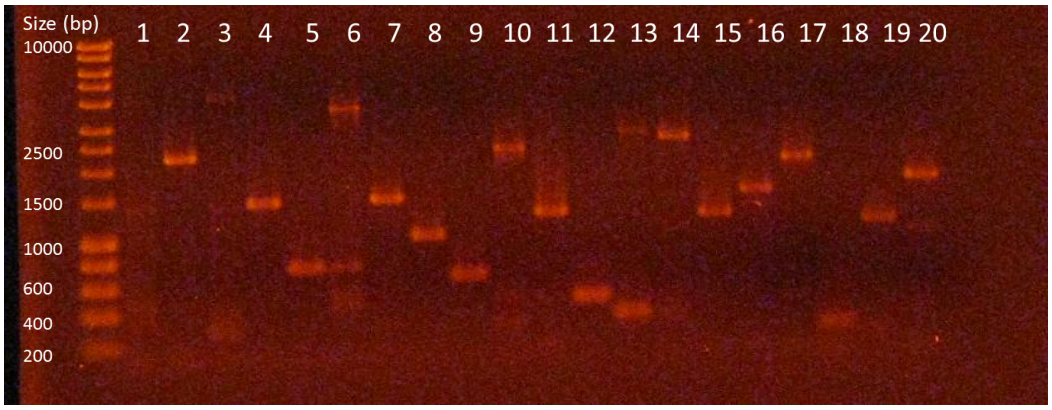


Figure 3.1: Representative gel electrophoresis results using *L. garvieae* DNA before inverse PCR.

A: Genomic DNA samples isolated from individual *L. garvieae* mutants prior to restriction enzyme digestion. Large intact DNA can be seen above the highest molecular weight marker. Lanes 1-20 on each image represent a different bacterial mutant with Hyperladder 1kb (Bioline) as molecular weight marker.
B: The same DNA visualised post-digestion with *Hind*III restriction enzyme. The intact DNA has been digested and the resulting products form a smear of smaller DNA fragments.

A



B

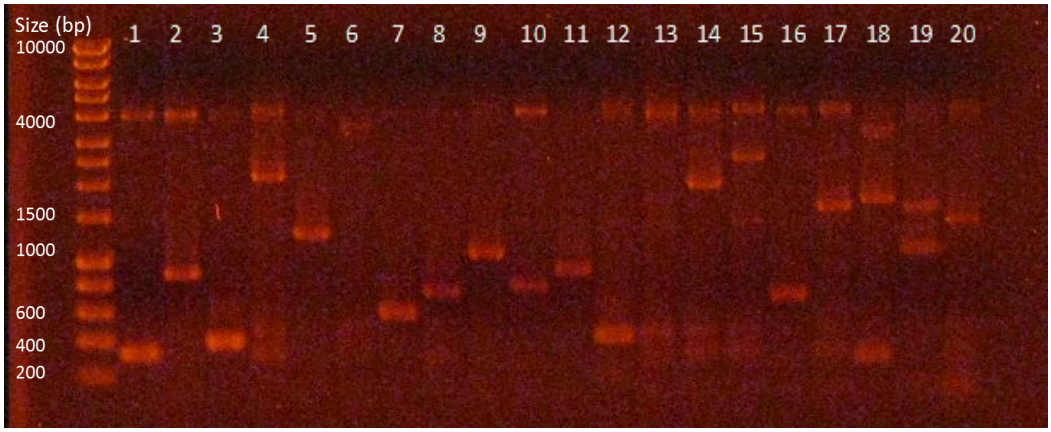


Figure 3.2: Gel electrophoresis following inverse PCR to amplify sequences flanking IS*S1* insertion elements.

Lanes 1-20 represent DNA from 20 individual bacterial colonies.

A*: L. garvieae* mutants grown on BHI/Ery solid media (input pool). Amplified products generating unique patterns were observed for each mutant analysed, suggesting the plasmid had inserted randomly throughout the *L. garvieae* genome. Well 1 appears to have no product, indicating that the fragments generated by digestion were too large to be re-ligated and amplified during inverse PCR.

B: *L. garvieae* mutants grown in fish serum then harvested from BHI/Ery solid media (output pool).
Amplified products generating unique banding patterns were observed for each mutant analysed, suggesting that the plasmid had inserted randomly throughout the *L. garvieae* genome. 11 lanes show an amplified product at 4000bp, which may suggest the presence of intact pGh9:IS*S1* plasmidand that the ligation reaction prior to the inverse PCR was partially incomplete for these DNA samples. Well 6 appears to have no product, where the fragments generated by digestion may have been too large to be re-ligated and amplified correctly by inverse PCR. Sample 19 has generated 2 products, which indicates the likely presence of tandem transposition, resulting in duplicate copies of the IS*S1* element being integrated into the genome.

3.2 PIMMS analysis of *L. garvieae* before and after growth in salmonid serum

Genomic DNA extracted from the MP1-5 input and output bacterial populations was subject to PIMMS as previously described (Blanchard 2016). Sequencing of the inverse PCR products was conducted at the London Genome Centre (Queen Mary University of London). The resulting raw FASTQ sequence data was analysed using freely available software in a Linux system and each sequence read was assessed for sequence quality of >30 Phred score.

Data was processed using the PIMMS bioinformatic pipeline (Blanchard 2015) and reads mapped to the *L. garvieae* 02106 genome. The *L. garvieae* 02106 genome sequence information was generated by MicrobesNG (University of Birmingham) and annotated protein sequence generated using PROKKA (Seemann, 2014). Matched reads were defined as those sequence reads containing the ISS1 flanking region, and mapped reads were defined as sequence reads containing the ISS1 and *L. garvieae* 02106 genome information, which could then be mapped back to the reference genome, to confirm the location of the mutation within the genome for each individual sequence analysed.

A 'true' insertional event was defined as one with ≥3 occurrences within each of the mutant pools indicating the detection by genome sequencing was not due to chance (Klein *et al.*, 2012). A total of 44,831 unique insertions or bacterial mutants were identified in the input pool, ranging between 6984 and 10725 mutants across the input pools MP1-5 (Table 3.1). This was calculated to be equivalent to a mutation every 47bp within the genome of the input pools with an average read depth of 8. Fewer unique insertions (33,421) were identified in the output pools (following growth in fish serum) and the number of insertions in

the output pools (MP1-5) ranged from 6041 to 7139 mutants per pool (Table 3.2). This was calculated to be equivalent to a mutation every 70bp within the fish serum output pools with an average read depth of 10.

Table 3.1: Metrics of analysed sequencing data for input pools. Values represent the number of sequence reads and corresponding percentages associated with each stage of the bioinformatics pipeline for each mutant pool.

Pool Number	Total Number of Reads	Matched Reads (%)	Mapped Reads (%)	Unique Insertions with ≥3 Occurrences	Average Plasmid Inter-Insertion Distance	Average Read Depth
1	372068	174373 (46.87)	72317 (82.38)	6984	301	9
2	426818	167350 (39.21)	82730 (84.82)	9125	230	8
3	584477	227662 (38.95)	87605 (80.96)	10752	196	6
4	625140	243628 (38.97)	112368 (83.83)	9395	162	7
5	598174	218394 (36.51)	77411 (79.54)	9797	215	6
Combined pool total	2606677	1031407 (40.10)	432431 (82.31)	44831	47	8

Table 3.2: Metrics of analysed sequencing data for output pools. Values represent the number of sequence reads and corresponding percentages associated with each stage of the bioinformatics pipeline for each mutant pool.

Pool Number	Total Number of Reads	Matched Reads (%)	Mapped Reads (%)	Unique Insertions with ≥3 Occurrences	Average Plasmid Inter-Insertion Distance	Average Read Depth
1	441762	176995 (40.07)	58839 (77.86)	7139	295	7
2	504838	207915 (41.18)	76246 (76.59)	6576	320	9
3	543060	216876 (39.94)	71431 (77.48)	6798	309	10
4	494057	198136 (40.10)	64249 (74.32)	6867	306	9
5	524528	237715 (45.32)	68358 (79.78)	6041	348	11
Combined pool total	2508245	1037637 (41.32)	339123 (77.21)	33421	70	10

3.3 Essential genes in the *L. garvieae* genome

A total of 2063 coding sequences were identified within the annotated *L. garvieae* 02106 genome. A gene was deemed essential for bacterial growth in a particular condition if no ISS1 insertions were identified throughout the coding sequence in the input or output bacterial mutant pools. In the input pools, bacterial that were grown on BHI/ERY solid media, a total of 282 genes were identified as essential, compared with 398 genes for the output pool, after the same population was subsequently grown in fish serum, and then re-harvested from BHI/ERY solid media (Figure 3.3). A total of 257 genes were identified as essential for growth of *L. garvieae* 02106 in both growth conditions.

Further analysis was also performed to identify bacterial mutants where mutations were only found within the terminal 15% of the coding sequence and these are referred to as 'truncated' mutations in this analysis. Insertion within only the terminal 15% of the gene may indicate essentiality of the gene product which is likely to be produced, as the correspondingly truncated protein would likely retain functionality. 89 truncated sequences were identified in the bacteria grown in the input pools and 90 in the output pools (Figure 3.3). Only genes not identified in any pool were reported as essential, without considering genes which had significant up- or down-regulation in one medium compared to the other.

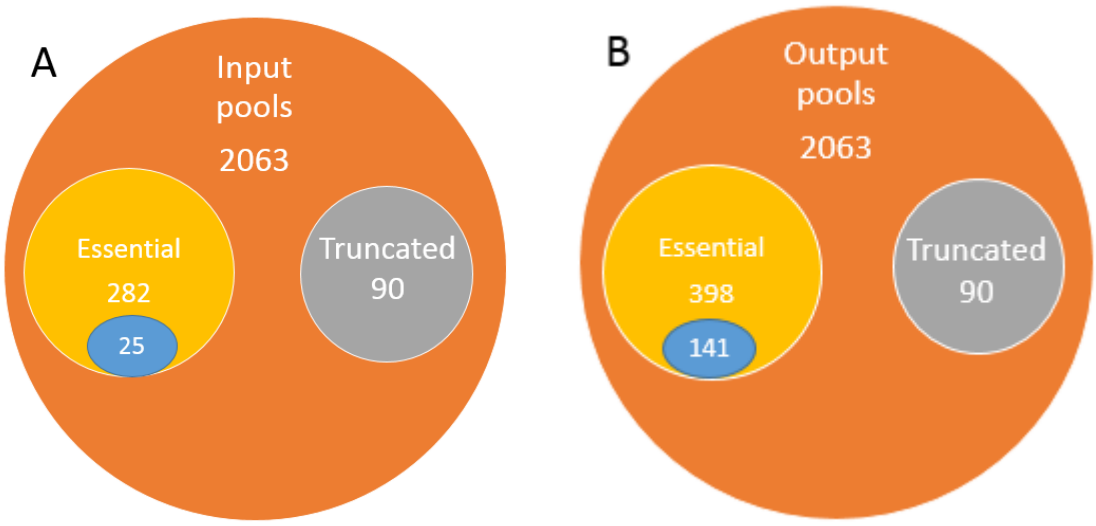


Figure 3.3: Modified Venn diagrams showing the distribution of essential and truncated genes across the two growth media used in this study.

Genes present in *Lactococcus garvieae* grown in the input pools and output pools (A and B) respectively. 2063 genes in total were identified in the bacterium (orange circles), of which 282 were essential in the input pools, and 398 were essential in the output pools (yellow circles). Only 25 genes were essential in the input only and 141 genes were found to be exclusively essential in the output pools following growth in fish serum (blue circles). In addition, 90 genes were found to be essential where mutations could only be detected in the final 15% of the coding sequence (referred to as truncated genes) in each pool (grey circles), 39 of which were shared between the two pools.

3.4 Analysis of essential genes for *L. garvieae* growth in the input and output pools

Essential and truncated genes from both input and output pools were categorised using the Rapid Annotation using Subsystem Technology (RAST) online resource (Overbeek *et al.*, 2014), which collates data from various online sources (KEGG annotations for information on metabolic pathways (Kanehisa *et al.*, 2012); GenBank which collates annotated DNA sequences (Benson *et al.*, 2013); and Swiss-Prot which provides a database of annotated protein sequences (UniProt, 2013) to enable genes to be grouped according to the functions of their encoded proteins. As such, this provides a very broad indication of their function. Many RAST categories exist, from Protein Metabolism and Cell Division, to Sulphur Metabolism and Virulence and Defence.

The 282 essential genes for growth and survival of *L. garvieae* 02106 in the input pools were assigned across 17 such categories, versus 18 categories for the 398 essential genes for the output pools grown in fish serum. The majority of essential genes in *L. garvieae* 02106 growing in both growth conditions related to protein metabolism (28.6% in the input pools; 12.7% in the output pools) or were deemed hypothetical (16.1% in mutants in the input pools; 36% in the output pools) (Tables 3.3 and 3.4). Of the large numbers of hypothetical proteins identified as essential (92 in the input pool and 43 in the output pool in total), 38 were essential in both pools. Other differences arose in categories observed between input and output with there being one gene, *pth*, involved in the 'Dormancy and Sporulation' category in *L. garvieae* input pools and two, *dnaE* and *polC_2*, in 'Phages, Prophages, Transposable Elements, Plasmids' category, with these categories not featuring at all with genes essential for growth in the output pools. *dnaE* and *polC_2* were also categorised into the 'DNA

Metabolism' category, with between 20 and 25 other essential genes in the pools belonging to two or three RAST categories. This is in accordance with the multiple functions possible for a single gene meaning that they can play a role in several metabolic pathways and functions.

Table 3.3: All essential coding sequences for *L. garvieae* in input pools and their associated RAST categories[#].

RAST Category	Count	Gene[#]
Amino Acids and Derivatives	5	*Alr*, argR_2, aroA_2, ftsZ, metK*
Carbohydrates	18	*aldC_2, alr, eno, fba_1, fba_3, gap*, gpsA*, gtaB, lacF, lacG, pfkA, pgcA, pgl, ptsI, pyk, rpe, sacX, tkt_2*
Cell Division and Cell Cycle	12	*cdaA, dnaB, dnaD, dnaG*, ftsA, ftsE, ftsL*, ftsX, gpsB, pbpX_1, tsaB*, tsaD*
Cell Wall and Capsule	17	*epsE, epsH, femA, glmS, glmU, murB, murD, murE, murF_2, murG, LAG_00151, rfbA, rfbC, tagG_1, tagH_1, tsaB*, tsaE*
Cofactors, Vitamins, Prosthetic Groups, Pigments	14	*birA, coaBC_1, coaBC_2, coaE, dhfR, gap*, hpt*, nadE, panT*, pdxK, ribF, thiN, thyA*, tilS**
DNA Metabolism	12	*dnaC, dnaE*, dnaG*, dnaN, hup, ligA,* LAG_02062, LAG_00596*, parC*, pare*, polC_2*, ssb*
Dormancy and Sporulation	1	*pth*
Fatty Acids, Lipids, and Isoprenoids	17	*accB, accD*, acpP, acpS, fabD, fabF, fabI, fabZ_1, fabZ_2, fni, gpsA*, mvaS,* LAG_00316*, pgsA, plsC, thrB, uppS*
Hypothetical	43	*atpA, atpB, atpE, atpF, atpG, atpH, glpE_2, hslR, ileS, immR_1,* LAG_00006, LAG_00037, LAG_00093, LAG_00114, LAG_00156, LAG_00159, LAG_00346, LAG_00464, LAG_00477, LAG_00545, LAG_01139, LAG_01157, LAG_01316, LAG_01426, LAG_01550, LAG_01733, LAG_01795, LAG_01881, LAG_02040, LAG_02041, LAG_02042, LAG_02051, LAG_02052, LAG_02055, LAG_02059, LAG_02060, *mnmA, pglJ, pssM, ptsH, pyrH, trxA, ykoT*
Membrane Transport	4	*ecfA1, ecfA2, ecfT, panT**
Nucleosides and Nucleotides	9	*Gmk, hpt*,* LAG_00721, LAG_00807*, nrdE1, nrdF2, nrdH*, thyA*, tmk*
Phages, Prophages, Transposable Elements, Plasmids	2	*dnaE*, polC_2**
Phosphorous Metabolism	5	*ppaC, pstA2, pstB3_1, pstB3_2, pstC*
Protein Metabolism	76	*asnS, aspS, bglH_6, def, der_1, der_2, efp, fmt, frr, gatA, gatC, groS, grpE*, hisS, hrcA*, infA, infB, leuS, lysS, obg, pheS, prfB, proS, pth*, rbgA, rplB, rplC, rplD, rplE, rplF, rplI, rplJ, rplK, rplL, rplM, rplN, rplO, rplP, rplR, rplS, rplT*, rplU, rplV, rplW, rplX, rpmA, rpmB, rpmC, rpmD, rpmF, rpmH, rpmI*, rpsA, rpsB, rpsC, rpsD, rpsE, rpsF, rpsG*, rpsH, rpsI, rpsJ, rpsK, rpsL*, rpsM, rpsP, rpsQ, rpsS, rpsZ, thrS, trmD*, tsaB*, tsf, tuf*, tyrS, valS*
RNA Metabolism	17	*Cca, ftsL*, greA,* LAG_01465*, nusA, rimP, rnj1, rnpA, rnz, rplGA, rpoA, rpoB*, rpoC*, rpoE, rsmH, tilS*, trmD**
Stress Response	3	*grpE*, hrcA*, nrdH**
Virulence, Disease and Defence	11	*accD*, infC, parC*, pare*, rplT*, rpmI*, rpoB*, rpoC*, rpsG*, rps[2]L*, tuf**

[#]Each gene was associated to its RAST category based on the subsystem of function (Overbeek et al. 2005). *indicates genes identified to belong to multiple RAST categories

Table 3.4: All essential coding sequences for *L. garvieae* growth in fish serum and their associated RAST categories[#].

RAST Category	Count	Gene
Amino Acids and Derivatives	7	*alr*, aroA_2, cysE, ftsZ, metK, mtnN, proC*
Carbohydrates	28	*aldC_2, alr*, eno, fba_1, fba_3, galE, gap*, gnd, gpmA_1, gpsA*, gtaB, hprK, lacF, lacG, pdhD, pfkA, pgi, pgk, pgl, prs, prs2, pta, ptsI, pyk, rpe, sacX, tkt_2, zwf*
Cell Division and Cell Cycle	18	*cdaA, cdaR, divIVA, dnaB, dnaD, dnaG*, ftsA, ftsE, ftsK_1, ftsL*, ftsX, gpsB, mreC, pbpX_1, recU, rpsU, tsaB*, tsaD*
Cell Wall and Capsule	24	*dgs, epsE, epsH, femA, femB, femX, gale, glmS, glmU,* LAG_00151, *murB, murD, murE, murF_2, murG, rfbA, rfbC, rmlB, tagB, tagD_2, tagG_1, tagH_1, tsaB*, tsaE*
Cofactors, Vitamins, Prosthetic Groups, Pigments	16	*birA, coaA, coaBC_1, coaBC_2, ftsH, gap, gltX, hpt, nadD_1, nadE, panT*, pdxK, thiN, thlA, thyA*, tilS**
DNA Metabolism	22	*addA, dnaC, dnaG*, dnaI, dnaN, dnaX_1, dnaX_2, gyrB, hhaIM, hup,* LAG_00596, LAG_02062, *ligA, parC*, pare*, priA, recG, recO, recR, recU, ssb xseB*
Fatty Acids, Lipids, and Isoprenoids	19	*accB, accD*, acpP, cdsA, fabD, fabF, fabG_1, fabI, fabZ_1, fabZ_2, fni, gpsA*,* LAG_00316, *pgsA, plsC, plsY, thlA, thrB, uppS*
Hypothetical	92	*acuR, atpA, atpB, atpE, atpF, atpG, atpH, cpsY, cspL, epsJ, fabH, gdpP, glnR, glpE_2, hslR, ileS, immR_1,* LAG_00006, LAG_00035, LAG_00037, LAG_00042, LAG_00094, LAG_00114, LAG_00142, LAG_00144, LAG_00156, LAG_00159, LAG_00161, LAG_00162, LAG_00180, LAG_00296, LAG_00346, LAG_00464, LAG_00484, LAG_00524, LAG_00533, LAG_00543, LAG_00644, LAG_00754, LAG_00904, LAG_01103, LAG_01139, LAG_01157, LAG_01143, LAG_01191, LAG_01204, LAG_01222, LAG_01307, LAG_01316, LAG_01341, LAG_01362, LAG_01374, LAG_01407, LAG_01426, LAG_01427, LAG_01483, LAG_01550, LAG_01722, LAG_01742, LAG_01763, LAG_01779, LAG_01795, LAG_01881, LAG_01909, LAG_02040, LAG_02041, LAG_02042, LAG_02051, LAG_02052, LAG_02055, LAG_02059, LAG_02060, *mnmA, murJ, pglJ, ppm1, pssM, ptsH, pyrH, rfbX, secA_1, secY, sepF, tig, walR_1, xerS, yabA, yhbY, ykoT, yvcJ, yxeN, znuC*
Membrane Transport	3	*ecfA2, ftsY, panT**
Nucleosides and Nucleotides	15	*Gmk,* LAG_00721, *guaA, hpt*, mtnN, nrdE1, nrdF2, nrdH*, nrdR, prs, prs2, tdk, thyA*, tmk, yumC*'*
Phosphorous Metabolism	6	*phoU, pstA2, pstB3_1, pstB3_2, pstC, pstS1_2*
Protein Metabolism	91	*asnS, aspS, bglH_6, def, der_1, der_2, dnaK, dps, efp, engB, fmt, frr, ftsY, gatA, gatC, gltX, glyQ, glyS, groS, grpE*, hrcA*, infA, infB, leuS, lysS, map, metG, obg, pheT_2, prfB, proS, rbgA, rim, rimI_2, rplA, rplB, rplC, rplD, rplE, rplF, rplI, rplJ, rplK, rplL, rplM, rplN, rplO, rplP, rplQ, rplR, rplS, rplT, rplU, rplV, rplW, rplX, rpmA, rpmC, rpmD, rpmF, rpmH, rpmI, rpsA, rpsB, rpsC, rpsD, rpsE, rpsF, rpsG, rpsH, rpsI, rpsJ, rpsK, rpsL*, rpsM, rpsP, rpsQ, rpsS, rpsU, rpsZ, smpB, spsB, thrS, trmD*, trpS2, tsaB*, tsf, tuf*, typA, tyrS, valS*
Regulation and Cell Signalling	2	*hprK, secG*
Respiration	1	*nfr2*
RNA Metabolism	24	*Cca, ftsL*, greA,* LAG_01465, *mnmG*, nusA, nusB, nusG, rimP, rnc, rnhC, rnj2, rnpA, rnz, rplGA, rpoA, rpoB*, rpoC*, rpoE, rpoZ, rsmH, tadA_2, tilS*, trmD**
Stress Response	6	*dnaK, dps, grpE, hrcA, nrdH, smpB*
Sulfur Metabolism	2	*trxB, yumC**
Virulence, Disease and Defence	14	*accD*, copY, gyrB, infC, misCA, parC*, pare*, rplT*, rpmI*, rpoB*, rpoC*, rpsG*, rpsL*, tuf**

[#]Each gene was associated to its RAST category based on the subsystem of function (Overbeek et al. 2005). *indicates genes identified to belong to multiple RAST categories

3.5 Essential genes identified as unique to either input or output pools

To identify genes which were unique in either the input or output population of bacterial mutants, genes identified as essential in both growth conditions were discounted (Tables 3.5 and 3.6).This revealed clear differences between the two populations with just 13 RAST categories with only 25 individual genes represented in the input pools and 18 RAST categories with 141 individual genes represented for the output pools. This reflects fundamental differences between the nutrient sources used to generate the input and output pools, showing that many genes are conditionally essential depending on the media used for bacterial growth (Tables 3.5 and 3.6). Some of these were in RAST categories which were not identified in the alternative pool, for example one gene, *nfr2*, belonged to the category 'Respiration', two others belonged to 'Regulation and Cell Signalling' (*hprK* and *secG*), and a further two essential genes came under 'Sulphur Metabolism' (*trxB* and *yumC*, with *yumC* also being in the 'Nucleosides and Nucleotides' category), none of which featured as categories for essential genes in the input pools. Following growth in fish serum, 14 essential genes were involved in the 'Virulence and Defence' category, compared to 11 in the input pools before selection. All 11 of those genes found to be essential in the input pools were shared in both pools, but the 3 other genes *copY, gyrB* and *misCA* in that RAST category were only essential for growth in the output pools (Table 3.6).

Under the hypothetical category, just 5 genes were found to be unique to the input compared to 54 genes being unique for growth after screening in fish serum (Tables 3.5 and 3.6). Other categories significantly more represented by essential genes in the output pools than the input pools include the six genes in the 'Cell Division and Cell Cycle' category (*cdaR, divIVA, ftsK_1, mreC, recU* and

rpsU) which does not even feature as a category when shared essential genes are excluded from considerations of essential genes in the input pools; the 'Carbohydrates' category with 11 essential genes for growth in fish serum but just one gene, *pgcA,* essential only in the input pools; and the 'Protein Metabolism' category which contains 4 genes essential for growth in the input pools but 19 genes essential for growth in the output pools.

Table 3.5: Essential coding sequences identified as unique within the *L. garvieae* input pools and their associated RAST categories

RAST Category	Count	Gene
Amino Acids and Derivatives	1	*argR_2*
Carbohydrates	1	*pgcA*
Cofactors, Vitamins, Prosthetic Groups, Pigments	3	*coaE, dhfR, ribF,*
DNA Metabolism	2	*dnaE*, polC_2**
Dormancy and Sporulation	1	*pth**
Fatty acids, Lipids, and Isoprenoids	2	*acpS, mvaS*
Hypothetical	5	LAG_00477, LAG_00093, LAG_00545, LAG_01733*, trxA*
Membrane transport	2	*ecfA1, ecfT*
Nucleosides and Nucleotides	1	LAG_00807
Phages, Prophages, Trasposable Elements, Plasmids	2	*dnaE*, polC_2**
Phosphorous Metabolism	1	*ppaC*
Protein Metabolism	4	*hisS, pheS, pth*, rpmB*
RNA Metabolism	1	*rnj1*

Table 3.6: Essential coding sequences identified as unique within the for *L. garvieae* output pools and their associated RAST categories

RAST Category	Count	Gene
Amino Acids and Derivatives	3	*cysE, mtnN, proC*
Carbohydrates	11	*gale*, gnd, gpmA_1, hprK, pdhD, pgi, pgk, prs, prs2, pta, zwf*
Cell Division and Cell Cycle	6	*cdaR, divIVA, ftsK_1, mreC, recU*, rpsU**
Cell Wall and Capsule	7	*dgs, femB, femX, gale*, rmlB, tagB, tagD_2*
Cofactors, Vitamins, Prosthetic Groups, Pigments	5	*coaA, ftsH, gltX*, nadD_1, thlA**
DNA Metabolism	12	*addA, dnaI, dnaX_1, dnaX_2, gyrB*, hhaIM, priA, recG, recO, recR, recU*, xseB*
Fatty Acids, Lipids, and Isoprenoids	4	*cdsA, fabG_1, plsY, thlA**
Hypothetical	54	*acuR, cpsY, cspL, epsJ, fabH, gdpP, glnR,* LAG_00035, LAG_00042, LAG_00094, LAG_00142, LAG_00144, LAG_00161, LAG_00162, LAG_00180, LAG_00296, LAG_00484, LAG_00524, LAG_00533, LAG_00543, LAG_00644, LAG_00754, LAG_00904, LAG_01103, LAG_01143, LAG_01191, LAG_01204, LAG_01222, LAG_01307, LAG_01341, LAG_01362, LAG_01374, LAG_01407, LAG_01427, LAG_01483, LAG_01722, LAG_01742, LAG_01763, LAG_01779, LAG_01909, *murJ, ppm1, rfbX, secA_1, secY, sepF, tig, walR_1, xerS, yabA, yhbY, yvcJ, yxeN, znuC*
Membrane Transport	1	*ftsY*
Nucleosides and Nucleotides	7	*guaA, mtnN, nrdR, prs, prs2, tdk, yumC*
Phosphorous Metabolism	2	*phoU, pstS1_2*
Protein Metabolism	19	*dnaK, dps, engB, ftsY, gltX*, glyQ, glyS, map, metG, pheT_2, rimI_2, rim, rplA, rplQ, rpsU*, smpB, spsB, trpS2, typA*
Regulation and Cell Signalling	2	*hprK, secG*
Respiration	1	*Nfr2*
RNA Metabolism	8	*mnmG, nusB, nusG, rnc, rnhC, rnj2, rpoZ, tadA_2*
Stress Response	3	*dnaK, dps, smpB*
Sulfur Metabolism	2	*trxB, yumC*
Virulence, Disease and Defence	3	*copY, gyrB*, misCA*

3.6 Truncated sequences important for *L. garvieae* growth

Comparing the genes deemed to encode truncated sequences, the 90 truncated coding sequences identified in the input pools were spread across 18 RAST categories, with the same number of truncated sequences in the output pools being spread across 20 RAST categories (Tables 3.7 and 3.8). 39 of these genes were truncated in both pools. Again, the majority of the truncated sequences in both growth conditions were identified in either the 'Hypothetical' category or the 'Protein Metabolism' category (21% Hypothetical and 18% Protein Metabolism in the input pools compared with 32% Hypothetical and 12% Protein Metabolism in the output pools). Altogether, assuming the truncated sequences to be included as 'essential', this study found 371 genes essential for the growth and survival of *L. garvieae* 02106 in the input pools compared to 488 genes essential in the output pools.

Table 3.7: Truncated coding sequences in *L. garvieae* in the input pools and their associated RAST category. Each protein coding sequence deemed important for *L. garvieae* growth in the input pools that was deemed truncated i.e. insertions within the C-terminal 15% of the encoded protein.

RAST Category	Count	Gene
Amino Acids and Derivatives	1	LAG_01197
Carbohydrates	6	*coaA, iscS_2*, pgk, prs2*, rpsR, tpiA,*
Cell Division and Cell Cycle	4	*dgs*, ftsK_1, ftsW, glmM*,*
Cell Wall and Capsule	12	*ddl, femX, glmM*, ltaS1, mraY, murC, murF_1,* LAG_01479, *prfA, rmlB, rmlD_1, tagO,*
Cofactors, Vitamins, Prosthetic Groups, Pigments	8	*bioY2, coaD, fpgS, gltX*, nadD_1, nadK, pgi, prs*,*
DNA Metabolism	7	*dnaA, dnaI, dnaX_1, hhaIM, recR, topA, zwf,*
Fatty Acids, Lipids, and Isoprenoids	3	*accA, accC, galK_1,*
Hypothetical	19	*cobQ, cpsY, epsJ, murJ,* LAG_01152, LAG_01176, LAG_00142, LAG_01422, LAG_01484, LAG_00484, LAG_00524, LAG_00754, LAG_00811, LAG_00904, *rfbX, secA_1, tig, yrrK, znuB,*
Membrane Transport	3	*Ffh*,* LAG_01485, *prs**
Miscellaneous	2	*cysS*, gpmA_1,*
Nucleosides and Nucleotides	6	*adk, cmk, iscS_2*, prs2*, trxB*, yumC,*
Phosphorous Metabolism	1	*phoU*
Protein Metabolism	16	*alaS, cysS*, dnaX_2, engB, ffh*, ftsY, gatB, gltX*, glyS,* LAG_01762, *rplA, rplQ, rpmE2, rsgA_2, serS, smpB,*
Regulation and Cell Signalling	1	*secY*
RNA Metabolism	4	*dgs*, nusG, rnj2, rpoZ,*
Stress Response	1	*sodA*
Sulfur Metabolism	1	*trxB**
Virulence, Disease and Defence	3	*gyrB, sigA, yhbY*

[#]Each gene was associated to its RAST category based on the subsystem of function (Overbeek et al. 2005). *indicates genes identified to belong to multiple RAST categories

Table 3.8 Truncated coding sequences for *L. garvieae* grown in fish serum and their associated RAST category[#]. Each protein coding sequence deemed important for *L. garvieae* growth in fish serum that was deemed truncated i.e. insertions within the C-terminal 15% of the encoded protein.

RAST Category	Count	Gene
Amino Acids and Derivatives	3	*argR_2, iscS_2*, serS**
Carbohydrates	5	*galK_1, lacC_1, rpiA, tkt_1, tpiA*
Cell Division and Cell Cycle	5	*ezrA, divIB, ftsW, rodA, sigA**
Cell Wall and Capsule	8	*ddl, ltaS1,* LAG_01971, *mraY, murC, murF_1, rmlD_1, tagO*
Cofactors, Vitamins, Prosthetic Groups, Pigments	5	*coaD, coaE, fpgS*, nadK, ribF*
DNA Metabolism	6	*dnaA, recA, recF, ruvB, topA, uvrB*
Dormancy and Sporulation	1	*pth**
Fatty Acids, Lipids, and Isoprenoids	4	*accA, accC, acpS, mvaS*
Hypothetical	29	*arlR_1, atpC, cobQ, cspLA_1, cysS, glmM,* LAG_00043, LAG_00477, LAG_00545, LAG_00656, LAG_00900, LAG_01152, LAG_01224, LAG_01484, LAG_01485, LAG_01836, LAG_01905, *penA, pgcA, ppaX, scpB,* spxA_2, *spxA_3, spxA_11, tcyC, yrrK, ytpP, yusO, znuB*
Membrane Transport	3	*bioY2, ecfT, ffh**
Miscellaneous	1	*iscS_2**
Nucleosides and Nucleotides	5	*Adk, cmk, guaB, pyrG, trxA**
Phages, Prophages, Transposable Elements, Plasmids	1	*dnaE*
Phosphorous Metabolism	1	*ppaC*
Protein Metabolism	11	*alaS, ffh*, fus*, gatB, groL, pth*, rpmE2, rpsO, rpsR, rsgA_2, serS**
Regulation and Cell Signalling	1	*yjbM*
RNA Metabolism	4	*iscS_2*, rnj1, rsuA_2*, sigA**
Stress Response	1	*sodA*
Sulfur Metabolism	1	*trxA**
Virulence, Disease and Defence	3	*Fus*, fpgS*, rsuA_2**

[#]Each gene was associated to its RAST category based on the subsystem of function (Overbeek et al. 2005). *indicates genes identified to belong to multiple RAST categories

3.7 Analysis of subcellular location of genes essential for growth in fish serum

Each of the genes identified as essential for growth of *L. garvieae* 02106 in the output pools (and therefore essential for growth in fish serum which may indicate a role in contributing to septicaemia in clinical lactococcosis in fish), were initially assessed using the SignalP software (Petersen *et al.*, 2011) and PSORTb (Yu *et al.*, 2010) to determine surface or secreted genes and understand their subcellular location. SignalP was used to ascertain which, if any, encoded a signal peptide. If present, a signal peptide is indicative of protein that will be exported from the bacterial cell cytoplasm either as a membrane protein, cell wall associated protein or a truly secreted protein. As such, some proteins containing a signal peptide have potential as targets for vaccination (Kovjazin and Carmon, 2014). Out of the 398 sequences essential for growth in fish serum, three (cdaR, ftsH and pstS1_2) were identified to have a signal peptide (Table 3.9). PSORTb is one of the most accurate predictors of subcellular localisation of bacterial protein (Yu *et al.*, 2010), and was used to complement the findings of SignalP by identifying additional genes encoding protein with a cell wall or extracellular localisation and consequently potential as targets for vaccination, diagnostics and immune responses. Analysis identified four genes with these localisations: *divIB* and *spsB* with predicted cell wall localisations; and LAG_01374 and *sodA* with predicted extracellular localisations (Table 3.9). Of these, *divIB* and *sodA* were identified from the truncated subset of genes, meaning that mutations were only identified in the final 15% of the coding sequence.

In order to identify additional genes with a potential impact on bacterial growth in fish serum, EdgeR analysis was performed to examine the read depth (the

total number of insertions per coding sequence) in each pool as a proxy for the prevalence of a given mutation in a coding sequence (Robinson, McCarthy and Smyth, 2010). This identified nine genes, mutations of which were detected within the output pool data set at statistically significantly lower numbers than in the input pool, three of which (LAG_00167, *ancA* and tcyB) expressed signal peptide (Table 3.10). Although not essential, the data supports the view that these genes are likely to have phenotypic importance. Of these, two were identified as likely to be surface or extracellularly expressed: *ancA* and LAG_00167.

In total four genes were chosen to further investigate based on their likely subcellular localisations and identification as essential for growth in the output pool, after selection in fish serum: *divIB* and *spsB* identified directly from PIMMS comparisons, and *ancA* and LAG_00167 identified by EdgeR analysis.

Table 3.9. Coding sequences which were essential after screening in fish serum and their associated RAST categories of interest from PIMMS data.

Gene	**RAST Category**	**Putative Function**	**Subcellular localisation*** **
cdaR	Cell Division and Cell Cycle	CdaA regulatory protein CdaR**	Unknown
*divIB**	Cell Division and Cell Cycle	Cell division protein DivIB	Cell wall localisation/ possibly many localisation sites
ftsH	Cofactors, Vitamins, Prosthetic Groups, Pigments	ATP-dependent zinc metalloprotease FtsH**	Cytoplasmic membrane
LAG_01374	Hypothetical protein	Hypothetical protein	Extracellular localisation
pstS1_2	Phosphorous Metabolism	Phosphate-binding protein PstS 1**	Unknown
*sodA**	Stress Response	Superoxide dismutase [Mn]	Extracellular localisation
spsB	Protein Metabolism	Signal peptidase IB	Cell wall localisation/possibly many localisation sites

*Truncated genes
** Signal peptide detected using BLASTp and SignalP
***Subcellular localisation by PSORTb

Table 3.10. Genes with statistically significant fold change differences after screening in fish serum[1]

Locus	Gene	RAST Category	Function	Subcellular Localisation***	Log-FC	FDR*	Input vs Output
LAG_00167	NA	Hypothetical	Hypothetical protein**	Unknown	-2.39538	0.03414	DOWN
LAG_00168	*ancA*	Virulence, Disease and Defence	Cellulosome-anchoring protein**	Cell wall	-2.03501	0.02552	DOWN
LAG_00243	*penA*	Cell Wall and Capsule	Penicillin-binding protein 2B	Cytoplasmic membrane	-3.56023	0.03414	DOWN
LAG_00472	*artM_2*	-	Arginine transport ATP-binding protein ArtM	Cytoplasmic membrane	-3.71231	0.03414	DOWN
LAG_00473	*tcyB*	-	L-cystine transport system permease protein TcyB**	Cytoplasmic membrane	-4.09013	6.34106 e-07	DOWN
LAG_00611	*purB*	Nucleosides and Nucleotides	Adenylosuccinate lyase	Cytoplasmic	-3.61624	0.03414	DOWN
LAG_00899	*acuR*	-	Transcriptional regulator AcuR	Cytoplasmic	-4.56277	0.03414	DOWN
LAG_01618	*treA*	Carbohydrates	Trehalose-6-phosphate hydrolase	Cytoplasmic	-2.94243	0.03414	DOWN
LAG_01994	*clpE*	-	ATP-dependent Clp protease; ATP-binding subunit ClpE	Cytoplasmic	-1.22193	0.03414	DOWN

[1]Results derived from EdgeR analysis. EdgeR developed by (Robinson, McCarthy and Smyth, 2010). NA = no gene name applicable. FDR = false discovery rate. * p-value adjusted Benjamini and Hochberg's procedure (Benjamini & Hochberg 1995). **indicates presence of a signal peptide. Where no RAST category is present (denoted -), RAST was unable to assign a category to that gene. ***Subcellular localisation by PSORTb

3.8 Homology of the essential genes of *L. garvieae*

The products of the four selected genes in strain 02106 were compared with other *L. garvieae* strains used in this study (00021, 03017 and 03084) (Verner-Jeffreys *et al.*, 2011) using Clustal Omega (Sievers and Higgins, 2017) (Figures 3.4-3.7). Clustal Omega carries out multiple sequence alignment enabling assessment of the degree of similarity between proteins from different sources. Three of the genes of interest (*ancA, divIB* and *spsB*) could be identified in strain 02106 and 3 other virulence *L. garvieae* strains previously isolated from cases of clinical disease in fish (00021, 03017 and 03084) or alignment with >95% similarity across strains. However LAG_00167 from 02106 could only be identified in strain 0021 from these draft genomes, although this was with 100% similarity (Figure 3.6).

To compare the sequence similarity of the selected four virulence genes with other *L. garvieae* strains and other lactococcal species of clinical importance the same four genes from strain 02106 were aligned against those found in other genomes identified using BLASTp (Figures 3.4-3.7). Similar sequences found in other strains and species would have the potential to be targeted with the same specific molecule as that developed against *L. garvieae* 02106, making future work on these proteins more relevant to infections with other lactococcal strains and species, potentially in different host organisms. Proteins with over 70% identity (aligned amino acids) in other strains, species and hosts were considered for comparison as this was considered a high enough match for the immune system or a diagnostic molecule to recognise as the same sequence and hence act as a multivalent molecule, but low enough to allow for the inevitable degree of variation between relevant proteins from other bacterial species located from many different sources.

This enabled comparison of DivIB from 02106 with the homologous cell division protein FtsQ in four other strains of *L. garvieae,* two identified with 100% identity to the protein from the 02106 strain (*L. garvieae* PAQ102015-99 from a commercial trout farm in the USA (Accession number: OAL09416.1) (Nelson *et al.*, 2016), and another strain 8831 from lactococcosis in rainbow trout in Spain WP_019293242.1) (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011), and two shared 98% identity to the 02106 strain (*L. garvieae* TB25 from lactococcosis in Italian rainbow trout (WP_019292071.1) (Ricci *et al.*, 2012) and strain 21881 isolated from a case of human septicaemia (WP_019292071.1) (Aguado-Urda, López-Campos, Blanco, *et al.*, 2011; Aguado-Urda, López-Campos, Gibello, *et al.*, 2011) (Figure 3.5)).

spsB was aligned with three other signal peptidase I proteins in strains of *L. garvieae* using Clustal Omega: UNIUD074 from lactococcosis in Italian rainbow trout (WP_019299792.1) (Reimundo *et al.*, 2011) and DSM20684, an unpublished genome taken from a mastitic cow in Italy (PCS00250.1) (Sun et al., 2017, Unpublished), and 21881 from the same case of human septicaemia (WP_019291501.1) (Aguado-Urda, López-Campos, Blanco, *et al.*, 2011) in which the DivIB homologue was also identified and aligned very similarly. All three of these proteins had 99% identity with the signal peptidase B protein from *L. garvieae* 02106 (Figure 3.7)).

ancA was aligned with two hypothetical proteins in strains of *L. garvieae*: 8831 from rainbow trout in Spain with 100% alignment (WP_019293013.1) (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011), and PAQ102015-99 from the commercial US trout farm with 98% identity (OAL09117.1) (Nelson *et al.*, 2016) (Figure 3.4).

Finally LAG_00167 aligned with strains of *L. garvieae* from a wide variety of sources, including human cholecystitis (Kim, Kang and Park, 2015) and a grey lemur (Denapaite *et al.*, 2016). Alignments were produced against *L. garvieae* A1 from soil (WP_081165648.1) (Altin, Nikerel and Şahin, 2017), 8831 from rainbow trout in Spain (WP_019293014.1) (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011), PAQ-102015-99 from the commercial US trout farm (OAL09116.1) (Nelson *et al.*, 2016) and TB25 from rainbow trout in Italy (WP_019336008.1) (Ricci *et al.*, 2012). The protein also aligned with an example of *L. petauri,* strain 159469 with 71% identity, which was isolated from an abscess in a sugar glider (WP_086582781.1) (Goodman *et al.*, 2017) as the closest alignment to a non-*L. garvieae* species for interest (Figure 3.5).

```
Lgv 02106            MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPVDEDGQTVKEEIQEDTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
Lgv 00021            MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPVDEDGQTVKEEIQEDTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
Lgv 8831             MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPVDEDGQTVKEEIQEDTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
Lgv PAQ102015-99     MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPVDEDGQTVKEEIQEDTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
Lgv 03017            MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPIDEEGQTVKEDIQENTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
Lgv 03084            MINLRKAAVFTGLCFIALAAHAAQADTAEVPVDNHPMGYYAEVQTEENPMTAPIDAQGNLAPIDEEGQTVKEDIQENTETPKVSSRVRRAIADDAETAQASLRNAPSDLVSNDTSLPRKD
                     ************************************************************:**:******:***:****************************************

Lgv 02106            AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLSTSTVMINDAEYVPKDSVGTMPYWD
Lgv 00021            AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLSTSTVMINDAEYVPKDSVGTMPYWD
Lgv 8831             AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLSTSTVMINDAEYVPKDSVGTMPYWD
Lgv PAQ102015-99     AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLSTSTVMINDAEYVPKDSVGTMPYWD
Lgv 03017            AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLTTGTVMINDAEYVPKDSVGTMPYWD
Lgv 03084            AVDIASWQDWMTQSDFNQLKAQGVKTVIVKLTESTTYINPAAKAQIQMAKNAGLTVAVYHFSHFSESGKTAQATVNNTARAEANFFANVAKQYGLTTGTVMINDAEYVPKDSVGTMPYWD
                     ******************************************************************************************:*.**********************

Lgv 02106            WTVASQNFADQLKKQGFVSTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVKFVNLPVKNPNPSPF
Lgv 00021            WTVASQNFADQLKKQGFVSTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVKFVNLPVKNPNPSPF
Lgv 8831             WTVASQNFADQLKKQGFVSTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVKFVNLPVKNPNPSPF
Lgv PAQ102015-99     WTVASQNFADQLKKQGFVSTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVKFVNLPVKNPNPSPF
Lgv 03017            WTVASQNFADQLKKQGFVNTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVNFVNLPVKNPNPSPF
Lgv 03084            WTVASQNFADQLKKQGFVNTRHYASKAWAVDGVGQMEPSKLGAKNMWIAQYLYGKPSASNLQNTQFGSWQYTSQMYFTNFSRRSPLDVSIDYANIFSGDLPRISVNFVNLPVKNPNPSPF
                     ******************.*****************************************************************************************:**************

Lgv 02106            KDISQSIYKNYINWNYKVGITTGYTPTTYNPNANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYTPNGTVTRGQMAAFLHRTAKAMGKAPASGTYTSS
Lgv 00021            KDISQSIYKNYINWNYKVGITTGYTPTTYNPNANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYTPNGTVTRGQMAAFLHRTAKAMGKAPASGTYTSS
Lgv 8831             KDISQSIYKNYINWNYKVGITTGYTPTTYNPNANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYTPNGTVTRGQMAAFLHRTAKAMGKAPASGTYTSS
Lgv PAQ102015-99     KDISQSIYKNYINWNYKVGITTGYTPTTYNPNANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYTPNGTVTRGQMAAFLHRTAKAMGKAPASGTYTSS
Lgv 03017            KDISQSIYKNYINWNYKVGITTGYTPTTYNPDANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYNPNGNVTRGQMAAFLHRTAKAMGKAPASGTYTSS
Lgv 03084            KDISQSIYKNYINWNYKVGITTGYTPTTYNPDANVTRGEMAVFLHRLAGSPAYTPPFNVYTDVNQYKNQILWLTAANISNGTAPHYNPNGNVTRGQMAAFLHRTAKAMGKAPASGTYTSS
                     ******************************:*********************************************************.***.****************************

Lgv 02106            FKDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYDTLK
Lgv 00021            FKDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYDTLK
Lgv 8831             FKDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYDTLK
Lgv PAQ102015-99     FKDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYDTLK
Lgv 03017            FTDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYNTLK
Lgv 03084            FTDINNNMFKNDINWLKTKGITTGYTPTTFRPDASISRGEMAAFLNRFYNTLK
                     *.*********************************************:***
```

Figure 3.4. Sequence alignment of *L. garvieae* strain 02106 *ancA*.
L. garvieae 02106 >LAG_00168 (*ancA*) was compared with 3 other clinical *L. garvieae* strains (00021, 03017 and 03084) used in this study using Clustal Omega (Sievers and Higgins, 2017) with over 95% similarity between the sequences. The protein sequence also aligned with *L. garvieae* 8831 (Accession number WP_019293013.1) isolated from rainbow trout in Spain (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011) with 100% identity, and with 98% identity to a protein expressed by *L. garvieae* PAQ102015-99 (OAL09117.1), isolated from a commercial trout farm in the USA (Nelson *et al.*, 2016). (*) represents positions with a conserved residue between strains. (:) represents amino acid group conservation with very closely related properties – equivalent to >0.5 in the Gonnet PAM 250 matrix. (.) represents amino acid group conservation with poorly related properties as equivalent to <0.5 and >0 in the Gonnet PAM 250 matrix (Sievers and Higgins, 2017). Red represents the location of signal peptide across all strains used for the alignment (Petersen *et al.*, 2011).

```
Lgv 02106          MSEENLTPWQKKHLEYQRRKAAENQEKSEEPKKRKFFKKKEDIEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEHSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv 00021          MSEENLTPWQKKHLEYQRRKAAENQEKSEEPKKRKFFKKKEDIEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEHSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv 8831           MSEENLTPWQKKHLEYQRRKAAENQEKSEEPKKRKFFKKKEDIEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEHSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv PAQ102015-99  MSEENLTPWQKKHLEYQRRKAAENQEKSEEPKKRKFFKKKEDIEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEHSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv TB25           MSEENLTPWQKKHLEYQRRKADENQEKSEEPKKRKFFKKKEDSEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEPSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv 21881          MSEENLTPWQKKHLEYQRRKADENQEKSEEPKKRKFFKKKEDSEADSPEVQEEIEQQESFVEAEESEQGYSDDFVEDFEEQEPEPSFFEGSFEVFKKMWPVLFLAILLFLTSIYAVSPIS
Lgv 03017          MSEENLTPWQKKNLEYQRRKAAENQEKSEEPKKRKFLKKKEETEADSPEVQEEIEQQESFVEAESFEETYSDDFVEDFEEQEPEPSFFEGSFEVFKKMWPVLLLAILLFLTSIYAVSPIS
Lgv 03084          MSEENLTPWQKKNLEYQRRKAAENQEKSEEPKKRKFLKKKEETEADSPEVQEEIEQQESFVEAESFEETYSDDFVEDFEEQEPEPSFFEGSFEVFKKMWPVLLLAILLFLTSIYAVSPIS
                   ************:******** ***************:****: *********************. *: *************** *****************:*****************

Lgv 02106          KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKDQETAKDKLSKLPVLKNFSDEEVEKF
Lgv 00021          KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKDQETAKDKLSKLPVLKNFSDEEVEKF
Lgv 8831           KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKDQETAKDKLSKLPVLKNFSDEEVEKF
Lgv PAQ102015-99  KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKDQETAKDKLSKLPVLKNFSDEEVEKF
Lgv TB25           KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKNQEIAKDKLSSLPILKNFSDEEVEKF
Lgv 21881          KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNKRAIENSIVQQFPRVKSVNLHVSFPNNIEAKVTEFEKVAYVEQKGKTYQVLESGHILKNQEIAKDKLSSLPILKNFSDEEVEKF
Lgv 03017          KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNRRAIENSIVQEFPRVKSVNLQVSFPNNIEAKVTEFEKVAYVEQKGKNYQVLENGHILKDQEIAKDKVSNLPLLKNFSDDEVEKF
Lgv 03084          KIGTFTVSGNKNESFESIVQASRLKPTDRIYGVLRNRRAIENSIVQEFPRVKSVNLQVSFPNNIEAKVTEFEKVAYVEQKGKNYQVLENGHILKDQEIAKDKVSNLPLLKNFSDDEVEKF
                   ************************************:*********:*********:*************************.*****.*****:** ****:*.**:******:*****

Lgv 02106          ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv 00021          ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv 8831           ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv PAQ102015-99  ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv TB25           ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv 21881          ITAYMKLKPEIRGLITTVTKTPTKATKDFIALDMSDGNQVRVSLSQITEKVPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv 03017          ITAFMKLKPEIRGLVTTVTKTPTKATNDFIALDMSDGNQVRVSLSQITEKMPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
Lgv 03084          ITAFMKLKPEIRGLVTTVTKTPTKATNDFIALDMSDGNQVRVSLSQITEKMPYYPSIAKQLQAPQVIDMEAGIYAKPKEDYLADLKNPEGNKKNSENTTEITATQ
                   ***:**********:***********:***********************:*****************************************************
```

Figure 3.5. Sequence alignment of *L. garvieae* strain 02106 >LAG_00471 (*divIB*).
L. garvieae 02106 >LAG_00471 (*divIB*) was compared with 3 other clinical *L. garvieae* strains (00021, 03017 and 03084) used in this study using Clustal Omega (Sievers and Higgins, 2017), with over 95% similarity in the protein sequence between strains. The protein also aligned with 100% identity with a DivIB protein from *L. garvieae* 8831 (WP_019293242.1), isolated from rainbow trout in Spain (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011), and with *L. garvieae* PAQ102015-99 (OAL09416.1) from a commercial trout farm in the US (Nelson *et al.*, 2016). 98% identity was observed with *L. garvieae* TB25 (WP_019292071.1) from lactococcosis in Italian rainbow trout (Ricci *et al.*, 2012), and with *L. garvieae* 21881 (WP_019292071.1) isolated from a case of human septicaemia (Aguado-Urda, López-Campos, Blanco, *et al.*, 2011). (*) represents positions with a conserved residue between strains. (:) represents amino acid group conservation with very closely related properties – equivalent to >0.5 in the Gonnet PAM 250 matrix. (.) represents amino acid group conservation with poorly related properties as equivalent to <0.5 and >0 in the Gonnet PAM 250 matrix (Sievers and Higgins, 2017). No signal peptide was identified in the protein from any strain used in this alignment.

```
Lgv A1                  MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDKEKEKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPVELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lgv 02106               MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDK--EKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPDELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lgv 00021               MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDK--EKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPDELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lgv 8831                MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDK--EKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPDELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lgv PAQ102015-99        MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDK--EKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPDELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lgv TB25                MTIYKYKKYIKIFSILVTIVSCFYISSGNVLAIDK--EKVTFNISATQEGGPAASSNIVYENVQTAYENIMKGTIPDELEKTVLWNAALSDNQQFIELGSGLKLGQGITHDSAEAKKIIQ
Lpt 159469              MTFYKNKNYIKVFSLLFVMLISVYSVK-STYATEADNGEVTFNISATQQGEPAASSSIAYENIQTAYENIMKGNIPNELEKSVIWNTSLTNKENFINLGDGLRLGQGITHSSEEAKKIIQ
                        **:** *:***:**:*..:: ..*  . .. * :    :*********:* *****.*.***:**********.** ****:*:**::*:::::**:**.**:*******.* *******

Lgv A1                  ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lgv 02106               ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lgv 00021               ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lgv 8831                ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lgv PAQ102015-99        ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lgv TB25                ILFQSNFEIFQFLNGNPRESMSDIKSFLTDENGQGSAKIEKGLLAVISNSTIINLVDLTENNQNISVDLDGTNSGVSFEFVGVSDNSKSKVGTYVLENNQKIAYKITVSKDLLKDGEQVL
Lpt 159469              ILFQSNFDIFQFLNGSSHKTMSDIKSLITDENGKGSAQAERGLLAVISNAMIISFVDLASNNQNISVDLDGTSSGISLEFTGIPENSQNASGAYILENNQKIGYKITISKDLLKESEQVF
                        *******:*******. :::******::*****:***: *:********: **.:***:.************.**:*:**.*: :**:.  *:*:*******.****:******:.***:

Lgv A1                  SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lgv 02106               SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lgv 00021               SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lgv 8831                SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lgv PAQ102015-99        SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lgv TB25                SILTPSNVIIESSSVPLEKKSVLPTIIPENYYQGLAVTSDNYELLKPQIFSVTSEKLKSTFSNENYYTLPQSDEDIVVTGELSVSPIVTEEVNFLFTTVPLTAQLNLHSFNMQDGSNVKQ
Lpt 159469              SIQTPPNVVIDSSSVPLQKKSLLPSVIPEAYYQGLTVTSDNYELLQQQVFSMTSEKLKSTYTNENYYTLPRSDEDITITGTLSVSPNVPEEVNFLFNTLPLTAQLNLHNFNMQDGSNVKQ
                        ** ** **:*:******:***:**::*** *****:*********: *:**:********::********:*****.:** ***** * *******.*:*********.***********

Lgv A1                  PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISSHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGEIEGIPMAVNPQNWNRDFQAIQSKNQS
Lgv 02106               PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISSHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGESEGIPMAVNPQNWNRDFQAIQSKNQS
Lgv 00021               PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISSHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGESEGIPMAVNPQNWNRDFQAIQSKNQS
Lgv 8831                PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISSHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGESEGIPMAVNPQNWNRDFQAIQSKNQS
Lgv PAQ102015-99        PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGESEGIPMAVNPQNWNRDFQAIQSKNQS
Lgv TB25                PSNFQVTAQVGEGTTAASALAAPLSSAGINFVLIDGEENKLVKDAQYVLGKKQDNKYYISSHSGWKEVKQKDLTQLNTDDYTVMSGGNIYNFGESEGIPMAVNPQNWNRDFQAIQSKNQS
Lpt 159469              PSSFQITVQVGEGVGAASIISAPLSSAGINFVMIDGEKNKLISGAQYVLGKKEADKYYISSDKGWKEVEQSNLSHLNLDDYILLSGGNIYNLDDNQAIPMAVNSQNWDRDFQAIQSRNQS
                        **.**:*.*****. *** ::***********:****:***:..********: :***** *..*****:*.:*::** *** ::*******:.: :.*********:********:***

Lgv A1                  LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQSQAVGLNGQIPGYIAGTNEFNILSVTSNTGSLKINVKNSIIFPIALIIFVIVLIGLVLIWRF
Lgv 02106               LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQSQAVGLNGQIPGYIAGTNEFNILSVTSNTDSLKINVKKSIIFPIVLIIFVIVLIGLVLIWRF
Lgv 00021               LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQSQAVGLNGQIPGYIAGTNEFNILSVTSNTDSLKINVKKSIIFPIVLIIFVIVLIGLVLIWRF
Lgv 8831                LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQSQAVGLNGQIPGYIAGTNEFNILSVTSNTDSLKINVKKSIIFPIVLIIFVIVLIGLVLIWRF
Lgv PAQ102015-99        LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQSQAVGLNGQIPGYIAGTNEFNILSVTSNTDSLKINVKKSIIFPIVLIIFVIVLIGLVLIWRF
Lgv TB25                LLGIRGLGQGNQYFLMQVKAPSGYNKIDQPHYFTVHNDKDSTQISRNSDSIGFAQNQAVGLNGQIPGYIAGTNEFNILSVTSNTDSLKINVKKSIIFPIVLIIFVIVLIGLVLIWRF
Lpt 159469              LLGIRGLGQGKQYFVMQVKAPEGYSKVDQPHYFTVHNNKNNLQSPRNSDSIGFATEQAMKLNGQIPGYMAGTNEFNALSVTSDIGNLGINIKS-IIIPIMLIILFIIFIGVLLVWKL
                        **********:***:******.**.*:**********:*:. *  ********* .**: ********:******* *****: ..* **:*. **:** ***:.*::**::*:*::
```

Figure 3.6. Sequence alignment of L. garvieae strain 02106 >LAG_00167.
L. garvieae 02106 >LAG_00167 was compared with other clinical *L. garvieae* strains used in this study using Clustal Omega (Sievers and Higgins, 2017). 100% alignment was observed between *L. garvieae* 02106 and *L. garvieae* 00021, as well as with *L. garvieae* 8831 (WP_019293014.1) isolated from an outbreak of lactococcosis in trout in Spain (Aguado-Urda, López-Campos, Gibello, *et al.*, 2011). The protein also aligned with 99% identity to other hypothetical proteins from *L. garvieae* TB25 (WP_019336008.1) isolated from rainbow trout showing signs of lactococcosis in Italy (Ricci *et al.*, 2012), the *L. garvieae* PAQ102015-9 strain (OAL09116.1) from a commercial trout farm in the USA (Nelson *et al.*, 2016), and *L. garvieae* A1 (WP_081165648.1) isolated from soil (Altin, Nikerel and Şahin, 2017). The protein sequence in *L. gravieae* 02106 aligned at 71% identity with a strain of *L. petauri* (WP_086582781.1) from an abscess in a sugar glider, which was the closest alignment of the protein with a non-*L. garvieae* strain. Red highlights the location of signal peptide identified using SignalP (Petersen *et al.*, 2011).

```
Lgv 03017          MENTTQTKQTNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv 03084          MENTTQTKQTNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv UNIUDO74       MENTTQTKQTNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv DSM20684       MENTTQTKQTNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv 02106          MENTTQNKQPNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv 00021          MENTTQNKQPNAFTRFIKEWGIFLAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
Lgv 21881          MENTTQNKQPNAFTRFVKEWGIFIAIITIAILSRIFIWSLVVVDGHSMDPNLADKQRLVLIKTASINRFDIVVAKETETVNGQTETKDVVKRVVGMPGDEIKFDKDQLYINGKKTDEPYL
                   ******.** ******:******:*****************************************************************************************

Lgv 03017          ADFKKQLSNNELEKTYQNYALTSELSEANRAFFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv 03084          ADFKKQLSNNELEKTYQNYALTSELSEANRAFFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv UNIUDO74       ADFKKQLSNNELEKTYQNYALTSELSEANRAFFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv DSM20684       ADFKKQLSNNELEKTYQNYALTSELSEANRAFFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv 02106          ADFKKQLSNNELEKTYQNYALTSELSEANRAYFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv 00021          ADFKKQLSNNELEKTYQNYALTSELSEANRAYFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
Lgv 21881          ADFKKQLSNNELEKTYQNYALTSELSEANRAYFVQLAQQAQAFTTDATGNPTFTIKVPEGEYLLLGDNRIVSRDSRAVGTFKRSDIVGRTMFRVWPINKISTLN
                   ******************************:*****************************************************************************
```

Figure 3.7. Sequence alignment of L. garvieae strain 02106 >LAG_02029 (spsB).
L. garvieae 02106 >LAG_02029 (*spsB*) was aligned with 3 other clinical *L. garvieae* strains (00021, 03017 and 03084) used in this study using Clustal Omega (Sievers and Higgins, 2017), with over 95% similarity between strains. The protein also aligned with 99% identity in *L. garvieae* UNIUD074 (WP_019299792.1), isolated from rainbow trout in Italy (Reimundo *et al.*, 2011), to a draft genome of *L. garvieae* DSM20684 (PCS00250.1) from a mastitic cow in Italy (Sun et al., 2017), and with *L. garvieae* 21881 (WP_019291501.1) from a case of human septicaemia (Aguado-Urda, López-Campos, Blanco, *et al.*, 2011).

3.9 Involvement of essential genes in metabolic pathways

The Kyoto Encyclopedia of Genes and Genomes (KEGG) software was used to determine if genes *LAG_00167*, *ancA, divIB* and *spsB* could be assigned function within metabolic pathways, to determine putative roles in growth in fish serum. Each pathway identified could categorise genes in two ways: either by the normalised insertions mapped (NIM) or by the first unique insertion position in the gene as a centile of gene length. The NIM values are obtained using the PIMMS data, and represent the number of insertions of the ISS1 element across the coding sequence relative to others in the population, also taking the variability of the number of mapped sequence reads into account for each experiment. The NIM values were converted to a score based on the number of insertions present, between the coding sequence with the fewest insertions (lowest score) and the coding sequence with the most insertions (highest score) as a centile for comparison within the KEGG programme. The first unique insertion position is location of the ISS1 insertion closest to the start codon of the gene, expressed as a centile of gene length. Insertion close to the start of sequence will result in a decreased likelihood of producing a functional gene product due to early termination and production of a truncated protein. The first unique insertion position could be considered more important in the study of essential genes, because whilst the NIM gives information on the number of insertions in a gene, it cannot give as reliable and indication of whether the gene could encode a functional protein before the first site of mutation in the sequence.

To highlight differences in these comparison parameters, both analysis outputs are displayed for analysis of *divIB* (Figures 3.8 and 3.9). This gene could not be assigned to a metabolic pathway within KEGG, but its orthologue *ftsQ* was

identified as part of the cell cycle pathway of *Caulobacter crescentus*, an organism frequently used to model the bacterial cell cycle. In this cell cycle pathway, protein FtsQ was found to be part of a complex associated with FtsA, FtsW, MurG and FtsZ and the actions of Z ring formation in bacterial division (Figures 3.8 and 3.9). All four of the genes encoding these associated proteins were annotated in the input and output pools for *L. garvieae* used in this study. *ftsQ* has a low number (<20-30%) of normalised insertions mapped (NIM) in both input and output pools relative to the other genes in this study, but a more considerable difference was noted between input and output pools when comparing the first unique insertion position in the gene: 5.9% in the input pool and 88.2% in the output pool.

In contrast to *divIB*, *spsB* was identified as being involved in the protein export pathway (Figure 3.10) and also matched with *spsB* identified in *S. aureus* in the quorum sensing pathway (data not shown), which is involved in cell-cell communication to coordinate growth, division, and defence including the formation of bacterial biofilms (Nadell *et al.*, 2008). No other proteins in the *S. aureus* quorum sensing pathway could be identified in the *L. garvieae* 02106 proteome and there are no reports of *L. garvieae* forming biofilms in current literature. However, in the protein export pathway, two prokaryotic signal peptidases were identified (SPaseI and SPaseII), with SPaseI being encoded by *spsB.* The first unique insertion position of the ISS1 element was found to be at the 72nd centile in the input pool, and there are no insertions in the gene found within the output pool (highlighted in red in the KEGG pathway, Figure 3.10). Other proteins in the *L. garvieae* 02106 genome were also identified in this protein export pathway, including *secG* which was also found to be essential for growth in the output pool, but not in the input pool.

Neither the hypothetical protein LAG_00167 nor *ancA* (LAG_00168) were identified within bacterial pathways available for analysis through the KEGG software, indicating that they may not have an involvement in core metabolic pathways or that they are less commonly found in other bacterial species on which the KEGG pathways are based.

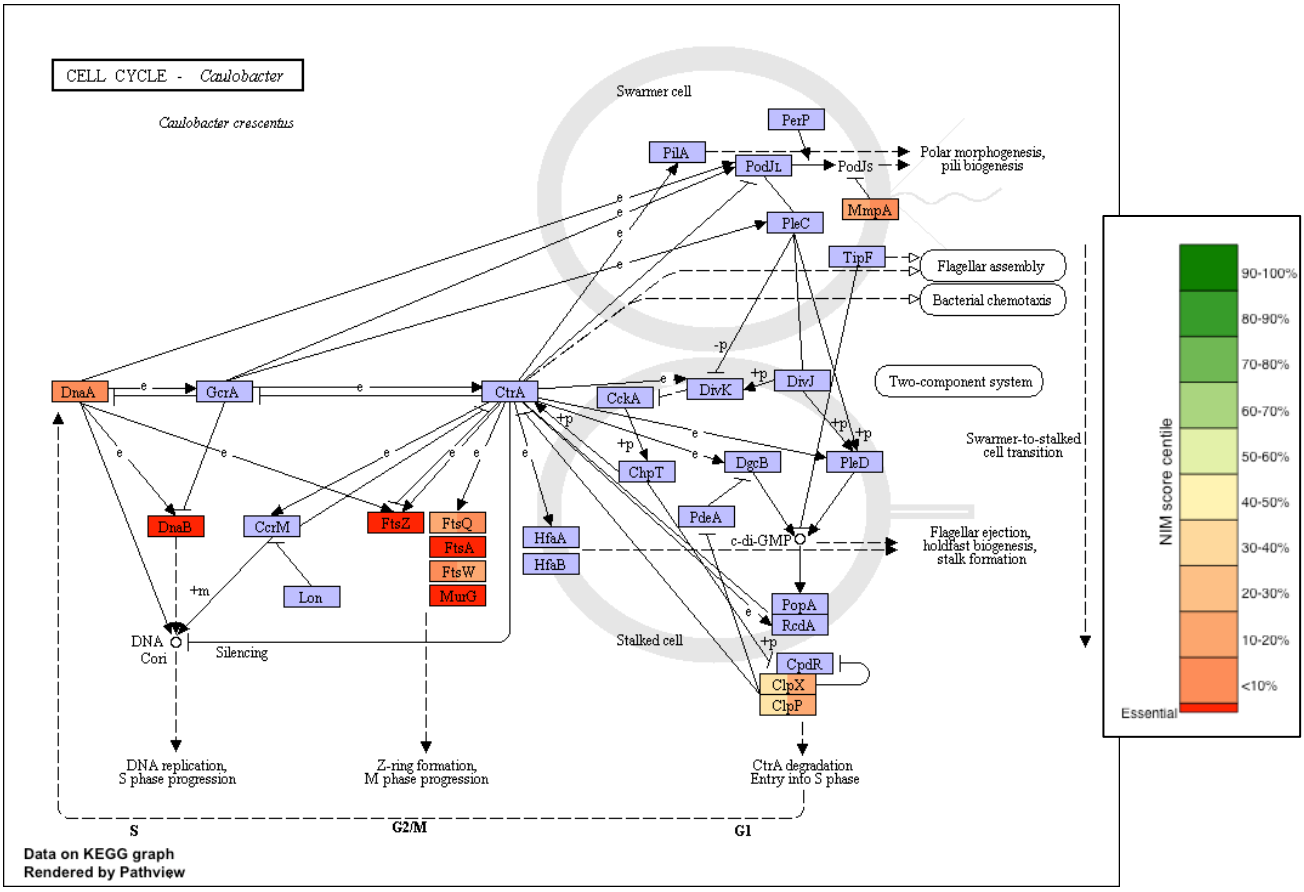


Figure 3.8: NIM analysis of the cell cycle pathway of *C. crescentus* and the role of the DivIB orthologue FtsQ in the model bacterial cell cycle.
All proteins involved in the model cell cycle pathway are shown in individual boxes, which are divided in two to show any differences between the input pool (left hand side) and output pool (right hand side). Lilac denotes proteins known to be involved in the metabolic pathway but which were not identified in the pools of *L. garvieae* 02106 used in this study. Genes are linked by arrows indicating the interaction of their products within the pathway. Solid arrows indicate one gene having a molecular interaction or relation on another gene in the direction of the arrow; interrupted arrows indicate an indirect or unknown link. Lines ending with 'T'-head instead of an arrowhead indicate where one protein inhibits the other. Empty-filled arrows point to a link to or from another map of a different pathway. 'e' indicates where the interaction between two genes involves expression. +m indicates where the encoded protein is methylated. +p indicates where a protein is phosphorylated. Inset right: colour-coded key where red indicates that the gene is essential in that pool with zero insertions throughout the gene length and green indicates the genes with the highest number of insertions throughout their length. The NIM 'score' is assigned on a gene-specific basis relative to all other genes in the pool. FtsQ has a NIM score in the 10-20% centile, whilst in the output pool the NIM score is in the <10% centile. The lower this value, the more likely the protein is to play an essential role in the pathway.

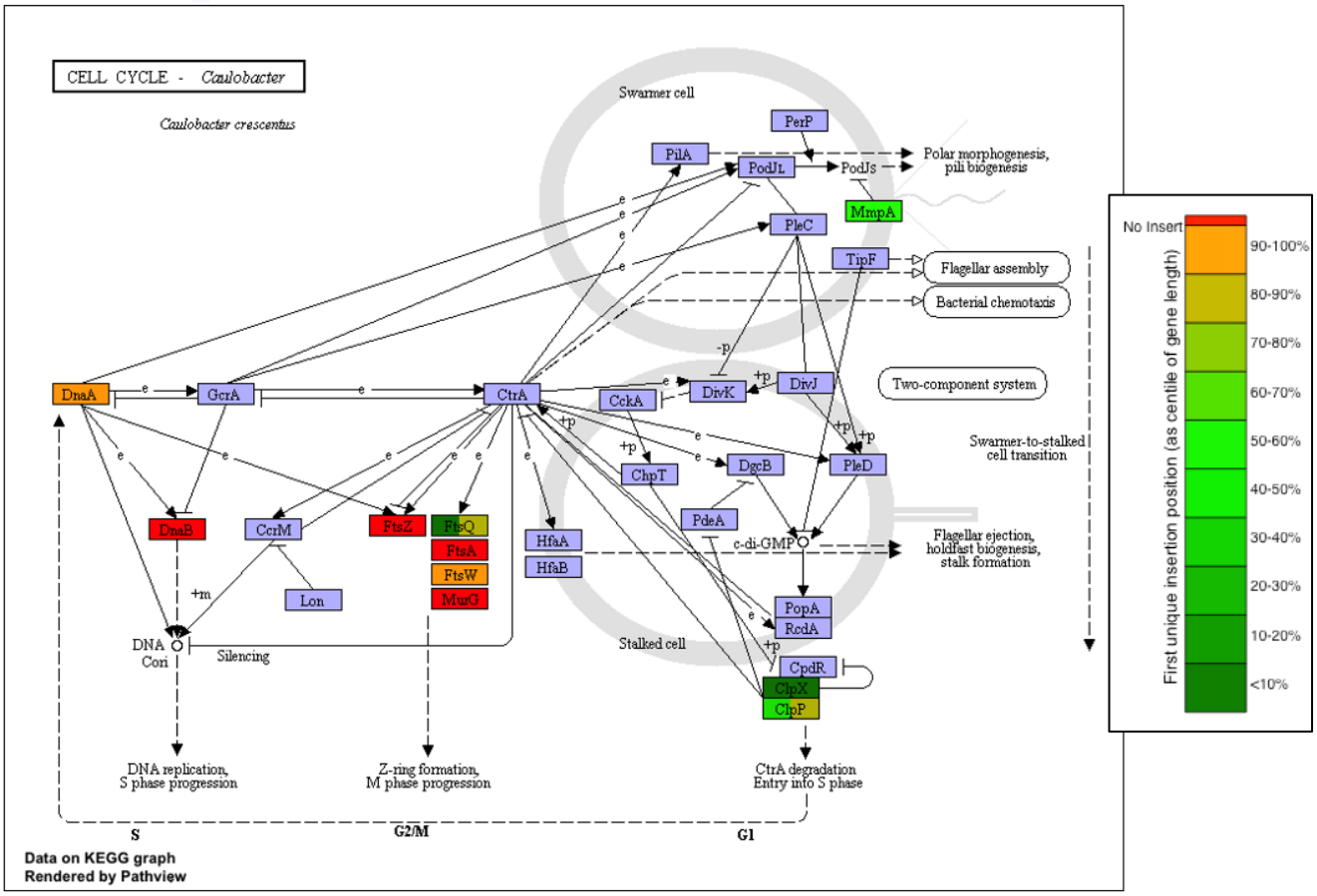


Figure 3.9: First unique insertion analysis of the cell cycle pathway of *C. crescentus* and the role of the DivIB orthologue FtsQ in the model bacterial cell cycle.

Inset right: colour-coded key where red indicates that zero insertions occurred throughout the coding sequence, and various shades of green indicate the position of the first unique insertion of the ISS1 element in the gene, where darker greens indicate an earlier insertion and paler greens to orange indicate later insertions in the sequence. In the input pool, the gene encoding FtsQ has a first unique insertion position at <10% of its length (dark green), compared to a first insertion point at 80-90% of the gene in the output pool (mustard yellow). The lower this value, the earlier the gene in the pool has been disrupted and thus the less likely it is to be essential, as the bacteria with this insertion have grown despite having a disrupted version of the gene and hence a disrupted and potentially non-functional version of the resultant protein. The later in the gene the first insertion occurs, the more likely this gene is to be essential or truncated, as the majority of the gene can be encoded to potentially functional protein (either complete or truncated) for the bacteria to survive. Lilac denotes proteins known to be involved in the metabolic pathway but which were not identified in the pools of *L. garvieae* 02106 used in this study. Genes are linked by arrows indicating the interaction of their products within the pathway.

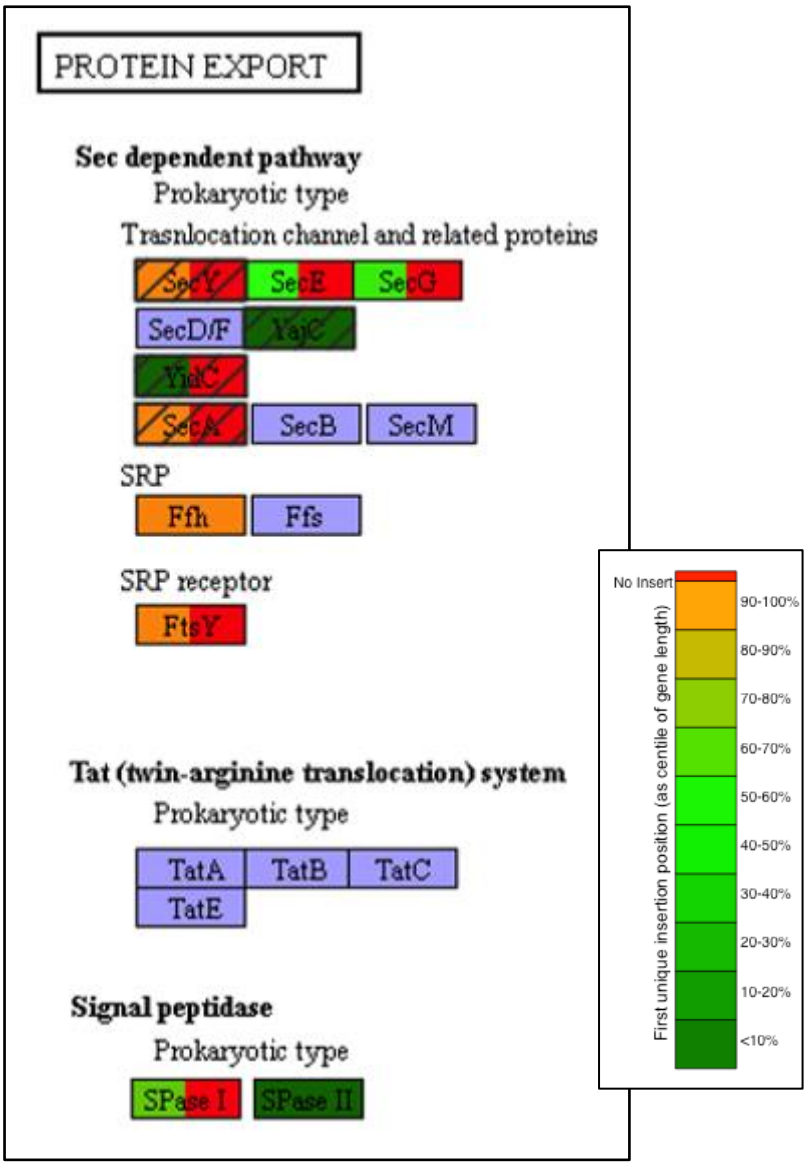


Figure 3.10: Analysis of the first unique insertion positions of the ISS1 element in the protein export pathway and the role of two prokaryotic signal peptidases, which KEGG identified as encoded by gene *spsB*.
Inset right: colour-coded key where red indicates that zero insertions occurred throughout the coding sequence, and various shades of green indicate the position of the first unique insertion of the ISS1 element in the gene, where darker greens indicate an earlier insertion and paler greens to orange indicate later insertions in the sequence. SPase I was encoded with a first unique insertion position at 30-40% (bright green) and no insertions (red) in *spsB* in input and output pools respectively, whereas SPase II was encoded with a first insertion at <10% of the *spsB* gene length in both input and output pools. Lilac denotes proteins known to be involved in the metabolic pathway but which were not identified in the pools of *L. garvieae* 02106 used in this study.

3.10 Further investigation of LAG_00167 and *ancA*

As LAG_00167 and *ancA* could not be identified within the KEGG metabolic pathway analysis, each protein was further investigated using the STRING database (Szklarczyk *et al.*, 2017) which identifies associations between different proteins in the genome in order to link putative functions and is particularly useful for predicting the function of hypothetical proteins. Associations can be by neighbourhood, where the genes encoding two proteins are closely positioned in the genome, or by co-occurrence if two proteins are often seen expressed together or not at all, but rarely expressed alone. STRING can also associate genes by 'fusion', if at least one organism has orthologues of the gene which has fused into one single gene encoding a protein, or by 'textmining' of protein names across abstracts in PubMed, as well as by co-expression, experimental evidence and pathway databases.

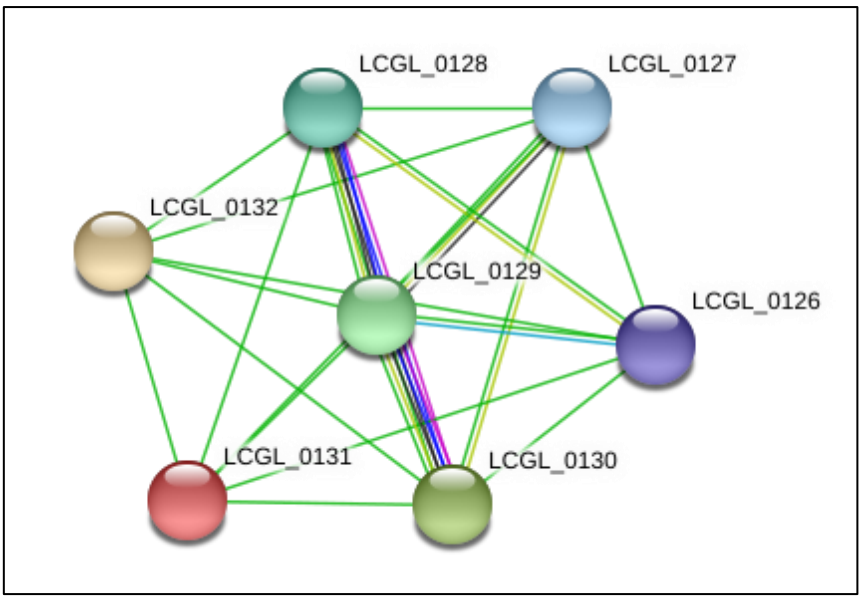
STRING compares a protein sequence with the known protein sequences within organisms in its database, and in this case the closest organism to *L. garvieae* 02106 was the fish *L. garvieae* Lg2 strain (Accession number: PRJDA18707), isolated from a clinical case of disease in yellowtail and therefore this strain was used for the comparison (Kawanishi *et al.*, 2006; Morita *et al.*, 2011).

The LAG_00167 equivalent in the Lg2 genome, LCGL_0131, was annotated as a conserved hypothetical protein. Six genes were found to encode proteins with functional links to LCGL_0131 in the Lg2 genome (Figure 3.11), between which were significantly more interactions than expected compared to a random selection of genes from the genome. These six proteins included another conserved hypothetical protein, one repeat unit transporter, one UDP-galactopyranose mutase, and three putative glycosyltransferases, all of which

were assigned to the 'neighbourhood' channel being consistently associated with the region of the genome of LCGL_0131. UDP-galactopyranose mutase is essential among many pathogenic microbes for biosynthesis of galactofuranose, an essential cell wall component in bacteria (Tanner *et al.*, 2014), and glycosyltransferases also play a structural role in the formation of glycosidic bonds (Gloster, 2014).

For *ancA*, the equivalent protein sequence in the Lg2 genome in the STRING database was LCGL_0133, also identified as a conserved hypothetical protein. Ten predicted functional partners were identified in the Lg2 genome (Figure 3.12), ranging from cell surface proteins to various phage proteins and other conserved hypothetical proteins. These also had significantly more interactions between each other than would be seen between random genes in the genome. Unlike with LAG_00167, the majority of these proteins were associated by co-occurrence, with only two (an inosine-5'-monophosphate dehydrogenase and a 30S ribosomal protein) belonging to the neighbourhood channel. Inosine-5'-monophosphate dehydrogenase has been targeted as a molecule for antimicrobial development as it is a critical enzyme for the synthesis of the nucleotide guanine and additionally a potential target in cancer research, parasitic and viral infections and also autoimmune conditions (Mazzolari, Maddis and Carini, 2016)

A



B

Your Input:

LCGL_0131 *Conserved hypothetical protein (600 aa)*

Predicted Functional Partners:

	Neighborhood	Gene Fusion	Cooccurence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
LCGL_0132 *Conserved hypothetical protein (457 aa)*	●								0.859
LCGL_0130 *Repeat unit transporter (481 aa)*	●								0.859
LCGL_0129 *UDP-galactopyranose mutase (378 aa)*	●								0.859
LCGL_0128 *Putative glycosyltransferase (342 aa)*	●								0.767
LCGL_0127 *Putative glycosyltransferase (280 aa)*	●								0.488
LCGL_0126 *Putative glycosyltransferase (335 aa)*	●								0.484

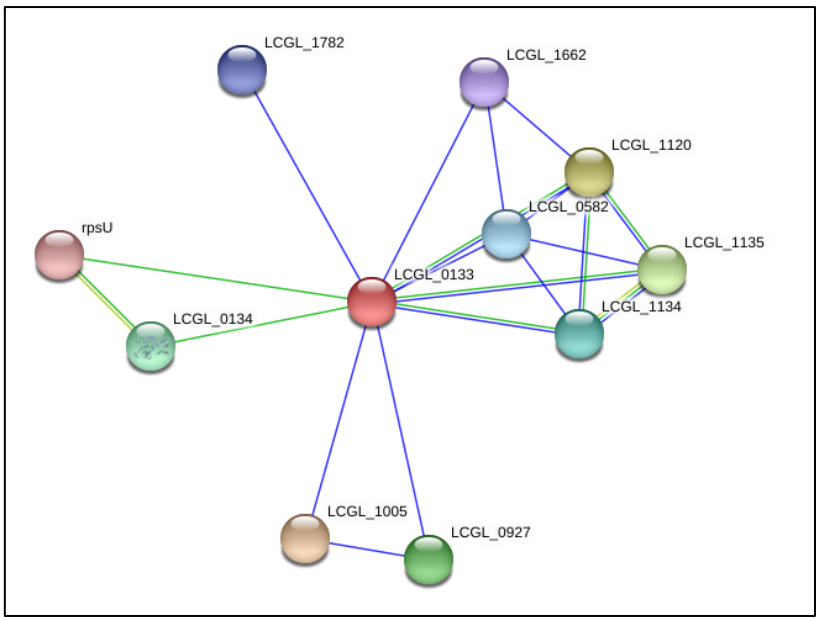
Figure 3.11: Proteins with links to LCGL_0131, the equivalent to LAG_00167 in the Lg2 genome

Interactions between genes are represented by lines of different colours connecting genes. Interactions are either known (blue line: from curated databases; pink line: experimentally determined), predicted (green line: by gene neighbourhood; dark blue line: by gene co-occurrence), or 'other' interaction (yellow line: by textmining from databases; black line: from co-expression of proteins together but not separately; and lilac line: association by protein homology.

A. STRING web showing six proteins with functional links to LCGL_0131 (red node), with increased interactions found between them versus random genes in the genome. These proteins include LGCL_0126, LGCL_0127, LGCL_0128, LGCL_0129, LGCL_0130 and LGCL_0132. All were associated to LCGL_0131 by gene neighbourhood.

B. Table listing the predicted functional partners of LCGL_0131, all associated by the neighbourhood in the genome in which they are present. The predicted functional partners to LCGL_0131 include another hypothetical protein LCGL_0132, a repeat unit transporter LCGL_0130, a UDP-galactopyranose mutase LCGL_0129, and three putative glycosyltransferases LCGL_0126, LGCL_0127 and LGCL_0128.

A



B

Your Input:

		Neighborhood	Gene Fusion	Cooccurence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
LCGL_0133	*Conserved hypothetical protein (484 aa)*									

Predicted Functional Partners:

		Neighborhood	Gene Fusion	Cooccurence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
LCGL_1005	*Cell surface protein (702 aa)*			●						0.676
LCGL_1120	*Phage minor tail protein (1593 aa)*			●						0.650
LCGL_1135	*Phage terminase large subunit (411 aa)*			●						0.612
LCGL_0927	*Conserved hypothetical protein (225 aa)*			●						0.608
LCGL_0134	*Inosine-5'-monophosphate dehydrogenase (493 aa)*	●								0.592
LCGL_1134	*Phage portal protein (502 aa)*			●						0.555
LCGL_0582	*Nicotinamide mononucleotide transporter protein (235 aa)*			●						0.536
LCGL_1782	*Aminopeptidase (846 aa)*			●						0.530
LCGL_1662	*Conserved hypothetical protein (362 aa)*			●						0.512
rpsU	*30S ribosomal protein S21 (61 aa)*	●								0.412

Figure 3.12: Proteins with links to LCGL_0133, the equivalent to *ancA*, LAG_00168, in the Lg2 genome

Interactions between genes are represented by lines of different colours connecting genes. Interactions are either predicted (green line: by gene neighbourhood; dark blue line: by gene co-occurrence), or 'other' interaction (yellow line: by textmining from databases)

A. STRING web showing ten proteins with functional links to LCGL_0133 (red node), with increased interactions found between them versus random genes in the genome. These proteins include LGCL_1005, LGCL_1120, LGCL_1135, LGCL_0927, LGCL_0134, LGCL_1134, LGCL_0582, LGCL_1782, LGCL_1662 and rpsU.

B. Table listing the predicted functional partners of LCGL_0133, mainly associated by co-occurrence. These include a range of proteins including a cell surface protein LCGL_1005, inosine-5'-monophosphate dehydrogenase LCGL_0134 and aminopeptidase LCGL_1782.

3.11 Development of site-directed mutagenesis for genes of interest

The four genes of interest above (*divIB, spsB, ancA* and LAG_00167) were selected for generation of knockout or impaired function mutants to test the effect of mutation on bacterial growth and potential virulence.

Primer targets were designed to remove the internal part of the gene and subsequently knockout function (Table 2.1), with EcoRI/HindIII restriction enzyme sites at the start and end of the amplified sequences for direct cloning into the pGh9 plasmid. This plasmid was used for the generation of the PIMMS mutants, with the ISS1 element removed using EcoRI/HindIII digestion to provide a compatible site for gene ligation (Figure 3.13).

PCR products were amplified using phusion polymerase and separated on 1% agarose/TAE gels by electrophoresis (Figure 3.14). Amplified product was extracted from gels using the QIAquick PCR Purification Kit (Qiagen), and digested with the relevant restriction enzyme to generate compatible ends for ligation. *divIB* fragments were digested with *EcoR*I, *BamH*I and *Hind*III; *spsB, ancA* and LAG_00167 fragments were digested with *EcoR*I, *EcoR*V and *Hind*III.

Once digested, fragments were again gel purified and ligated using T4 DNA ligase at 4°C overnight (Figure 3.15). The resulting product showed concatenation, indicating that further optimisation of the ligation reaction using different concentrations of DNA ligase may be necessary in future studies. The fragments corresponding to the correct size of the two fragments after ligation were ligated into pGh9 plasmid and desalted prior to electroporation into commercially available electrocompetent *E. coli* Top10F with bacterial selection performed on agar containing 200µg/ml erythromycin. However no colonies were observed, indicating that future optimisation was required.

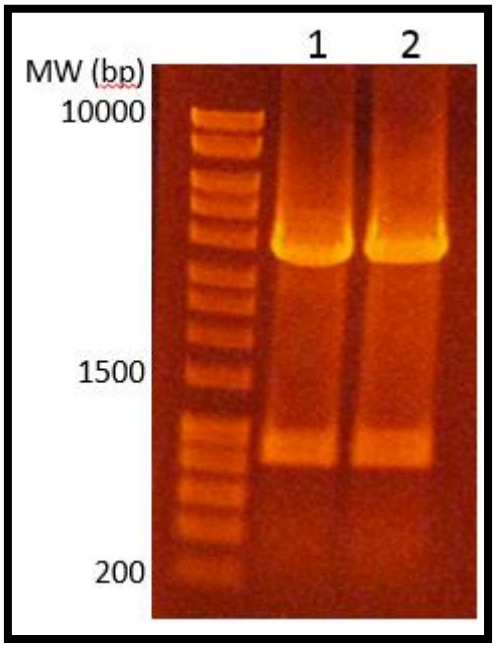


Figure 3.13: Gel electrophoresis image showing the excision of the IS*S1* element from the pGh9 plasmid

pGh9:IS*S1* plasmid following digestion with restriction endonucleases *Eco*RI and *Hind*III showing the excised IS*S1* element at 808bp. The pGh9 plasmid vector is shown at 3752bp in size.

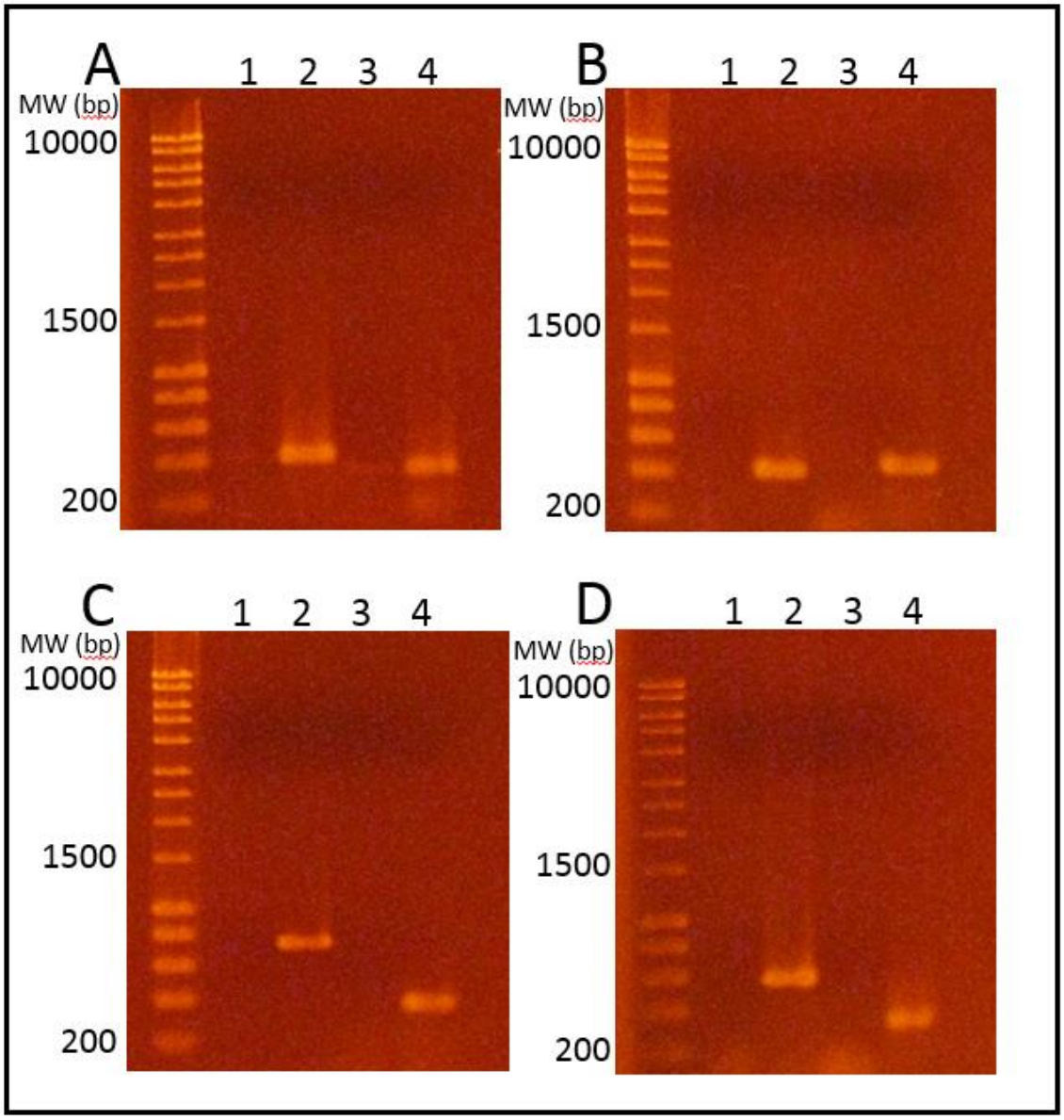


Figure 3.14: Gel electrophoresis demonstrating amplicons of specific genes
Wells are numbered 1-4, with 1: Negative control for fragment 1; 2: Fragment 1; 3: Negative control for fragment 2; 4: Fragment 2.Hyperladder 1kb (Bioline) is used as molecular weight marker (bp). Fragments vary in size (range 338bp-742bp) depending on primer pair used (Table 2.1).

A: *divIB* amplicons generated using primers 1090/1091 (Fragment 1) and 1104/1105 (Fragment 2);
B: *spsB* amplicons generated using primers 1096/1097 (Fragment 1) and 1098/1099 (Fragment 2);
C: LAG_00167 amplicons generated using primers 1106/1107 (Fragment 1) and 1108/1109 (Fragment 2);
D: *ancA* amplicons generated using primers 1112/1113 (Fragment 1) and 1116/1117 (Fragment 2).

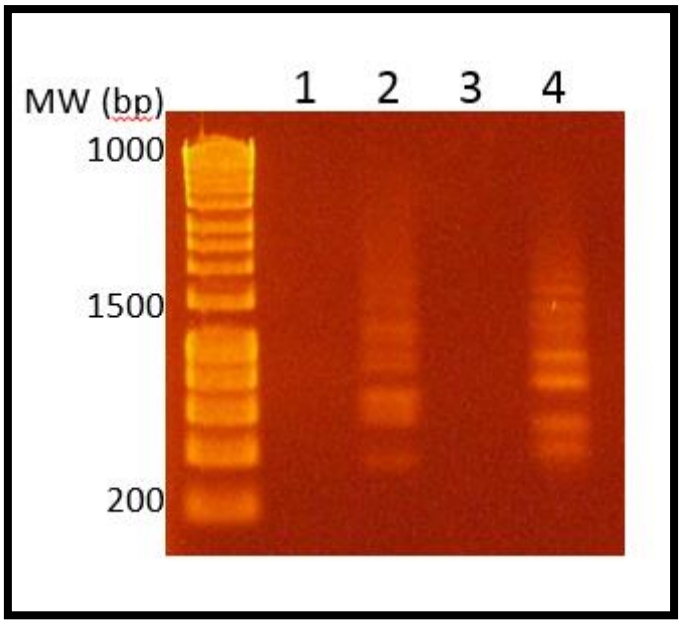


Figure 3.15: Ligation of restriction enzyme treated fragments

Representative image showing ligation products for LAG_00167 and *ancA* fragments as shown in figure 3.14. Multiple fragments of DNA of different sizes can be seen, likely due to concatenation of the DNA.

4.0 Discussion

At the time of this study, there are no commercial vaccines available for use against *L. garvieae* infection or alternatives to antibiotics for treatment of disease. To reduce reliance on antibiotics and maintain food safety, this study made the first steps towards potential prophylaxis development by identifying genes essential for the growth of *L. garvieae* clinical strain 02106 in fish serum using the PIMMS laboratory protocol (Blanchard *et al.*, 2016).

4.1 PIMMS based analysis of genes essential for *L. garvieae* growth

Generating a map of the essential genome often relies on mutagenesis strategies to disrupt genes, which are then seen as essential if the mutation of that gene prevents the mutated bacteria from survival or proliferation. If the gene were non-essential then those bacteria would remain within the population, and this is the principle on which identification of essential genes was defined using PIMMS in this study. There is a known sequence bias which exists with the use of all transposons (Coulter *et al.*, 1998), however analysis of the insertional location in this study found no overt bias of the pGh9:*ISS1* mutagen to any particular region of the *L. garvieae* 02106 coding sequence. The specific genes with a high number of insertion elements were identified in both the input and output pool populations, and tended to have a large number of unique insertion points throughout the entire coding sequence. For example, the gene with the highest number of unique insertion positions, LAG_00934*,* found 213 unique insertions across its length from the 0.3 centile to the 100 gene centile in the input pool populations and 155 unique insertion positions from 0.7 centile to 99.4 gene centile in the output. This suggests a broad spread of insertions which can be interpreted as no overt bias existing when the mutagen is used and

complements other studies where similar results have been obtained with the pGh9:ISS1 transposon (Lampe, Grant and Robertson, 1998; Lampe, 2010; Green *et al.*, 2012).

In this study, PIMMS was able to identify 39,045 unique mutations in a total of 309,931 mutants in the *L. garvieae* input pool, and 26,075 unique mutations out of 261,011 mutants in the *L. garvieae* output pool. At a ratio of 1 mutation for every 10 mutants, these values are lower than the values for rate of unique mutations obtained for *S. uberis* in a similar PIMMS-based study, where 80,617 mutations were identified in around 100,000 mutants, or around 8 mutations for every 10 mutants (Blanchard *et al.*, 2016). One explanation for the differences in the number of sequences obtained for analysis could be from the use of different methods to generate the sequencing libraries at different institutions. In the PIMMS *S. uberis* study, sequencing libraries were generated using the Illumina TruSeq Nano library compared with the enzymatic based the NEBNext Ultra kit used in this study and the DNA size purification systems prior to analysis also differed. However, the values for matched and mapped reads were almost identical between the two studies, with a mean of 38% for *S. uberis* compared to 40% and 41% in the input and output pools of *L. garvieae* respectively (Tables 3.1 and 3.2) indicating that the previous success of PIMMS in *S. uberis* can be replicated with similar efficiency in *Lactococcus garvieae*.

The *S. uberis* study used bovine milk and serum to replicate the environment in which the mastitic pathogen may replicate to cause disease in cattle. As *L. garvieae* is a pathogen known to cause mastitis in dairy cattle (Bar *et al.*, 2008; Medrano-Galarza *et al.*, 2012), a similar approach may be used to identify genes important for *L. garvieae* proliferation in the mammary gland and targeted for future control strategies.

A number of genes were identified in this study that were essential for bacterial growth in fish serum and also were identified as essential for growth of *S. uberis* in milk containing serum. This included *ftsH, ftsW* and *ezrA* identified as essential for growth in media and fish serum and categorised under the 'Cell Division and Cell Cycle' RAST category. Given these genes have been in two closely related bacterial species, this may provide a future target for a number of streptococcal and lactococcal species.

In the present study, fish serum was used to replicate *L. garvieae* infection of live fish, mimicking bacterial survival and replication in the blood to cause septicaemia. Serum does not include blood cells to mimic the whole blood environment, but will contain other proteins present including some elements of complement, so parts of the innate immune response can still be initiated within the serum environment. Serum is also a more easily reproducible environment for potential future studies as blood cells can degrade over time and are difficult to obtain in large numbers from live animals. Additional genes essential for the growth and proliferation within fish are also likely to be identified through whole blood or direct *in vivo* challenge of bacterial mutants into fish, but such analysis was beyond the scope of this project.

The PIMMS bioinformatic pipeline can only recognise and analyse coding sequences and therefore the role of promoter or regulatory sequences, which may be of equal importance biologically, was unable to be assessed in this study. This development would be an important addition for TIS based analysis using PIMMS alongside the use of a complete annotated genome for comparative analysis, which was unavailable at the time of this study for *L. garvieae* 02106.

Comparison with other TIS based evaluation of genes essential for *L. garvieae* proliferation reveals one study where Signature-Tagged Mutagenesis (STM) was used to investigate *L. garvieae* UNIUD074, isolated from an Italian outbreak of lactococcosis in rainbow trout (Reimundo *et al.*, 2011), to identify genes essential for growth and survival using a live rainbow trout model. A total of 1250 different UNIUD074-tagged Tn917 mutants were screened in live fish and harvested 72 hours post-infection, to identify which mutations were critical for bacterial survival (Menéndez *et al.*, 2007). Several of the genes identified by Menendez *et al.* proved to be homologous to hypothetical proteins found in the present study, with hypothesized functions involving transcriptional regulators and calcium ion transport. Some of which included the enzyme acetolactate synthase encoded by *alsS,* the transcription regulator encoded by *xre,* D-Alanine-D-alanyl carrier protein encoded by *dltA, glnP* encoding a glutamine ABC transporter, and the DNA processing protein DprA, showing some similarity in identified genes between the studies with shared homology to the same genes in *L. lactis* subsp. *lactis* (Menéndez *et al.*, 2007). However direct comparisons with the genes identified in this study could not be made, as the corresponding gene sequences were not available within this publication.

4.2 Analysis of genes determined to be essential for *L. garvieae* survival

Determining the essential genes for growth using the PIMMS data is a relatively simple process. If the gene is deemed essential for bacterial survival in the particular environment tested, then disruption by pGh9:ISS1 results in that mutant being absent in the pool from that environment. Similarly, a gene found with multiple insertions is unlikely to be essential for growth in the condition examined, however the position of the insertion is important, particularly when

insertion elements are identified only within the terminal part of the sequence and for this reason, the arbitrary cut-off of identification of a mutation from15% from the C-terminus of the gene was also used to identify potential genes of interest.

4.2.1 The use of RAST to categorise essential genes in the *L. garvieae* genome

In order to broadly group genes with similar functions, essential genes identified in the PIMMS analysis were categorised by functional role using the Rapid Annotation of microbial genomes using Subsystems Technology (RAST) software (Overbeek *et al.*, 2014). RAST (http://rast.nmpdr.org/) annotates the genome based on information from multiple online repositories, searching databases of literature, annotations from metabolic pathway programmes (Kanehisa *et al.*, 2012), and other databases including GenBank (Benson *et al.*, 2013) and SwissProt (UniProt, 2013) to obtain putative gene characterisation. Grouping genes by function (Overbeek *et al.*, 2014) makes it much easier to target focus on smaller numbers of genes, under headings such as 'DNA metabolism', 'Cell Division and Cell Cycle', and 'Virulence, Disease and Defence'.

In the input pools, the majority of essential genes belonged to the Protein Metabolism category (28.6%), followed by the hypothetical protein category (16.1%). Following selection in fish serum, the output pools also contained high numbers of essential genes in these categories (23.3% and 23.6% respectively). It is unsurprising that genes involved in protein metabolism are so frequently considered essential, as producing and processing proteins is vital for growth and division, and the synthesis of signalling molecules and antigens. Given it has been estimated that a third of the essential genome can be comprised of genes with unknown roles it was also unsurprising to identify a high proportion of unknown

or hypothetical functional sequences within this data (Glass *et al.*, 2006). Programmes such as DEG (Database of Essential Genes), which contains a list of all known essential genes, Position-Specific Iterated BLAST (PSI-BLAST), (Altschul *et al.*, 1997) and STRING, which associates encoded proteins by linked function can be used to investigate hypothetical proteins (Szklarczyk *et al.*, 2015), however functional data through comparison of individual knockout mutants with their wildtype counterparts also provides key information.

There were 11 common genes identified in the Virulence, Disease and Defence category when *L. garvieae* 02106 was grown in media and fish serum, with an additional three genes *copY, gyrB* and *misCA,* only essential in the fish serum output population. *copY* codes for a transcriptional repressor which identifies with the CopY/TcrY family of copper transport repressors by protein BLAST (BLASTp) analysis. Copper is regarded as important as a cofactor for a number of enzymatic reactions, although free copper can be highly reactive and toxic, so its transport is tightly controlled in many bacteria and their hosts (Argüello, Raimunda and Padilla-Benavides, 2013). This result is unsurprising, given the micronutrient poor environment of serum, compared to the nutrient rich bacterial media. Using a specifically low-copper medium to grow the mutant pools in could add evidence for the importance of *copY* for growth, and provide a target for future bacterial growth restriction application to reduce the scale of outbreaks in aquaculture. The gene *gyrB* encodes a DNA gyrase subunit B, and aligns with many examples of DNA topoisomerase subunit B using protein BLASTp. These enzymes facilitate the winding of DNA, with deficiencies compromising transcription and replication (Champoux, 2001). The gene *misCA* encodes a membrane protein insertase, with a similar sequence found in protein translocase component YidC, another membrane protein insertase, in other *L.*

garvieae strains and in *L. lactis*. These enzymes integrate proteins into the cytoplasmic membrane of the bacteria (Wickles *et al.*, 2014), so perhaps allow bacteria to persist in the host environment.

Additionally, investigation of genes involved in stress responses, induced in through limited nutrition or changes of environment on entering a host from the environment could be important to investigate further. Adapting to this change of environment is likely to improve the ability of these bacteria to survive. Fish serum may contain elements of complement from the innate immune system, which would be found in the live fish and may invoke stress response mechanisms. 6 genes were assigned to the RAST category of 'Stress Response' in bacteria from the output pools compared to 3 from the input pools. The common genes shared as essential in both growth conditions in this category were *grpE, hrcA* and *nrdH*. Being common in both media suggests that they may encode proteins for core stress responses in any media or environment or may have been misaligned by RAST, as there were also identified in multiple RAST categories. The additional three genes under the Stress Response category identified as essential for growth in fish serum were *dnaK, dps* and *smpB*. *dnaK* encodes a molecular chaperone of the same name, *dps* a protein for protection of DNA against oxidative stress, and *smpB* encodes an SsrA-binding protein. By associating with proteins, chaperones prevent the protein from misfolding and are responsible for correct protein folding and proteostasis in the cell. In *S. intermedius*, the DnaK chaperone system is important for growth, resistance to temperature fluctuation and resistance to cytotoxicity against certain cell lines (Tomoyasu *et al.*, 2012). *S. aureus* DnaK knockout mutants have been found to exhibit reduced growth and survival rates in a mouse host (Singh et al., 2007; Tomoyasu et al., 2012), which could have a parallel in *L. garvieae* in the fish

host. Resistance to temperature fluctuation may be particularly relevant in the aquaculture environment, given changing water temperatures and the poikilothermic nature of fish. The involvement of this gene in pathogenicity has also been described for *Salmonella enterica* serovar *typhimurium* (*S. typhimurium*), where lack of DnaK causes reduced expression of pathogenicity islands and the DnaK null mutant showed no ability to cause systemic infection (Takaya et al., 2004). This could be a potential protein for further investigation in *L. garvieae* as targeting the encoded protein from this gene could make the bacterium less able to survive both in the aquatic environment and in the host.

Dps produces a protein for protection during starvation, and is found in multiple *Lactococcus* species including *L. garvieae, L. lactis*, and *L. piscium*, with the dps protein belonging to the Ferritin-like superfamily of proteins which store iron. In *Lactococcus*, the protein has also been found to contribute to hydrogen peroxide sensitivity, and binds to DNA to prevent oxidative stress by hydroxyl radicals (Stillman et al., 2005). The damage caused by these radicals includes DNA strand breakage, inactivation of protein and peroxidation of lipids (Krieg and Hoffman, 1986). If targeting this gene makes the bacteria more vulnerable to starvation and unable to store iron, then it could be important for bacterial survival in any environment with limited availability of nutrients. Free iron concentration may be limited in serum, which could reflect the differences observed.

Another intriguing gene identified by the RAST analysis was *pth*, which was essential for *L. garvieae* survival in the input pools however was only identified in one unique insertion position at the 94.2 centile of the coding sequence in the comparative output pools. The gene is of interest is categorised in the RAST category 'Dormancy and Sporulation', however, *L. garvieae* does not produce

spores. Many Gram-positive bacteria are capable of surviving for long periods of time in an aquatic environment even under conditions of starvation, in which time a state of dormancy or 'viable but non-culturable' state may be entered. In this state, even plating onto a solid media or inoculating into a liquid media may be unable to produce viable cells (Currás *et al.*, 2002). The *pth* gene has been reported as encoding a peptidyl-tRNA hydrolase (Sharma *et al.*, 2014), previously identified in *Streptococcus mutans* (Ajdic *et al.*, 2002) and *Streptococcus pyogenes* (Ferretti *et al.*, 2001), and has been shown to rescue 'stalled ribosomes' where the protein produced by the ribosome is prevented from release at the ribosome exit tunnel. Peptidyl-tRNA is a product of this ribosome stalling, and is cleaved in part by the hydrolase enzyme. The accumulation of peptidyl-tRNA molecules would lead to cell death, and as a result the peptidyl-tRNA hydrolase has been considered as a potential target for antimicrobial drugs (Sharma *et al.*, 2014) which could be relevant for development of new antimicrobials to combat *L. garvieae* in aquaculture, reducing reliance on other classes where resistance is increasing.

Of the truncated genes identified as important for growth in fish serum, *guaB* is particularly interesting, as it is shown to encode an inosine-5'-monophosphate dehydrogenase (IMPDH), an enzyme critical for the de novo synthesis of the nucleotide guanine and a target drugs against bacterial, parasitic and viral infections, as well as for therapies against cancers and autoimmune diseases using IMPDH inhibitors (Mazzolari, Maddis and Carini, 2016). As a truncated essential sequence in *L. garvieae* 02106, where two unique insertions of the ISS1 element were identified between the 96th and 100th centile using PIMMS, the gene may be a potential future target for antimicrobial therapy in aquaculture.

4.2.2 Assessment of phenotypically important genes

The EdgeR software was used to generate a comprehensive list of statistically differentially expressed genes across the pools, highlighting additional genes which could still be important even if they were not considered 'essential' using the PIMMS data. A total of 9 genes were identified which were all downregulated after growth in fish serum, 8 of these with a fold difference of greater than 2, indicating a significant decrease in the proportion of bacterial mutants detected after growth in fish serum compared the original input pool (Table 3.10). One gene, *artM*, encodes an arginine transport ATP-binding protein with arginine identified as an important amino acid for pathogenesis in bacteria (Xiong *et al.*, 2016). Arginine restriction may represent a potential mechanism to control growth and survival of *L. garvieae* and perhaps choosing a feed source with low levels of arginine could be investigated as a way to reduce bacterial growth in the environment and risk of clinical disease.

4.2.3 Selecting genes of interest from the *L. garvieae* genome

4.2.3.1 Using PSORTb and SignalP to identify genes of interest in the *L. garvieae* genome

Genes important for *L. garvieae* virulence in fish were identified by screening essential genes from the output pool to identify those with extracellular or cell wall localisations, or signal peptide expression, as these are most easily accessible by the immune system and extracellular environment. This was completed using PSORTb, an online tool which predicts subcellular localisation of proteins (Yu *et al.*, 2010), and SignalP to determine which genes encoded a signal peptide. Signal peptides drive proteins towards the cell membrane and into secretory pathways to exert an action outside of the cell (Emanuelsson *et al.*, 2007), so proteins with signal peptide are generally located in the cell

membrane, cell wall or are extracellular proteins and are often involved in host-based interactions (Kovjazin and Carmon, 2014).From the genes identified by EdgeR as significantly downregulated in fish serum, three encoded signal peptide when analysed by SignalP (Table 3.10). These were LAG_00167, *ancA,* and *tcyB,* which were highlighted for further investigation along with the essential genes identified as encoding signal peptide.

Two genes essential for *L. garvieae* survival in fish serum were identified which expressed signal peptides: *cdaR* and *pstS1_2. cdaR* was categorised using RAST under 'Cell Division and Cell Cycle', and encodes a cyclic di-AMP synthase A regulator, which is involved in the homeostasis of a proposed essential bacterial signalling nucleotide cyclic di-AMP in *Bacillis subtilis* (Mehne *et al.*, 2013). The gene *pstS1_2* is in the 'Phosphate Metabolism' RAST category and encodes a phosphate-binding protein. Phosphate limitation is known to slow growth rates in bacteria (Zimmerman *et al.*, 2014), and up-regulates proteins related to acquisition and storage of phosphate (Lamarche *et al.*, 2008), and *pstS1_2* could play a role in this. Both *cdaR* and *psts1_2* had 'Unknown' subcellular localisations with PSORTb, but as both expressed a signal peptide and *psts1_2* action could be targeted by removing phosphate in the environment, these had potential as targets to control lactococcosis in aquaculture.

Six additional genes deemed essential for growth in fish serum were identified with particularly interesting features using this process along with *pstS1_2* and *cdaR*: *ftsH,* LAG_01374, *spsB, ezrA, divIB* and *sodA* (Table 3.9), with the latter three being truncated sequences. Both *spsB* and *divIB* were likely to have a cell wall localisation, with hypothetical protein LAG_01374 and *sodA* being extracellularly expressed.

The gene *sodA* encodes a superoxide dismutase and was allocated to the Stress Response RAST category. The encoded protein is important in many bacterial species for surviving stress induced by ethanol, paraquat and low temperatures (Benov and Fridovich, 1995; Lüders, Fallet and Franco-Lara, 2009; Esteve-Gassent *et al.*, 2015). The role of *sodA* in surviving temperature fluctuations could be significant as *L. garvieae* is a cold-water pathogen in aquaculture, but this study cultured the bacteria at higher temperatures than would be found in a poikilothermic fish host. The gene has been investigated in a number of bacteria as a potential vaccine candidate, with a recombinant vaccine using the gene from group A streptococcus eliciting strong antibody responses in a mouse model (McMillan *et al.*, 2004). The same study found that levels of SodA antibody were elevated in human hospital patients, likely as markers of recent or recurrent infection by streptococcal bacteria, so the antibody against this protein could potentially act as a proxy for disease detection in fish. SodA has also been considered essential for *S. pneumoniae* colonisation of a host (Mahdi *et al.*, 2015), and inactivation of the gene has found to significantly reduce the virulence in many streptococcal species (Poyart *et al.*, 2001; Tang *et al.*, 2012). This presents the SodA protein as a potential vaccine candidate or diagnostic marker for current, recent, or recurring infection with virulent *L. garvieae*.

The cell division protein FtsH was identified as a membrane bound ATP-dependent zinc (Zn^{2+}) metalloprotease (Tomoyasu, Yamanaka, *et al.*, 1993; Tomoyasu, Yuki, *et al.*, 1993; Akiyama, Yoshihisa and Ito, 1995). It is likely that there is little zinc available for growth in fish serum as a source of nutrients and that the bacteria will need this for replication, hence the gene being essential for bacterial survival in fish serum. The gene was identified in the input pools with the presence of four insertions of the ISS1 element at just one unique position

(at the 2.2 percentile) in the input pool and therefore this gene was not considered an essential gene *L. garvieae* survival. *ftsH* is present with over 95% homology in other strains of *L. garvieae* with 99% identical alignment (Nishiki *et al.*, 2016), as well as being in multiple *L. lactis* strains (Radziwill-Bienkowska *et al.*, 2016). In *Streptococcus suis*, the *ftsH* gene was identified as producing a cell division protease and it was also found to be essential in PIMMS based analysis of *S. uberis* 0140J when grown in Todd-Hewitt Broth, milk and milk with serum (Blanchard, 2015). The metalloprotease has multiple potential roles associated with cell division and requires cofactors for function. For example, the protein FtsH has been implicated in the zinc-dependent degradation of both EzrA in *B. subtilis* (Mielich-Süss *et al.,* 2013), and FtsZ in *E. coli* (Srinivasan *et al.,* 2008). Interestingly, FtsZ was identified as essential for *L. garvieae* 02106 growth in both input and output pools in this study, with *ezrA* being deemed essential in the same bacteria grown in fish serum. In other studies, the proteins encoded by these two genes have been found to interact, with EzrA, a septation ring formation regulator, regulating the polymerisation of FtsZ which would normally form a 'Z ring' to initiate septation in the process of bacterial cell division much like tubulin in eukaryotic cells (Lutkenhaus *et al.*, 1997; Singh *et al.*, 2007; Srinivasan *et al.*, 2008), with both genes highly conserved amongst the other *Lactococcus* species (Nishiki *et al.*, 2016). With all of these genes identified as essential in the *L. garvieae* 02106 genome, targeting *ftsH* could ultimately interfere with the functioning of all three genes, which could represent parts of a cell division pathway and an alternative method of control of bacterial cell division and lactococcosis.

Using SignalP, *ftsH* was determined to not encode a signal peptide. However, PSORTb suggested the opposite, highlighting some of the ambiguity in using

bioinformatics software as different programmes. Signal P identifies signal peptides using the degree of hydrophobicity of the protein, its hydrophobic movement and its abundance of amino acids and truncates the protein sequences to just 70 amino acids to enable the sequence to be read efficiently, which can make the result less representative of the whole protein. However, should this feature be disabled, the Hidden Markov Model which forms the basis of the software would be much less sensitive (Emanuelsson *et al.*, 2007). In comparison, PSORTb has a higher specificity than sensitivity so generates few false positive results, but a higher degree of false negatives (Gardy *et al.*, 2003). Manual analysis of these ambiguous proteins can be extremely useful in working out which information can be considered true in addition to individual gene/protein characterisation studies.

4.3 Investigating *divIB, spsB, ancA,* and LAG_00167 as important genes in the virulence of *L. garvieae* 02106 in fish

Of the 17 genes of interest identified from the PIMMS analysis and the EdgeR results, four genes, *divIB, spsB, ancA,* and LAG_00167, were selected for further analysis of their potential role in bacterial virulence and survival in fish serum, and were also considered for the development of a site-directed mutagenesis protocol. Both *divIB* and *spsB* were recognised as essential (*divIB* as truncated) with cell wall protein localisation and *ancA* and LAG_00167 were identified by the EdgeR analysis with *ancA* determined to be cell wall expressed and the subcellular localisation of LAG_00167 unable to be determined.

The four genes were aligned against other *L. garvieae* strains and other related species using the Clustal Omega software (Sievers and Higgins, 2017) (Figures 3.4-3.7) to assess how similar protein sequences were between organisms. Sequence conservation is important when considering the potential of the

proteins as either part of a multivalent vaccine versus being a specific diagnostic target.

Within the *divIB* gene, two unique insertions of the *IS*S1 element were identified by PIMMS which were located in the final 15% of the coding sequence: the first at the 88.2 centile, and the second at the 98 centile. *divIB* has been characterised with a role of cell division protein DivIB, and homologous to the FtsQ orthologue in Gram-negative bacteria (Harry *et al.*, 1994). The gene is relatively well-studied, and has been identified in multiple Gram-positive species including *S. aureus, Bacillus subtilis* and *Pneumococcus* (Le Gouëllec *et al.*, 2008). In *S. aureus,* the DivIB protein is important as part of a cell division checkpoint by binding peptidoglycan at the β subdomain and minimising the effects of poor septation in division (Bottomley *et al.*, 2014). The gene aligned with over 95% similarity to all other *L. garvieae* strains investigated in this study which indicates high conservation between strains including *L. garvieae* 21881 (98% similarity), which was isolated from a case of human septicaemia, indicating potential for this protein to be targeted in human as well as fish bacteraemic infections. Furthermore due to the high gene conservation, this could provide an attractive *L. garvieae*-specific monovalent vaccine or have potential usage as a specific molecule to diagnose infection and allow differentiation of clinically indistinguishable streptococcal and lactococcal based infections in future studies.

Identified as essential for growth in fish serum from the PIMMS comparative analysis, the cell wall protein *spsB* produces signal peptidase IB and are enzymes which cleave signal peptides from their protein for release (Paetzel, 2014). Efforts have even been made to develop antibiotics whose action is based upon the inhibition of signal peptidase, SPaseI (Paetzel, 2014), which could be

relevant to developing additional antibiotics for use in aquaculture to optimise food production. The expression of signal peptidases on the cell surface makes them relatively accessible for drugs, also contributing to their potential as effective targets and with a high degree of conservation between strains (Figure 3.7), this gene also has potential for future diagnostic or therapeutic applications.

The gene *ancA* was identified through EdgeR analysis and encodes a cellulosome-anchoring protein although little information in relation to the function of this gene in *L. garvieae*. Cellulosomes are large complexes of extracellular enzymes, which anchor to the cell surface by means of the anchoring protein (Doi *et al.*, 2003) and from here they can affect molecules in the surroundings. STRING based analysis was performed to determine additional information about this protein using the *ancA* equivalent in *L. garvieae* Lg2 (LCGL_0133) and 10 other proteins in the database were identified as linked to *AncA* mostly by co-occurrence, with two of the ten being linked by neighbourhood (LCGL_0134, encoding an inosine-5'-monophosphate dehydrogenase (IMPDH), and rpsU, encoding a 30S ribosomal subunit) (Figure 3.12). Association by co-occurrence indicates that the proteins involved tend to be expressed together, and increases the chances they are functionally linked and inter-reliant (Szklarczyk *et al.*, 2017). The variety of proteins with functional links to *ancA* illustrates how challenging it can be to confidently determine the function of a particular protein or gene, even with the wealth of tools and databases available.

Denoted as a hypothetical protein, LAG_00167 was identified as a gene of interest using EdgeR analysis based on statistically significant reduction in the numbers of bacterial mutants identified after growth in fish serum (Table 3.10). A total of 30 unique mutation positions were identified from the 4th to the 96th centile in the *L. garvieae* input pool, and insertions in 4 unique positions after screening in fish serum from the 48th centile to the 72nd centile. The LAG_00167 gene was found to be unique to lactococcus. Using STRING, the corresponding gene in the Lg2 genome was LCGL_0131 which had associations with 6 other genes encoding another hypothetical protein, and five with known functions which could provide clues about the role of LAG_00167 (Figure 3.11). All were associated by neighbourhood to LCGL_0131, meaning that they are consistently observed in the same region of the genome as each other. This is the case for conserved and co-transcribed 'operons': adjacent genes with similar functions which are all controlled by an operator gene. The functions of the associated proteins include one repeat unit transporter, one UDP-galactopyranose mutase, and three putative glycosyltransferases. UDP-galactopyranose mutase is a key enzyme in the biosynthesis of galactofuranose, by catalysing the conversion of UDP-galactopyranose into galactofuranose. This is an essential cell wall component in the bacterial cell wall, and even a cell surface virulence factor in protozoa parasites (Tanner *et al.*, 2014), and may therefore represent a potential target for alternative antibiotic therapy against lactococcosis. Similarly, glycosyltransferases are enzymes which catalyse the formation of glycosidic bonds, which also play a structural role (Gloster, 2014). According to the PROKKA based genome annotation the LAG_00167 gene is adjacent to *ancA* (LAG_00168) in the 00021 and 02106 draft genomes, however the gene was not identified in all other *L. garvieae* genomes used for comparative analysis and

therefore this gene may be of limited value for future diagnostic or therapuetica pplications due to its lack of conservation between strains.

Without being able to assess their participation in metabolic pathways using KEGG, other resources needed to be employed to gain further insight into the roles of *ancA* and LAG_00167. Other than using STRING, one other database which can be used to assess hypothetical protein function is the Database of Essential Genes (DEG), where the user can enter the amino acid or nucleotide sequence of interest for comparison against known essential gene and protein sequences in the database. DEG does not contain lactococcal species, and the sequence for LAG_00167 matches most closely to another essential hypothetical sequence in *S. agalactiae* A909 with only 33% identity (aligned amino acid residues). This highlights the difficulty in determining the function of unknown or hypothetical proteins and determining their potential role in virulence.

4.3.1 Investigating the involvement of the selected genes in metabolic pathways in *L. garvieae*

One way to access more information on specific genes and to develop ways of targeting them is to consider the metabolic pathways in which they play a role. A metabolic pathway represents a chain of reactions which links proteins which are all involved in some process in metabolism, for example in the export of protein, or the metabolism of folate, or the process of cell division. The product of one reaction often catalyses the next reaction, and so on (Karp, 2001). Many databases exist which contain this information for multiple species of bacteria and the largest of these databases is the Kyoto Encyclopaedia of Genes and Genomes (KEGG), which is frequently updated and contains data from multiple

species (Ogata *et al.*, 1999). As KEGG pathways represent a gene's involvement in metabolic processes, genes which do not play a role in a core metabolic process will not be represented on the database. Equally, if the genes in question are unique to a species, mis-assigned due to draft genome annotation or only transiently expressed in an organism due to a particular environmental condition or stressor, they may not be present. Identifying the involvement of genes in specific pathways may help to understand how many seemingly unrelated genes can actually be interdependent, just as *ftsH, ezrA* and *ftzZ* appear to be (Singh *et al.*, 2007). Targeting one gene in a pathway or network may have an effect on multiple other genes, or targeting an alternative gene may indirectly block the function of an actual gene of interest.

KEGG was used in this study to ascertain other genes which could contribute to the action of *divIB* and *spsB*. KEGG can generate colour-coded pathways according to two different ways of measuring the essential nature of genes, the data for which are provided by PIMMS in the inputted species.

It is clear from the KEGG pathways shown (Figures 3.8-3.10) that many proteins involved in the pathways identified between *divIB* and *spsB* were not identified in draft annotation of the *L. garvieae* 02106 genome, so the pathways appear to be either incomplete or an alternative functional pathway may exist for these species.

KEGG analysis of *divIB* illustrated its involvement in the cell cycle pathway through its orthologue FtsQ in the Gram-negative *Caulobacter crescentus,* in which many studies have been carried out to learn more about the cell cycle. Using the position of the first insertion, the KEGG pathway illustrates the truncated nature of the DivIB protein, with the first insertion at <10% of the

gene length in the input pool, versus 80-90% of gene length in the output pool of fish serum (Figure 3.9). In the pathway, FtsQ can be seen to be part of a complex with FtsA, FtsW, and MurG for Z-ring formation, with close association to FtsZ which has previously been found to be associated with FtsA and Z ring formation (Lutkenhaus, Pichoff and Du, 2012). All of these proteins were identified from the *L. garvieae* 02106 genome, with FtsA and MurG being essential in both media with zero insertion mutants identified. Therefore, there could be potential to impact the function of many genes in the pathway if *divIB* or a similarly important gene within this pathway was targeted to disrupt function.

When assessing the involvement of *spsB* in metabolic pathways, KEGG presented a very different style of figure, showing the SPase I protein as one of two SPases involved in prokaryotic protein export (Figure 3.10). The gene had insertions in the last 70-80% of the gene in the input pool (at 72% according to PIMMS, hence it was not considered essential in this medium), however in fish serum no insertions of the gene were observed, and it was considered essential. Alongside SPaseI in the KEGG figure was SPaseII, another signal peptidase which does not share the same pattern of insertion with the pGh9 mutagen as SPaseI. This may mean that a knock-out mutant of SPaseI could still functionally secrete protein, as the alternative protein, SPaseII, could carry out the signal peptidase function.

4.4 Future work

Each of the genes and their related proteins discussed above have potential vaccine applications for future control or alternatively diagnosis of lactococcal infections. Attempts at site-directed mutagenesis in order to generate knock-out

mutants of each of the genes *divIB, spsB, ancA* and LAG_00167 were not successful within the limited time frame of this study.

This study used a draft annotation of the *L. garvieae* 02106 genome, and future work could produce a greater wealth of information if the genome annotation were completed. The genes identified as important in this study could undergo further *in vitro* analysis by developing a knock-out mutant of each gene and assessing its growth rate relative to a wild type variety to estimate how the mutant may respond *in vivo*. In accordance with an essential minimal genome, around a third of all genes identified by PIMMS had a hypothetical function, which present challenges for further investigation to establish more about their roles.

The use of serum in the present study to identify genes that were important for bacterial growth, was a useful tool to identify a panel of genes which may directly relate to the virulence of *L. garvieae* in live fish. A development of this in future would be to perform an *in vivo* challenge using knock-out mutants of the essential genes identified by PIMMS in live trout. Those genes determined to be essential under the 'Virulence, Disease and Defence' RAST category in fish serum (such as *copY, gyrB* and *misCA* which were only essential in serum) could be interesting to assess in order to validate their position under this category, as well as mutants of the four genes taken forward for further analysis.

Another way of performing a similar assessment of a wider number of genes would be to use the mutant banks generated with pGh9:ISS1 directly in fish and to harvest back the organs to determine which strains survived using PIMMS. This would be more relevant to disease status than using serum however it is likely that 'bottlenecks' that may occur, such as obtaining enough bacterial

mutants back for analysis and which tissue to target in order to get the best return of bacteria.

To test the potential of the selected genes as vaccination or diagnostic targets, antisera could be generated against the proteins and used in a diagnostic ELISA as a precursor for more specific test. This could be particularly relevant for DivIB which could be used to distinguish an *L. garvieae* infection from a clinically similar streptococcal infection or even an *L. lactis* infection, given that the DivIB protein generated by these species was quite different in structure between these species. Also interesting as a target in a future study could be FtsH, after discovering its involvement with other essential proteins (FtsZ and EzrA) from the *L. garvieae* genome. Generation of recombinant proteins or protein modelling work may allow protein interaction studies to be performed, particularly important for identifying substrates for enzymes like *ancA* which could provide significant new information on this gene.

Given *L. garvieae* causes mastitis in dairy cattle and is considered an emerging pathogen in the dairy industry, PIMMS analysis could be used to identify genes important for causing mastitis in cattle through the construction of a pGh9:ISS1 mutant bank in a strain derived from cattle, with the phenotypic studies carried out using bacteria grown in cows' milk rather than serum.

4.5 Conclusion

This study was the first to identify potential genes of interest directly related to growth in serum of a lactococcal species using PIMMS-based comparative analysis and successfully identified almost 400 genes that were categorised as important for survival and potential virulence of fish pathogen *L. garvieae* 02106 in fish serum as a proxy for bacterial virulence in the live host.

The findings have identified genes with potential as targets for a lactococcosis vaccination, for use in diagnostics to differentiate lactococcosis from infection with other streptococci, and as potential alternative control methods to the continued use of antimicrobials in aquaculture practices. Using an array of bioinformatics techniques including RAST, SignalP, PSORTb, KEGG, and STRING, further information on the importance, location and significance of a number of genes as well as putative function was obtained. Both *divIB* and *spsB* were found to be highly conserved between *L. garvieae* species, but no other related bacterial species and with their protein products predicted to be localised to the bacterial cell wall, these genes have most potential for further investigation as monovalent vaccination candidates or specific diagnostic targets. This could present either gene as a potential specific diagnostic target for lactococcosis, which is typically non-distinguishable from clinical streptococcosis caused by other related bacteria. Comparatively little information could be uncovered on *ancA*, and whilst hypothetical protein LAG_00167 may have a structural role in the bacteria, the exact functions of these proteins is yet to be elucidated, although they appear to be important for *L. garvieae* survival in fish serum.

With *divIB* and *spsB* also being found with almost completely identical sequences in *L. garvieae* infections in humans, these could present exciting genes of relevance to human medicine, where lactococcosis is considered an emerging disease (Aguado-Urda, López-Campos, Blanco, *et al.*, 2011). A very similar sequence to *spsB* was also identified in a mastitic cow, so this gene may also have relevance to the dairy industry where *L. garvieae* is known to have a role in mastitis.

394 genes remain in the essential genome which are yet to be further investigated, some of which may have the potential to improve the wealth of

tools we have available to combat the growing threat of lactococcal infection in aquaculture over the next few decades. In the face of an increasing human population with higher than ever demands on the production of fish as a food source, these genes could play a significant role in the development of therapeutics, prophylactics or diagnostics in any species at risk of infection. The impact of this on aquaculture productivity, the reduction in antibiotic usage, resistance development and drug costs could make a great positive difference to the industry. Hence in terms of improving trout health, food security and reducing the risk of lactococcosis spread to humans, these findings could contribute significantly to future progress.

References

Agnew, W. and Barnes, A. C. (2007) 'Streptococcus iniae: An aquatic pathogen of global veterinary significance and a challenging candidate for reliable vaccination', *Veterinary Microbiology*, pp. 1–15. doi: 10.1016/j.vetmic.2007.03.002.

Aguado-Urda, M., López-Campos, G. H., Blanco, M. M., *et al.* (2011) 'Genome sequence of Lactococcus garvieae 21881, isolated in a case of human septicemia', *Journal of Bacteriology*, 193(15), pp. 4033–4034. doi: 10.1128/JB.05090-11.

Aguado-Urda, M., López-Campos, G. H., Gibello, A., *et al.* (2011) 'Genome sequence of Lactococcus garvieae 8831, isolated from rainbow trout lactococcosis outbreaks in Spain', *Journal of Bacteriology*, pp. 4263–4264. doi: 10.1128/JB.05326-11.

Aguado-Urda, M. *et al.* (2012) 'Characterization of Plasmids in a human clinical strain of Lactococcus garvieae', *PLoS ONE*, 7(6). doi: 10.1371/journal.pone.0040119.

Ajdic, D. *et al.* (2002) 'Genome sequence of Streptococcus mutans UA159, a cariogenic dental pathogen', *Proceedings of the National Academy of Sciences*, 99(22), pp. 14434–14439. doi: 10.1073/pnas.172501299.

Akiyama, Y., Yoshihisa, T. and Ito, K. (1995) 'FtsH, a membrane-bound ATPase, forms a complex in the cytoplasmic membrane of Escherichia coli', *Journal of Biological Chemistry*, 270(40), pp. 23485–23490. doi: 10.1074/jbc.270.40.23485.

Altin, G., Nikerel, E. and Şahin, F. (2017) 'Draft genome sequence of

magnesium-dissolving Lactococcus garvieae A1, isolated from soil', *Genome Announcements*, 5(21). doi: 10.1128/genomeA.00386-17.

Altschul, S. F. *et al.* (1990) 'Basic local alignment search tool', *Journal of Molecular Biology*, 215(3), pp. 403–410. doi: 10.1016/S0022-2836(05)80360-2.

Altschul, S. F. *et al.* (1997) 'Gapped BLAST and PSI-BLAST: A new generation of protein database search programs', *Nucleic Acids Research*, pp. 3389–3402. doi: 10.1093/nar/25.17.3389.

Amoroso, G. *et al.* (2016) 'Skeletal anomaly assessment in diploid and triploid juvenile Atlantic salmon (Salmo salar L.) and the effect of temperature in freshwater', *Journal of Fish Diseases*, 39(4), pp. 449–466. doi: 10.1111/jfd.12438.

Anderson, E. D. *et al.* (1996) 'Genetic immunization of rainbow trout (Oncorhynchus mykiss) against infectious hematopoietic necrosis virus.', *Molecular marine biology and biotechnology*, 5(2), pp. 114–22. Available at: http://www.ncbi.nlm.nih.gov/pubmed/8680524.

Argüello, J. M., Raimunda, D. and Padilla-Benavides, T. (2013) 'Mechanisms of copper homeostasis in bacteria', *Frontiers in Cellular and Infection Microbiology*, 3. doi: 10.3389/fcimb.2013.00073.

Aslibekyan, S., Almeida, M. and Tintle, N. (2014) 'Pathway analysis approaches for rare and common variants: Insights from genetic analysis workshop 18', *Genetic Epidemiology*, 38(SUPPL.1). doi: 10.1002/gepi.21831.

Atrazhev, A. M. and Elliott, J. F. (1996) 'Simplified desalting of ligation reactions immediately prior to electroporation into E. coli', *BioTechniques*.

Austin, B. and Austin, D. A. (2012) *Bacterial fish pathogens: Disease of farmed*

and wild fish, *Bacterial Fish Pathogens: Disease of Farmed and Wild Fish*. doi: 10.1007/978-94-007-4884-2.

Avci, H. *et al.* (2014) 'Experimental Lactococcus garvieae infection in rainbow trout, Oncorhynchus mykiss, Walbaum 1792: A comparative histopathological and immunohistochemical study', *Journal of Fish Diseases*, 37(5), pp. 481–495. doi: 10.1111/jfd.12132.

Aziz, R. K. *et al.* (2008) 'The RAST Server: Rapid Annotations using Subsystems Technology', *BMC Genomics*, 9(1), p. 75. doi: 10.1186/1471-2164-9-75.

Balayut, E. A. (1989) *Aquaculture Systems and Practices: a Selected Review*, *Food & Agriculture Organization*. Available at: http://www.fao.org/docrep/t8598e/t8598e00.htm.

Barnett, T. C. *et al.* (2015) 'Streptococcal toxins: Role in pathogenesis and disease', *Cellular Microbiology*, pp. 1721–1741. doi: 10.1111/cmi.12531.

Bastardo, A. *et al.* (2012) 'Effectiveness of bivalent vaccines against Aeromonas hydrophila and Lactococcus garvieae infections in rainbow trout Oncorhynchus mykiss (Walbaum)', *Fish and Shellfish Immunology*, 32(5), pp. 756–761. doi: 10.1016/j.fsi.2012.01.028.

Baureder, M. and Hederstedt, L. (2012) 'Genes important for catalase activity in enterococcus faecalis', *PLoS ONE*, 7(5). doi: 10.1371/journal.pone.0036725.

Benov, L. and Fridovich, I. (1995) 'Superoxide dismutase protects against aerobic heat shock in Escherichia coli', *Journal of Bacteriology*, 177(11), pp. 3344–3346. doi: 10.1128/jb.177.11.3344-3346.1995.

Benson, D. A. *et al.* (2013) 'GenBank', *Nucleic Acids Research*, 41(D1). doi: 10.1093/nar/gks1195.

Bercovier, H., Ghittino, C. and Eldar, A. (1997) 'Immunization with bacterial antigens: infections with streptococci and related organisms', *Developments in Biological Standardization*, 90, pp. 153–160.

Besson, M. *et al.* (2014) 'Economic values of growth and feed efficiency for fish farming in recirculating aquaculture system with density and nitrogen output limitations: A case study with African catfish (clarias gariepinus)', *Journal of Animal Science*, 92(12), pp. 5394–5405. doi: 10.2527/jas2014-8266.

Blanchard, A. (2015) 'The Use of Random Mutagenesis in the Functional Annotation of the Streptococcus uberis Genome', (July).

Blanchard, A. M. *et al.* (2016) 'PIMMS (Pragmatic Insertional Mutation Mapping System) laboratory methodology a readily accessible tool for identification of essential genes in Streptococcus', *Frontiers in Microbiology*, 7(OCT), pp. 1–12. doi: 10.3389/fmicb.2016.01645.

Bostock, J. *et al.* (2010) 'Aquaculture: global status and trends.', *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 365(1554), pp. 2897–2912. doi: 10.1098/rstb.2010.0170.

Bottomley, A. L. *et al.* (2014) 'Staphylococcus aureusDivIB is a peptidoglycan-binding protein that is required for a morphological checkpoint in cell division', *Molecular Microbiology*, 94(5), pp. 1041–1064. doi: 10.1111/mmi.12813.

Cabello, F. C. *et al.* (2013) 'Antimicrobial use in aquaculture re-examined: Its relevance to antimicrobial resistance and to animal and human health', *Environmental Microbiology*, 15(7), pp. 1917–1942. doi: 10.1111/1462-2920.12134.

Champoux, J. J. (2001) 'DNA topoisomerases: structure, function, and

mechanism.', *Annual review of biochemistry*, 70, pp. 369–413. doi: 10.1146/annurev.biochem.70.1.369.

Chan, J. F. W. *et al.* (2011) 'Primary infective spondylodiscitis caused by Lactococcus garvieae and a review of human L. garvieae infections', *Infection*, 39(3), pp. 259–264. doi: 10.1007/s15010-011-0094-8.

Chao, M. C. *et al.* (2016) 'The design and analysis of transposon insertion sequencing experiments', *Nature Reviews Microbiology*. Nature Publishing Group, 14(2), pp. 119–128. doi: 10.1038/nrmicro.2015.7.

Christie, K. E. (1997) 'Immunization with viral antigens: infectious pancreatic necrosis.', *Developments in biological standardization*, 90, pp. 191–9. Available at: http://www.ncbi.nlm.nih.gov/pubmed/9270848.

Cipriano, R. C., Ford, L. A. and Jones, T. E. (1994) 'Relationship between resistance of salmonids to furunculosis and recovery of Aeromonas salmonicida from external mucus.', *Journal of wildlife diseases*, 30(4), pp. 577–80. doi: 10.7589/0090-3558-30.4.577.

Coulter, S. N. *et al.* (1998) 'Staphylococcus aureus genetic loci impacting growth and survival in multiple infection environments', *Molecular Microbiology*, 30(2), pp. 393–404. doi: 10.1046/j.1365-2958.1998.01075.x.

Currás, M. *et al.* (2002) 'Dormancy as a survival strategy of the fish pathogen Streptococcus parauberis in the marine environment', *Diseases of Aquatic Organisms*, 52(2), pp. 129–136. doi: 10.3354/dao052129.

Dang, H. T. *et al.* (2012) 'Development of a novel PCR assay based on the 16S-23S rRNA internal transcribed spacer region for the detection of Lactococcus garvieae', *Journal of Fish Diseases*, 35(7), pp. 481–487. doi: 10.1111/j.1365-

2761.2012.01382.x.

Defoirdt, T., Sorgeloos, P. and Bossier, P. (2011) 'Alternatives to antibiotics for the control of bacterial disease in aquaculture', *Current Opinion in Microbiology*, pp. 251–258. doi: 10.1016/j.mib.2011.03.004.

Denapaite, D. *et al.* (2016) 'Highly Variable *Streptococcus oralis* Strains Are Common among Viridans Streptococci Isolated from Primates', *mSphere*, 1(2), pp. e00041-15. doi: 10.1128/mSphere.00041-15.

Doi, R. H. *et al.* (2003) 'Cellulosomes from mesophilic bacteria', *Journal of Bacteriology*, pp. 5907–5914. doi: 10.1128/JB.185.20.5907-5914.2003.

Egan, S. A. *et al.* (2010) 'Identification of sortase A (SrtA) substrates in Streptococcus uberis: Evidence for an additional hexapeptide (LPXXXD) sorting motif', *Journal of Proteome Research*, 9(2), pp. 1088–1095. doi: 10.1021/pr901025w.

Eldar, A. and Ghittino, C. (1999) 'Lactococcus garvieae and Streptococcus iniae infections in rainbow trout Oncorhynchus mykiss: Similar, but different diseases', *Diseases of Aquatic Organisms*, 36(3), pp. 227–231. doi: 10.3354/dao036227.

Ellis, T. *et al.* (2015) 'Aquaculture statistics for the UK , with a focus on England and Wales 2012', p. 18. Available at: https://www.gov.uk/government/uploads/system/uploads/attachment_data/file/405469/Aquaculture_Statistics_UK_2012.pdf.

Emanuelsson, O. *et al.* (2007) 'Locating proteins in the cell using TargetP, SignalP and related tools', *Nature Protocols*, 2(4), pp. 953–971. doi: 10.1038/nprot.2007.131.

EMBL, SIB Swiss Institute of Bioinformatics and Protein Information Resource (PIR) (2013) 'UniProt', in *Nucleic acids research*, p. 41: D43-D47.

Esteve-Gassent, M. D. *et al.* (2015) 'Absence of sodA increases the levels of oxidation of key metabolic determinants of Borrelia burgdorferi', *PLoS ONE*, 10(8). doi: 10.1371/journal.pone.0136707.

European Commission (2016) *Facts and figures on the Common Fisheries Policy*. doi: 10.2771/607841.

FAO (2015) 'An Overview of Recently Published Global Aquaculture Statistics'.

Ferretti, J. J. *et al.* (2001) 'Complete genome sequence of an M1 strain of Streptococcus pyogenes', *Proceedings of the National Academy of Sciences*, 98(8), pp. 4658–4663. doi: 10.1073/pnas.071559398.

Fl??rez, A. B. *et al.* (2012) 'Genome sequence of Lactococcus garvieae IPLA 31405, a bacteriocin-producing, tetracycline-resistant strain isolated from a raw-milk cheese', *Journal of Bacteriology*, pp. 5118–5119. doi: 10.1128/JB.00975-12.

Fulde, M. and Valentin-Weigand, P. (2013) 'Epidemiology and pathogenicity of zoonotic streptococci', *Current Topics in Microbiology and Immunology*, 368, pp. 49–81. doi: 10.1007/82-2012-277.

Gardy, J. L. *et al.* (2003) 'PSORT-B: Improving protein subcellular localization prediction for Gram-negative bacteria', *Nucleic Acids Research*, 31(13), pp. 3613–3617. doi: 10.1093/nar/gkg602.

Gibello, A. *et al.* (2016) 'The zoonotic potential of Lactococcus garvieae: An overview on microbiology, epidemiology, virulence factors and relationship with its presence in foods', *Research in Veterinary Science*, pp. 59–70. doi:

10.1016/j.rvsc.2016.09.010.

Gibson, D. G. *et al.* (2010) 'Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome', *Science*, 329(5987), pp. 52–56. doi: 10.1126/science.1190719.

Glass, J. I. *et al.* (2006) 'Essential genes of a minimal bacterium', *Proceedings of the National Academy of Sciences*, 103(2), pp. 425–430. doi: 10.1073/pnas.0510013103.

Gloster, T. M. (2014) 'Advances in understanding glycosyltransferases from a structural perspective', *Current Opinion in Structural Biology*, pp. 131–141. doi: 10.1016/j.sbi.2014.08.012.

Goodman, L. B. *et al.* (2017) 'Lactococcus petauri sp. nov., isolated from an abscess of a sugar glider', *International Journal of Systematic and Evolutionary Microbiology*, 67(11), pp. 4397–4404. doi: 10.1099/ijsem.0.002303.

Le Gouëllec, A. *et al.* (2008) 'Roles of pneumococcal DivIB in cell division', *Journal of Bacteriology*, 190(13), pp. 4501–4511. doi: 10.1128/JB.00376-08.

Green, B. *et al.* (2012) 'Insertion site preference of Mu, Tn5, and Tn7 transposons.', *Mobile DNA*, 3(1), p. 3. doi: 10.1186/1759-8753-3-3.

Harry, E. J. *et al.* (1994) 'Conservation of the 168 divIB gene in Bacillus subtilis W23 and B. licheniformis, and evidence for homology to ftsQ of Escherichia coli', *Gene*, 147(1), pp. 85–89. doi: 10.1016/0378-1119(94)90043-4.

Holbourn, K. P., Shone, C. C. and Acharya, K. R. (2006) 'A family of killer toxins: Exploring the mechanism of ADP-ribosylating toxins', *FEBS Journal*, pp. 4579–4593. doi: 10.1111/j.1742-4658.2006.05442.x.

Johnson, J. R. (1991) 'Virulence factors in Escherichia coli urinary tract infection.', *Clinical microbiology reviews*, 4(1), pp. 80–128. doi: 10.1128/CMR.4.1.80.Updated.

Joyce, A. R. *et al.* (2006) 'Experimental and computational assessment of conditionally essential genes in Escherichia coli', *Journal of Bacteriology*, 188(23), pp. 8259–8271. doi: 10.1128/JB.00740-06.

Kanehisa, M. *et al.* (2012) 'KEGG for integration and interpretation of large-scale molecular data sets', *Nucleic Acids Research*, 40(D1). doi: 10.1093/nar/gkr988.

Karp, P. D. (2001) 'Pathway databases: a case study in computational symbolic theories', *Science (New York, NY)*, 293(5537), pp. 2040–2044. doi: 10.1126/science.1064621.

Kawanishi, M. *et al.* (2005) 'Drug resistance and pulsed-field gel electrophoresis patterns of Lactococcus garvieae isolates from cultured Seriola (yellowtail, amberjack and kingfish) in Japan', *Letters in Applied Microbiology*, 40(5), pp. 322–328. doi: 10.1111/j.1472-765X.2005.01690.x.

Kawanishi, M. *et al.* (2006) 'Differences between Lactococcus garvieae isolated from the genus Seriola in Japan and those isolated from other animals (trout, terrestrial animals from Europe) with regard to pathogenicity, phage susceptibility and genetic characterization', *Journal of Applied Microbiology*, 101(2), pp. 496–504. doi: 10.1111/j.1365-2672.2006.02951.x.

Kawanishi, M. *et al.* (2007) 'Characterization of Lactococcus garvieae isolated from radish and broccoli sprouts that exhibited a KG+ phenotype, lack of virulence and absence of a capsule', *Letters in Applied Microbiology*, 44(5), pp. 481–487. doi: 10.1111/j.1472-765X.2007.02114.x.

Keseler, I. M. *et al.* (2011) 'EcoCyc: A comprehensive database of Escherichia coli biology', *Nucleic Acids Research*, 39(SUPPL. 1). doi: 10.1093/nar/gkq1143.

Kietzman, C. C. *et al.* (2016) 'Dynamic capsule restructuring by the main pneumococcal autolysin LytA in response to the epithelium.', *Nature communications*, 7, p. 10859. doi: 10.1038/ncomms10859.

Kim, C. H. *et al.* (2000) 'DNA vaccines encoding viral glycoproteins induce nonspecific immunity and Mx protein synthesis in fish.', *Journal of virology*, 74(15), pp. 7048–7054. doi: 10.1128/JVI.74.15.7048-7054.2000.

Kim, J. H., Kang, D. H. and Park, S. C. (2015) 'Draft Genome Sequence of Human-Pathogenic Lactococcus garvieae LG-ilsanpaik-gs201105 That Caused Acute Acalculous Cholecystitis', *Genome Announc*, 3(3). doi: 10.1128/genomeA.00464-15.

Klein, B. A. *et al.* (2012) 'Identification of essential genes of the periodontal pathogen Porphyromonas gingivalis', *BMC Genomics*, 13(1), p. 578. doi: 10.1186/1471-2164-13-578.

Kline, K. A. *et al.* (2009) 'Bacterial Adhesins in Host-Microbe Interactions', *Cell Host and Microbe*, pp. 580–592. doi: 10.1016/j.chom.2009.05.011.

Kovjazin, R. and Carmon, L. (2014) 'The use of signal peptide domains as vaccine candidates', *Human Vaccines and Immunotherapeutics*, 10(9), pp. 2733–2740. doi: 10.4161/21645515.2014.970916.

Krieg, N. R. and Hoffman, P. S. (1986) 'Microaerophily and oxygen toxicity.', *Annual review of microbiology*, 40, pp. 107–130. doi: 10.1146/annurev.mi.40.100186.000543.

Kusuda R, H. M. (1988) 'Extracellular and intracellular toxins of Streptococcus

sp. isolated from yellowtail.', *Bull Eur Assoc Fish Pathol*, (8), pp. 9–10. Available at: https://eafp.org/download/1988-Volume8/Issue 1/08_1 p9.PDF.

L??ders, S., Fallet, C. and Franco-Lara, E. (2009) 'Proteome analysis of the Escherichia coli heat shock response under steady-state conditions', *Proteome Science*, 7, p. 36. doi: 10.1186/1477-5956-7-36.

Lamarche, M. G. *et al.* (2008) 'The phosphate regulon and bacterial virulence: A regulatory network connecting phosphate homeostasis and pathogenesis', *FEMS Microbiology Reviews*, pp. 461–473. doi: 10.1111/j.1574-6976.2008.00101.x.

Lampe, D. J. (2010) 'Bacterial genetic methods to explore the biology of mariner transposons', *Genetica*, 138(5), pp. 499–508. doi: 10.1007/s10709-009-9401-z.

Lampe, D. J., Grant, T. E. and Robertson, H. M. (1998) 'Factors affecting transposition of the Himar1 mariner transposon in vitro', *Genetics*, 149(1), pp. 179–187. doi: 9584095.

Langridge, G. C. *et al.* (2009) 'Simultaneous assay of every Salmonella Typhi gene using one million transposon mutants', *Genome Research*, 19(12), pp. 2308–2316. doi: 10.1101/gr.097097.109.

Leigh, J. A. *et al.* (2010) 'Sortase anchored proteins of Streptococcus uberis play major roles in the pathogenesis of bovine mastitis in dairy cattle', *Veterinary Research*, 41(5). doi: 10.1051/vetres/2010036.

Lutkenhaus, J. and Addinall, S. G. (1997) 'Bacterial cell division and the Z ring.', *Annual review of biochemistry*, 66, pp. 93–116. doi: 10.1146/annurev.biochem.66.1.93.

Lutkenhaus, J., Pichoff, S. and Du, S. (2012) 'Bacterial cytokinesis: From Z ring to divisome', *Cytoskeleton*, pp. 778–790. doi: 10.1002/cm.21054.

M. Halveson (2011) *An entirely synthetic fish: how rainbow trout beguiled America and overran the world*.

Ma, K., Khan, S. and Miyan K (2011) 'Aquaculture as a food production system: A review', *Review Article Biology and Medicine*, 3(2), pp. 291–302.

Mackie, A. *et al.* (2014) 'Addition of Escherichia coli K-12 growth observation and gene essentiality data to the ecocyc database', *Journal of Bacteriology*, 196(5), pp. 982–988. doi: 10.1128/JB.01209-13.

Maguin, E. and Ge, L. De (1996) 'Efficient Insertional Mutagenesis in Lactococci and Other Gram-Positive Bacteria', 178(3), pp. 931–935.

Mahdi, L. K. *et al.* (2015) 'Characterization of pneumococcal genes involved in bloodstream invasion in a mouse model', *PLoS ONE*, 10(11). doi: 10.1371/journal.pone.0141816.

Maki, T. *et al.* (2008) 'Drug resistance mechanism of the fish-pathogenic bacterium Lactococcus garvieae', *Journal of Fish Diseases*, 31(6), pp. 461–468. doi: 10.1111/j.1365-2761.2008.00927.x.

Marraffini, L. A., DeDent, A. C. and Schneewind, O. (2006) 'Sortases and the Art of Anchoring Proteins to the Envelopes of Gram-Positive Bacteria', *Microbiology and Molecular Biology Reviews*, 70(1), pp. 192–221. doi: 10.1128/MMBR.70.1.192-221.2006.

Martin, V. J. J. and Mohn, W. W. (1999) 'An alternative inverse PCR (IPCR) method to amplify DNA sequences flanking Tn5 transposon insertions', *Journal of Microbiological Methods*, 35(2), pp. 163–166. doi: 10.1016/S0167-7012(98)00115-8.

Mashoof, S. and Criscitiello, M. (2016) 'Fish Immunoglobulins', *Biology*, 5(4), p.

45. doi: 10.3390/biology5040045.

Mazzolari, A., Maddis, D. De and Carini, M. (2016) 'Inosine 5´-monophosphate dehydrogenase inhibitors as antimicrobial agents: recent progress and future perspectives', *Future Medicinal Chemistry*, 7, pp. 1415–1429. doi: 10.1017/CBO9781107415324.004.

McMillan, D. J. *et al.* (2004) 'Immune response to superoxide dismutase in group A streptococcal infection', *FEMS Immunology and Medical Microbiology*, 40(3), pp. 249–256. doi: 10.1016/S0928-8244(04)00003-3.

Mehne, F. M. P. *et al.* (2013) 'Cyclic Di-AMP homeostasis in bacillus subtilis: Both lack and high level accumulation of the nucleotide are detrimental for cell growth', *Journal of Biological Chemistry*, 288(3), pp. 2004–2017. doi: 10.1074/jbc.M112.395491.

Melorose, J., Perroy, R. and Careas, S. (2015) 'World population prospects', *United Nations*, 1(6042), pp. 587–92. doi: 10.1017/CBO9781107415324.004.

Menéndez, A. *et al.* (2007) 'Genes required for Lactococcus garvieae survival in a fish host', *Microbiology*, 153(10), pp. 3286–3294. doi: 10.1099/mic.0.2007/007609-0.

Menéndez, A., Mayo, B. and Guijarro, J. A. (2006) 'Construction of transposition insertion libraries and specific gene inactivation in the pathogen Lactococcus garvieae', *Research in Microbiology*, 157(6), pp. 575–581. doi: 10.1016/j.resmic.2005.11.016.

Meyburgh, C., Bragg, R. and Boucher, C. (2017) 'Lactococcus garvieae: an emerging bacterial pathogen of fish', *Diseases of Aquatic Organisms*, 123(1), pp. 67–79. doi: 10.3354/dao03083.

Michel, C., Kerouault, B. and Martin, C. (2003) 'Chloramphenicol and florfenicol susceptibility of fish-pathogenic bacteria isolated in France: Comparison of minimum inhibitory concentration, using recommended provisory standards for fish bacteria', *Journal of Applied Microbiology*, 95(5), pp. 1008–1015. doi: 10.1046/j.1365-2672.2003.02093.x.

Mielich-Süss, B., Schneider, J. and Lopez, D. (2013) 'Overproduction of flotillin influences cell differentiation and shape in Bacillus subtilis', *mBio*, 4(6). doi: 10.1128/mBio.00719-13.

Miyauchi, E. *et al.* (2012a) 'Comparative genomic analysis of Lactococcus garvieae strains isolated from different sources reveals candidate virulence genes', *International Journal of Microbiology*. doi: 10.1155/2012/728276.

Miyauchi, E. *et al.* (2012b) 'Comparative genomic analysis of Lactococcus garvieae strains isolated from different sources reveals candidate virulence genes', *International Journal of Microbiology*, 2012. doi: 10.1155/2012/728276.

Morita, H. *et al.* (2011a) 'Complete genome sequence and comparative analysis of the fish pathogen lactococcus garvieae', *PLoS ONE*, 6(8), pp. 1–8. doi: 10.1371/journal.pone.0023184.

Morita, H. *et al.* (2011b) 'Complete genome sequence and comparative analysis of the fish pathogen lactococcus garvieae', *PLoS ONE*, 6(8). doi: 10.1371/journal.pone.0023184.

Moumene, M. *et al.* (2016) 'Complete genome sequence and description of Lactococcus garvieae M14 isolated from Algerian fermented milk', *New Microbes and New Infections*, 10, pp. 122–131. doi: 10.1016/j.nmni.2016.01.009.

MSD Animal Health (2017) 'MSD ANIMAL HEALTH IN NEDERLAND', *MSD Animal*

Health, pp. 1–8. Available at: http://www.msd-animal-health.nl/binaries/Bedrijfsbrochure_MSD_AH_-_nederlands_-_final_tcm100-186622.pdf.

Mushegian, A. R. and Koonin, E. V (1996) 'A minimal gene set for cellular life derived by comparison of complete bacterial genomes.', *Proceedings of the National Academy of Sciences of the United States of America*, 93(19), pp. 10268–10273. doi: 10.1073/pnas.93.19.10268.

Musher, D. M. (1992) 'Infections Caused by Streptococcus pneumoniae: Clinical Spectrum, Pathogenesis, Immunity, and Treatment', *Clinical Infectious Diseases*, 14(4), pp. 801–809. doi: 10.1093/clinids/14.4.801.

Nadell, C. D. *et al.* (2008) 'The evolution of quorum sensing in bacterial biofilms', *PLoS Biology*, 6(1), pp. 0171–0179. doi: 10.1371/journal.pbio.0060014.

Nelson, M. C. *et al.* (2016) 'Draft Genome Sequence of *Lactococcus garvieae* Strain PAQ102015-99, an Outbreak Strain Isolated from a Commercial Trout Farm in the Northwestern United States', *Genome Announcements*, 4(4), pp. e00781-16. doi: 10.1128/genomeA.00781-16.

Nishiki, I. *et al.* (2016) 'Complete Genome Sequence of Nonagglutinating *Lactococcus garvieae* Strain 122061 Isolated from Yellowtail in Japan', *Genome Announcements*, 4(4), pp. e00592-16. doi: 10.1128/genomeA.00592-16.

Noga, E. J. (2010) *Fish disease: diagnosis and treatment.*, *Fish disease: diagnosis and treatment*.

North, B. P. *et al.* (2006) 'Stocking density practices of commercial UK rainbow trout farms', *Aquaculture*. doi: 10.1016/j.aquaculture.2006.05.043.

Ogata, H. *et al.* (1999) 'KEGG: Kyoto encyclopedia of genes and genomes', *Nucleic Acids Research*, pp. 29–34. doi: 10.1093/nar/27.1.29.

van Opijnen, T., Bodi, K. L. and Camilli, A. (2009) 'Tn-seq: High-throughput parallel sequencing for fitness and genetic interaction studies in microorganisms', *Nature Methods*, 6(10), pp. 767–772. doi: 10.1038/nmeth.1377.

van Opijnen, T. and Camilli, A. (2013) 'Transposon insertion sequencing: a new tool for systems-level analysis of microorganisms.', *Nature reviews. Microbiology*, 11(7), pp. 435–42. doi: 10.1038/nrmicro3033.

Van Opijnen, T. and Camilli, A. (2012) 'A fine scale phenotype-genotype virulence map of a bacterial pathogen', *Genome Research*, 22(12), pp. 2541–2551. doi: 10.1101/gr.137430.112.

Overbeek, R. *et al.* (2005) 'The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes', *Nucleic Acids Research*, 33(17), pp. 5691–5702. doi: 10.1093/nar/gki866.

Overbeek, R. *et al.* (2014) 'The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST)', *Nucleic Acids Research*, 42(D1). doi: 10.1093/nar/gkt1226.

Paetzel, M. (2014) 'Structure and mechanism of Escherichia coli type I signal peptidase', *Biochimica et Biophysica Acta - Molecular Cell Research*, pp. 1497–1508. doi: 10.1016/j.bbamcr.2013.12.003.

Pérez-Sánchez, T. *et al.* (2011) 'Identification and characterization of lactic acid bacteria isolated from rainbow trout, Oncorhynchus mykiss (Walbaum), with inhibitory activity against Lactococcus garvieae', *Journal of Fish Diseases*, 34(7),

pp. 499–507. doi: 10.1111/j.1365-2761.2011.01260.x.

Petersen, T. N. *et al.* (2011) 'SignalP 4.0: discriminating signal peptides from transmembrane regions', *Nature Methods*, 8(10), pp. 785–786. doi: 10.1038/nmeth.1701.

Poyart, C. *et al.* (2001) 'Contribution of Mn-cofactored superoxide dismutase (SodA) to the virulence of Streptococcus agalactiae', *Infection and Immunity*, 69(8), pp. 5098–5106. doi: 10.1128/IAI.69.8.5098-5106.2001.

Pray, L. (2008) 'Transposons: The jumping genes.', *Nature Education*, 1(1), p. 204. Available at: http://www.nature.com/scitable/topicpage/transposons-the-jumping-genes-518.

Press, C. M. L. and Evensen, O. (1999) 'The morphology of the immune system in teleost fishes', *Fish and Shellfish Immunology*, 9(4), pp. 309–318. doi: 10.1006/fsim.1998.0181.

Pridgeon, J. (2012) 'Major bacterial diseases in aquaculture and their vaccine development.', *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources*, 7(048). doi: 10.1079/PAVSNNR20127048.

Ra, C. H. *et al.* (2009) 'Evaluation of optimal culture conditions for recombinant ghost bacteria vaccine production with the antigen of Streptococcus iniae GAPDH', *Journal of Microbiology and Biotechnology*, 19(9), pp. 982–986. doi: 10.4014/jmb.0901.007.

Radziwill-Bienkowska, J. M. *et al.* (2016) 'Adhesion of the genome-sequenced Lactococcus lactis subsp. cremoris IBB477 strain is mediated by specific molecular determinants', *Applied Microbiology and Biotechnology*, 100(22), pp. 9605–9617. doi: 10.1007/s00253-016-7813-0.

Rasmussen, M. *et al.* (2014) 'Lactococcus garvieae endocarditis presenting with subdural haematoma.', *BMC Cardiovascular Disorders*, 14(13), pp. 1471–2261. doi: 10.1186/1471-2261-14-13.

Ravelo, C. *et al.* (2006) 'Use of adjuvanted vaccines to lengthen the protection against lactococcosis in rainbow trout (Oncorhynchus mykiss)', *Aquaculture*, 251(2–4), pp. 153–158. doi: 10.1016/j.aquaculture.2005.05.027.

Reimundo, P. *et al.* (2011) 'Genome sequence of Lactococcus garvieae UNIUD074, isolated in Italy from a lactococcosis outbreak', *Journal of Bacteriology*, pp. 3684–3685. doi: 10.1128/JB.05210-11.

Ricci, G. *et al.* (2012) 'Genome sequences of Lactococcus garvieae TB25, isolated from italian cheese, and Lactococcus garvieae LG9, isolated from italian rainbow trout', *Journal of Bacteriology*, pp. 1249–1250. doi: 10.1128/JB.06655-11.

Robinson, M. D., McCarthy, D. J. and Smyth, G. K. (2010) 'edgeR: a Bioconductor package for differential expression analysis of digital gene expression data.', *Bioinformatics (Oxford, England)*, 26(1), pp. 139–40. doi: 10.1093/bioinformatics/btp616.

Rogers, Y.-H. and Venter, J. C. (2005) 'Genomics: Massively parallel sequencing', *Nature*, 437(7057), pp. 326–327. doi: 10.1038/437326a.

Romero, J., Feijoó, C. G. and Navarrete, P. (2012) 'Antibiotics in aquaculture – Use, abuse and alternatives', *Health and Environment in Aquaculture*, pp. 160–198. doi: 10.5772/28157.

Salama, N. R., Shepherd, B. and Falkow, S. (2004) 'Global transposon mutagenesis and essential gene analysis of Helicobacter pylori', *Journal of*

Bacteriology, 186(23), pp. 7926–7935. doi: 10.1128/JB.186.23.7926-7935.2004.

Seemann, T. (2014) 'Prokka: Rapid prokaryotic genome annotation', *Bioinformatics*, 30(14), pp. 2068–2069. doi: 10.1093/bioinformatics/btu153.

Sharma, S. *et al.* (2014) 'Structural and functional insights into peptidyl-tRNA hydrolase', *Biochimica et Biophysica Acta - Proteins and Proteomics*, pp. 1279–1288. doi: 10.1016/j.bbapap.2014.04.012.

Sievers, F. and Higgins, D. G. (2017) 'Clustal Omega for making accurate alignments of many protein sequences', *Protein Science*. doi: 10.1002/pro.3290.

Singh, J. K. *et al.* (2007) 'A membrane protein, EzrA, regulates assembly dynamics of FtsZ by interacting with the C-terminal tail of FtSZ', *Biochemistry*, 46(38), pp. 11013–11022. doi: 10.1021/bi700710j.

Slater, J. D. *et al.* (2003) 'Mutagenesis of Streptococcus equi and Streptococcus suis by transposon Tn917', *Veterinary Microbiology*, 93(3), pp. 197–206. doi: 10.1016/S0378-1135(03)00030-0.

Sommerset, I. *et al.* (2005) 'Vaccines for fish in aquaculture.', *Expert review of vaccines*, 4(1), pp. 89–101. doi: 10.1586/14760584.4.1.89.

Spellerberg, B. *et al.* (1999) 'Identification of genetic determinants for the hemolytic activity of streptococcus agalactiae by iss1 transposition', *Journal of Bacteriology*, 181(10), pp. 3212–3219.

Srinivasan, R., Rajeswari, H. and Ajitkumar, P. (2008) 'Analysis of degradation of bacterial cell division protein FtsZ by the ATP-dependent zinc-metalloprotease FtsH in vitro', *Microbiological Research*, 163(1), pp. 21–30. doi: 10.1016/j.micres.2006.03.001.

Subasinghe, R. P. (2005) 'Epidemiological approach to aquatic animal health management: Opportunities and challenges for developing countries to increase aquatic production through aquaculture', in *Preventive Veterinary Medicine*, pp. 117–124. doi: 10.1016/j.prevetmed.2004.11.004.

Szklarczyk, D. *et al.* (2015) 'STRING v10: Protein-protein interaction networks, integrated over the tree of life', *Nucleic Acids Research*, 43(D1), pp. D447–D452. doi: 10.1093/nar/gku1003.

Szklarczyk, D. *et al.* (2017) 'The STRING database in 2017: Quality-controlled protein-protein association networks, made broadly accessible', *Nucleic Acids Research*, 45(D1), pp. D362–D368. doi: 10.1093/nar/gkw937.

Tang, Y. *et al.* (2012) 'Inactivation of the sodA gene of Streptococcus suis type 2 encoding superoxide dismutase leads to reduced virulence to mice', *Veterinary Microbiology*, 158(3–4), pp. 360–366. doi: 10.1016/j.vetmic.2012.02.028.

Tanner, J. J. *et al.* (2014) 'Structure, mechanism, and dynamics of UDP-galactopyranose mutase', *Archives of Biochemistry and Biophysics*, pp. 128–141. doi: 10.1016/j.abb.2013.09.017.

Tomoyasu, T., Yuki, T., *et al.* (1993) 'The Escherichia coli FtsH protein is a prokaryotic member of a protein family of putative ATPases involved in membrane functions, cell cycle control, and gene expression', *Journal of Bacteriology*, 175(5), pp. 1344–1351.

Tomoyasu, T., Yamanaka, K., *et al.* (1993) 'Topology and subcellular localization of FtsH protein in Escherichia coli', *Journal of Bacteriology*, 175(5), pp. 1352–1357.

Tomoyasu, T. *et al.* (2012) 'Role of streptococcus intermedius DnaK chaperone

system in stress tolerance and pathogenicity', *Cell Stress and Chaperones*, 17(1), pp. 41–55. doi: 10.1007/s12192-011-0284-4.

Torkamani, A., Topol, E. J. and Schork, N. J. (2008) 'Pathway analysis of seven common diseases assessed by genome-wide association', *Genomics*, 92(5), pp. 265–272. doi: 10.1016/j.ygeno.2008.07.011.

Troell, M. *et al.* (2014) 'Does aquaculture add resilience to the global food system?', *Proceedings of the National Academy of Sciences*, 111(37), pp. 13257–13263. doi: 10.1073/pnas.1404067111.

Tucker, T., Marra, M. and Friedman, J. M. (2009) 'Massively Parallel Sequencing: The Next Big Thing in Genetic Medicine', *American Journal of Human Genetics*, pp. 142–154. doi: 10.1016/j.ajhg.2009.06.022.

Türe et al. (2014) 'Comparison of Experimental Susceptibility of Rainbow Trout (Oncorhynchus mykiss), Turbot (Psetta maxima), Black Sea Trout (Salmo trutta labrax) and Sea Bass (Dicentrarchus labrax) to Lactococcus garvieae', *Turkish Journal of Fisheries and Aquatic Science*, 14, pp. 713–726. doi: 10.4194/1303-2712-v14.

Ture, M. and Altinok, I. (2016) 'Detection of putative virulence genes of Lactococcus garvieae', *Diseases of Aquatic Organisms*, 119(1), pp. 59–66. doi: 10.3354/dao02981.

UniProt (2013) 'Update on activities at the Universal Protein Resource (UniProt) in 2013.', *Nucleic acids research*, 41(Database issue), pp. D43–7. doi: 10.1093/nar/gks1068.

Vela, A. I. *et al.* (2000) 'Phenotypic and genetic characterization of Lactococcus garvieae isolated in Spain from lactococcosis outbreaks and comparison with

isolates of other countries and sources', *Journal of Clinical Microbiology*, 38(10), pp. 3791–3795.

Vendrell, D. *et al.* (2006) 'Lactococcus garvieae in fish: A review', *Comparative Immunology, Microbiology and Infectious Diseases*, 29(4), pp. 177–198. doi: 10.1016/j.cimid.2006.06.003.

Verner-Jeffreys, D. W. *et al.* (2011) 'Evaluation of the biolog microlog 1 system for the identification of gram positive cocci pathogenic for fish', *Bulletin of the European Association of Fish Pathologists*, 31(5), pp. 171–181.

Wang, C. Y. C. *et al.* (2007) 'Lactococcus garvieae infections in humans: Possible association with aquaculture outbreaks', *International Journal of Clinical Practice*, 61(1), pp. 68–73. doi: 10.1111/j.1742-1241.2006.00855.x.

Ward, P. N. *et al.* (2001) 'Identification and disruption of two discrete loci encoding hyaluronic acid capsule biosynthesis genes hasA, hasB, and hasC in Streptococcus uberis', *Infection and Immunity*, 69(1), pp. 392–399. doi: 10.1128/IAI.69.1.392-399.2001.

Wendlandt, S. *et al.* (2015) 'Multidrug resistance genes in staphylococci from animals that confer resistance to critically and highly important antimicrobial agents in human medicine', *Trends in Microbiology*, pp. 44–54. doi: 10.1016/j.tim.2014.10.002.

Wickles, S. *et al.* (2014) 'A structural model of the active ribosome-bound membrane protein insertase YidC', *eLife*, 3(July2014), pp. 1–17. doi: 10.7554/eLife.03035.

Wong, T. T. and Zohar, Y. (2015) 'Production of reproductively sterile fish: A mini-review of germ cell elimination technologies', *General and Comparative*

Endocrinology, 221, pp. 3–8. doi: 10.1016/j.ygcen.2014.12.012.

Woynarovich, A., Hoitsy, G. and Moth-Poulsen, T. (2011) 'Small-scale rainbow trout farming', *FAO fisheries and aquaculture*, p. 81p. Available at: http://search.proquest.com/docview/1268652225?accountid=14643%5Cnhttp://mlbsfx.sibi.usp.br:3410/sfxlcl41?url_ver=Z39.88-2004&rft_val_fmt=info:ofi/fmt:kev:mtx:book&genre=book&sid=ProQ:Aquatic+Science+&+Fisheries+Abstracts+(ASFA)+Aquaculture+Abstracts&atitl.

Xiong, L. *et al.* (2016) 'Arginine metabolism in bacterial pathogenesis and cancer therapy', *International Journal of Molecular Sciences*, 17(3), pp. 1–18. doi: 10.3390/ijms17030363.

Xu, K. *et al.* (2015) 'Development and application of biological technologies in fish genetic breeding', *Science China Life Sciences*, pp. 187–201. doi: 10.1007/s11427-015-4798-3.

Yáñez, J. M., Houston, R. D. and Newman, S. (2014) 'Genetics and genomics of disease resistance in salmonid species', *Frontiers in Genetics*. doi: 10.3389/fgene.2014.00415.

Yoshida, T. *et al.* (1996) 'Phenotypic variation associated with an anti-Phagocytic factor in the bacterial fish pathogen Enterococcus seriolicida', *Diseases of Aquatic Organisms*, 25(1–2), pp. 81–86.

Ytrestøyl, T., Aas, T. S. and Åsgård, T. (2015) 'Utilisation of feed resources in production of Atlantic salmon (Salmo salar) in Norway', *Aquaculture*, 448, pp. 365–374. doi: 10.1016/j.aquaculture.2015.06.023.

Yu, N. Y. *et al.* (2010) 'PSORTb 3.0: Improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for

all prokaryotes', *Bioinformatics*, 26(13), pp. 1608–1615. doi: 10.1093/bioinformatics/btq249.

Zhang, Y. A. *et al.* (2010) 'IgT, a primitive immunoglobulin class specialized in mucosal immunity', *Nature Immunology*, 11(9), pp. 827–835. doi: 10.1038/ni.1913.

Zhou, L. *et al.* (2010) 'A novel multivalent vaccine based on secretary antigen-delivery induces protective immunity against Vibrio anguillarum and Aeromonas hydrophila', *Journal of Biotechnology*, 146(1–2), pp. 25–30. doi: 10.1016/j.jbiotec.2009.12.010.

Zimmerman, A. E. *et al.* (2014) 'Phosphate supply explains variation in nucleic acid allocation but not C: P stoichiometry in the western North Atlantic', *Biogeosciences*, 11(6), pp. 1599–1611. doi: 10.5194/bg-11-1599-2014.

Zlotkin, A. *et al.* (1998) 'Identification of Lactococcus garvieae by PCR', *Journal of Clinical Microbiology*, 36(4), pp. 983–985.

Zuily, S., Mami, Z. and Meune, C. (2011) 'Lactococcus garvieae endocarditis', *Archives of Cardiovascular Diseases*, 104(2), pp. 138–139. doi: 10.1016/j.acvd.2010.05.005.

Appendices
Appendix 1

Table documenting credits gained during this MRes

Date	Event	Duration/ days	Credits
30/06/2017	SVMS Open Day	1	1
21/08/2017 – 05/09/2017	Veterinary Medicine UCAS Tutoring at Cardiff Sixth Form (UoN ambassador and tutor)	12	6
15/09/2017	SVMS Open Day	1	1
20/10/2017	Fellowship Day - RCVS (conference)	1	2
22/10/2017	Dog breeding reform group symposium (conference)	1	2
08/11/2017	Interprofessional Masterclass - Emergency Medicine	0.5	1
13/12/2017	Interprofessional masterclass - Pain, QMC	0.5	1
11/04/2018	Interprofessional masterclass - careers and leadership	0.5	1
24/03/2018	Offer holder day SVMS	1	1
Submitted 04/04/2018	ATP	N/A	5
Various	Central Short Courses (1 credit each unless otherwise stated): - Active listening - Video presentation - Small group teaching - Lecturing for learning - Foundations of teaching in HE - Assessing and giving feedback (2 credits)	N/A	7
Total credits (20 required)			28

Appendix 2

Table of annotations of each coding sequence for the PIMMS input pool of the *L. garvieae* 02106 genome used in this study

Locus	Gene	Start	Stop	CDS length	Product	Total number of insertions	Number of unique insertion positions	Unique insertions per1KbCDS (>=3)	First unique insertion centile	Last unique insertion centile %	Normalised Reads Mapped (NRM) score	Normalised Insertions Mapped (NIM) score
LAG_00001	parB	309	1097	789	Putative chromosome-partitioning protein ParB	132	17	21.546	5.3	95.9	471.96	60.783
LAG_00002	dnaA	1352	2710	1359	Chromosomal replication initiator protein DnaA	28	2	1.472	95.3	98.4	58.123	4.152
LAG_00003	dnaN	2874	4016	1143	DNA polymerase III subunit beta	0	0	0			0	0
LAG_00004	rexB	4060	7383	3324	ATP-dependent helicase/deoxyribonuclease subunit B	49	10	3.008	1.5	93.5	41.586	8.487
LAG_00005	addA	7376	10939	3564	ATP-dependent helicase/nuclease subunit A	77	14	3.928	3.1	94.1	60.948	11.082
LAG_00006	NA	10941	11144	204	hypothetical protein	0	0	0			0	0
LAG_00007	ychF	11260	12375	1116	Ribosome-binding ATPase YchF	32	3	2.688	34.9	76.4	80.89	7.583
LAG_00008	pth	12485	13057	573	Peptidyl-tRNA hydrolase	0	0	0			0	0
LAG_00009	mfd	13054	16539	3486	Transcription-repair-coupling factor	152	24	6.885	1.2	80.3	123.005	19.422
LAG_00010	hslR	16659	16931	273	Heat shock protein 15	0	0	0			0	0
LAG_00011	NA	16959	17330	372	hypothetical protein	33	4	10.753	76.9	97.6	250.253	30.334
LAG_00012	pnp_1	17327	17608	282	Polyribonucleotide nucleotidyltransferase	23	5	17.73	5.7	86.5	230.084	50.018
LAG_00013	hpaH	17605	19041	1437	Anthranilate 3-monooxygenase oxygenase component	71	13	9.047	5.8	75.9	139.383	25.521
LAG_00014	NA	19022	20323	1302	hypothetical protein	28	5	3.84	20.8	83.2	60.667	10.833
LAG_00015	tilS	20320	21573	1254	tRNA(Ile)-lysidine synthase	0	0	0			0	0
LAG_00016	hpt	21566	22105	540	Hypoxanthine-guanine phosphoribosyltransferase	0	0	0			0	0
LAG_00017	ftsH	22218	24263	2046	ATP-dependent zinc metalloprotease FtsH	4	1	0.489	2.2	2.2	5.515	1.379
LAG_00018	NA	24488	24561	74	tRNA-Glu	0	0	0			0	0
LAG_00019	NA	24566	24655	90	tRNA-Ser	0	0	0			0	0
LAG_00020	NA	24664	24739	76	tRNA-Met	0	0	0			0	0
LAG_00021	NA	24760	24834	75	tRNA-Phe	0	0	0			0	0
LAG_00022	NA	24837	24907	71	tRNA-Gly	0	0	0			0	0
LAG_00023	NA	24947	25020	74	tRNA-Ile	0	0	0			0	0
LAG_00024	NA	25140	25217	78	tRNA-Asn	0	0	0			0	0
LAG_00025	NA	26502	26825	324	hypothetical protein	80	11	33.951	0.9	98.8	696.552	95.776
LAG_00026	NA	27385	27696	312	hypothetical protein	192	19	60.897	2.2	99	1736.021	171.794
LAG_00027	NA	28167	28535	369	hypothetical protein	123	13	35.23	4.6	97	940.345	99.386
LAG_00028	NA	28532	29800	1269	hypothetical protein	556	57	44.917	5.5	94.8	1236.008	126.713
LAG_00029	NA	30063	30458	396	hypothetical protein	295	24	60.606	0.3	95.2	2101.528	170.972
LAG_00030	NA	30857	32623	1767	hypothetical protein	375	50	28.297	1.3	93.8	598.691	79.826
LAG_00031	NA	32620	32751	132	hypothetical protein	27	3	22.727	29.5	100	577.03	64.114
LAG_00032	NA	32748	33077	330	hypothetical protein	34	9	27.273	1.8	99.1	290.652	76.937
LAG_00033	NA	33167	33436	270	hypothetical protein	77	11	40.741	10.4	94.4	804.517	114.931
LAG_00034	NA	33433	33585	153	hypothetical protein	46	5	32.68	20.9	95.4	848.154	92.191
LAG_00035	NA	33582	33734	153	hypothetical protein	29	3	19.608	46.4	90.8	534.706	55.314
LAG_00036	NA	33724	34011	288	hypothetical protein	75	8	27.778	6.9	84	734.644	78.362
LAG_00037	NA	34008	34190	183	hypothetical protein	0	0	0			0	0
LAG_00038	NA	34190	34483	294	hypothetical protein	93	6	20.408	3.4	77.6	892.368	57.572
LAG_00039	NA	34600	34785	186	hypothetical protein	6	1	5.376	4.3	4.3	91.001	15.167
LAG_00040	NA	34867	35484	618	hypothetical protein	321	19	30.744	2.8	94	1465.294	86.731
LAG_00041	NA	35630	35896	267	hypothetical protein	97	6	22.472	4.1	89.5	1024.87	63.394
LAG_00042	NA	35939	36145	207	hypothetical protein	58	6	28.986	19.8	98.1	790.435	81.769

LAG_00043	NA	36413	36796	384	hypothetical protein	46	5	13.021	69.8	97.7	337.936	36.732
LAG_00044	NA	36808	37359	552	hypothetical protein	188	22	39.855	2.9	92.8	960.787	112.432
LAG_00045	NA	37533	37772	240	hypothetical protein	199	18	75	6.7	92.1	2339.107	211.578
LAG_00046	NA	37857	39170	1314	hypothetical protein	644	44	33.486	1.6	99.6	1382.607	94.464
LAG_00047	NA	39187	39777	591	hypothetical protein	158	23	38.917	11.8	97	754.185	109.786
LAG_00048	NA	39807	40205	399	hypothetical protein	264	29	72.682	9	96	1866.549	205.038
LAG_00049	NA	40267	41121	855	hypothetical protein	441	44	51.462	0.1	99.6	1455.059	145.176
LAG_00050	Int-Tn_1	41576	42757	1182	Transposase from transposon Tn916	561	61	51.607	1.9	99.5	1338.917	145.586
LAG_00051	NA	43133	43206	74	tRNA-Lys	23	3	40.541	4.1	89.2	876.808	114.366
LAG_00052	recO	43356	44150	795	DNA repair protein RecO	74	13	16.352	4	92.1	262.587	46.13
LAG_00053	pdhD	44185	45606	1422	Dihydrolipoyl dehydrogenase	104	14	9.845	11.2	95.4	206.32	27.774
LAG_00054	pdhC	45630	47216	1587	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenas	146	18	11.342	5.8	98.3	259.528	31.997
LAG_00055	pdhB	47209	48189	981	Pyruvate dehydrogenase E1 component subunit beta	58	10	10.194	3.4	80.6	166.789	28.757
LAG_00056	pdhA	48192	49316	1125	Pyruvate dehydrogenase E1 component subunit alpha	90	5	4.444	22.3	87.4	225.683	12.538
LAG_00057	NA	49348	50343	996	Lipoate--protein ligase 1	122	11	11.044	1.1	63.6	345.548	31.156
LAG_00058	glpQ	50548	51318	771	Glycerophosphodiester phosphodiesterase	45	9	11.673	2.5	89.9	164.652	32.93
LAG_00059	NA	51330	51968	639	hypothetical protein	27	4	6.26	30.4	100	119.199	17.659
LAG_00060	trpS2	51986	53017	1032	Tryptophan--tRNA ligase 2	3	1	0.969	1.7	1.7	8.201	2.734
LAG_00061	osmC	53436	53876	441	Peroxiredoxin OsmC	165	15	34.014	0.7	98	1055.489	95.954
LAG_00062	mgtA	54232	56829	2598	Magnesium-transporting ATPase, P-type 1	302	43	16.551	0.2	99.9	327.926	46.691
LAG_00063	plsX	56865	57857	993	Phosphate acyltransferase	154	17	17.12	2.2	99.6	437.502	48.296
LAG_00064	ybiV_1	57972	58781	810	Sugar phosphatase YbiV	133	23	28.395	12.2	74	463.207	80.103
LAG_00065	ybiT_1	58857	60485	1629	putative ABC transporter ATP-binding protein YbiT	103	11	6.753	0.7	98.5	178.371	19.049
LAG_00066	NA	60768	61253	486	hypothetical protein	48	9	18.519	31.1	97.3	278.621	52.241
LAG_00067	tipA	61272	62009	738	HTH-type transcriptional activator TipA	119	22	29.81	1.4	98.8	454.882	84.096
LAG_00068	yueB	62110	64806	2697	ESX secretion system protein YueB	217	39	14.461	1.8	99.3	226.98	40.794
LAG_00069	NA	64853	65383	531	hypothetical protein	37	4	7.533	30.7	45.8	196.569	21.251
LAG_00070	NA	65611	66486	876	Penicillin acylase	145	18	20.548	14.4	98.4	466.952	57.966
LAG_00071	naiP	66740	67960	1221	Putative niacin/nicotinamide transporter NaiP	143	24	19.656	1	100	330.391	55.45
LAG_00072	Int-Tn_2	68238	69500	1263	Transposase from transposon Tn916	357	42	33.254	4.2	98.7	797.394	93.811
LAG_00073	NA	69588	69848	261	hypothetical protein	28	5	19.157	13.8	79.3	302.64	54.043
LAG_00074	repB	69850	70455	606	Replication protein RepB	103	16	26.403	2.6	93.6	479.483	74.483
LAG_00075	NA	70578	71159	582	hypothetical protein	299	31	53.265	5.7	99.8	1449.294	150.261
LAG_00076	NA	71156	72235	1080	hypothetical protein	373	37	34.259	0.6	98.8	974.301	96.647
LAG_00077	NA	72237	72554	318	hypothetical protein	78	12	37.736	12.3	97.8	691.952	106.454
LAG_00078	NA	72766	73548	783	hypothetical protein	243	29	37.037	1.4	99	875.493	104.483
LAG_00079	NA	73555	73908	354	hypothetical protein	138	15	42.373	1.1	100	1099.725	119.535
LAG_00080	dinB_1	74037	74639	603	DNA polymerase IV	87	16	26.534	1.3	98.5	407.015	74.853
LAG_00081	NA	74636	74815	180	hypothetical protein	101	14	77.778	7.2	87.2	1582.913	219.414
LAG_00082	NA	74958	76190	1233	hypothetical protein	571	70	56.772	0.2	98.8	1306.415	160.156
LAG_00083	NA	76387	76974	588	hypothetical protein	166	29	49.32	0.7	98	796.414	139.133
LAG_00084	pinR	77411	77719	309	Serine recombinase PinR	252	24	77.67	13.3	99.4	2300.649	219.109
LAG_00085	NA	78180	78473	294	hypothetical protein	194	18	61.224	2	99	1861.498	172.716
LAG_00086	NA	78836	79756	921	hypothetical protein	411	46	49.946	0.4	97.2	1258.898	140.899
LAG_00087	NA	79965	81119	1155	hypothetical protein	603	67	58.009	0.9	98.5	1472.799	163.644
LAG_00088	hhaIM	81138	82379	1242	Modification methylase HhaI	3	1	0.805	99.5	99.5	6.814	2.271
LAG_00089	rpmGA	83364	83513	150	50S ribosomal protein L33 1	10	2	13.333	35.3	92	188.069	37.614
LAG_00090	rpmF	83544	83717	174	50S ribosomal protein L32	0	0	0			0	0
LAG_00091	zosA	84092	85885	1794	Zinc-transporting ATPase	24	4	2.23	8.6	65.4	37.74	6.29
LAG_00092	NA	85896	87164	1269	putative AAA domain-containing protein	137	13	10.244	16	97.4	304.556	28.899
LAG_00093	NA	87187	87660	474	L-methionine sulfoximine/L-methionine sulfone acetyltransferase	0	0	0			0	0
LAG_00094	NA	87797	88261	465	hypothetical protein	22	2	4.301	54.6	67.1	133.468	12.133
LAG_00095	prmA	88286	89239	954	Ribosomal protein L11 methyltransferase	122	14	14.675	2.3	93.9	360.761	41.399
LAG_00096	rsmE	89242	89997	756	Ribosomal RNA small subunit methyltransferase E	16	4	5.291	33.1	84.4	59.704	14.926

LAG_00097	relA	90122	92347	2226	Bifunctional (p)ppGpp synthase/hydrolase RelA	133	20	8.985	2.6	99.3	168.552	25.346
LAG_00098	dtd	92402	92851	450	D-aminoacyl-tRNA deacylase	59	11	24.444	28.2	98.2	369.869	68.959
LAG_00099	NA	92869	93480	612	D-ribitol-5-phosphate phosphatase	111	15	24.51	2	93.3	511.658	69.143
LAG_00100	plsC	93603	94223	621	1-acyl-sn-glycerol-3-phosphate acyltransferase	0	0	0			0	0
LAG_00101	secA_1	94323	96896	2574	Protein translocase subunit SecA	8	2	0.777	95.4	95.5	8.768	2.192
LAG_00102	aroF	96996	98024	1029	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive	135	21	20.408	0.6	90.9	370.106	57.572
LAG_00103	ptsH	98181	98447	267	Phosphocarrier protein HPr	0	0	0			0	0
LAG_00104	ptsI	98447	100174	1728	Phosphoenolpyruvate-protein phosphotransferase	0	0	0			0	0
LAG_00105	NA	100296	100595	300	Nucleoid-associated protein	56	8	26.667	1.7	98.7	526.593	75.228
LAG_00106	NA	100748	100833	86	tRNA-Leu	3	1	11.628	57	57	98.408	32.803
LAG_00107	menH_1	100917	101852	936	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	190	21	22.436	0.3	90.3	572.646	63.292
LAG_00108	NA	101911	102021	111	hypothetical protein	13	1	9.009	28.8	28.8	330.391	25.415
LAG_00109	rnpA	102222	102590	369	Ribonuclease P protein component	0	0	0			0	0
LAG_00110	misCA	102587	103402	816	Membrane protein insertase MisCA	18	5	6.127	5.8	98.8	62.229	17.286
LAG_00111	NA	103427	104338	912	hypothetical protein	10	3	3.289	50.1	96.4	30.932	9.28
LAG_00112	rpmH	104459	104593	135	50S ribosomal protein L34	0	0	0			0	0
LAG_00113	ydhF	104743	105654	912	Oxidoreductase YdhF	67	11	12.061	0.2	100	207.247	34.026
LAG_00114	NA	105844	106110	267	hypothetical protein	0	0	0			0	0
LAG_00115	yrrK	106110	106538	429	Putative pre-16S rRNA nuclease	4	1	2.331	96.7	96.7	26.303	6.576
LAG_00116	NA	106553	106876	324	hypothetical protein	13	2	6.173	6.2	93.5	113.19	17.414
LAG_00117	NA	107017	108624	1608	hypothetical protein	86	11	6.841	1.7	92	150.876	19.298
LAG_00118	codY	108761	109552	792	GTP-sensing transcriptional pleiotropic repressor CodY	25	3	3.788	63	76.4	89.048	10.686
LAG_00119	gatC	109698	110003	306	Glutamyl-tRNA(Gln) amidotransferase subunit C	0	0	0			0	0
LAG_00120	gatA	110003	111475	1473	Glutamyl-tRNA(Gln) amidotransferase subunit A	0	0	0			0	0
LAG_00121	gatB	111477	112910	1434	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	5	1	0.697	98.5	98.5	9.836	1.967
LAG_00122	mepA	112924	114279	1356	Multidrug export protein MepA	155	22	16.224	0.6	99.5	322.463	45.769
LAG_00123	cspC	114406	114603	198	Cold shock protein CspC	38	3	15.152	38.9	65.7	541.41	42.743
LAG_00124	NA	114715	115233	519	5-formyltetrahydrofolate cyclo-ligase	51	6	11.561	21.2	94.2	277.211	32.613
LAG_00125	gluP	115223	115915	693	Rhomboid protease GluP	87	14	20.202	4.9	95.8	354.156	56.991
LAG_00126	dut	115947	116399	453	Deoxyuridine 5'-triphosphate nucleotidohydrolase	97	13	28.698	4	95.8	604.062	80.957
LAG_00127	mggB	116489	117850	1362	Mannosylglucosyl-3-phosphoglycerate phosphatase	332	37	27.166	1	98.5	687.653	76.636
LAG_00128	NA	117834	118436	603	hypothetical protein	113	12	19.9	4	60.2	528.651	56.14
LAG_00129	rlmN	118533	119603	1071	putative dual-specificity RNA methyltransferase RlmN	198	24	22.409	3.2	90.3	521.536	63.216
LAG_00130	arcA	119813	121042	1230	Arginine deiminase	140	13	10.569	0.3	93.3	321.093	29.816
LAG_00131	arcB	121169	122212	1044	Ornithine carbamoyltransferase, catabolic	68	13	12.452	8.5	99.7	183.745	35.128
LAG_00132	arcD1_1	122409	123872	1464	Arginine/ornithine antiporter ArcD1	147	18	12.295	0.3	83.1	283.26	34.685
LAG_00133	arcC1	123970	124920	951	Carbamate kinase 1	139	13	13.67	8	93.1	412.328	38.563
LAG_00134	proX	124972	125463	492	Prolyl-tRNA editing protein ProX	62	9	18.293	20.3	94.5	355.496	51.604
LAG_00135	vioD	125474	126604	1131	Capreomycidine synthase	98	16	14.147	2.1	99.5	244.44	39.909
LAG_00136	NA	126682	127293	612	Putative NAD(P)H nitroreductase	141	19	31.046	6	98.7	649.944	87.581
LAG_00137	hexs-b	127400	128380	981	Hexaprenyl-diphosphate synthase large subunit ((2E,6E)-farnesyl-diphosphate spec	167	20	20.387	2.5	96.4	480.237	57.513
LAG_00138	menA_1	128384	129286	903	1,4-dihydroxy-2-naphthoate octaprenyltransferase	491	30	33.223	0.4	96	1533.918	93.722
LAG_00139	feoB	129480	131585	2106	Fe(2+) transporter FeoB	3053	88	41.785	0.8	99.7	4089.561	117.878
LAG_00140	NA	131598	132059	462	hypothetical protein	102	13	28.139	8.2	89.2	622.826	79.38
LAG_00141	NA	132232	133902	1671	hypothetical protein	28	7	4.189	40.2	81.9	47.27	11.818
LAG_00142	NA	133902	134270	369	hypothetical protein	7	1	2.71	87.5	87.5	53.516	7.645
LAG_00143	rpmB	134556	134750	195	50S ribosomal protein L28	0	0	0			0	0
LAG_00144	NA	134932	135582	651	hypothetical protein	22	5	7.68	6.1	86.9	95.334	21.667
LAG_00145	ctpE	135686	138004	2319	putative cation-transporting ATPase E	155	26	11.212	3.7	90	188.556	31.629
LAG_00146	rfbA	138156	139025	870	Glucose-1-phosphate thymidylyltransferase 1	0	0	0			0	0
LAG_00147	rfbC	139026	139622	597	putative dTDP-4-dehydrorhamnose 3,5-epimerase	0	0	0			0	0
LAG_00148	NA	139672	139881	210	hypothetical protein	12	2	9.524	36.7	57.1	161.202	26.867
LAG_00149	rmlB	139904	140947	1044	dTDP-glucose 4,6-dehydratase	12	2	1.916	95.6	97.9	32.426	5.404
LAG_00150	rmlD_1	140963	141859	897	dTDP-4-dehydrorhamnose reductase	5	1	1.115	96.8	96.8	15.725	3.145

LAG_00151	NA	141970	143121	1152	hypothetical protein	0	0	0			0	0
LAG_00152	epsE	143143	144084	942	Putative glycosyltransferase EpsE	0	0	0			0	0
LAG_00153	tagG_1	144081	144890	810	Teichoic acid translocation permease protein TagG	0	0	0			0	0
LAG_00154	tagH_1	144901	146061	1161	Teichoic acids export ATP-binding protein TagH	0	0	0			0	0
LAG_00155	pssM	146058	146948	891	Exopolysaccharide glucosyl ketal-pyruvate-transferase	0	0	0			0	0
LAG_00156	NA	146959	148293	1335	hypothetical protein	0	0	0			0	0
LAG_00157	epsJ	148312	151245	2934	putative glycosyltransferase EpsJ	5	1	0.341	99.3	99.3	4.807	0.961
LAG_00158	pglJ	151329	152570	1242	N-acetylgalactosamine-N, N'-diacetylbacillosaminyl-diphospho-undecaprenol 4-alph	0	0	0			0	0
LAG_00159	NA	152567	153442	876	hypothetical protein	0	0	0			0	0
LAG_00160	ppm1	153445	154176	732	Polyprenol monophosphomannose synthase	20	5	6.831	28.6	90.4	77.077	19.269
LAG_00161	NA	154176	154535	360	hypothetical protein	21	4	11.111	36.1	53.3	164.56	31.345
LAG_00162	NA	154593	155390	798	hypothetical protein	82	10	12.531	7.5	77.3	289.881	35.351
LAG_00163	epsH	155427	156413	987	Putative glycosyltransferase EpsH	0	0	0			0	0
LAG_00164	cpsY	156415	157422	1008	Exopolysaccharide phosphotransferase CpsY	3	1	0.992	98.7	98.7	8.396	2.799
LAG_00165	rfbX	157499	158908	1410	Putative O-antigen transporter	6	2	1.418	98.8	99.9	12.004	4.001
LAG_00166	NA	158983	160356	1374	hypothetical protein	128	22	16.012	13.5	99.1	262.804	45.169
LAG_00167	NA	160361	162148	1788	hypothetical protein	191	30	16.779	4.1	95.5	301.352	47.333
LAG_00168	ancA	162569	164170	1602	Cellulosome-anchoring protein	491	52	32.459	7.9	97.8	864.624	91.569
LAG_00169	guaB	164339	165820	1482	Inosine-5'-monophosphate dehydrogenase	64	10	6.748	9.9	99.2	121.826	19.035
LAG_00170	rpsU	165946	166122	177	30S ribosomal protein S21	8	1	5.65	70.6	70.6	127.504	15.938
LAG_00171	comGA	166308	167252	945	ComG operon protein 1	221	24	25.397	1	91	659.734	71.645
LAG_00172	NA	167191	168210	1020	hypothetical protein	214	34	33.333	0.4	98.1	591.864	94.034
LAG_00173	pulG	168229	168534	306	Type II secretion system protein G	67	11	35.948	1.6	94.4	617.677	101.41
LAG_00174	NA	168786	169190	405	hypothetical protein	118	15	37.037	2	87.4	821.931	104.483
LAG_00175	NA	169171	169611	441	hypothetical protein	146	17	38.549	2.5	96.6	933.948	108.747
LAG_00176	znuA_1	169843	170688	846	High-affinity zinc uptake system binding-protein ZnuA	131	17	20.095	1.8	99.1	436.827	56.687
LAG_00177	NA	170759	171643	885	putative RNA pseudouridine synthase	121	12	13.559	1.2	96.7	385.701	38.251
LAG_00178	pbpF_1	171719	174007	2289	Penicillin-binding protein 1F	202	27	11.796	2.8	99.5	248.951	33.276
LAG_00179	oatA	174176	176011	1836	O-acetyltransferase OatA	227	27	14.706	4.3	98.4	348.788	41.486
LAG_00180	NA	176208	176405	198	hypothetical protein	4	1	5.051	43.4	43.4	56.991	14.248
LAG_00181	nusG	176514	177074	561	Transcription termination/antitermination protein NusG	9	2	3.565	90.4	97.9	45.257	10.057
LAG_00182	yeeO	177121	178398	1278	putative FMN/FAD exporter YeeO	170	17	13.302	18.2	91.4	375.255	37.525
LAG_00183	mscL	178436	178816	381	Large-conductance mechanosensitive channel	49	7	18.373	3.7	95.3	362.81	51.83
LAG_00184	rpsJ	179142	179450	309	30S ribosomal protein S10	0	0	0			0	0
LAG_00185	rplC	179465	180088	624	50S ribosomal protein L3	0	0	0			0	0
LAG_00186	rplD	180111	180737	627	50S ribosomal protein L4	0	0	0			0	0
LAG_00187	rplW	180737	181033	297	50S ribosomal protein L23	0	0	0			0	0
LAG_00188	rplB	181049	181882	834	50S ribosomal protein L2	0	0	0			0	0
LAG_00189	rpsS	182096	182374	279	30S ribosomal protein S19	0	0	0			0	0
LAG_00190	rplV	182390	182737	348	50S ribosomal protein L22	0	0	0			0	0
LAG_00191	rpsC	182750	183403	654	30S ribosomal protein S3	0	0	0			0	0
LAG_00192	rplP	183407	183823	417	50S ribosomal protein L16	0	0	0			0	0
LAG_00193	rpmC	183820	184029	210	50S ribosomal protein L29	0	0	0			0	0
LAG_00194	rpsQ	184048	184308	261	30S ribosomal protein S17	0	0	0			0	0
LAG_00195	rplN	184330	184698	369	50S ribosomal protein L14	0	0	0			0	0
LAG_00196	rplX	184856	185161	306	50S ribosomal protein L24	0	0	0			0	0
LAG_00197	rplE	185181	185723	543	50S ribosomal protein L5	0	0	0			0	0
LAG_00198	rpsZ	185743	185928	186	30S ribosomal protein S14 type Z	0	0	0			0	0
LAG_00199	NA	186154	187758	1605	hypothetical protein	513	53	33.022	2.4	100	901.676	93.156
LAG_00200	spxA_1	188109	188510	402	Regulatory protein Spx	206	19	47.264	2	96.3	1445.604	133.332
LAG_00201	ldhB	188611	189564	954	L-lactate dehydrogenase 2	273	29	30.398	7.1	99.6	807.277	85.755
LAG_00202	rmlD_2	189561	190427	867	dTDP-4-dehydrorhamnose reductase	170	16	18.454	2.2	97.5	553.144	52.061
LAG_00203	NA	190428	190538	111	hypothetical protein	18	4	36.036	18	53.2	457.465	101.659
LAG_00204	rpsH	190761	191159	399	30S ribosomal protein S8	0	0	0			0	0

LAG_00205	rplF	191247	191783	537	50S ribosomal protein L6	0	0	0			0	0
LAG_00206	rplR	191926	192273	348	50S ribosomal protein L18	0	0	0			0	0
LAG_00207	rpsE	192294	192788	495	30S ribosomal protein S5	0	0	0			0	0
LAG_00208	rpmD	192799	192981	183	50S ribosomal protein L30	0	0	0			0	0
LAG_00209	tmpC_1	193119	194168	1050	Membrane lipoprotein TmpC	129	18	17.143	7.5	82.7	346.584	48.361
LAG_00210	rplO	194370	194822	453	50S ribosomal protein L15	0	0	0			0	0
LAG_00211	secY	194893	196209	1317	Protein translocase subunit SecY	16	3	2.278	93.5	96.7	34.272	6.426
LAG_00212	adk	196361	197008	648	Adenylate kinase	21	3	4.63	90.6	100	91.422	13.06
LAG_00213	znuB	197057	197866	810	High-affinity zinc uptake system membrane protein ZnuB	20	2	2.469	95.2	97.3	69.655	6.966
LAG_00214	znuC	197859	198581	723	High-affinity zinc uptake system ATP-binding protein ZnuC	8	2	2.766	10.8	26.4	31.215	7.804
LAG_00215	zitR_1	198603	199046	444	Transcriptional regulator ZitR	17	4	9.009	22.3	94.6	108.013	25.415
LAG_00216	infA	199248	199466	219	Translation initiation factor IF-1	0	0	0			0	0
LAG_00217	rpsM	199653	200018	366	30S ribosomal protein S13	0	0	0			0	0
LAG_00218	rpsK	200036	200419	384	30S ribosomal protein S11	0	0	0			0	0
LAG_00219	rpoA	200471	201409	939	DNA-directed RNA polymerase subunit alpha	0	0	0			0	0
LAG_00220	rplQ	201425	201805	381	50S ribosomal protein L17	3	1	2.625	92.9	92.9	22.213	7.404
LAG_00221	ctc	202195	203679	1485	S-layer protein	651	65	43.771	4.9	99.1	1236.696	123.48
LAG_00222	NA	203689	204141	453	hypothetical protein	404	23	50.773	0.9	98.5	2515.889	143.231
LAG_00223	NA	204389	204461	73	tRNA-Thr	14	3	41.096	32.9	63	541.02	115.933
LAG_00224	radA	204794	206011	1218	DNA repair protein RadA	252	27	22.167	2.8	98.5	583.662	62.535
LAG_00225	yacL	206143	207219	1077	putative PIN and TRAM-domain containing protein YacL	239	24	22.284	2.3	97.4	626.023	62.864
LAG_00226	NA	207242	207871	630	hypothetical protein	100	16	25.397	2.9	97.6	447.783	71.645
LAG_00227	ald	208058	209179	1122	Alanine dehydrogenase	219	28	24.955	1.2	98.2	550.63	70.4
LAG_00228	NA	209210	209704	495	hypothetical protein	179	10	20.202	2.2	98.8	1020.131	56.991
LAG_00229	gltX	209850	211289	1440	Glutamate--tRNA ligase	33	1	0.694	99.8	99.8	64.649	1.959
LAG_00230	adh	211316	212269	954	Alcohol dehydrogenase	145	20	20.964	18.9	98.7	428.773	59.141
LAG_00231	NA	212518	218886	6369	hypothetical protein	714	103	16.172	1.9	99	316.253	45.622
LAG_00232	pepX	218959	221256	2298	Xaa-Pro dipeptidyl-peptidase	338	41	17.842	0.7	100	414.93	50.332
LAG_00233	NA	221433	221639	207	hypothetical protein	20	4	19.324	17.4	93.2	272.564	54.513
LAG_00234	fnr_1	221983	222645	663	Anaerobic regulatory protein	84	12	18.1	2.9	92.9	357.416	51.059
LAG_00235	gla	222894	223763	870	Glycerol facilitator-aquaporin gla	93	10	11.494	1.1	94.7	301.559	32.426
LAG_00236	metQ	224306	225157	852	putative D-methionine-binding lipoprotein MetQ	295	27	31.69	2.3	99.4	976.766	89.399
LAG_00237	metN	225179	226255	1077	Methionine import ATP-binding protein MetN	214	18	16.713	7.1	100	560.54	47.148
LAG_00238	metP	226256	226951	696	Methionine import system permease protein MetP	183	20	28.736	12.2	91.1	741.737	81.064
LAG_00239	pepV_1	226972	228393	1422	Beta-Ala-Xaa dipeptidase	121	14	9.845	2	97.6	240.046	27.774
LAG_00240	NA	228492	228779	288	hypothetical protein	4	1	3.472	66.3	66.3	39.181	9.795
LAG_00241	hcaR	228951	229856	906	Hca operon transcriptional activator HcaR	152	17	18.764	22.5	99.2	473.286	52.933
LAG_00242	gpmA_1	229954	230655	702	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	16	1	1.425	99.9	99.9	64.297	4.019
LAG_00243	penA	230782	232938	2157	Penicillin-binding protein 2B	129	24	11.127	24	99.7	168.713	31.388
LAG_00244	NA	232976	233908	933	hypothetical protein	204	20	21.436	13.8	98.6	616.818	60.472
LAG_00245	cysL	234067	234909	843	HTH-type transcriptional regulator CysL	239	28	33.215	4.4	94.8	799.795	93.7
LAG_00246	NA	234872	235789	918	Monoacylglycerol lipase	222	30	32.68	2.4	98.6	682.211	92.191
LAG_00247	recR	236057	236659	603	Recombination protein RecR	13	3	4.975	85.1	98.7	60.818	14.035
LAG_00248	ddl	236672	237721	1050	D-alanine--D-alanine ligase	15	2	1.905	96.1	99	40.3	5.373
LAG_00249	ricR	237961	238227	267	Copper-sensing transcriptional repressor RicR	73	8	29.963	26.2	96.3	771.294	84.525
LAG_00250	murF_1	238333	239664	1332	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	26	2	1.502	97.7	99.9	55.065	4.236
LAG_00251	oppA	239979	241652	1674	Oligopeptide-binding protein OppA	309	38	22.7	0.5	97.7	520.728	64.038
LAG_00252	oppB	241726	242643	918	Oligopeptide transport system permease protein OppB	228	19	20.697	2.4	98.6	700.649	58.387
LAG_00253	dppC	242659	243693	1035	Dipeptide transport system permease protein DppC	114	11	10.628	0.4	62.4	310.723	29.982
LAG_00254	oppD	243710	244771	1062	Oligopeptide transport ATP-binding protein OppD	176	16	15.066	3.3	92.9	467.516	42.501
LAG_00255	oppF	244771	245706	936	Oligopeptide transport ATP-binding protein OppF	210	27	28.846	1.6	90.4	632.924	81.376
LAG_00256	NA	245859	246302	444	hypothetical protein	67	9	20.27	21.4	92.1	425.697	57.183
LAG_00257	prfC	246410	247981	1572	Peptide chain release factor 3	147	22	13.995	3.7	96.7	263.799	39.48
LAG_00258	ltaS	248139	250742	2604	Lipoteichoic acid synthase	309	49	18.817	0.7	93.1	334.754	53.084

LAG_00259	cshA	250964	252583	1620	ATP-dependent RNA helicase CshA	114	12	7.407	1	95.1	198.517	20.897
LAG_00260	sipW	253310	254470	1161	Signal peptidase I W	87	17	14.643	11.1	95.7	211.395	41.307
LAG_00261	NA	254445	255509	1065	hypothetical protein	92	14	13.146	1.7	96.2	243.695	37.084
LAG_00262	NA	255611	256633	1023	hypothetical protein	178	17	16.618	0.7	87.4	490.854	46.879
LAG_00263	cna_1	256672	259734	3063	Collagen adhesin	217	34	11.1	2.8	88.1	199.858	31.314
LAG_00264	era	260748	261659	912	GTPase Era	23	5	5.482	45.1	98.5	71.144	15.466
LAG_00265	mutM	261850	262674	825	Formamidopyrimidine-DNA glycosylase	54	8	9.697	8.7	88.2	184.649	27.355
LAG_00266	recA	262775	263926	1152	Protein RecA	25	6	5.208	65.3	99.6	61.22	14.693
LAG_00267	cycA	263963	265327	1365	D-serine/D-alanine/glycine transporter	183	30	21.978	10.5	98.5	378.205	62.001
LAG_00268	NA	265532	265906	375	hypothetical protein	61	6	16	31.7	84.5	458.888	45.137
LAG_00269	NA	265890	266246	357	hypothetical protein	75	10	28.011	0.3	81.2	592.654	79.021
LAG_00270	NA	266304	266822	519	hypothetical protein	226	22	42.389	0.6	95.4	1228.427	119.581
LAG_00271	yjbK	266952	267515	564	Putative triphosphatase YjbK	123	14	24.823	14.2	88.1	615.225	70.026
LAG_00272	yjbM	267866	268546	681	GTP pyrophosphokinase YjbM	21	3	4.405	23.3	50.4	86.992	12.427
LAG_00273	nadK	268533	269345	813	NAD kinase	7	2	2.46	98.6	99.4	24.289	6.94
LAG_00274	rluD_1	269558	270439	882	Ribosomal large subunit pseudouridine synthase D	322	34	38.549	3.2	99.7	1029.901	108.747
LAG_00275	NA	270966	271724	759	Putative peptidyl-prolyl cis-trans isomerase	212	25	32.938	0.8	96.8	787.957	92.919
LAG_00276	lysP_1	271944	273479	1536	Lysine-specific permease	323	41	26.693	0.8	98.7	593.225	75.301
LAG_00277	artP	273492	274295	804	Arginine-binding extracellular protein ArtP	358	35	43.532	4.6	98.3	1256.132	122.806
LAG_00278	nfr2	274352	274948	597	NADH-dependent flavin reductase subunit 2	28	4	6.7	5.7	76.2	132.31	18.901
LAG_00279	apbE_1	274941	275900	960	FAD:protein FMN transferase	99	15	15.625	0.8	97.9	290.919	44.079
LAG_00280	NA	275920	277518	1599	hypothetical protein	364	41	25.641	0.4	97.4	642.187	72.334
LAG_00281	lysS	277614	279101	1488	Lysine--tRNA ligase	0	0	0			0	0
LAG_00282	NA	279520	281358	1839	hypothetical protein	249	37	20.12	5.1	99.5	381.967	56.758
LAG_00283	NA	281373	281861	489	hypothetical protein	78	12	24.54	21.9	99.4	449.981	69.228
LAG_00284	NA	281883	282671	789	hypothetical protein	100	17	21.546	0.3	96.8	357.545	60.783
LAG_00285	kdgT	283022	284029	1008	2-keto-3-deoxygluconate permease	196	18	17.857	0.7	97.9	548.534	50.376
LAG_00286	thiI	284119	285339	1221	putative tRNA sulfurtransferase	163	20	16.38	8.8	93.7	376.6	46.209
LAG_00287	ribZ_1	285405	286832	1428	Riboflavin transporter RibZ	302	40	28.011	0.3	99.4	596.605	79.021
LAG_00288	nhaK_1	286853	288943	2091	Sodium, potassium, lithium and rubidium/H(+) antiporter	428	52	24.868	0	99.4	577.428	70.155
LAG_00289	NA	289022	289489	468	hypothetical protein	100	11	23.504	11.8	83.3	602.785	66.306
LAG_00290	tyrS	289614	290873	1260	Tyrosine--tRNA ligase	0	0	0			0	0
LAG_00291	pbpF_2	291010	293433	2424	Penicillin-binding protein 1F	234	32	13.201	5.1	98.4	272.328	37.241
LAG_00292	ogt_1	293512	294021	510	Methylated-DNA--protein-cysteine methyltransferase	71	10	19.608	3.3	95.1	392.732	55.314
LAG_00293	ogt_2	294011	294415	405	Methylated-DNA--protein-cysteine methyltransferase, constitutive	50	10	24.691	16.8	88.6	348.276	69.655
LAG_00294	NA	294432	295115	684	hypothetical protein	71	12	17.544	0.3	73.4	292.827	49.492
LAG_00295	pepA	295226	296293	1068	Glutamyl aminopeptidase	97	14	13.109	30.7	99.1	256.217	36.98
LAG_00296	NA	296494	296781	288	hypothetical protein	16	3	10.417	23.3	96.9	156.724	29.386
LAG_00297	ytpP	296778	297098	321	Thioredoxin-like protein YtpP	30	4	12.461	27.1	93.5	263.648	35.153
LAG_00298	pheT_1	297100	297723	624	Phenylalanine--tRNA ligase beta subunit	30	7	11.218	19.9	93.9	135.627	31.646
LAG_00299	ssbA	297793	298182	390	Single-stranded DNA-binding protein A	40	5	12.821	5.9	95.4	289.337	36.167
LAG_00300	NA	298239	298769	531	hypothetical protein	115	17	32.015	0.6	84.7	610.958	90.316
LAG_00301	groS	298887	299168	282	10 kDa chaperonin	0	0	0			0	0
LAG_00302	groL	299198	300823	1626	60 kDa chaperonin	16	4	2.46	37.9	99.6	27.759	6.94
LAG_00303	yycJ	300873	301685	813	Putative metallo-hydrolase YycJ	107	16	19.68	2	91.1	371.28	55.518
LAG_00304	walK_1	301682	303100	1419	Sensor histidine kinase WalK	217	40	28.189	8.8	97.9	431.405	79.522
LAG_00305	walR_1	303093	303794	702	Transcriptional regulatory protein WalR	9	1	1.425	0.9	0.9	36.167	4.019
LAG_00306	tmk	304005	304634	630	Thymidylate kinase	0	0	0			0	0
LAG_00307	dnaX_1	304660	305523	864	DNA polymerase III subunit gamma/tau	7	2	2.315	96.8	100	22.856	6.53
LAG_00308	NA	305536	306309	774	hypothetical protein	58	10	12.92	4.3	99.1	211.395	36.447
LAG_00309	yabA	306334	306675	342	Initiation-control protein YabA	16	2	5.848	5.8	14.9	131.978	16.497
LAG_00310	rsmI	306672	307538	867	Ribosomal RNA small subunit methyltransferase I	109	17	19.608	23.3	97.8	354.663	55.314
LAG_00311	tcyK	307668	308510	843	L-cystine-binding protein TcyK	166	20	23.725	2.7	98.1	555.506	66.928
LAG_00312	NA	308530	308718	189	hypothetical protein	118	9	47.619	1.6	96.8	1761.28	134.335

LAG_00313	galK_1	308883	309815	933	Galactokinase	4	1	1.072	98.4	98.4	12.094	3.024
LAG_00314	teaD	309963	310376	414	TRAP-T-associated universal stress protein TeaD	102	15	36.232	4.1	66.2	695.037	102.211
LAG_00315	thrB	310559	311506	948	Homoserine kinase	0	0	0			0	0
LAG_00316	NA	311478	312434	957	Phosphomevalonate kinase	0	0	0			0	0
LAG_00317	fni	312427	313482	1056	Isopentenyl-diphosphate delta-isomerase	0	0	0			0	0
LAG_00318	sodA	313535	314143	609	Superoxide dismutase [Mn]	25	2	3.284	93.9	94.9	115.806	9.264
LAG_00319	cshB	314263	315603	1341	DEAD-box ATP-dependent RNA helicase CshB	103	16	11.931	1.5	97.2	216.679	33.659
LAG_00320	NA	315603	316187	585	hypothetical protein	265	32	54.701	0.9	100	1277.904	154.313
LAG_00321	glvR	316207	316947	741	HTH-type transcriptional regulator GlvR	210	30	40.486	5.5	99.5	799.483	114.212
LAG_00322	licB_1	317162	317488	327	Lichenan-specific phosphotransferase enzyme IIB component	80	12	36.697	2.8	95.7	690.161	103.524
LAG_00323	licC_1	317513	318853	1341	Lichenan permease IIC component	451	55	41.014	0.3	98.1	948.759	115.702
LAG_00324	bglA	319054	320556	1503	Aryl-phospho-beta-D-glucosidase BglA	319	45	29.94	1	98.1	598.742	84.462
LAG_00325	bglC	320556	321992	1437	Aryl-phospho-beta-D-glucosidase BglC	287	39	27.14	1.1	97.3	563.421	76.562
LAG_00326	licB_2	322084	322404	321	Lichenan-specific phosphotransferase enzyme IIB component	72	10	31.153	1.2	85.7	632.755	87.883
LAG_00327	licA	322439	322771	333	Lichenan-specific phosphotransferase enzyme IIA component	83	14	42.042	26.7	99.1	703.141	118.602
LAG_00328	NA	322913	322983	71	tRNA-Cys	0	0	0			0	0
LAG_00329	NA	323427	324494	1068	hypothetical protein	555	49	45.88	0.7	97	1465.987	129.429
LAG_00330	lmrA	324631	326376	1746	Multidrug resistance ABC transporter ATP-binding and permease protein	450	58	33.219	1.6	96	727.071	93.711
LAG_00331	ponA_1	326419	328560	2142	Penicillin-binding protein 1A/1B	515	49	22.876	1.3	99.7	678.26	64.533
LAG_00332	NA	328560	329681	1122	hypothetical protein	202	25	22.282	2.7	98.7	507.887	62.857
LAG_00333	ligA	329785	331752	1968	DNA ligase	0	0	0			0	0
LAG_00334	dagK_1	331749	332753	1005	Diacylglycerol kinase	70	13	12.935	5.1	96.2	196.49	36.491
LAG_00335	NA	333064	334809	1746	hypothetical protein	242	35	20.046	5.6	88	391.002	56.55
LAG_00336	sugC	334952	336088	1137	Trehalose import ATP-binding protein SugC	159	22	19.349	7.3	95.4	394.498	54.585
LAG_00337	por	336349	339996	3648	Pyruvate synthase	606	85	23.3	0.1	96.8	468.626	65.731
LAG_00338	cdaA	340111	340938	828	Cyclic di-AMP synthase CdaA	0	0	0			0	0
LAG_00339	cdaR	340938	341891	954	CdaA regulatory protein CdaR	27	2	2.096	81.3	85.7	79.841	5.914
LAG_00340	glmM	341922	343283	1362	Phosphoglucosamine mutase	6	1	0.734	99.3	99.3	12.427	2.071
LAG_00341	tsaE	343477	343932	456	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	0	0	0			0	0
LAG_00342	mshD	343929	344444	516	Mycothiol acetyltransferase	142	13	25.194	0.4	95	776.331	71.073
LAG_00343	brpA	344568	345914	1347	Biofilm regulatory protein A	148	21	15.59	4.3	97.5	309.958	43.98
LAG_00344	NA	345977	346052	76	tRNA-Arg	0	0	0			0	0
LAG_00345	NA	346209	346799	591	hypothetical protein	225	23	38.917	8.8	95.9	1073.998	109.786
LAG_00346	NA	346811	347155	345	hypothetical protein	0	0	0			0	0
LAG_00347	NA	347436	347642	207	hypothetical protein	27	4	19.324	8.2	61.4	367.961	54.513
LAG_00348	NA	347654	347869	216	hypothetical protein	51	3	13.889	1.4	68.5	666.077	39.181
LAG_00349	truA	348095	348829	735	tRNA pseudouridine synthase A	28	5	6.803	36.6	76.6	107.468	19.191
LAG_00350	pdxK	348822	349655	834	Pyridoxine/pyridoxal/pyridoxamine kinase	0	0	0			0	0
LAG_00351	hmpT	349652	350134	483	Thiamine precursor transporter HmpT	24	4	8.282	14.7	81.6	140.176	23.363
LAG_00352	NA	350115	350657	543	hypothetical protein	29	6	11.05	5	93.6	150.663	31.172
LAG_00353	pyrG	351142	352746	1605	CTP synthase	28	5	3.115	35.8	99.4	49.214	8.788
LAG_00354	maa	352852	353469	618	Maltose O-acetyltransferase	238	19	30.744	0.3	98.2	1086.417	86.731
LAG_00355	NA	353506	353682	177	hypothetical protein	8	2	11.299	4	23.2	127.504	31.876
LAG_00356	dnaE	353789	356905	3117	DNA polymerase III subunit alpha	0	0	0			0	0
LAG_00357	NA	356915	357568	654	hypothetical protein	96	13	19.878	3.5	98.6	414.097	56.076
LAG_00358	NA	357736	358572	837	DegV domain-containing protein	49	9	10.753	29.2	93.5	165.15	30.334
LAG_00359	lipC	358565	359389	825	Spore germination lipase LipC	233	30	36.364	17.7	94.7	796.728	102.583
LAG_00360	NA	359379	359963	585	hypothetical protein	131	15	25.641	1.5	91.8	631.719	72.334
LAG_00361	hup	360081	360356	276	DNA-binding protein HU	0	0	0			0	0
LAG_00362	iscS_1	360573	361745	1173	Cysteine desulfurase IscS	217	33	28.133	2	97.5	521.879	79.364
LAG_00363	cysK	361856	362776	921	Cysteine synthase	150	25	27.144	2.9	87.2	459.452	76.575
LAG_00364	NA	362961	363890	930	Autolysin	108	10	10.753	16.7	100	327.604	30.334
LAG_00365	NA	363993	364619	627	putative metallo-hydrolase	111	13	20.734	4	99.5	499.417	58.49
LAG_00366	ponA_2	364623	366710	2088	Penicillin-binding protein 1A	207	30	14.368	2.4	99.3	279.671	40.532

LAG_00367	recU	366742	367392	651	Holliday junction resolvase RecU	19	4	6.144	11.2	74.3	82.334	17.334
LAG_00368	NA	367665	368192	528	hypothetical protein	82	8	15.152	16.5	80.3	438.115	42.743
LAG_00369	spxA_2	368329	368721	393	Regulatory protein Spx	5	1	2.545	77.6	77.6	35.891	7.178
LAG_00370	NA	368745	369026	282	hypothetical protein	14	3	10.638	25.2	75.2	140.051	30.011
LAG_00371	suhB	368992	369780	789	Fructose-1, 6-bisphosphatase/inositol-1-monophosphatase	94	13	16.477	1	97.1	336.093	46.481
LAG_00372	murAA	369853	371136	1284	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	73	8	6.231	11.4	82.9	160.386	17.577
LAG_00373	NA	371129	371314	186	hypothetical protein	36	6	32.258	16.1	93.5	546.007	91.001
LAG_00374	tig	371468	372751	1284	Trigger factor	17	2	1.558	87.7	88.2	37.35	4.394
LAG_00375	NA	372908	373240	333	HTH-type transcriptional regulator	124	12	36.036	4.5	91.9	1050.475	101.659
LAG_00376	hchA_1	373237	373914	678	Molecular chaperone Hsp31 and glyoxalase 3	114	19	28.024	0.3	95.6	474.333	79.056
LAG_00377	NA	373914	374834	921	hypothetical protein	271	29	31.488	0.2	99.3	830.076	88.827
LAG_00378	yjjG	374932	375621	690	Pyrimidine 5'-nucleotidase YjjG	143	17	24.638	0.1	95.4	584.649	69.504
LAG_00379	NA	375673	375744	72	tRNA-Arg	0	0	0			0	0
LAG_00380	rnz	375931	376863	933	Ribonuclease Z	0	0	0			0	0
LAG_00381	ephD	376844	377491	648	putative oxidoreductase EphD	103	8	12.346	22.7	92.9	448.405	34.828
LAG_00382	recJ	377524	379758	2235	Single-stranded-DNA-specific exonuclease RecJ	146	21	9.396	1.2	74.8	184.282	26.506
LAG_00383	apt	379748	380260	513	Adenine phosphoribosyltransferase	132	12	23.392	9.2	100	725.88	65.989
LAG_00384	rpoE	380386	380946	561	putative DNA-directed RNA polymerase subunit delta	0	0	0			0	0
LAG_00385	mltG	381052	382767	1716	Endolytic murein transglycosylase	126	16	9.324	13.3	90.9	207.139	26.303
LAG_00386	greA	382792	383265	474	Transcription elongation factor GreA	0	0	0			0	0
LAG_00387	ctsR	383385	383837	453	Transcriptional regulator CtsR	41	7	15.453	6.2	90.9	255.325	43.592
LAG_00388	clpC	383827	386277	2451	ATP-dependent Clp protease ATP-binding subunit ClpC	248	40	16.32	2.9	96.6	285.441	46.039
LAG_00389	hpf_1	386400	386957	558	Ribosome hibernation promotion factor	65	14	25.09	3.2	67.2	328.615	70.779
LAG_00390	pflB	387205	389538	2334	Formate acetyltransferase	372	52	22.279	1	99.3	449.625	62.851
LAG_00391	coaE	389777	390382	606	Dephospho-CoA kinase	0	0	0			0	0
LAG_00392	yjhB	390429	391619	1191	Putative metabolite transport protein YjhB	246	34	28.547	1.6	93.5	582.682	80.533
LAG_00393	ftsW	391895	393118	1224	putative peptidoglycan glycosyltransferase FtsW	21	2	1.634	95.8	99.2	48.4	4.61
LAG_00394	cfiB	393551	396970	3420	2-oxoglutarate carboxylase small subunit	681	75	21.93	2	98	561.732	61.865
LAG_00395	clpP	397016	397615	600	ATP-dependent Clp protease proteolytic subunit	54	8	13.333	31.8	95.8	253.893	37.614
LAG_00396	NA	397795	398172	378	hypothetical protein	86	14	37.037	1.1	96.3	641.822	104.483
LAG_00397	NA	398232	398762	531	hypothetical protein	102	12	22.599	1.3	92.8	541.893	63.752
LAG_00398	spxA_3	398924	399322	399	Regulatory protein Spx	53	7	17.544	20.6	91	374.724	49.492
LAG_00399	dtd3	399458	400231	774	D-aminoacyl-tRNA deacylase	96	14	18.088	2.3	89.9	349.896	51.026
LAG_00400	rnmV	400228	400773	546	Ribonuclease M5	45	12	21.978	6.4	86.1	232.503	62.001
LAG_00401	drrA	400770	401696	927	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA	364	41	44.229	1.8	95.9	1107.72	124.771
LAG_00402	yadH	401689	402459	771	Inner membrane transport permease YadH	188	28	36.316	0.5	90.1	687.878	102.45
LAG_00403	rbsR_1	402520	403488	969	Ribose operon repressor	244	30	30.96	4.9	97.2	710.353	87.339
LAG_00404	scrB	403488	404903	1416	Sucrose-6-phosphate hydrolase	71	13	9.181	19.1	96.9	141.45	25.899
LAG_00405	treP	405086	407023	1938	PTS system trehalose-specific EIIBC component	218	28	14.448	0.3	98.5	317.33	40.758
LAG_00406	gmuE	407046	407915	870	Putative fructokinase	189	22	25.287	2.3	98	612.845	71.336
LAG_00407	rsmA	408033	408980	948	Ribosomal RNA small subunit methyltransferase A	18	2	2.11	26.6	71	53.564	5.952
LAG_00408	NA	408981	409562	582	hypothetical protein	89	16	27.491	8.6	99.8	431.395	77.554
LAG_00409	NA	409660	410106	447	Acetyltransferase	50	6	13.423	8.1	97.8	315.552	37.866
LAG_00410	tqsA	410216	411337	1122	AI-2 transport protein TqsA	239	21	18.717	13.3	97.4	600.915	52.8
LAG_00411	corC_1	411383	412711	1329	Magnesium and cobalt efflux protein CorC	292	25	18.811	2.9	89.1	619.821	53.067
LAG_00412	bmr3	412824	414284	1461	Multidrug resistance protein 3	274	35	23.956	0.5	75.6	529.064	67.581
LAG_00413	pflA	414351	415145	795	Pyruvate formate-lyase 1-activating enzyme	85	12	15.094	34.8	99.7	301.62	42.582
LAG_00414	ppaC	415291	416235	945	putative manganese-dependent inorganic pyrophosphatase	0	0	0			0	0
LAG_00415	NA	416235	416999	765	hypothetical protein	129	18	23.529	0.5	99.9	475.704	66.377
LAG_00416	pepT	417002	418243	1242	Peptidase T	329	28	22.544	2	99	747.279	63.598
LAG_00417	yjeM_1	418583	420184	1602	Inner membrane transporter YjeM	212	32	19.975	1.3	96.3	373.32	56.35
LAG_00418	murE	420245	421696	1452	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L- lysine ligase	0	0	0			0	0
LAG_00419	NA	421890	422768	879	hypothetical protein	107	16	18.203	29.2	87.8	343.402	51.35
LAG_00420	NA	423049	423384	336	hypothetical protein	32	4	11.905	33.6	90.5	268.67	33.584

LAG_00421	NA	423381	423548	168	hypothetical protein	28	4	23.81	2.4	76.2	470.172	67.167
LAG_00422	NA	423557	424111	555	hypothetical protein	169	21	37.838	2.3	91.7	859.017	106.742
LAG_00423	murJ	424225	425943	1719	Lipid II flippase MurJ	6	1	0.582	100	100	9.847	1.641
LAG_00424	pepO	426039	427922	1884	Neutral endopeptidase	161	26	13.8	0.8	92.7	241.076	38.931
LAG_00425	NA	427916	428227	312	DNA base-flipping protein	14	2	6.41	11.5	25	126.585	18.084
LAG_00426	rpoB	428511	432101	3591	DNA-directed RNA polymerase subunit beta	0	0	0			0	0
LAG_00427	rpoC	432421	436068	3648	DNA-directed RNA polymerase subunit beta'	0	0	0			0	0
LAG_00428	ytlR	436161	437069	909	Putative lipid kinase YtlR	240	27	29.703	0.1	100	744.827	83.793
LAG_00429	mecA	437316	437999	684	Adapter protein MecA	36	4	5.848	15.4	59.8	148.475	16.497
LAG_00430	tagO	438003	439259	1257	putative undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase	33	2	1.591	89.2	92.5	74.061	4.489
LAG_00431	NA	439337	440107	771	putative ABC transporter ATP-binding protein	56	11	14.267	1.7	99.7	204.9	40.248
LAG_00432	sufB_1	440179	441435	1257	FeS cluster assembly protein SufB	79	13	10.342	6.1	97.6	177.296	29.175
LAG_00433	sufS	441435	442646	1212	Cysteine desulfurase SufS	102	16	13.201	1.1	93.7	237.414	37.241
LAG_00434	iscU	442671	443126	456	Iron-sulfur cluster assembly scaffold protein IscU	34	5	10.965	12.9	93.2	210.34	30.932
LAG_00435	sufB_2	443151	444548	1398	FeS cluster assembly protein SufB	157	29	20.744	11.4	96.4	316.811	58.519
LAG_00436	NA	444845	445489	645	hypothetical protein	291	27	41.86	4.2	99.7	1272.745	118.09
LAG_00437	ybiT_2	445636	447192	1557	putative ABC transporter ATP-binding protein YbiT	342	48	30.829	0.3	99.7	619.649	86.968
LAG_00438	ybiR	447358	448533	1176	Inner membrane protein YbiR	542	52	44.218	0.2	99.7	1300.17	124.74
LAG_00439	comEA	448591	449235	645	ComE operon protein 1	101	17	26.357	17.1	100	441.743	74.353
LAG_00440	comEC	449255	451465	2211	ComE operon protein 3	765	89	40.253	1.1	99.7	976.07	113.556
LAG_00441	axe1-6A	451620	452396	777	Carbohydrate acetyl esterase/feruloyl esterase	148	16	20.592	2.2	100	537.34	58.091
LAG_00442	atpE	452592	452807	216	ATP synthase subunit c	0	0	0			0	0
LAG_00443	atpB	452862	453575	714	ATP synthase subunit a	0	0	0			0	0
LAG_00444	atpF	453589	454095	507	ATP synthase subunit b	0	0	0			0	0
LAG_00445	atpH	454110	454637	528	ATP synthase subunit delta	0	0	0			0	0
LAG_00446	atpA	454703	456211	1509	ATP synthase subunit alpha	0	0	0			0	0
LAG_00447	atpG	456223	457104	882	ATP synthase gamma chain	0	0	0			0	0
LAG_00448	atpD	457164	458573	1410	ATP synthase subunit beta	22	1	0.709	3.4	3.4	44.016	2.001
LAG_00449	atpC	458591	459016	426	ATP synthase epsilon chain	22	4	9.39	69.5	96.9	145.687	26.489
LAG_00450	NA	459203	459874	672	hypothetical protein	295	33	49.107	1.9	97.9	1238.4	138.533
LAG_00451	NA	459906	460727	822	hypothetical protein	262	39	47.445	5.1	99.5	899.162	133.845
LAG_00452	NA	460816	461733	918	L-2-hydroxyisocaproate dehydrogenase	186	24	26.144	1.5	99.9	571.582	73.753
LAG_00453	gpmA_2	461847	462551	705	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	91	12	17.021	2.1	80.7	364.133	48.018
LAG_00454	vanYB	462535	463320	786	D-alanyl-D-alanine carboxypeptidase	139	22	27.99	13.4	100	498.885	78.96
LAG_00455	NA	463352	463756	405	hypothetical protein	66	9	22.222	4.4	71.9	459.724	62.69
LAG_00456	hrcA	463895	464932	1038	Heat-inducible transcription repressor HrcA	0	0	0			0	0
LAG_00457	grpE	464966	465508	543	Protein GrpE	0	0	0			0	0
LAG_00458	dnaK	465586	467412	1827	Chaperone protein DnaK	22	4	2.189	55.7	99	33.97	6.176
LAG_00459	spxA_4	467561	467959	399	Regulatory protein Spx	100	13	32.581	7.3	68.7	707.026	91.913
LAG_00460	glcR	468137	468838	702	HTH-type transcriptional repressor GlcR	111	16	22.792	7.1	97.7	446.061	64.297
LAG_00461	lacC_1	468835	469761	927	Tagatose-6-phosphate kinase	67	8	8.63	24.9	100	203.893	24.345
LAG_00462	fruA_1	469776	471680	1905	PTS system fructose-specific EIIABC component	169	31	16.273	11.3	100	250.265	45.907
LAG_00463	rpmE2	471792	472034	243	50S ribosomal protein L31 type B	3	1	4.115	96.7	96.7	34.828	11.609
LAG_00464	NA	472251	472802	552	hypothetical protein	0	0	0			0	0
LAG_00465	arlR_1	472904	473599	696	Response regulator ArlR	16	3	4.31	32.9	93.4	64.851	12.16
LAG_00466	arlS_1	473687	475177	1491	Signal transduction histidine-protein kinase ArlS	132	21	14.085	6.8	99.7	249.749	39.733
LAG_00467	glnP	475573	477144	1572	Glutamine transport system permease protein GlnP	592	72	45.802	0.6	99.2	1062.374	129.208
LAG_00468	artM_1	477145	477882	738	Arginine transport ATP-binding protein ArtM	122	18	24.39	11.7	86.3	466.35	68.806
LAG_00469	murD	478022	479383	1362	UDP-N-acetylmuramoylalanine--D-glutamate ligase	0	0	0			0	0
LAG_00470	murG	479385	480479	1095	UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecapr	0	0	0			0	0
LAG_00471	divIB	480479	481516	1038	Cell division protein DivIB	43	4	3.854	5.9	98.8	116.864	10.871
LAG_00472	artM_2	481612	482349	738	Arginine transport ATP-binding protein ArtM	230	16	21.68	6.9	98.8	879.184	61.161
LAG_00473	tcyB	482363	484507	2145	L-cystine transport system permease protein TcyB	383	47	21.911	0.3	99.9	503.709	61.813

LAG_00474	NA	484746	485402	657	putative membrane protein	33	6	9.132	3.8	62.9	141.696	25.763
LAG_00475	aroE	485476	486342	867	Shikimate dehydrogenase (NADP(+))	67	12	13.841	4.6	60	218.004	39.045
LAG_00476	aroB	486326	487387	1062	3-dehydroquinate synthase	96	12	11.299	17.2	99.4	255.009	31.876
LAG_00477	NA	487384	487497	114	hypothetical protein	0	0	0			0	0
LAG_00478	NA	487816	488742	927	hypothetical protein	176	21	22.654	7.8	98.1	535.601	63.907
LAG_00479	NA	488749	489339	591	hypothetical protein	49	11	18.613	20.1	89	233.893	52.507
LAG_00480	aroC	489341	490510	1170	Chorismate synthase	89	16	13.675	12	83.1	214.591	38.578
LAG_00481	NA	490644	490994	351	hypothetical protein	34	3	8.547	30.2	85.2	273.263	24.111
LAG_00482	yxdL	491022	491810	789	ABC transporter ATP-binding protein YxdL	116	15	19.011	5.1	94.7	414.753	53.632
LAG_00483	bceB	491803	493776	1974	Bacitracin export permease protein BceB	505	47	23.81	3.4	91.4	721.693	67.167
LAG_00484	NA	493777	493995	219	hypothetical protein	4	1	4.566	90	90	51.526	12.881
LAG_00485	graR	494105	494761	657	Response regulator protein GraR	126	18	27.397	11	96.7	541.02	77.289
LAG_00486	graS	494748	495638	891	Sensor histidine kinase GraS	257	27	30.303	0.4	89.3	813.699	85.486
LAG_00487	NA	495628	496185	558	hypothetical protein	85	14	25.09	13.6	99.8	429.727	70.779
LAG_00488	aroA_1	496305	497615	1311	3-phosphoshikimate 1-carboxyvinyltransferase	179	20	15.256	1.5	97.3	385.175	43.036
LAG_00489	aroK	497606	498091	486	Shikimate kinase	191	18	37.037	16.9	87.9	1108.678	104.483
LAG_00490	pspB_1	498088	498684	597	Putative phosphoserine phosphatase 2	59	4	6.7	4.4	98.7	278.796	18.901
LAG_00491	recD2	498681	501122	2442	ATP-dependent RecD-like DNA helicase	225	35	14.333	7.5	98.7	259.923	40.433
LAG_00492	NA	501169	501378	210	hypothetical protein	96	7	33.333	21	96.7	1289.615	94.034
LAG_00493	rny_1	501809	502318	510	Ribonuclease Y	78	10	19.608	4.9	90.6	431.452	55.314
LAG_00494	rpsT	502469	502702	234	30S ribosomal protein S20	16	3	12.821	58.1	96.2	192.891	36.167
LAG_00495	NA	502938	503597	660	hypothetical protein	151	24	36.364	0.6	99.4	645.418	102.583
LAG_00496	ung	503594	504253	660	Uracil-DNA glycosylase	63	12	18.182	4.4	95.9	269.28	51.292
LAG_00497	ybhL	504357	505061	705	Inner membrane protein YbhL	182	18	25.532	22.6	94.5	728.267	72.026
LAG_00498	yitU	505118	505942	825	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YitU	98	13	15.758	0.6	96.6	335.105	44.453
LAG_00499	pbuO	506306	507727	1422	Guanine/hypoxanthine permease PbuO	285	36	25.316	1.3	98.1	565.397	71.419
LAG_00500	NA	507805	508905	1101	hypothetical protein	155	21	19.074	3.5	96.3	397.148	53.807
LAG_00501	coiA	508981	509985	1005	Competence protein CoiA	278	29	28.856	0.4	97.8	780.346	81.403
LAG_00502	pepF1	509969	511774	1806	Oligoendopeptidase F, plasmid	139	27	14.95	2	90.7	217.123	42.175
LAG_00503	prmC_1	511774	512457	684	Release factor glutamine methyltransferase	53	8	11.696	3.7	71.6	218.589	32.995
LAG_00504	prsA	512555	513463	909	Foldase protein PrsA	4	1	1.1	49.6	49.6	12.414	3.103
LAG_00505	alaS	513713	516331	2619	Alanine--tRNA ligase	6	2	0.764	97.8	99.4	6.463	2.154
LAG_00506	rpiR_1	516671	517462	792	HTH-type transcriptional regulator RpiR	282	36	45.455	0.5	97.5	1004.459	128.229
LAG_00507	glpF_1	517480	517737	258	putative glycerol uptake facilitator protein	63	4	15.504	6.2	49.6	688.857	43.737
LAG_00508	pspB_2	517846	518403	558	Putative phosphoserine phosphatase 2	116	18	32.258	7.5	98	586.451	91.001
LAG_00509	bglH_1	518707	520140	1434	Aryl-phospho-beta-D-glucosidase BglH	334	43	29.986	1	96.9	657.061	84.592
LAG_00510	smpB	520208	520675	468	SsrA-binding protein	6	2	4.274	91.9	99.4	36.167	12.056
LAG_00511	pstS1_1	520856	521749	894	Phosphate-binding protein PstS 1	290	30	33.557	3.9	90.5	915.1	94.666
LAG_00512	pstS1_2	521979	522830	852	Phosphate-binding protein PstS 1	5	1	1.174	35.4	35.4	16.555	3.311
LAG_00513	pstC	522845	523768	924	Phosphate transport system permease protein PstC	0	0	0			0	0
LAG_00514	pstA2	523768	524655	888	Phosphate transport system permease protein PstA 2	0	0	0			0	0
LAG_00515	pstB3_1	524674	525477	804	Phosphate import ATP-binding protein PstB 3	0	0	0			0	0
LAG_00516	pstB3_2	525491	526252	762	Phosphate import ATP-binding protein PstB 3	0	0	0			0	0
LAG_00517	phoU	526308	526961	654	Phosphate-specific transport system accessory protein PhoU	10	1	1.529	98.3	98.3	43.135	4.314
LAG_00518	serS	526992	528263	1272	Serine--tRNA ligase	6	1	0.786	99.1	99.1	13.307	2.218
LAG_00519	NA	528605	529282	678	hypothetical protein	150	20	29.499	0.9	96.2	624.122	83.216
LAG_00520	NA	529353	529733	381	hypothetical protein	51	11	28.871	5.2	94	377.619	81.447
LAG_00521	manZ_1	529839	530936	1098	PTS system mannose-specific EIID component	186	21	19.126	4.6	97.6	477.88	53.954
LAG_00522	sorA_1	530959	531762	804	PTS system sorbose-specific EIIC component	43	5	6.219	2	85.7	150.876	17.544
LAG_00523	manX_1	531793	532782	990	PTS system mannose-specific EIIAB component	38	5	5.051	2.4	80.2	108.282	14.248
LAG_00524	NA	533284	533793	510	hypothetical protein	3	1	1.961	100	100	16.594	5.531
LAG_00525	cmk	533823	534485	663	Cytidylate kinase	3	1	1.508	97.4	97.4	12.765	4.255
LAG_00526	NA	534559	535083	525	hypothetical protein	95	13	24.762	7.4	99.8	510.473	69.854
LAG_00527	NA	535209	536255	1047	hypothetical protein	171	30	28.653	5.9	97.4	460.742	80.832

LAG_00528	NA	536308	536577	270	hypothetical protein	60	7	25.926	21.9	87.8	626.896	73.138
LAG_00529	msrA2	536637	537179	543	Peptide methionine sulfoxide reductase MsrA 2	83	15	27.624	6.8	91.3	431.208	77.929
LAG_00530	Int-Tn_3	537349	538530	1182	Transposase from transposon Tn916	151	21	17.766	13.6	95.6	360.386	50.12
LAG_00531	NA	538623	539030	408	hypothetical protein	52	10	24.51	5.1	57.1	359.544	69.143
LAG_00532	NA	539152	539334	183	hypothetical protein	36	4	21.858	49.2	88.5	554.957	61.662
LAG_00533	NA	539415	539522	108	hypothetical protein	11	1	9.259	9.3	9.3	287.327	26.121
LAG_00534	NA	539522	539872	351	hypothetical protein	67	9	25.641	1.7	90.6	538.488	72.334
LAG_00535	NA	539919	540167	249	hypothetical protein	80	8	32.129	17.3	97.2	906.356	90.636
LAG_00536	NA	540453	540866	414	hypothetical protein	88	11	26.57	20.8	91.5	599.64	74.955
LAG_00537	NA	540992	541276	285	hypothetical protein	35	4	14.035	26	78.6	346.443	39.593
LAG_00538	NA	541463	542017	555	hypothetical protein	110	16	28.829	10.6	94.6	559.124	81.327
LAG_00539	immR_1	542027	542410	384	HTH-type transcriptional regulator ImmR	0	0	0			0	0
LAG_00540	NA	542681	542887	207	hypothetical protein	14	3	14.493	2.4	27.1	190.795	40.885
LAG_00541	NA	542930	543205	276	hypothetical protein	68	2	7.246	5.4	73.9	695.037	20.442
LAG_00542	NA	543290	543472	183	hypothetical protein	24	2	10.929	6.6	12	369.972	30.831
LAG_00543	NA	543469	543744	276	hypothetical protein	14	4	14.493	47.5	64.5	143.096	40.885
LAG_00544	NA	543746	543997	252	hypothetical protein	9	2	7.937	27	43.7	100.751	22.389
LAG_00545	NA	543981	544250	270	hypothetical protein	0	0	0			0	0
LAG_00546	NA	544344	544673	330	hypothetical protein	64	6	18.182	11.2	95.8	547.11	51.292
LAG_00547	NA	544670	546379	1710	hypothetical protein	126	19	11.111	4.4	95.6	207.866	31.345
LAG_00548	NA	546986	548083	1098	hypothetical protein	160	18	16.393	10.5	93.4	411.08	46.246
LAG_00549	NA	548486	548737	252	hypothetical protein	40	6	23.81	3.6	89.3	447.783	67.167
LAG_00550	NA	549152	549484	333	hypothetical protein	72	10	30.03	10.5	81.1	609.953	84.716
LAG_00551	qacC	549985	550314	330	Quaternary ammonium compound-resistance protein QacC	125	9	27.273	17.9	97	1068.573	76.937
LAG_00552	NA	550508	550831	324	hypothetical protein	123	9	27.778	7.4	100	1070.948	78.362
LAG_00553	NA	550969	553128	2160	hypothetical protein	168	26	12.037	7.6	98.7	219.414	33.957
LAG_00554	NA	553128	553829	702	hypothetical protein	123	22	31.339	2.1	95.6	494.284	88.408
LAG_00555	mccF	554356	555327	972	Microcin C7 self-immunity protein MccF	310	31	31.893	0.5	96.2	899.712	89.971
LAG_00556	msrR	555525	556895	1371	Regulatory protein MsrR	222	27	19.694	0.1	99.9	456.798	55.556
LAG_00557	malG	556936	557790	855	Maltose transport system permease protein MalG	233	29	33.918	4.4	98.7	768.773	95.684
LAG_00558	malF	557792	559141	1350	Maltose transport system permease protein MalF	381	43	31.852	0.1	99.8	796.158	89.855
LAG_00559	malX_1	559213	560448	1236	Maltose/maltodextrin-binding protein	319	38	30.744	3.9	97.3	728.082	86.731
LAG_00560	bbmA	560702	562456	1755	Intracellular maltogenic amylase	282	38	21.652	0.1	89	453.294	61.082
LAG_00561	malL	562709	564316	1608	Oligo-1,6-glucosidase	113	18	11.194	4.7	90.2	198.244	31.579
LAG_00562	malP	564341	566605	2265	Maltose phosphorylase	207	30	13.245	0.6	96	257.816	37.365
LAG_00563	pgmB	566598	567263	666	Beta-phosphoglucomutase	119	11	16.517	9.6	93.1	504.059	46.594
LAG_00564	malR	567290	568270	981	HTH-type transcriptional regulator MalR	62	13	13.252	1	100	178.292	37.384
LAG_00565	arlR_2	568440	569117	678	Response regulator ArlR	82	5	7.375	15	85.5	341.187	20.804
LAG_00566	arlS_2	569153	570535	1383	Signal transduction histidine-protein kinase ArlS	288	35	25.307	5.4	99.3	587.46	71.393
LAG_00567	dxs	570599	572341	1743	1-deoxy-D-xylulose-5-phosphate synthase	180	29	16.638	4.8	99	291.329	46.936
LAG_00568	yusV	572909	573691	783	putative siderophore transport system ATP-binding protein YusV	82	7	8.94	11.5	88	295.434	25.22
LAG_00569	yfhA_1	573681	574631	951	putative siderophore transport system permease protein YfhA	30	6	6.309	0.6	89.1	88.992	17.798
LAG_00570	feuC	574628	575566	939	Iron-uptake system permease protein FeuC	153	15	15.974	28.6	98.2	459.657	45.064
LAG_00571	fhuD	575578	576519	942	Iron(3+)-hydroxamate-binding protein FhuD	58	9	9.554	7.6	98.5	173.694	26.953
LAG_00572	hpr	576821	577396	576	HTH-type transcriptional regulator Hpr	27	4	6.944	7.6	32.8	132.236	19.591
LAG_00573	fabH	577396	578373	978	3-oxoacyl-[acyl-carrier-protein] synthase 3	4	1	1.022	13.7	13.7	11.538	2.884
LAG_00574	acpP	578461	578682	222	Acyl carrier protein	0	0	0			0	0
LAG_00575	fabD	578781	579704	924	Malonyl CoA-acyl carrier protein transacylase	0	0	0			0	0
LAG_00576	fabG_1	579783	580514	732	3-oxoacyl-[acyl-carrier-protein] reductase FabG	6	1	1.366	50.3	50.3	23.123	3.854
LAG_00577	fabF	580572	581789	1218	3-oxoacyl-[acyl-carrier-protein] synthase 2	0	0	0			0	0
LAG_00578	accB	581882	582355	474	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	0	0	0			0	0
LAG_00579	fabZ_1	582369	582803	435	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	0	0	0			0	0
LAG_00580	accC	582999	584363	1365	Biotin carboxylase	17	3	2.198	96.6	97.5	35.134	6.2
LAG_00581	csbB	584946	585881	936	Putative glycosyltransferase CsbB	335	47	50.214	0.9	99.4	1009.665	141.654

LAG_00582	accD	586195	587061	867	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	0	0	0			0	0
LAG_00583	accA	587054	587809	756	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	25	3	3.968	93.1	98.3	93.288	11.195
LAG_00584	NA	587872	588114	243	hypothetical protein	49	5	20.576	3.7	97.5	568.85	58.046
LAG_00585	spxA_5	588258	588608	351	Regulatory protein Spx	53	6	17.094	2.3	86	425.968	48.223
LAG_00586	exoA	588639	589499	861	Exodeoxyribonuclease	108	14	16.26	1	84.6	353.858	45.87
LAG_00587	metG	589729	591717	1989	Methionine--tRNA ligase	40	6	3.017	79.1	99.8	56.733	8.51
LAG_00588	sdh	591750	592595	846	Serine 3-dehydrogenase	242	23	27.187	10.2	99.4	806.962	76.695
LAG_00589	NA	592738	592977	240	hypothetical protein	44	7	29.167	12.1	71.7	517.189	82.28
LAG_00590	bacC	592970	593689	720	Dihydroanticapsin 7-dehydrogenase	148	16	22.222	9.4	73.3	579.879	62.69
LAG_00591	queT	593807	594364	558	Queuosine precursor transporter QueT	270	26	46.595	5	100	1365.016	131.446
LAG_00592	yidA_1	594419	595204	786	Sugar phosphatase YidA	136	23	29.262	1.3	98.7	488.118	82.549
LAG_00593	NA	595356	596138	783	hypothetical protein	117	20	25.543	1.7	100	421.534	72.057
LAG_00594	NA	596257	596682	426	Putative universal stress protein	22	4	9.39	6.6	75.6	145.687	26.489
LAG_00595	ftsK_1	596810	599173	2364	DNA translocase FtsK	3	1	0.423	89.5	89.5	3.58	1.193
LAG_00596	NA	599170	600171	1002	hypothetical protein	0	0	0			0	0
LAG_00597	gpsB	600284	600673	390	Cell cycle protein GpsB	0	0	0			0	0
LAG_00598	rlmL	601130	602287	1158	Ribosomal RNA large subunit methyltransferase K/L	149	21	18.135	4.6	93.3	362.983	51.159
LAG_00599	mapZ	602309	604153	1845	Mid-cell-anchored protein Z	308	36	19.512	0.6	100	470.937	55.045
LAG_00600	murR	604208	604951	744	HTH-type transcriptional regulator MurR	199	27	36.29	1.5	95	754.551	102.376
LAG_00601	NA	605091	606005	915	6-phosphogluconate dehydrogenase, NAD(+)-dependent, decarboxylating	247	22	24.044	0.2	98.8	761.525	67.828
LAG_00602	bglF_1	606012	607898	1887	PTS system beta-glucoside-specific EIIBCA component	516	63	33.386	1.3	98.5	771.411	94.184
LAG_00603	bglH_2	607888	609324	1437	Aryl-phospho-beta-D-glucosidase BglH	554	57	39.666	0.8	97.9	1087.58	111.899
LAG_00604	xylB_1	609369	610868	1500	Xylulose kinase	498	53	35.333	0.3	96.1	936.583	99.677
LAG_00605	arsC	610941	611333	393	Glutaredoxin arsenate reductase	69	12	30.534	12.7	90.1	495.296	86.138
LAG_00606	pepQ	611376	612461	1086	Xaa-Pro dipeptidase	160	22	20.258	0.6	82.3	415.622	57.148
LAG_00607	ccpA	612664	613659	996	Catabolite control protein A	26	4	4.016	1.6	97.2	73.641	11.329
LAG_00608	cspL	613864	614064	201	Cold shock protein 2	4	1	4.975	65.7	65.7	56.14	14.035
LAG_00609	NA	614236	614309	74	tRNA-Met	8	1	13.514	77	77	304.977	38.122
LAG_00610	aroD	614427	615116	690	3-dehydroquinate dehydratase	105	12	17.391	0.4	91.7	429.288	49.061
LAG_00611	purB	615228	616523	1296	Adenylosuccinate lyase	185	25	19.29	0.8	99	402.694	54.418
LAG_00612	hlyU	616665	616988	324	Transcriptional activator HlyU	34	6	18.519	0.3	88	296.034	52.241
LAG_00613	cadA	617001	619034	2034	Cadmium, zinc and cobalt-transporting ATPase	424	54	26.549	4.1	99.8	588.062	74.895
LAG_00614	NA	619105	619911	807	hypothetical protein	199	28	34.696	8.1	99.8	695.645	97.88
LAG_00615	uvrC	620049	621827	1779	UvrABC system protein C	176	28	15.739	1.3	98.7	279.09	44.401
LAG_00616	NA	621941	622288	348	hypothetical protein	32	6	17.241	7.8	67.8	259.405	48.639
LAG_00617	mutY	622391	623464	1074	Adenine DNA glycosylase	109	16	14.898	17.2	93.5	286.306	42.027
LAG_00618	pepV_2	623575	624981	1407	Beta-Ala-Xaa dipeptidase	98	18	12.793	3.7	96.4	196.49	36.09
LAG_00619	NA	625224	626285	1062	hypothetical protein	341	42	39.548	6.4	96.8	905.812	111.566
LAG_00620	murQ	626282	627172	891	N-acetylmuramic acid 6-phosphate etherase	239	33	37.037	2.8	98.9	756.708	104.483
LAG_00621	NA	627196	629121	1926	PTS system EIIBC component	430	54	28.037	0.8	99.5	629.826	79.094
LAG_00622	acpS	629226	629588	363	Holo-[acyl-carrier-protein] synthase	0	0	0			0	0
LAG_00623	alr	629611	630723	1113	Alanine racemase	0	0	0			0	0
LAG_00624	spxA_6	630866	631297	432	Regulatory protein Spx	142	17	39.352	0.7	94	927.284	111.013
LAG_00625	pnuC	631411	632118	708	Nicotinamide riboside transporter PnuC	147	17	24.011	0.6	96.6	585.723	67.737
LAG_00626	sugE	632163	632483	321	Quaternary ammonium compound-resistance protein SugE	66	10	31.153	1.2	95.3	580.026	87.883
LAG_00627	NA	632972	633685	714	hypothetical protein	179	17	23.81	0.6	93.4	707.234	67.167
LAG_00628	folD	633769	634638	870	Bifunctional protein FolD protein	44	6	6.897	0.1	90.3	142.673	19.455
LAG_00629	xseA	634713	635966	1254	Exodeoxyribonuclease 7 large subunit	67	13	10.367	6.9	89.1	150.725	29.245
LAG_00630	xseB	635976	636200	225	Exodeoxyribonuclease 7 small subunit	11	2	8.889	75.1	84.9	137.917	25.076
LAG_00631	garK	636307	637362	1056	Glycerate 2-kinase	101	14	13.258	2.1	99.6	269.815	37.4
LAG_00632	NA	637475	637651	177	hypothetical protein	49	8	45.198	2.3	92.1	780.964	127.504
LAG_00633	NA	637777	638628	852	Farnesyl diphosphate synthase	153	15	17.606	5.9	92.5	506.594	49.666
LAG_00634	tlyA	638625	639434	810	Hemolysin A	51	9	11.111	27.8	88.4	177.621	31.345
LAG_00635	argR_1	639431	639877	447	Arginine repressor	31	5	11.186	31.5	88.8	195.642	31.555

LAG_00636	recN	639889	641553	1665	DNA repair protein RecN	178	28	16.817	8	95.1	301.588	47.441
LAG_00637	NA	641561	642520	960	hypothetical protein	173	23	23.958	0.2	99.5	508.374	67.587
LAG_00638	femA	642578	643795	1218	Aminoacyltransferase FemA	0	0	0			0	0
LAG_00639	femB	643795	644841	1047	Aminoacyltransferase FemB	14	3	2.865	36.6	99.3	37.722	8.083
LAG_00640	yumC	644941	645921	981	Ferredoxin--NADP reductase 2	21	5	5.097	89.2	97.9	60.389	14.378
LAG_00641	NA	645982	646536	555	hypothetical protein	60	12	21.622	2.9	92.6	304.977	60.995
LAG_00642	mutS2	646542	648878	2337	Endonuclease MutS2	334	41	17.544	5.7	93.8	403.177	49.492
LAG_00643	trxA	648965	649279	315	Thioredoxin	0	0	0			0	0
LAG_00644	NA	649475	649678	204	hypothetical protein	8	1	4.902	11.8	11.8	110.629	13.829
LAG_00645	NA	649768	649839	72	tRNA-Gln	0	0	0			0	0
LAG_00646	femX	649900	651069	1170	Lipid II:glycine glycyltransferase	3	1	0.855	98.3	98.3	7.233	2.411
LAG_00647	rsmH	651159	652130	972	Ribosomal RNA small subunit methyltransferase H	0	0	0			0	0
LAG_00648	ftsL	652163	652543	381	Cell division protein FtsL	0	0	0			0	0
LAG_00649	pbpX_1	652540	654834	2295	Penicillin-binding protein 2x	0	0	0			0	0
LAG_00650	mraY	654922	655914	993	Phospho-N-acetylmuramoyl-pentapeptide- transferase	10	2	2.014	98.3	99.9	28.409	5.682
LAG_00651	ywaC	656139	656792	654	GTP pyrophosphokinase YwaC	248	29	44.343	0.6	99.4	1069.75	125.092
LAG_00652	phoP_1	656792	657187	396	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP	127	13	32.828	2.3	97	904.725	92.61
LAG_00653	cssS	657197	658582	1386	Sensor histidine kinase CssS	531	61	44.012	0.6	96.8	1080.786	124.158
LAG_00654	rplS	658676	659026	351	50S ribosomal protein L19	0	0	0			0	0
LAG_00655	NA	659219	659344	126	hypothetical protein	72	6	47.619	27	97.6	1612.019	134.335
LAG_00656	NA	659489	659725	237	hypothetical protein	12	3	12.658	4.2	68.4	142.837	35.709
LAG_00657	NA	659941	660513	573	hypothetical protein	180	28	48.866	0.3	99.5	886.189	137.852
LAG_00658	nlhH	660778	661731	954	Carboxylesterase NlhH	242	40	41.929	0.1	97	715.608	118.282
LAG_00659	ybbH_1	661886	662614	729	putative HTH-type transcriptional regulator YbbH	212	32	43.896	4.8	90.3	820.383	123.831
LAG_00660	malX_2	662720	664771	2052	PTS system maltose-specific EIICB component	780	89	43.372	1.4	98.7	1072.323	122.355
LAG_00661	patB	664821	665990	1170	Cystathionine beta-lyase PatB	381	45	38.462	3.6	98.8	918.644	108.501
LAG_00662	NA	666035	666565	531	hypothetical protein	108	14	26.365	9.6	89.8	573.77	74.378
LAG_00663	mrp	666754	667092	339	Iron-sulfur cluster carrier protein	20	5	14.749	9.7	95	166.433	41.608
LAG_00664	NA	667158	667775	618	hypothetical protein	232	21	33.981	0.6	98.1	1059.029	95.86
LAG_00665	liaS	667772	668752	981	Sensor histidine kinase LiaS	140	16	16.31	0.4	98.8	402.594	46.011
LAG_00666	vraR	668770	669405	636	Response regulator protein VraR	94	16	25.157	11.6	98	416.945	70.969
LAG_00667	NA	669486	670289	804	Putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	166	21	26.119	0.9	96.9	582.452	73.684
LAG_00668	NA	670351	670941	591	Putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	34	8	13.536	5.6	46.4	162.293	38.187
LAG_00669	yugI	670943	671338	396	General stress protein 13	8	2	5.051	24.7	29.8	56.991	14.248
LAG_00670	ydjZ	671356	671961	606	TVP38/TMEM64 family inner membrane protein YdjZ	85	10	16.502	12.5	90.3	395.69	46.552
LAG_00671	rodA	672066	673379	1314	Peptidoglycan glycosyltransferase RodA	89	14	10.654	27.8	99.7	191.075	30.057
LAG_00672	NA	673523	673954	432	hypothetical protein	80	13	30.093	38.2	98.6	522.414	84.892
LAG_00673	NA	674127	675347	1221	Secreted 45 kDa protein	240	30	24.57	0.5	90.5	554.503	69.313
LAG_00674	lptB	675498	676397	900	Lipopolysaccharide export system ATP-binding protein LptB	404	34	37.778	6.6	92.9	1266.331	106.572
LAG_00675	NA	676390	677658	1269	hypothetical protein	473	45	35.461	12.8	99.1	1051.496	100.037
LAG_00676	spxA_7	677701	678135	435	Regulatory protein Spx	86	16	36.782	2.8	95.2	557.722	103.762
LAG_00677	carB	678720	681905	3186	Carbamoyl-phosphate synthase large chain	544	83	26.051	0.2	99.7	481.683	73.492
LAG_00678	rluE	681996	682529	534	Ribosomal large subunit pseudouridine synthase E	194	20	37.453	1.9	86.3	1024.87	105.657
LAG_00679	NA	682557	683354	798	hypothetical protein	285	31	38.847	0.6	97.4	1007.512	109.589
LAG_00680	NA	683351	684451	1101	hypothetical protein	321	34	30.881	0.5	98.1	822.481	87.116
LAG_00681	NA	684473	685702	1230	hypothetical protein	237	36	29.268	1.7	100	543.565	82.567
LAG_00682	pyrK	686134	686919	786	Dihydroorotate dehydrogenase B (NAD(+)), electron transfer subunit	54	9	11.45	1.9	86.9	193.811	32.302
LAG_00683	pyrDB	686919	687854	936	Dihydroorotate dehydrogenase B (NAD(+)), catalytic subunit	197	28	29.915	5.3	98.5	593.743	84.39
LAG_00684	pyrF	687847	688566	720	Orotidine 5'-phosphate decarboxylase	206	26	36.111	5	95.8	807.129	101.871
LAG_00685	rsmG	688599	689312	714	Ribosomal RNA small subunit methyltransferase G	102	15	21.008	5.7	95.8	403.005	59.265
LAG_00686	hepT	689312	690271	960	Heptaprenyl diphosphate synthase component 2	179	24	25	1.5	89.3	526.005	70.526
LAG_00687	NA	690262	690792	531	hypothetical protein	120	15	28.249	29.4	96.4	637.522	79.69
LAG_00688	NA	690789	691184	396	hypothetical protein	120	14	35.354	18.2	99.5	854.859	99.734
LAG_00689	gtaB	691287	692213	927	UTP--glucose-1-phosphate uridylyltransferase	0	0	0			0	0

LAG_00690	gpsA	692237	693256	1020	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	0	0	0			0	0
LAG_00691	guaD	693476	693958	483	Guanine deaminase	25	4	8.282	20.3	71.4	146.016	23.363
LAG_00692	speG	693978	694475	498	Spermidine N(1)-acetyltransferase	40	8	16.064	1.2	67.3	226.589	45.318
LAG_00693	NA	694489	694977	489	hypothetical protein	70	8	16.36	11.5	95.1	403.829	46.152
LAG_00694	kcsA	695008	695343	336	pH-gated potassium channel KcsA	78	7	20.833	10.7	72.6	654.883	58.772
LAG_00695	cfa	695406	696599	1194	Cyclopropane-fatty-acyl-phospholipid synthase	190	23	19.263	1.1	77.1	448.908	54.342
LAG_00696	NA	696798	697151	354	hypothetical protein	36	6	16.949	44.4	75.7	286.885	47.814
LAG_00697	NA	697184	697483	300	hypothetical protein	112	8	26.667	39	97.3	1053.186	75.228
LAG_00698	NA	697531	697899	369	hypothetical protein	64	9	24.39	16.3	85.4	489.285	68.806
LAG_00699	NA	698059	698343	285	hypothetical protein	71	9	31.579	7	88.1	702.784	89.085
LAG_00700	NA	698391	698759	369	hypothetical protein	63	8	21.68	16.8	54.7	481.64	61.161
LAG_00701	NA	698814	699206	393	hypothetical protein	69	10	25.445	0.5	46.8	495.296	71.782
LAG_00702	NA	699306	699950	645	hypothetical protein	156	23	35.659	0.8	96.6	682.297	100.595
LAG_00703	NA	700473	700661	189	hypothetical protein	51	9	47.619	0.5	52.9	761.231	134.335
LAG_00704	NA	700912	701490	579	hypothetical protein	82	11	18.998	1	69.1	399.525	53.595
LAG_00705	NA	701500	702672	1173	TelA-like protein	128	15	12.788	3.1	93.2	307.837	36.075
LAG_00706	nagA_1	702768	703919	1152	N-acetylglucosamine-6-phosphate deacetylase	39	7	6.076	0.3	98.4	95.504	17.142
LAG_00707	pfkA	704164	705192	1029	ATP-dependent 6-phosphofructokinase	0	0	0			0	0
LAG_00708	pyk	705302	706810	1509	Pyruvate kinase	0	0	0			0	0
LAG_00709	ldhA	707037	708014	978	L-lactate dehydrogenase 1	63	11	11.247	2.9	97.5	181.723	31.729
LAG_00710	NA	708119	709165	1047	hypothetical protein	588	71	67.813	0.4	99.5	1584.305	191.302
LAG_00711	NA	709575	710528	954	hypothetical protein	247	33	34.591	2.5	93.1	730.393	97.583
LAG_00712	NA	710528	711598	1071	hypothetical protein	219	28	26.144	3.2	98.9	576.85	73.753
LAG_00713	xylG	711582	713111	1530	Xylose import ATP-binding protein XylG	207	30	19.608	3.9	95.1	381.669	55.314
LAG_00714	NA	713394	715019	1626	hypothetical protein	146	22	13.53	3.3	95.2	253.303	38.169
LAG_00715	queG	715123	716178	1056	Epoxyqueuosine reductase	91	18	17.045	3.6	98.9	243.1	48.086
LAG_00716	prfB	716230	717327	1098	Peptide chain release factor 2	0	0	0			0	0
LAG_00717	ftsE	717537	718229	693	Cell division ATP-binding protein FtsE	0	0	0			0	0
LAG_00718	ftsX	718222	719157	936	Cell division protein FtsX	0	0	0			0	0
LAG_00719	nrdF2	719257	720243	987	Ribonucleoside-diphosphate reductase subunit beta nrdF2	0	0	0			0	0
LAG_00720	nrdE1	720258	722426	2169	Ribonucleoside-diphosphate reductase subunit alpha 1	0	0	0			0	0
LAG_00721	NA	722480	722899	420	Putative NrdI-like protein	0	0	0			0	0
LAG_00722	nrdH	722896	723114	219	Glutaredoxin-like protein NrdH	0	0	0			0	0
LAG_00723	plsY	723223	723861	639	Glycerol-3-phosphate acyltransferase	10	1	1.565	0.3	0.3	44.148	4.415
LAG_00724	parE	724091	726028	1938	DNA topoisomerase 4 subunit B	0	0	0			0	0
LAG_00725	polC_1	726073	726894	822	DNA polymerase III PolC-type	12	2	2.433	4.3	95	41.183	6.864
LAG_00726	NA	726897	727358	462	Acetyltransferase	32	7	15.152	17.5	89.4	195.396	42.743
LAG_00727	parC	727404	729887	2484	DNA topoisomerase 4 subunit A	0	0	0			0	0
LAG_00728	gyrA	729900	732518	2619	DNA gyrase subunit A	9	2	0.764	2.2	98.5	9.694	2.154
LAG_00729	apbE_2	732520	733590	1071	FAD:protein FMN transferase	512	47	43.884	0.3	97.8	1348.617	123.799
LAG_00730	NA	733602	734333	732	hypothetical protein	119	17	23.224	1	87.4	458.611	65.516
LAG_00731	NA	734384	735151	768	hypothetical protein	195	28	36.458	17.1	96.9	716.278	102.85
LAG_00732	natA_1	735164	736030	867	ABC transporter ATP-binding protein NatA	179	28	32.295	1.3	99.3	582.428	91.106
LAG_00733	pcrA	736241	738535	2295	ATP-dependent DNA helicase PcrA	206	31	13.508	0.7	97.7	253.217	38.105
LAG_00734	tag	738539	739105	567	DNA-3-methyladenine glycosylase 1	126	20	35.273	5.6	94	626.896	99.507
LAG_00735	NA	739303	740559	1257	hypothetical protein	336	45	35.8	1	98.8	754.071	100.992
LAG_00736	NA	740648	741100	453	hypothetical protein	116	14	30.905	10.6	98.7	722.384	87.184
LAG_00737	truB	741227	742132	906	tRNA pseudouridine synthase B	150	23	25.386	2.3	88.5	467.059	71.616
LAG_00738	ribF	742134	743045	912	Riboflavin biosynthesis protein RibF	0	0	0			0	0
LAG_00739	tpiA	743180	743938	759	Triosephosphate isomerase	4	1	1.318	95.1	95.1	14.867	3.717
LAG_00740	asD	744009	745601	1593	Bifunctional aspartate aminotransferase and L-aspartate beta-decarboxylase	413	49	30.76	0.4	98.6	731.379	86.774
LAG_00741	NA	745759	746346	588	hypothetical protein	143	18	30.612	5.1	99	686.068	86.358
LAG_00742	hemN	746391	747515	1125	Oxygen-independent coproporphyrinogen-III oxidase-like protein	265	33	29.333	1.2	99.5	664.51	82.75
LAG_00743	NA	747565	748392	828	hypothetical protein	126	17	20.531	20.3	97.9	429.288	57.92

LAG_00744	endA	748501	749394	894	DNA-entry nuclease	273	38	42.506	0.4	98.3	861.457	119.91
LAG_00745	lytG	749481	750119	639	Exo-glucosaminidase LytG	160	27	42.254	2.8	92.3	706.362	119.199
LAG_00746	NA	750250	750942	693	hypothetical protein	119	20	28.86	0.6	98.3	484.42	81.415
LAG_00747	strB1	751344	752327	984	Inosamine-phosphate amidinotransferase 1	170	25	25.407	3.7	99.3	487.374	71.673
LAG_00748	gph_1	752381	752980	600	Phosphoglycolate phosphatase	249	23	38.333	0.8	100	1170.729	108.14
LAG_00749	NA	752992	753726	735	hypothetical protein	161	21	28.571	5.2	95.9	617.941	80.601
LAG_00750	gyrB	753888	755846	1959	DNA gyrase subunit B	12	1	0.51	97.5	97.5	17.28	1.44
LAG_00751	xerD_1	755932	757056	1125	Tyrosine recombinase XerD	442	48	42.667	0.6	98.9	1108.353	120.364
LAG_00752	NA	757187	757765	579	hypothetical protein	294	28	48.359	2.1	97.4	1432.442	136.423
LAG_00753	NA	757818	758408	591	hypothetical protein	160	17	28.765	14	95.6	763.732	81.146
LAG_00754	NA	758420	758773	354	hypothetical protein	3	1	2.825	94.9	94.9	23.907	7.969
LAG_00755	NA	759067	759861	795	hypothetical protein	255	28	35.22	0.8	97.6	904.86	99.357
LAG_00756	NA	760016	760246	231	hypothetical protein	51	10	43.29	8.7	94.4	622.826	122.123
LAG_00757	NA	760259	760510	252	hypothetical protein	75	11	43.651	20.6	95.2	839.593	123.14
LAG_00758	NA	760527	760676	150	hypothetical protein	37	6	40	6.7	100	695.855	112.841
LAG_00759	NA	760893	761669	777	hypothetical protein	179	22	28.314	15.1	89.8	649.891	79.875
LAG_00760	NA	761670	762635	966	hypothetical protein	228	26	26.915	7.3	95.9	665.834	75.928
LAG_00761	NA	762868	763194	327	hypothetical protein	110	17	51.988	0.9	96.6	948.972	146.659
LAG_00762	NA	763194	763979	786	hypothetical protein	288	42	53.435	0.6	96.6	1033.661	150.742
LAG_00763	NA	763963	764247	285	hypothetical protein	125	12	42.105	11.2	73	1237.295	118.78
LAG_00764	NA	764244	764648	405	hypothetical protein	118	15	37.037	16	88.6	821.931	104.483
LAG_00765	NA	764755	765036	282	hypothetical protein	63	11	39.007	7.8	88.7	630.231	110.04
LAG_00766	NA	765141	765530	390	hypothetical protein	151	22	56.41	1.8	97.7	1092.246	159.135
LAG_00767	spxA_8	765648	766046	399	Regulatory protein Spx	199	22	55.138	13	95.7	1406.982	155.546
LAG_00768	NA	766237	766638	402	hypothetical protein	166	16	39.801	7	99.8	1164.904	112.28
LAG_00769	NA	766936	768066	1131	hypothetical protein	481	57	50.398	5.7	99.6	1199.75	142.174
LAG_00770	NA	768286	768918	633	hypothetical protein	236	28	44.234	1.6	98.1	1051.76	124.785
LAG_00771	NA	769003	769078	76	tRNA-Arg	31	4	52.632	28.9	78.9	1150.685	148.475
LAG_00772	NA	769203	769751	549	hypothetical protein	121	20	36.43	4.4	99.3	621.758	102.77
LAG_00773	NA	769963	770454	492	hypothetical protein	278	33	67.073	5.9	96.3	1593.999	189.216
LAG_00774	NA	770444	771727	1284	hypothetical protein	451	67	52.181	2.3	95	990.877	147.203
LAG_00775	NA	771729	773324	1596	hypothetical protein	775	94	58.897	0.1	97.5	1369.863	166.151
LAG_00776	NA	773308	774198	891	hypothetical protein	243	33	37.037	1.9	98.9	769.373	104.483
LAG_00777	NA	774341	774910	570	hypothetical protein	274	31	54.386	4.2	97.9	1356.076	153.425
LAG_00778	NA	774921	775787	867	hypothetical protein	280	28	32.295	0.6	98.2	911.06	91.106
LAG_00779	cgkA	775865	776323	459	Kappa-carrageenase	135	21	45.752	10	99.6	829.716	129.067
LAG_00780	NA	776336	776680	345	hypothetical protein	315	32	92.754	3.8	98.6	2575.726	261.661
LAG_00781	NA	776677	776952	276	hypothetical protein	92	15	54.348	3.3	87	940.345	153.317
LAG_00782	NA	776952	777302	351	hypothetical protein	133	15	42.735	5.7	98.6	1068.939	120.557
LAG_00783	NA	777299	777661	363	hypothetical protein	222	22	60.606	0.3	100	1725.26	170.972
LAG_00784	NA	777672	778319	648	hypothetical protein	305	35	54.012	2.9	94.1	1327.801	152.371
LAG_00785	NA	778389	778832	444	hypothetical protein	196	18	40.541	3.2	91.4	1245.321	114.366
LAG_00786	NA	778877	779158	282	hypothetical protein	124	11	39.007	1.4	96.8	1240.455	110.04
LAG_00787	NA	779158	781857	2700	hypothetical protein	1013	131	48.519	0.1	99.5	1058.41	136.872
LAG_00788	NA	781858	782703	846	hypothetical protein	478	51	60.284	0.8	99.3	1593.917	170.062
LAG_00789	NA	782700	784802	2103	hypothetical protein	843	95	45.174	0.4	99.4	1130.828	127.436
LAG_00790	NA	784792	786135	1344	hypothetical protein	521	63	46.875	0.8	99.6	1093.57	132.236
LAG_00791	NA	786176	786538	363	hypothetical protein	124	15	41.322	9.4	92.3	963.659	116.572
LAG_00792	sle1	786522	787646	1125	N-acetylmuramoyl-L-alanine amidase sle1	430	55	48.889	0.8	100	1078.262	137.917
LAG_00793	NA	787721	788407	687	hypothetical protein	309	36	52.402	1.9	99	1268.849	147.827
LAG_00794	NA	788645	789109	465	hypothetical protein	117	15	32.258	15.5	89.9	709.808	91.001
LAG_00795	NA	789113	789919	807	hypothetical protein	159	22	27.261	17.2	98.1	555.817	76.906
LAG_00796	NA	790827	790949	123	hypothetical protein	123	8	65.041	15.4	100	2821.034	183.482
LAG_00797	pspB_3	791063	791659	597	Putative phosphoserine phosphatase 2	322	36	60.302	12.1	99	1521.563	170.113

LAG_00798	NA	791985	793511	1527	hypothetical protein	486	52	34.054	0.1	95.9	897.854	96.067
LAG_00799	NA	794046	794495	450	hypothetical protein	74	12	26.667	5.3	97.3	463.903	75.228
LAG_00800	emrB_1	794492	796018	1527	Multidrug export protein EmrB	244	29	18.991	6.9	99.2	450.774	53.576
LAG_00801	NA	796018	796734	717	hypothetical protein	87	14	19.526	5.3	89.7	342.301	55.083
LAG_00802	niaX	796933	797478	546	Niacin transporter NiaX	95	10	18.315	7.3	90.3	490.839	51.667
LAG_00803	rpiR_2	797554	798312	759	HTH-type transcriptional regulator RpiR	125	15	19.763	21.1	99.5	464.597	55.752
LAG_00804	ribZ_2	798476	799870	1395	Riboflavin transporter RibZ	199	29	20.789	10.5	96.7	402.427	58.645
LAG_00805	deoB	799952	801187	1236	Phosphopentomutase	72	12	9.709	1.4	93	164.332	27.389
LAG_00806	NA	801224	801460	237	hypothetical protein	61	5	21.097	9.7	60.3	726.089	59.515
LAG_00807	NA	801400	801489	90	hypothetical protein	0	0	0			0	0
LAG_00808	punA	801480	802295	816	Purine nucleoside phosphorylase 1	79	14	17.157	2.7	90.6	273.115	48.4
LAG_00809	deoD	802379	803077	699	Purine nucleoside phosphorylase DeoD-type	58	11	15.737	4.6	95.9	234.077	44.394
LAG_00810	fhs1	803207	804877	1671	Formate--tetrahydrofolate ligase 1	178	28	16.756	0.2	99.6	300.505	47.27
LAG_00811	NA	804891	805301	411	hypothetical protein	3	1	2.433	85.6	85.6	20.591	6.864
LAG_00812	yxeM_1	805468	806325	858	putative amino-acid-binding protein YxeM	30	5	5.828	10.8	65.5	98.638	16.44
LAG_00813	yxeN	806468	807355	888	putative amino-acid permease protein YxeN	3	1	1.126	25.9	25.9	9.531	3.177
LAG_00814	tcyC	807352	808113	762	L-cystine import ATP-binding protein TcyC	13	3	3.937	59.8	95.5	48.128	11.106
LAG_00815	NA	808106	808333	228	hypothetical protein	55	6	26.316	3.1	89.9	680.512	74.238
LAG_00816	trxB	808404	809324	921	Thioredoxin reductase	9	2	2.172	97.3	99.9	27.567	6.126
LAG_00817	secG	809438	809686	249	putative protein-export membrane protein SecG	7	2	8.032	69.1	83.5	79.306	22.659
LAG_00818	NA	809910	810371	462	hypothetical protein	257	27	58.442	8.9	81.4	1569.276	164.866
LAG_00819	mhqD	810692	811303	612	Putative hydrolase MhqD	187	27	44.118	1.8	97.9	861.982	124.457
LAG_00820	mhqA_1	811381	812550	1170	Putative ring-cleaving dioxygenase MhqA	394	54	46.154	1.3	99.5	949.989	130.202
LAG_00821	srrA_1	812597	813286	690	Transcriptional regulatory protein SrrA	257	29	42.029	4.2	99.1	1050.733	118.565
LAG_00822	walK_2	813296	814762	1467	Sensor protein kinase WalK	675	75	51.125	0.5	97.3	1298.022	144.225
LAG_00823	NA	814876	815826	951	hypothetical protein	483	52	54.679	0.7	98.1	1432.765	154.252
LAG_00824	yjeM_2	815993	817522	1530	Inner membrane transporter YjeM	667	93	60.784	0.9	99.9	1229.823	171.475
LAG_00825	NA	817679	817879	201	hypothetical protein	112	11	54.726	15.9	99.5	1571.919	154.385
LAG_00826	NA	817929	818171	243	hypothetical protein	168	20	82.305	0.8	99.2	1950.344	232.184
LAG_00827	NA	818416	819045	630	hypothetical protein	217	15	23.81	0.8	91.3	971.689	67.167
LAG_00828	rnr_1	819303	821738	2436	Ribonuclease R	616	73	29.967	0.4	97	713.365	84.538
LAG_00829	yecD	821763	822347	585	Isochorismatase family protein YecD	185	26	44.444	1.7	99.1	892.122	125.379
LAG_00830	NA	822697	824808	2112	hypothetical protein	1131	111	52.557	0.2	100	1510.696	148.265
LAG_00831	NA	824898	825218	321	hypothetical protein	66	10	31.153	1.6	97.8	580.026	87.883
LAG_00832	tagH_2	825534	827078	1545	Teichoic acids export ATP-binding protein TagH	512	63	40.777	2.1	100	934.867	115.032
LAG_00833	tagG_2	827103	827915	813	Teichoic acid translocation permease protein TagG	407	46	56.581	1.2	99.5	1412.252	159.616
LAG_00834	tagF	828018	830378	2361	Teichoic acid poly(glycerol phosphate) polymerase	857	113	47.861	0.2	99.9	1023.984	135.018
LAG_00835	NA	830382	831404	1023	hypothetical protein	401	46	44.966	2.2	97.8	1105.801	126.85
LAG_00836	tagD_1	831397	831831	435	Glycerol-3-phosphate cytidylyltransferase	85	11	25.287	5.7	94.3	551.236	71.336
LAG_00837	NA	831828	832250	423	hypothetical protein	137	11	26.005	2.1	57.2	913.668	73.36
LAG_00838	tarF_1	832271	833470	1200	Teichoic acid poly(glycerol phosphate) polymerase	241	36	30	0.2	88.8	566.558	84.631
LAG_00839	lytR_1	833515	834459	945	Transcriptional regulator LytR	217	32	33.862	2.3	99.5	647.793	95.527
LAG_00840	NA	834505	834879	375	hypothetical protein	73	10	26.667	1.9	86.9	549.161	75.228
LAG_00841	inlJ_1	834839	836902	2064	Internalin-J	490	68	32.946	2.7	99.8	669.722	92.941
LAG_00842	trmL	836977	837480	504	tRNA (cytidine(34)-2'-O)-methyltransferase	59	9	17.857	18.8	95.2	330.24	50.376
LAG_00843	dhfR	837969	838484	516	Dihydrofolate reductase	0	0	0			0	0
LAG_00844	clpX	838686	839924	1239	ATP-dependent Clp protease ATP-binding subunit ClpX	69	15	12.107	7.8	98.9	157.104	34.153
LAG_00845	engB	840105	840692	588	putative GTP-binding protein EngB	24	3	5.102	89.8	93.9	115.144	14.393
LAG_00846	folB	840676	841032	357	Dihydroneopterin aldolase	65	8	22.409	1.4	99.2	513.634	63.216
LAG_00847	folE	841089	842138	1050	GTP cyclohydrolase 1	45	7	6.667	15	95.9	120.901	18.807
LAG_00848	folP	842140	843213	1074	Dihydropteroate synthase	192	21	19.553	4.4	91.5	504.319	55.16
LAG_00849	folQ	843213	843707	495	putative DHNTP pyrophosphohydrolase	14	2	4.04	43	63.2	79.787	11.398
LAG_00850	fpgS	843704	844990	1287	Folylpolyglutamate synthase	17	2	1.554	97.4	99	37.263	4.384
LAG_00851	NA	845028	845666	639	Deoxyguanosine kinase	19	3	4.695	36	87.2	83.88	13.244

LAG_00852	glmS	845819	847636	1818	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	0	0	0			0	0
LAG_00853	NA	847740	848423	684	hypothetical protein	166	19	27.778	6.7	99.3	684.637	78.362
LAG_00854	menH_2	848489	849418	930	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	212	28	30.108	1.3	97.8	643.074	84.934
LAG_00855	NA	849707	850570	864	hypothetical protein	396	55	63.657	0.1	97.1	1292.974	179.58
LAG_00856	NA	850893	852626	1734	Fimbrial subunit type 1	878	96	55.363	6.2	100	1428.413	156.182
LAG_00857	NA	852760	856446	3687	hypothetical protein	1751	195	52.889	0.4	100	1339.742	149.2
LAG_00858	NA	856448	857080	633	hypothetical protein	255	27	42.654	3.6	100	1136.435	120.328
LAG_00859	NA	857208	859004	1797	hypothetical protein	734	76	42.293	0.2	99.6	1152.275	119.309
LAG_00860	spxA_9	859095	859424	330	Regulatory protein Spx	121	15	45.455	1.2	94.8	1034.379	128.229
LAG_00861	rex	859485	860138	654	Redox-sensing transcriptional repressor Rex	33	6	9.174	4.1	100	142.346	25.881
LAG_00862	gltC	860291	861184	894	HTH-type transcriptional regulator GltC	275	33	36.913	4.5	98	867.768	104.132
LAG_00863	mleA	861348	862970	1623	Malolactic enzyme	321	45	27.726	0.4	99.3	557.949	78.217
LAG_00864	citS	862988	864265	1278	Citrate-sodium symporter	263	39	30.516	1	98.1	580.541	86.088
LAG_00865	NA	864246	864422	177	hypothetical protein	27	4	22.599	6.2	79.1	430.327	63.752
LAG_00866	NA	864612	865466	855	hypothetical protein	298	37	43.275	0.5	97.9	983.237	122.08
LAG_00867	msrB	865608	866051	444	Peptide methionine sulfoxide reductase MsrB	87	13	29.279	0.9	77.9	552.77	82.598
LAG_00868	dkgB	866187	867026	840	2,5-diketo-D-gluconic acid reductase B	135	25	29.762	0.5	91	453.38	83.959
LAG_00869	NA	867208	867375	168	hypothetical protein	10	2	11.905	4.2	77.4	167.919	33.584
LAG_00870	dnaD	867437	868111	675	DNA replication protein DnaD	0	0	0			0	0
LAG_00871	nth	868089	868757	669	Endonuclease III	37	7	10.463	10.2	91	156.021	29.518
LAG_00872	trmK	868750	869427	678	tRNA (adenine(22)-N(1))-methyltransferase	102	11	16.224	16.4	91.9	424.403	45.769
LAG_00873	NA	869424	870194	771	GTP cyclohydrolase 1 type 2	195	27	35.019	3.5	99	713.491	98.791
LAG_00874	cof	870358	871122	765	HMP-PP phosphatase	146	17	22.222	1.2	99.5	538.393	62.69
LAG_00875	rlmCD_1	871165	872535	1371	23S rRNA (uracil-C(5))-methyltransferase RlmCD	221	31	22.611	2.7	99.7	454.74	63.787
LAG_00876	NA	872532	874262	1731	hypothetical protein	483	65	37.551	2.4	94.9	787.151	105.931
LAG_00877	ycgJ_1	874960	875577	618	putative methyltransferase YcgJ	38	6	9.709	51.8	94.3	173.462	27.389
LAG_00878	NA	875693	876874	1182	hypothetical protein	155	28	23.689	3.1	98.6	369.932	66.827
LAG_00879	lapB	876874	878115	1242	Lipopolysaccharide assembly protein B	167	28	22.544	1.9	99.2	379.318	63.598
LAG_00880	alsS	878315	879982	1668	Acetolactate synthase	236	33	19.784	8.7	98	399.139	55.812
LAG_00881	yddE	880125	880925	801	putative isomerase YddE	168	30	37.453	2	97.1	591.677	105.657
LAG_00882	NA	880986	882224	1239	Secreted 45 kDa protein	395	55	44.391	1.3	98.1	899.361	125.227
LAG_00883	NA	882590	883318	729	hypothetical protein	230	34	46.639	4.1	98.8	890.038	131.571
LAG_00884	gbpA	883353	884015	663	GlcNAc-binding protein A	171	23	34.691	1.5	90	727.597	97.864
LAG_00885	chiD	884047	885528	1482	Chitinase D	393	53	35.762	0.9	99.9	748.088	100.887
LAG_00886	crtK-2	885812	886297	486	Tryptophan-rich protein TspO	137	20	41.152	4.9	84.6	795.23	116.092
LAG_00887	NA	886385	887209	825	hypothetical protein	288	29	35.152	1.5	99.4	984.797	99.164
LAG_00888	spxA_10	887541	887777	237	Regulatory protein Spx	117	15	63.291	3.8	92	1392.662	178.546
LAG_00889	NA	887910	888551	642	hypothetical protein	215	35	54.517	3.6	99.8	944.739	153.795
LAG_00890	dosC	888564	889709	1146	Diguanylate cyclase DosC	338	58	50.611	2.5	99.7	832.033	142.775
LAG_00891	nagE	890006	891973	1968	PTS system N-acetylglucosamine-specific EIICBA component	435	52	26.423	3.9	98	623.552	74.54
LAG_00892	copB	892133	894169	2037	Copper-exporting P-type ATPase B	396	54	26.51	3.1	98.5	548.419	74.784
LAG_00893	NA	894194	894643	450	hypothetical protein	144	15	33.333	4	100	902.731	94.034
LAG_00894	NA	894804	895130	327	hypothetical protein	94	7	21.407	1.2	74.6	810.939	60.389
LAG_00895	NA	895123	895743	621	hypothetical protein	163	17	27.375	11.3	96.6	740.465	77.226
LAG_00896	NA	895740	896618	879	hypothetical protein	190	29	32.992	0.2	97.2	609.78	93.072
LAG_00897	uppP	896632	897471	840	Undecaprenyl-diphosphatase	156	15	17.857	0.5	73.6	523.906	50.376
LAG_00898	NA	897579	898220	642	hypothetical protein	135	22	34.268	3	98.9	593.208	96.671
LAG_00899	acuR	898407	898979	573	Transcriptional regulator AcuR	86	14	24.433	4	98.3	423.401	68.926
LAG_00900	NA	898999	899358	360	hypothetical protein	72	9	25	3.6	96.4	564.207	70.526
LAG_00901	rclA	899360	900718	1359	putative pyridine nucleotide-disulfide oxidoreductase RclA	299	43	31.641	1.5	96	620.669	89.26
LAG_00902	metC	900846	902000	1155	Cystathionine beta-lyase	221	26	22.511	5.4	98.6	539.782	63.504
LAG_00903	NA	902110	902658	549	hypothetical protein	197	9	16.393	0.7	84.3	1012.283	46.246
LAG_00904	NA	902659	902940	282	hypothetical protein	5	1	3.546	86.9	86.9	50.018	10.004
LAG_00905	NA	903007	904380	1374	hypothetical protein	403	50	36.39	4.5	98.4	827.421	102.658

LAG_00906	ahpC	904645	905208	564	Alkyl hydroperoxide reductase subunit C	131	17	30.142	5.5	98.2	655.24	85.031
LAG_00907	ahpF	905267	906796	1530	NADH dehydrogenase	401	58	37.908	0.7	99	739.369	106.941
LAG_00908	azoR	906961	907578	618	FMN-dependent NADH-azoreductase	87	15	24.272	2.1	98.5	397.136	68.472
LAG_00909	hpf_2	907689	908246	558	Ribosome hibernation promotion factor	172	20	35.842	1.3	98.6	869.566	101.112
LAG_00910	NA	908297	909133	837	hypothetical protein	196	30	35.842	4.9	99	660.6	101.112
LAG_00911	mngR_1	909358	909978	621	Mannosyl-D-glycerate transport/metabolism system repressor MngR	182	24	38.647	0.6	89.2	826.776	109.025
LAG_00912	opuAA	910183	911385	1203	Glycine betaine transport ATP-binding protein OpuAA	208	34	28.263	1.4	98.8	487.76	79.73
LAG_00913	gbuB	911378	913102	1725	Glycine betaine/carnitine transport permease protein GbuB	475	67	38.841	0.4	96.2	776.806	109.571
LAG_00914	aldC_1	913245	913943	699	Alpha-acetolactate decarboxylase	168	26	37.196	0.9	98.1	678.017	104.931
LAG_00915	dprA	914030	914899	870	DNA processing protein DprA	237	29	33.333	0.5	91.4	768.488	94.034
LAG_00916	topA	915088	917238	2151	DNA topoisomerase 1	3	1	0.465	88.2	88.2	3.934	1.311
LAG_00917	trmFO	917287	918630	1344	Methylenetetrahydrofolate--tRNA-(uracil-5-)- methyltransferase TrmFO	124	13	9.673	33.9	96.1	260.274	27.287
LAG_00918	NA	918704	918925	222	hypothetical protein	21	5	22.523	12.2	71.6	266.855	63.537
LAG_00919	xerS	918991	920052	1062	Tyrosine recombinase XerS	5	1	0.942	5.3	5.3	13.282	2.656
LAG_00920	NA	920833	921549	717	hypothetical protein	541	46	64.156	0.1	97.1	2128.562	180.987
LAG_00921	walR_2	921771	922448	678	Transcriptional regulatory protein WalR	369	55	81.121	0.6	99.4	1535.341	228.845
LAG_00922	srrB	922449	923348	900	Sensor protein SrrB	409	61	67.778	0.1	95.4	1282.003	191.203
LAG_00923	NA	923394	924170	777	hypothetical protein	407	55	70.785	0.8	99.7	1477.684	199.687
LAG_00924	yxlF_1	924172	925095	924	putative ABC transporter ATP-binding protein YxlF	741	73	79.004	1.1	98.9	2262.322	222.874
LAG_00925	NA	925563	926627	1065	hypothetical protein	490	65	61.033	4	98	1297.94	172.176
LAG_00926	NA	927188	928240	1053	putative zinc-binding alcohol dehydrogenase	548	62	58.879	0.4	98	1468.116	166.101
LAG_00927	NA	928253	928636	384	hypothetical protein	236	30	78.125	1	99.2	1733.76	220.393
LAG_00928	NA	928847	929284	438	putative HTH-type transcriptional regulator	198	26	59.361	4.3	99.1	1275.262	167.459
LAG_00929	asnA	929473	930477	1005	Aspartate--ammonia ligase	549	66	65.672	4.1	98.6	1541.042	185.262
LAG_00930	yjaB_1	930669	931118	450	putative N-acetyltransferase YjaB	160	26	57.778	4.4	99.8	1003.034	162.993
LAG_00931	ctpF	931199	933841	2643	putative cation-transporting ATPase F	1245	146	55.24	0.3	99.5	1328.864	155.835
LAG_00932	comR	934107	934679	573	HTH-type transcriptional repressor ComR	243	28	48.866	0.3	99.1	1196.355	137.852
LAG_00933	NA	934761	935426	666	Putative NAD(P)H nitroreductase	214	33	49.55	1.2	96.8	906.458	139.781
LAG_00934	NA	935596	938802	3207	hypothetical protein	1907	213	66.417	0.3	100	1677.49	187.365
LAG_00935	NA	938829	939518	690	hypothetical protein	498	60	86.957	3.6	98.3	2036.05	245.307
LAG_00936	NA	939515	939829	315	hypothetical protein	142	21	66.667	5.1	98.7	1271.704	188.069
LAG_00937	NA	939844	940098	255	hypothetical protein	188	19	74.51	3.5	90.6	2079.821	210.195
LAG_00938	NA	940134	940937	804	hypothetical protein	382	51	63.433	1.4	96.6	1340.342	178.946
LAG_00939	NA	940979	941800	822	hypothetical protein	324	48	58.394	1.9	97.9	1111.94	164.732
LAG_00940	NA	941885	944659	2775	hypothetical protein	1481	165	59.459	1.3	100	1505.568	167.737
LAG_00941	NA	945013	946302	1290	hypothetical protein	563	75	58.14	1.6	98.4	1231.195	164.014
LAG_00942	dltC	946289	946531	243	D-alanine--poly(phosphoribitol) ligase subunit 2	141	13	53.498	9.9	98.8	1636.896	150.919
LAG_00943	patA_1	946559	947773	1215	Peptidoglycan O-acetyltransferase	518	72	59.259	0.6	100	1202.712	167.172
LAG_00944	dltA	947773	949275	1503	D-alanine--poly(phosphoribitol) ligase subunit 1	690	95	63.207	0.7	98.5	1295.085	178.309
LAG_00945	NA	949475	950416	942	hypothetical protein	239	31	32.909	1.2	83	715.74	92.837
LAG_00946	proA	950578	951834	1257	Gamma-glutamyl phosphate reductase	415	55	43.755	3	94.9	931.368	123.434
LAG_00947	proB	951831	952655	825	Glutamate 5-kinase 1	284	40	48.485	1.9	97.3	971.119	136.777
LAG_00948	NA	952765	955704	2940	hypothetical protein	663	94	31.973	1.2	99.8	636.172	90.196
LAG_00949	NA	955730	956407	678	hypothetical protein	385	38	56.047	1.9	94.7	1601.914	158.111
LAG_00950	NA	956426	957670	1245	hypothetical protein	433	63	50.602	0.6	99.9	981.131	142.751
LAG_00951	NA	957701	959422	1722	hypothetical protein	679	76	44.135	1.3	100	1112.359	124.506
LAG_00952	NA	959563	959904	342	hypothetical protein	126	19	55.556	15.5	99.7	1039.328	156.724
LAG_00953	thiE	960042	960680	639	Thiamine-phosphate synthase	222	36	56.338	1.7	99.8	980.077	158.931
LAG_00954	thiD	960673	961473	801	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	364	42	52.434	0.6	99.3	1281.968	147.919
LAG_00955	thiM	961470	962231	762	Hydroxyethylthiazole kinase	280	36	47.244	0.9	81.8	1036.6	133.277
LAG_00956	rsgA_1	962548	963633	1086	Small ribosomal subunit biogenesis GTPase RsgA	291	42	38.674	6.1	99.6	755.912	109.101
LAG_00957	glcU_1	963813	964700	888	putative glucose uptake protein GlcU	206	29	32.658	2.4	99.5	654.429	92.128
LAG_00958	rbsD	964726	965121	396	D-ribose pyranase	54	11	27.778	10.4	96	384.686	78.362
LAG_00959	rbsK/rbiA	965133	966041	909	Bifunctional ribokinase/ribose-5-phosphate isomerase A	76	18	19.802	0.3	98.7	235.862	55.862

LAG_00960	rbsR_2	966043	967044	1002	Ribose operon repressor	323	44	43.912	1.1	98.5	909.375	123.878
LAG_00961	garB	967178	968500	1323	Glutathione amide reductase	348	44	33.258	1.4	99.2	742.041	93.821
LAG_00962	NA	968578	968850	273	hypothetical protein	92	13	47.619	2.9	87.9	950.678	134.335
LAG_00963	NA	968872	969132	261	hypothetical protein	42	9	34.483	1.9	86.2	453.959	97.277
LAG_00964	pox5	969151	970944	1794	Pyruvate oxidase	332	50	27.871	0.6	99.7	522.064	78.624
LAG_00965	lldD	971145	972242	1098	L-lactate dehydrogenase	371	50	45.537	0.5	96.6	953.191	128.462
LAG_00966	spxA_11	972287	972682	396	Regulatory protein Spx	81	14	35.354	2.5	95.7	577.03	99.734
LAG_00967	emrB_2	973035	974393	1359	Multidrug export protein EmrB	300	42	30.905	3.6	99.4	622.745	87.184
LAG_00968	NA	974524	975150	627	hypothetical protein	165	21	33.493	0.5	99.5	742.377	94.484
LAG_00969	pspE	975217	975540	324	Thiosulfate sulfurtransferase PspE	154	17	52.469	12.3	94.8	1340.862	148.017
LAG_00970	glpE_1	975540	975836	297	Thiosulfate sulfurtransferase GlpE	102	15	50.505	1.3	99.3	968.84	142.476
LAG_00971	bglK_1	975944	976816	873	Beta-glucoside kinase	338	40	45.819	4.7	100	1092.221	129.257
LAG_00972	gmuD_1	976816	978249	1434	6-phospho-beta-glucosidase GmuD	615	72	50.209	0.5	97.8	1209.858	141.642
LAG_00973	NA	978371	979543	1173	Endo-beta-N-acetylglucosaminidase	505	59	50.298	1.8	98.7	1214.511	141.893
LAG_00974	NA	979579	980859	1281	hypothetical protein	554	53	41.374	3.4	97.5	1220.025	116.717
LAG_00975	mngB_1	980876	983500	2625	Mannosylglycerate hydrolase	686	103	39.238	0.4	92	737.23	110.692
LAG_00976	gmuC_1	983531	984871	1341	PTS system oligo-beta-mannoside-specific EIIC component	370	52	38.777	2.2	100	778.361	109.391
LAG_00977	gmuR_1	985049	985762	714	HTH-type transcriptional regulator GmuR	96	11	15.406	25.2	98.2	379.299	43.461
LAG_00978	ideR	985911	986606	696	Iron-dependent repressor IdeR	73	10	14.368	3.3	96	295.884	40.532
LAG_00979	mntH	986678	988234	1557	Divalent metal cation transporter MntH	294	53	34.04	0.5	98.7	532.681	96.027
LAG_00980	NA	988270	988968	699	hypothetical protein	190	32	45.78	0.1	96.7	766.805	129.146
LAG_00981	NA	989064	989579	516	hypothetical protein	122	21	40.698	4.3	76.4	666.989	114.81
LAG_00982	nhaK_2	989710	991659	1950	Sodium, potassium, lithium and rubidium/H(+) antiporter	462	77	39.487	0.8	98.3	668.368	111.395
LAG_00983	ycgJ_2	991772	992503	732	putative methyltransferase YcgJ	287	38	51.913	0.1	98.6	1106.061	146.447
LAG_00984	NA	992632	993849	1218	hypothetical protein	332	48	39.409	2.4	99.7	768.952	111.174
LAG_00985	ndk	993959	994375	417	Nucleoside diphosphate kinase	105	18	43.165	2.6	99.3	710.332	121.771
LAG_00986	clpB	994517	997120	2604	Chaperone protein ClpB	640	91	34.946	1.2	99	693.342	98.585
LAG_00987	NA	997280	997909	630	hypothetical protein	246	28	44.444	0.5	99.8	1101.546	125.379
LAG_00988	ywnA	997998	998438	441	Putative HTH-type transcriptional regulator YwnA	295	16	36.281	1.8	99.1	1887.086	102.35
LAG_00989	NA	998584	999114	531	hypothetical protein	239	32	60.264	8.3	100	1269.731	170.006
LAG_00990	tetA_1	999163	1E+06	1167	Tetracycline resistance protein, class B	256	40	34.276	1.7	99.9	618.839	96.694
LAG_00991	gshAB	1E+06	1E+06	2262	Glutathione biosynthesis bifunctional protein GshAB	429	70	30.946	2.4	98.4	535.024	87.3
LAG_00992	NA	1E+06	1E+06	447	hypothetical protein	78	6	13.423	38.9	75.8	492.261	37.866
LAG_00993	yxeM_2	1E+06	1E+06	849	putative amino-acid-binding protein YxeM	156	19	22.379	4	84.1	518.352	63.133
LAG_00994	nylA	1E+06	1E+06	1476	6-aminohexanoate-cyclic-dimer hydrolase	356	47	31.843	4.9	95.1	680.412	89.83
LAG_00995	yjaB_2	1E+06	1E+06	420	putative N-acetyltransferase YjaB	165	24	57.143	6.4	99	1108.263	161.202
LAG_00996	NA	1E+06	1E+06	576	hypothetical protein	163	23	39.931	4.2	99.8	798.313	112.645
LAG_00997	NA	1E+06	1E+06	201	hypothetical protein	93	9	44.776	9	95.5	1305.254	126.315
LAG_00998	mhqA_2	1E+06	1E+06	897	Putative ring-cleaving dioxygenase MhqA	241	33	36.789	1.2	99.3	757.937	103.784
LAG_00999	murK	1E+06	1E+06	894	N-acetylmuramic acid/N-acetylglucosamine kinase	158	27	30.201	1.2	99.4	498.572	85.199
LAG_01000	NA	1E+06	1E+06	1089	hypothetical protein	426	57	52.342	0.7	94.9	1103.545	147.657
LAG_01001	NA	1E+06	1E+06	336	hypothetical protein	165	21	62.5	0.9	100	1385.329	176.315
LAG_01002	licC_2	1E+06	1E+06	1308	Lichenan permease IIC component	430	53	40.52	2.6	99.6	927.404	114.308
LAG_01003	NA	1E+06	1E+06	678	hypothetical protein	85	15	22.124	1.6	87.6	353.669	62.412
LAG_01004	NA	1E+06	1E+06	1041	hypothetical protein	233	42	40.346	0.9	99.3	631.413	113.817
LAG_01005	NA	1E+06	1E+06	1233	hypothetical protein	250	35	28.386	13.1	92.9	571.986	80.078
LAG_01006	NA	1E+06	1E+06	1506	Fumarate reductase flavoprotein subunit	404	56	37.185	5.2	98.8	756.771	104.899
LAG_01007	NA	1E+06	1E+06	1161	hypothetical protein	137	21	18.088	1.6	99.9	332.887	51.026
LAG_01008	NA	1E+06	1E+06	336	hypothetical protein	168	20	59.524	1.2	100	1410.517	167.919
LAG_01009	uvrA_1	1E+06	1E+06	2202	UvrABC system protein A	681	94	42.688	0.2	97.8	872.445	120.426
LAG_01010	licT_1	1E+06	1E+06	864	Transcription antiterminator LicT	551	67	77.546	1	100	1799.062	218.761
LAG_01011	bglH_3	1E+06	1E+06	1455	Aryl-phospho-beta-D-glucosidase BglH	856	99	68.041	0.1	99.7	1659.66	191.947
LAG_01012	bglF_2	1E+06	1E+06	1818	PTS system beta-glucoside-specific EIIBCA component	1372	140	77.008	0.3	99.9	2128.965	217.241
LAG_01013	NA	1E+06	1E+06	348	hypothetical protein	94	16	45.977	1.1	90.2	762.003	129.703

LAG_01014	NA	1E+06	1E+06	675	hypothetical protein	301	37	54.815	6.5	99.7	1257.972	154.634
LAG_01015	rplL	1E+06	1E+06	366	50S ribosomal protein L7/L12	0	0	0			0	0
LAG_01016	rplJ	1E+06	1E+06	516	50S ribosomal protein L10	0	0	0			0	0
LAG_01017	ribU	1E+06	1E+06	585	Riboflavin transporter RibU	78	10	17.094	4.1	98.3	376.138	48.223
LAG_01018	nhaK_3	1E+06	1E+06	2058	Sodium, potassium, lithium and rubidium/H(+) antiporter	537	72	34.985	0.5	98.6	736.101	98.695
LAG_01019	NA	1E+06	1E+06	447	hypothetical protein	153	18	40.268	11.9	100	965.589	113.599
LAG_01020	NA	1E+06	1E+06	798	hypothetical protein	267	34	42.607	2.9	100	943.88	120.194
LAG_01021	icaA_1	1E+06	1E+06	1335	Poly-beta-1,6-N-acetyl-D-glucosamine synthase	467	56	41.948	1.9	98.8	986.833	118.335
LAG_01022	NA	1E+06	1E+06	531	hypothetical protein	94	15	28.249	8.5	94.9	499.392	79.69
LAG_01023	ycdT	1E+06	1E+06	1143	putative diguanylate cyclase YcdT	495	68	59.493	1	98.4	1221.707	167.831
LAG_01024	NA	1E+06	1E+06	837	hypothetical protein	323	42	50.179	0.2	99.4	1088.643	141.557
LAG_01025	yhfK	1E+06	1E+06	669	putative sugar epimerase YhfK	222	32	47.833	1.6	99.1	936.128	134.937
LAG_01026	guaC	1E+06	1E+06	990	GMP reductase	425	48	48.485	1.1	98.2	1211.05	136.777
LAG_01027	NA	1E+06	1E+06	636	hypothetical protein	259	36	56.604	6.4	96.5	1148.817	159.681
LAG_01028	yutF	1E+06	1E+06	780	Acid sugar phosphatase	125	26	33.333	12.2	91.4	452.089	94.034
LAG_01029	NA	1E+06	1E+06	762	hypothetical protein	152	24	31.496	0.1	96.9	562.726	88.851
LAG_01030	tadA_1	1E+06	1E+06	441	tRNA-specific adenosine deaminase	60	7	15.873	21.8	68.7	383.814	44.778
LAG_01031	NA	1E+06	1E+06	336	hypothetical protein	42	8	23.81	5.7	88.4	352.629	67.167
LAG_01032	cdr	1E+06	1E+06	1644	Coenzyme A disulfide reductase	469	52	31.63	6.1	98	804.784	89.23
LAG_01033	ygaP	1E+06	1E+06	285	Inner membrane protein YgaP	117	14	49.123	13	90.9	1158.109	138.577
LAG_01034	NA	1E+06	1E+06	138	hypothetical protein	36	5	36.232	2.9	61.6	735.922	102.211
LAG_01035	NA	1E+06	1E+06	207	hypothetical protein	83	10	48.309	4.3	100	1131.139	136.282
LAG_01036	licC_3	1E+06	1E+06	1482	Lichenan permease IIC component	389	51	34.413	5.8	99	740.474	97.08
LAG_01037	NA	1E+06	1E+06	1098	hypothetical protein	1674	63	57.377	0.6	97.4	4300.92	161.863
LAG_01038	licB_3	1E+06	1E+06	324	Lichenan-specific phosphotransferase enzyme IIB component	160	14	43.21	4.3	88.9	1393.103	121.897
LAG_01039	NA	1E+06	1E+06	1008	hypothetical protein	319	49	48.611	3.7	97.8	892.768	137.134
LAG_01040	NA	1E+06	1E+06	426	hypothetical protein	65	7	16.432	9.2	91.3	430.439	46.355
LAG_01041	pyrC	1E+06	1E+06	1266	Dihydroorotase	246	36	28.436	9.1	99.4	548.163	80.219
LAG_01042	pyrE	1E+06	1E+06	630	Orotate phosphoribosyltransferase	97	17	26.984	3.8	98.1	434.35	76.123
LAG_01043	yheS	1E+06	1E+06	1905	putative ABC transporter ATP-binding protein YheS	247	31	16.273	8.4	99.7	365.772	45.907
LAG_01044	ybbH_2	1E+06	1E+06	852	putative HTH-type transcriptional regulator YbbH	141	20	23.474	1.3	98.9	466.861	66.221
LAG_01045	bsaA	1E+06	1E+06	489	Glutathione peroxidase BsaA	85	12	24.54	1.8	95.7	490.364	69.228
LAG_01046	rsuA_1	1E+06	1E+06	705	Ribosomal small subunit pseudouridine synthase A	155	22	31.206	6.4	96.2	620.227	88.032
LAG_01047	NA	1E+06	1E+06	1362	Magnesium transporter MgtE	176	32	23.495	2.5	97.1	364.539	66.28
LAG_01048	NA	1E+06	1E+06	207	hypothetical protein	15	4	19.324	1.9	88.4	204.423	54.513
LAG_01049	yloB	1E+06	1E+06	2757	Calcium-transporting ATPase	586	86	31.193	1	99.5	599.61	87.997
LAG_01050	NA	1E+06	1E+06	582	hypothetical protein	46	9	15.464	2.1	90.2	222.968	43.624
LAG_01051	potD	1E+06	1E+06	1068	Spermidine/putrescine-binding periplasmic protein	720	55	51.498	4.1	99.4	1901.82	145.278
LAG_01052	ydcV	1E+06	1E+06	801	Inner membrane ABC transporter permease protein YdcV	344	40	49.938	0.7	99.4	1211.53	140.876
LAG_01053	potB	1E+06	1E+06	795	Spermidine/putrescine transport system permease protein PotB	217	27	33.962	2.4	96.5	770.018	95.809
LAG_01054	potA	1E+06	1E+06	1272	Spermidine/putrescine import ATP-binding protein PotA	307	39	30.66	0.4	96.9	680.863	86.494
LAG_01055	yfnB_1	1E+06	1E+06	903	Putative HAD-hydrolase YfnB	193	21	23.256	0.3	98.6	602.945	65.605
LAG_01056	murB	1E+06	1E+06	909	UDP-N-acetylenolpyruvoylglucosamine reductase	0	0	0			0	0
LAG_01057	rluD_2	1E+06	1E+06	906	Ribosomal large subunit pseudouridine synthase D	66	13	14.349	19.5	89.7	205.506	40.478
LAG_01058	lspA	1E+06	1E+06	540	Lipoprotein signal peptidase	87	15	27.778	0.2	92	454.5	78.362
LAG_01059	dapE_1	1E+06	1E+06	1215	putative succinyl-diaminopimelate desuccinylase	479	41	33.745	0.5	98.3	1112.161	95.195
LAG_01060	acpB	1E+06	1E+06	1494	Capsule synthesis positive regulator AcpB	421	53	35.475	1.9	99	794.95	100.077
LAG_01061	spxA_12	1E+06	1E+06	405	Regulatory protein Spx	128	17	41.975	1.2	93.8	891.586	118.414
LAG_01062	cpdA_1	1E+06	1E+06	879	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	222	31	35.267	2.4	98.2	712.479	99.49
LAG_01063	NA	1E+06	1E+06	342	hypothetical protein	17	5	14.62	6.1	82.5	140.227	41.243
LAG_01064	NA	1E+06	1E+06	1749	hypothetical protein	394	63	36.021	2.9	97	635.499	101.615
LAG_01065	yerB	1E+06	1E+06	1029	Putative lipoprotein YerB	166	18	17.493	2.9	97.8	455.094	49.348
LAG_01066	mtlD	1E+06	1E+06	1152	Mannitol-1-phosphate 5-dehydrogenase	182	32	27.778	5.3	76.7	445.684	78.362
LAG_01067	mtlF	1E+06	1E+06	432	Mannitol-specific phosphotransferase enzyme IIA component	104	16	37.037	4.4	99.3	679.138	104.483

LAG_01068	mtlR	1E+06	1E+06	1935	Transcriptional regulator MtlR	502	75	38.76	0.7	98.9	731.865	109.342
LAG_01069	mtlA	1E+06	1E+06	1830	PTS system mannitol-specific EIICB component	371	52	28.415	1	99.9	571.914	80.161
LAG_01070	NA	1E+06	1E+06	423	hypothetical protein	126	20	47.281	2.1	97.6	840.308	133.382
LAG_01071	pcp	1E+06	1E+06	642	Pyrrolidone-carboxylate peptidase	192	22	34.268	2.5	99.5	843.674	96.671
LAG_01072	NA	1E+06	1E+06	933	hypothetical protein	160	26	27.867	6	95.5	483.779	78.614
LAG_01073	NA	1E+06	1E+06	675	hypothetical protein	110	19	28.148	5.3	98.8	459.724	79.407
LAG_01074	NA	1E+06	1E+06	414	Organic hydroperoxide resistance protein-like protein	59	12	28.986	18.8	99.3	402.031	81.769
LAG_01075	sarZ	1E+06	1E+06	441	HTH-type transcriptional regulator SarZ	99	17	38.549	0.7	99.1	633.293	108.747
LAG_01076	hchA_2	1E+06	1E+06	693	Molecular chaperone Hsp31 and glyoxalase 3	171	26	37.518	2.7	98.6	696.099	105.84
LAG_01077	NA	1E+06	1E+06	363	hypothetical protein	137	19	52.342	1.4	94.8	1064.688	147.657
LAG_01078	ycnE	1E+06	1E+06	285	Putative monooxygenase YcnE	102	14	49.123	1.8	86.7	1009.633	138.577
LAG_01079	NA	1E+06	1E+06	1482	hypothetical protein	374	42	28.34	0.3	99.7	711.921	79.948
LAG_01080	ytrE	1E+06	1E+06	672	ABC transporter ATP-binding protein YtrE	237	33	49.107	2.1	99.4	994.918	138.533
LAG_01081	inlA	1E+06	1E+06	1761	Internalin-A	642	72	40.886	3.1	99.2	1028.452	115.34
LAG_01082	NA	1E+06	1E+06	834	hypothetical protein	450	52	62.35	10.2	99.6	1522.14	175.892
LAG_01083	lepA	1E+06	1E+06	1824	Elongation factor 4	230	27	14.803	1.6	99.7	355.722	41.759
LAG_01084	NA	1E+06	1E+06	1488	hypothetical protein	402	51	34.274	0.3	98.9	762.134	96.689
LAG_01085	NA	1E+06	1E+06	1890	hypothetical protein	295	32	16.931	0.8	97.4	440.32	47.764
LAG_01086	NA	1E+06	1E+06	324	hypothetical protein	41	10	30.864	10.5	86.1	356.983	87.069
LAG_01087	NA	1E+06	1E+06	1035	hypothetical protein	192	29	28.019	15.7	97.6	523.322	79.043
LAG_01088	NA	1E+06	1E+06	612	hypothetical protein	112	19	31.046	5.7	98.9	516.268	87.581
LAG_01089	aldC_2	1E+06	1E+06	681	Alpha-acetolactate decarboxylase	0	0	0			0	0
LAG_01090	NA	1E+06	1E+06	732	hypothetical protein	82	12	16.393	5.2	95.5	316.017	46.246
LAG_01091	murF_2	1E+06	1E+06	1350	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	0	0	0			0	0
LAG_01092	cobQ	1E+06	1E+06	792	Cobyric acid synthase	141	5	6.313	90.8	100	502.229	17.81
LAG_01093	NA	1E+06	1E+06	1593	hypothetical protein	384	48	30.132	1.1	96.9	680.023	85.003
LAG_01094	NA	1E+06	1E+06	2658	hypothetical protein	732	95	35.741	1.2	99.5	776.899	100.827
LAG_01095	NA	1E+06	1E+06	702	putative ABC transporter ATP-binding protein	119	24	34.188	3.4	88.2	478.209	96.446
LAG_01096	nadE	1E+06	1E+06	825	NH(3)-dependent NAD(+) synthetase	0	0	0			0	0
LAG_01097	wecD	1E+06	1E+06	489	dTDP-fucosamine acetyltransferase	95	13	26.585	2.5	87.7	548.054	74.997
LAG_01098	pncB2	1E+06	1E+06	1464	Nicotinate phosphoribosyltransferase pncB2	20	3	2.049	1.5	99.9	38.539	5.781
LAG_01099	nadD_1	1E+06	1E+06	588	putative nicotinate-nucleotide adenylyltransferase	13	2	3.401	92.9	100	62.37	9.595
LAG_01100	rnr_2	1E+06	1E+06	2001	Ribonuclease R	41	6	2.999	22.9	90.4	57.802	8.459
LAG_01101	mnmC	1E+06	1E+06	1113	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC	212	24	21.563	2.1	92.8	537.34	60.831
LAG_01102	NA	1E+06	1E+06	525	hypothetical protein	99	13	24.762	1.1	95.6	531.966	69.854
LAG_01103	NA	1E+06	1E+06	168	hypothetical protein	20	4	23.81	7.1	91.1	335.837	67.167
LAG_01104	obg	1E+06	1E+06	1314	GTPase Obg	0	0	0			0	0
LAG_01105	sbcC	1E+06	1E+06	3138	Nuclease SbcCD subunit C	450	60	19.12	0.2	94.7	404.546	53.939
LAG_01106	sbcD	1E+06	1E+06	1173	Nuclease SbcCD subunit D	85	15	12.788	0.9	81.2	204.423	36.075
LAG_01107	yycN	1E+06	1E+06	462	putative N-acetyltransferase YycN	89	11	23.81	1.5	95.2	543.446	67.167
LAG_01108	menA_2	1E+06	1E+06	942	1,4-dihydroxy-2-naphthoate octaprenyltransferase	178	29	30.786	0.4	96.9	533.062	86.847
LAG_01109	yoaB_1	1E+06	1E+06	2676	Calcium-transporting ATPase 1	327	52	19.432	7.8	95	344.723	54.818
LAG_01110	NA	1E+06	1E+06	342	hypothetical protein	37	6	17.544	5	77.2	305.2	49.492
LAG_01111	bglK_2	1E+06	1E+06	885	Beta-glucoside kinase	83	12	13.559	28.4	96.5	264.572	38.251
LAG_01112	gmuD_2	1E+06	1E+06	1380	6-phospho-beta-glucosidase GmuD	211	32	23.188	0.7	95.3	431.332	65.415
LAG_01113	hexR_1	1E+06	1E+06	798	HTH-type transcriptional regulator HexR	172	20	25.063	2.1	99.2	608.042	70.703
LAG_01114	mngB_2	1E+06	1E+06	2619	Mannosylglycerate hydrolase	598	74	28.255	1	96.3	644.131	79.708
LAG_01115	manP	1E+06	1E+06	453	PTS system mannose-specific EIIBCA component	124	16	35.32	1.3	98.7	772.203	99.639
LAG_01116	fruA_2	1E+06	1E+06	1494	PTS system fructose-specific EIIB'BC component	315	41	27.443	3.6	99.5	594.796	77.418
LAG_01117	glpF_2	1E+06	1E+06	738	Glycerol uptake facilitator protein	83	14	18.97	4.2	87.1	317.271	53.516
LAG_01118	glpO	1E+06	1E+06	1830	Alpha-glycerophosphate oxidase	345	43	23.497	0.6	97.8	531.834	66.287
LAG_01119	glpK_1	1E+06	1E+06	1497	Glycerol kinase	400	44	29.392	5.8	90.6	753.783	82.916
LAG_01120	NA	1E+06	1E+06	1683	hypothetical protein	380	51	30.303	1.8	98.5	636.954	85.486
LAG_01121	acpA	1E+06	1E+06	1467	Capsule synthesis positive regulator AcpA	504	63	42.945	2.8	98.4	969.189	121.149

LAG_01122	eriC	1E+06	1E+06	1212	Chloride/fluoride channel protein	353	40	33.003	0.2	98.5	821.638	93.103
LAG_01123	NA	1E+06	1E+06	240	hypothetical protein	11	1	4.167	5.8	5.8	129.297	11.754
LAG_01124	glyS	1E+06	1E+06	2034	Glycine--tRNA ligase beta subunit	23	1	0.492	99.4	99.4	31.9	1.387
LAG_01125	glyQ	1E+06	1E+06	969	Glycine--tRNA ligase alpha subunit	8	1	1.032	0.6	0.6	23.29	2.911
LAG_01126	focA	1E+06	1E+06	780	putative formate transporter 1	72	12	15.385	1.9	93.8	260.403	43.401
LAG_01127	aes	1E+06	1E+06	1023	Acetyl esterase	229	33	32.258	1.2	98.7	631.492	91.001
LAG_01128	NA	1E+06	1E+06	1023	hypothetical protein	275	33	32.258	2.9	99.2	758.342	91.001
LAG_01129	yigZ	1E+06	1E+06	624	IMPACT family member YigZ	228	33	52.885	4.5	100	1030.762	149.189
LAG_01130	comFA	1E+06	1E+06	1257	ComF operon protein 1	315	44	35.004	1.9	98.2	706.942	98.747
LAG_01131	NA	1E+06	1E+06	645	hypothetical protein	1870	21	32.558	3.6	99.7	8178.811	91.848
LAG_01132	dgkA	1E+06	1E+06	462	Undecaprenol kinase	1486	19	41.126	8.2	84.8	9073.714	116.017
LAG_01133	ybeY	1E+06	1E+06	489	Endoribonuclease YbeY	19	2	4.09	3.5	100	109.611	11.538
LAG_01134	nudC	1E+06	1E+06	474	NADH pyrophosphatase	63	8	16.878	9.9	78.9	374.948	47.612
LAG_01135	NA	1E+06	1E+06	960	PhoH-like protein	163	28	29.167	0.3	95.6	478.988	82.28
LAG_01136	ald1_1	1E+06	1E+06	1107	Alanine dehydrogenase 1	276	38	34.327	0.5	97.9	703.347	96.838
LAG_01137	NA	1E+06	1E+06	282	hypothetical protein	51	9	31.915	11	98.6	510.187	90.033
LAG_01138	rpmA	1E+06	1E+06	285	50S ribosomal protein L27	0	0	0			0	0
LAG_01139	NA	1E+06	1E+06	345	hypothetical protein	0	0	0			0	0
LAG_01140	rplU	1E+06	1E+06	315	50S ribosomal protein L21	0	0	0			0	0
LAG_01141	dagK_2	1E+06	1E+06	909	Diacylglycerol kinase	132	21	23.102	1.8	92.4	409.655	65.172
LAG_01142	NA	1E+06	1E+06	1179	hypothetical protein	295	33	27.99	12.9	98.9	705.857	78.96
LAG_01143	NA	1E+06	1E+06	378	hypothetical protein	6	2	5.291	46.3	50.8	44.778	14.926
LAG_01144	NA	1E+06	1E+06	1299	hypothetical protein	217	18	13.857	2.2	74.1	471.258	39.091
LAG_01145	NA	1E+06	1E+06	813	Putative phosphatase	93	14	17.22	17.2	80.6	322.701	48.579
LAG_01146	NA	1E+06	1E+06	369	hypothetical protein	51	6	16.26	11.9	91.1	389.899	45.87
LAG_01147	moeZ	1E+06	1E+06	1014	putative adenylyltransferase/sulfurtransferase MoeZ	152	18	17.751	0.5	97.7	422.877	50.078
LAG_01148	NA	1E+06	1E+06	459	hypothetical protein	20	5	10.893	34	99.3	122.921	30.73
LAG_01149	NA	1E+06	1E+06	603	hypothetical protein	85	11	18.242	1.8	67.2	397.658	51.462
LAG_01150	cat3	1E+06	1E+06	645	Chloramphenicol acetyltransferase 3	184	23	35.659	0.8	97.5	804.76	100.595
LAG_01151	cpdA_2	1E+06	1E+06	879	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	125	20	22.753	1.9	96.2	401.171	64.187
LAG_01152	NA	1E+06	1E+06	531	hypothetical protein	6	2	3.766	85.1	94.4	31.876	10.625
LAG_01153	NA	1E+06	1E+06	1641	hypothetical protein	489	58	35.344	0.2	99.7	840.637	99.707
LAG_01154	natA_2	1E+06	1E+06	879	ABC transporter ATP-binding protein NatA	175	32	36.405	4.7	98.3	561.639	102.7
LAG_01155	bm3R1	1E+06	1E+06	567	HTH-type transcriptional repressor Bm3R1	85	15	26.455	0.4	95.9	422.906	74.631
LAG_01156	whiA	1E+06	1E+06	921	Putative sporulation transcription regulator WhiA	114	19	20.63	7.7	98.9	349.183	58.197
LAG_01157	NA	1E+06	1E+06	987	Putative gluconeogenesis factor	0	0	0			0	0
LAG_01158	yvcJ	1E+06	1E+06	891	Nucleotide-binding protein YvcJ	8	2	2.245	7.5	44.3	25.329	6.332
LAG_01159	clsA_1	1E+06	1E+06	1446	Major cardiolipin synthase ClsA	308	36	24.896	0.6	97.9	600.884	70.233
LAG_01160	ettA_1	1E+06	1E+06	1494	Energy-dependent translational throttle protein EttA	204	36	24.096	3.7	98	385.201	67.977
LAG_01161	NA	1E+06	1E+06	162	hypothetical protein	11	3	18.519	1.2	21.6	191.552	52.241
LAG_01162	yvbW_1	1E+06	1E+06	1335	putative amino acid permease YvbW	323	42	31.461	0.4	97.2	682.542	88.752
LAG_01163	NA	1E+06	1E+06	810	Putative phosphatase	145	19	23.457	16.5	99.1	505	66.172
LAG_01164	ccpB	1E+06	1E+06	924	Catabolite control protein B	164	22	23.81	2.4	97.3	500.703	67.167
LAG_01165	NA	1E+06	1E+06	774	hypothetical protein	140	18	23.256	5.3	98.4	510.264	65.605
LAG_01166	NA	1E+06	1E+06	1794	DegV domain-containing protein	348	43	23.969	2.5	99.7	547.224	67.617
LAG_01167	NA	1E+06	1E+06	414	hypothetical protein	144	19	45.894	1.4	96.4	981.229	129.468
LAG_01168	NA	1E+06	1E+06	1158	hypothetical protein	382	42	36.269	0.3	96.6	930.6	102.317
LAG_01169	NA	1E+06	1E+06	513	Stress response regulator gls24	24	5	9.747	4.1	65.9	131.978	27.495
LAG_01170	NA	1E+06	1E+06	186	hypothetical protein	88	7	37.634	1.6	81.7	1334.683	106.168
LAG_01171	NA	1E+06	1E+06	558	hypothetical protein	73	9	16.129	3.9	95.5	369.06	45.501
LAG_01172	NA	1E+06	1E+06	243	hypothetical protein	29	4	16.461	53.1	95.9	336.667	46.437
LAG_01173	NA	1E+06	1E+06	546	hypothetical protein	48	10	18.315	4.4	92.7	248.003	51.667
LAG_01174	tarF_2	1E+06	1E+06	285	Teichoic acid glycerol-phosphate transferase	62	4	14.035	36.1	94.7	613.699	39.593
LAG_01175	mnmG	1E+06	1E+06	1875	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	25	6	3.2	5.1	88.5	37.614	9.027

LAG_01176	NA	1E+06	1E+06	549	hypothetical protein	13	1	1.821	92.2	92.2	66.8	5.138
LAG_01177	NA	1E+06	1E+06	372	hypothetical protein	34	6	16.129	2.7	37.6	257.836	45.501
LAG_01178	mrnC	1E+06	1E+06	402	Mini-ribonuclease 3	20	4	9.95	5.2	78.9	140.35	28.07
LAG_01179	cysS	1E+06	1E+06	1353	Cysteine--tRNA ligase	4	1	0.739	99.6	99.6	8.34	2.085
LAG_01180	cysE	1E+06	1E+06	606	Serine acetyltransferase	6	1	1.65	35	35	27.931	4.655
LAG_01181	pnp_2	1E+06	1E+06	2280	Polyribonucleotide nucleotidyltransferase	364	39	17.105	0.9	97.9	450.376	48.255
LAG_01182	fecE	1E+06	1E+06	777	Fe(3+) dicitrate transport ATP-binding protein FecE	101	11	14.157	44.3	98.5	366.698	39.937
LAG_01183	yfhA_2	1E+06	1E+06	975	putative siderophore transport system permease protein YfhA	224	25	25.641	3.4	94.9	648.114	72.334
LAG_01184	hmuT	1E+06	1E+06	942	Hemin-binding periplasmic protein HmuT	201	23	24.416	7.6	97.9	601.94	68.879
LAG_01185	prs2	1E+06	1E+06	966	Ribose-phosphate pyrophosphokinase 2	8	2	2.07	95.2	99.6	23.363	5.841
LAG_01186	NA	1E+06	1E+06	351	hypothetical protein	79	12	34.188	3.1	85.5	634.933	96.446
LAG_01187	iscS_2	1E+06	1E+06	1062	Cysteine desulfurase IscS	33	4	3.766	95.6	99.8	87.659	10.625
LAG_01188	NA	1E+06	1E+06	345	hypothetical protein	49	6	17.391	1.2	88.4	400.669	49.061
LAG_01189	tuf	1E+06	1E+06	1188	Elongation factor Tu	0	0	0			0	0
LAG_01190	NA	1E+06	1E+06	183	hypothetical protein	80	7	38.251	15.8	94.5	1233.239	107.908
LAG_01191	NA	1E+06	1E+06	117	hypothetical protein	5	1	8.547	73.5	73.5	120.557	24.111
LAG_01192	ileS	1E+06	1E+06	2787	Isoleucine--tRNA ligase	0	0	0			0	0
LAG_01193	divIVA	1E+06	1E+06	852	Cell division protein DivIVA	3	1	1.174	19.6	19.6	9.933	3.311
LAG_01194	NA	1E+06	1E+06	798	hypothetical protein	25	4	5.013	44.4	76.2	88.378	14.141
LAG_01195	NA	1E+06	1E+06	246	hypothetical protein	4	1	4.065	53.3	53.3	45.87	11.468
LAG_01196	sepF	1E+06	1E+06	573	Cell division protein SepF	9	2	3.49	40.1	51	44.309	9.847
LAG_01197	NA	1E+06	1E+06	672	hypothetical protein	10	1	1.488	96.9	96.9	41.98	4.198
LAG_01198	ftsZ	1E+06	1E+06	1275	Cell division protein FtsZ	0	0	0			0	0
LAG_01199	ftsA	1E+06	1E+06	1362	Cell division protein FtsA	0	0	0			0	0
LAG_01200	NA	1E+06	1E+06	873	DegV domain-containing protein	52	8	9.164	2.5	87.6	168.034	25.851
LAG_01201	NA	1E+06	1E+06	729	Putative TrmH family tRNA/rRNA methyltransferase	48	7	9.602	1.4	77.4	185.747	27.088
LAG_01202	pepC	1E+06	1E+06	1311	Aminopeptidase C	125	23	17.544	0.9	95	268.977	49.492
LAG_01203	mtnN	1E+06	1E+06	681	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	48	8	11.747	6.6	55.2	198.839	33.14
LAG_01204	NA	1E+06	1E+06	279	hypothetical protein	12	3	10.753	28	83.9	121.335	30.334
LAG_01205	act	1E+06	1E+06	585	Methanol dehydrogenase activator	13	3	5.128	4.4	74.2	62.69	14.467
LAG_01206	glmU	1E+06	1E+06	1377	Bifunctional protein GlmU	0	0	0			0	0
LAG_01207	proC	1E+06	1E+06	792	Pyrroline-5-carboxylate reductase	60	8	10.101	24.1	90	213.715	28.495
LAG_01208	rpsO	1E+06	1E+06	270	30S ribosomal protein S15	8	1	3.704	26.7	26.7	83.586	10.448
LAG_01209	stkP	1E+06	1E+06	1959	Serine/threonine-protein kinase StkP	52	11	5.615	7.4	98.7	74.882	15.84
LAG_01210	NA	1E+06	1E+06	774	Putative protein phosphatase 2C-type	26	5	6.46	1.4	92.5	94.763	18.224
LAG_01211	rsmB	1E+06	1E+06	1272	Ribosomal RNA small subunit methyltransferase B	88	16	12.579	11.6	99.1	195.166	35.485
LAG_01212	fmt	1E+06	1E+06	930	Methionyl-tRNA formyltransferase	0	0	0			0	0
LAG_01213	NA	1E+06	1E+06	480	hypothetical protein	45	6	12.5	6.5	75.6	264.472	35.263
LAG_01214	yvdD	1E+06	1E+06	555	LOG family protein YvdD	57	7	12.613	19.5	90.5	289.728	35.581
LAG_01215	NA	1E+06	1E+06	657	Deoxyguanosine kinase	55	10	15.221	2	88.1	236.16	42.938
LAG_01216	priA	1E+06	1E+06	2328	Primosomal protein N'	64	14	6.014	0.9	92	77.554	16.965
LAG_01217	rpoZ	1E+06	1E+06	360	DNA-directed RNA polymerase subunit omega	5	1	2.778	96.9	96.9	39.181	7.836
LAG_01218	gmk	1E+06	1E+06	630	Guanylate kinase	0	0	0			0	0
LAG_01219	rny_2	1E+06	1E+06	1617	Ribonuclease Y	18	6	3.711	54.4	99.6	31.403	10.468
LAG_01220	metK	1E+06	1E+06	1194	S-adenosylmethionine synthase	0	0	0			0	0
LAG_01221	birA	1E+06	1E+06	750	Bifunctional ligase/repressor BirA	0	0	0			0	0
LAG_01222	NA	1E+06	1E+06	360	hypothetical protein	8	2	5.556	81.7	89.4	62.69	15.672
LAG_01223	NA	1E+06	1E+06	201	hypothetical protein	4	1	4.975	78.6	78.6	56.14	14.035
LAG_01224	NA	1E+06	1E+06	1089	hypothetical protein	25	4	3.673	46.6	99.7	64.762	10.362
LAG_01225	NA	1E+06	1E+06	1596	N-acetylmuramoyl-L-alanine amidase domain-containing protein	197	33	20.677	2.6	97	348.21	58.33
LAG_01226	ydjP	1E+06	1E+06	732	AB hydrolase superfamily protein YdjP	89	14	19.126	0.5	88	342.995	53.954
LAG_01227	bglH_4	1E+06	1E+06	1437	Aryl-phospho-beta-D-glucosidase BglH	230	31	21.573	0.4	95.6	451.522	60.857
LAG_01228	bglH_5	1E+06	1E+06	1446	Aryl-phospho-beta-D-glucosidase BglH	207	32	22.13	0.4	98.8	403.841	62.43
LAG_01229	bglF_3	1E+06	1E+06	1926	PTS system beta-glucoside-specific EIIBCA component	372	44	22.845	0.3	98.7	544.873	64.447

LAG_01230	licT_2	1E+06	1E+06	840	Transcription antiterminator LicT	160	14	16.667	3.1	86.1	537.34	47.017
LAG_01231	NA	1E+06	1E+06	492	hypothetical protein	81	15	30.488	4.1	95.5	464.438	86.007
LAG_01232	fba_1	1E+06	1E+06	897	Fructose-bisphosphate aldolase	0	0	0			0	0
LAG_01233	thrS	1E+06	1E+06	1941	Threonine--tRNA ligase	0	0	0			0	0
LAG_01234	NA	1E+06	1E+06	10509	hypothetical protein	733	105	9.991	1.8	99.9	196.766	28.186
LAG_01235	hemH	1E+06	1E+06	948	Ferrochelatase	83	19	20.042	9.2	95.9	246.989	56.54
LAG_01236	NA	1E+06	1E+06	7776	hypothetical protein	491	80	10.288	0.2	97.5	178.129	29.023
LAG_01237	NA	1E+06	1E+06	378	hypothetical protein	71	8	21.164	6.6	83.3	529.877	59.704
LAG_01238	NA	1E+06	1E+06	609	hypothetical protein	81	15	24.631	6.7	93.6	375.211	69.484
LAG_01239	upp	1E+06	1E+06	630	Uracil phosphoribosyltransferase	149	14	22.222	0.6	85.2	667.197	62.69
LAG_01240	napA	1E+06	1E+06	1128	Na(+)/H(+) antiporter	158	24	21.277	1.3	98.6	395.145	60.022
LAG_01241	NA	1E+06	1E+06	870	hypothetical protein	125	15	17.241	8.6	99.7	405.321	48.639
LAG_01242	yhaM	1E+06	1E+06	945	3'-5' exoribonuclease YhaM	126	13	13.757	2.5	89.7	376.138	38.808
LAG_01243	NA	1E+06	1E+06	1287	hypothetical protein	56	7	5.439	5.1	98.7	122.749	15.344
LAG_01244	rpe	1E+06	1E+06	660	Ribulose-phosphate 3-epimerase	0	0	0			0	0
LAG_01245	NA	1E+06	1E+06	207	hypothetical protein	4	1	4.831	17.4	17.4	54.513	13.628
LAG_01246	rsgA_2	1E+06	1E+06	882	Small ribosomal subunit biogenesis GTPase RsgA	8	1	1.134	96	96	25.588	3.198
LAG_01247	NA	1E+06	1E+06	495	hypothetical protein	39	8	16.162	38.8	99.8	222.263	45.592
LAG_01248	NA	1E+06	1E+06	207	hypothetical protein	28	3	14.493	36.2	99.5	381.589	40.885
LAG_01249	NA	1E+06	1E+06	774	hypothetical protein	99	14	18.088	5.2	99.2	360.83	51.026
LAG_01250	NA	1E+06	1E+06	195	hypothetical protein	22	3	15.385	4.6	70.3	318.27	43.401
LAG_01251	yocH	1E+06	1E+06	1032	Cell wall-binding protein YocH	110	22	21.318	2.7	98.4	300.692	60.138
LAG_01252	pheT_2	1E+06	1E+06	2409	Phenylalanine--tRNA ligase beta subunit	5	1	0.415	0.7	0.7	5.855	1.171
LAG_01253	pheS	1E+06	1E+06	1041	Phenylalanine--tRNA ligase alpha subunit	0	0	0			0	0
LAG_01254	NA	1E+06	1E+06	216	hypothetical protein	32	4	18.519	28.7	95.8	417.931	52.241
LAG_01255	purA	1E+06	1E+06	1290	Adenylosuccinate synthetase	91	14	10.853	29.7	99.8	199.003	30.616
LAG_01256	hslO	1E+06	1E+06	885	33 kDa chaperonin	56	9	10.169	7.1	90.8	178.506	28.688
LAG_01257	clcA	1E+06	1E+06	1545	H(+)/Cl(-) exchange transporter ClcA	186	23	14.887	0.3	97.5	339.62	41.996
LAG_01258	dus	1E+06	1E+06	996	putative tRNA-dihydrouridine synthase	113	12	12.048	1	100	320.057	33.988
LAG_01259	NA	1E+06	1E+06	243	hypothetical protein	25	6	24.691	1.6	96.3	290.23	69.655
LAG_01260	NA	1E+06	1E+06	882	hypothetical protein	173	23	26.077	5.4	99.4	553.332	73.564
LAG_01261	NA	1E+06	1E+06	864	hypothetical protein	58	11	12.731	20.1	83.8	189.375	35.916
LAG_01262	aspS	1E+06	1E+06	1749	Aspartate--tRNA ligase	0	0	0			0	0
LAG_01263	hisS	1E+06	1E+06	1284	Histidine--tRNA ligase	0	0	0			0	0
LAG_01264	pgsA	1E+06	1E+06	552	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	0	0	0			0	0
LAG_01265	NA	1E+06	1E+06	909	hypothetical protein	145	15	16.502	0.1	96.3	450	46.552
LAG_01266	albF	1E+06	1E+06	1284	Putative zinc protease AlbF	79	14	10.903	2.9	74.1	173.568	30.759
LAG_01267	albE	1E+06	1E+06	1245	Antilisterial bacteriocin subtilosin biosynthesis protein AlbE	276	21	16.867	0.4	99.7	625.386	47.584
LAG_01268	NA	1E+06	1E+06	363	hypothetical protein	4	1	2.755	6.9	6.9	31.086	7.771
LAG_01269	recF	1E+06	1E+06	1095	DNA replication and repair protein RecF	36	7	6.393	17.7	94.6	92.746	18.034
LAG_01270	NA	1E+06	1E+06	222	hypothetical protein	24	3	13.514	4.1	93.2	304.977	38.122
LAG_01271	arcD1_2	1E+06	1E+06	1461	Arginine/ornithine antiporter ArcD1	106	16	10.951	20.3	95.8	204.675	30.894
LAG_01272	galE	1E+06	1E+06	984	UDP-glucose 4-epimerase	3	1	1.016	0.3	0.3	8.601	2.867
LAG_01273	galT_1	1E+06	1E+06	1479	Galactose-1-phosphate uridylyltransferase	72	13	8.79	9.9	94.7	137.332	24.796
LAG_01274	galK_2	1E+06	1E+06	1200	Galactokinase	318	25	20.833	4.8	97.6	747.574	58.772
LAG_01275	galM	1E+06	1E+06	1029	Aldose 1-epimerase	49	10	9.718	1.1	81.2	134.335	27.415
LAG_01276	lacS	1E+06	1E+06	1398	Lactose permease	180	20	14.306	5.4	98.5	363.223	40.358
LAG_01277	hexR_2	1E+06	1E+06	738	HTH-type transcriptional regulator HexR	109	22	29.81	0.3	99.3	416.657	84.096
LAG_01278	nadR	1E+06	1E+06	873	Trifunctional NAD biosynthesis/regulator protein NadR	77	15	17.182	2.6	95.9	248.82	48.471
LAG_01279	ydcP_1	1E+06	1E+06	1290	putative protease YdcP	202	30	23.256	4.1	98.2	441.743	65.605
LAG_01280	NA	1E+06	1E+06	939	2-haloacrylate reductase	138	16	17.039	5.6	99.5	414.593	48.069
LAG_01281	ydcP_2	1E+06	1E+06	924	putative protease YdcP	90	15	16.234	0.8	75.3	274.776	45.796
LAG_01282	NA	1E+06	1E+06	279	hypothetical protein	16	3	10.753	6.1	87.5	161.78	30.334
LAG_01283	rlmA	1E+06	1E+06	822	23S rRNA (guanine(745)-N(1))-methyltransferase	134	23	27.981	3.6	99.5	459.877	78.934

LAG_01284	NA	1E+06	1E+06	627	CutC-like protein	98	12	19.139	12	95.5	440.927	53.991
LAG_01285	NA	1E+06	1E+06	1026	hypothetical protein	157	21	20.468	7.9	93.4	431.679	57.74
LAG_01286	ecsA	1E+06	1E+06	741	ABC-type transporter ATP-binding protein EcsA	162	26	35.088	0.7	99.2	616.744	98.984
LAG_01287	NA	1E+06	1E+06	846	hypothetical protein	136	17	20.095	8.2	90.5	453.499	56.687
LAG_01288	gph_2	1E+06	1E+06	642	Phosphoglycolate phosphatase	24	5	7.788	21.8	79	105.459	21.971
LAG_01289	inlJ_2	1E+06	1E+06	1749	Internalin-J	308	50	28.588	0.2	99.5	496.786	80.647
LAG_01290	NA	1E+06	1E+06	396	putative HIT-like protein	181	17	42.929	3.3	90.7	1289.412	121.105
LAG_01291	NA	1E+06	1E+06	228	hypothetical protein	72	7	30.702	1.8	57	890.853	86.611
LAG_01292	NA	1E+06	1E+06	357	hypothetical protein	21	4	11.204	19.3	50.1	165.943	31.608
LAG_01293	rplA	1E+06	1E+06	690	50S ribosomal protein L1	7	1	1.449	99.1	99.1	28.619	4.088
LAG_01294	rplK	1E+06	1E+06	480	50S ribosomal protein L11	0	0	0			0	0
LAG_01295	macB_1	1E+06	1E+06	630	Macrolide export ATP-binding/permease protein MacB	86	13	20.635	3.2	88.7	385.093	58.212
LAG_01296	NA	1E+06	1E+06	2073	hypothetical protein	349	53	25.567	2.1	99.2	474.935	72.125
LAG_01297	NA	1E+06	1E+06	399	hypothetical protein	90	6	15.038	39.8	90.2	636.323	42.422
LAG_01298	gloA	1E+06	1E+06	372	Lactoylglutathione lyase	49	6	16.129	7	89.2	371.588	45.501
LAG_01299	NA	1E+06	1E+06	216	hypothetical protein	4	1	4.63	53.7	53.7	52.241	13.06
LAG_01300	msrA	1E+06	1E+06	516	Peptide methionine sulfoxide reductase MsrA	111	10	19.38	10.9	95.9	606.85	54.671
LAG_01301	cvfB	1E+06	1E+06	861	Conserved virulence factor B	44	10	11.614	14.6	95	144.164	32.765
LAG_01302	frr	1E+06	1E+06	558	Ribosome-recycling factor	0	0	0			0	0
LAG_01303	pyrH	1E+06	1E+06	717	Uridylate kinase	0	0	0			0	0
LAG_01304	ackA_1	1E+06	1E+06	1194	Acetate kinase	93	19	15.913	4.4	98.5	219.729	44.891
LAG_01305	ackA_2	1E+06	1E+06	1194	Acetate kinase	163	20	16.75	0.2	94.3	385.116	47.253
LAG_01306	NA	1E+06	1E+06	936	hypothetical protein	40	6	6.41	4.1	98.9	120.557	18.084
LAG_01307	NA	1E+06	1E+06	231	hypothetical protein	11	2	8.658	35.1	59.3	134.335	24.425
LAG_01308	typA	1E+06	1E+06	1842	GTP-binding protein TypA/BipA	17	5	2.714	22.7	79.6	26.036	7.658
LAG_01309	NA	1E+06	1E+06	213	hypothetical protein	29	2	9.39	0.9	20.7	384.084	26.489
LAG_01310	glcK	1E+06	1E+06	966	Glucokinase	86	11	11.387	14.8	89	251.148	32.124
LAG_01311	glpE_2	1E+06	1E+06	381	Thiosulfate sulfurtransferase GlpE	0	0	0			0	0
LAG_01312	dps	1E+06	1E+06	447	DNA protection during starvation protein	13	2	4.474	60.6	79.2	82.043	12.622
LAG_01313	comC	1E+06	1E+06	651	Type 4 prepilin-like proteins leader peptide-processing enzyme	86	17	26.114	12.4	87.7	372.671	73.668
LAG_01314	dinB_2	1E+06	1E+06	1098	DNA polymerase IV	142	21	19.126	4.6	98.3	364.833	53.954
LAG_01315	murC	1E+06	1E+06	1332	UDP-N-acetylmuramate--L-alanine ligase	4	1	0.751	100	100	8.472	2.118
LAG_01316	NA	1E+06	1E+06	630	hypothetical protein	0	0	0			0	0
LAG_01317	rapA	1E+06	1E+06	3111	RNA polymerase-associated protein RapA	278	45	14.465	0.2	92.7	252.089	40.806
LAG_01318	yvbW_2	1E+06	1E+06	1341	putative amino acid permease YvbW	161	25	18.643	1.6	99.4	338.692	52.592
LAG_01319	pbpX_2	1E+06	1E+06	945	Putative penicillin-binding protein PbpX	108	11	11.64	28.3	90.4	322.404	32.837
LAG_01320	NA	1E+06	1E+06	777	hypothetical protein	37	6	7.722	30.5	99.5	134.335	21.784
LAG_01321	NA	1E+06	1E+06	789	hypothetical protein	44	8	10.139	5.3	95.8	157.32	28.604
LAG_01322	thiT	1E+06	1E+06	537	Thiamine transporter ThiT	58	9	16.76	6.5	90.7	304.693	47.28
LAG_01323	ybaK	1E+06	1E+06	480	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase YbaK	166	16	33.333	2.7	98.1	975.607	94.034
LAG_01324	NA	1E+06	1E+06	357	hypothetical protein	84	10	28.011	15.7	93.8	663.773	79.021
LAG_01325	NA	1E+06	1E+06	216	hypothetical protein	31	5	23.148	2.3	68.1	404.871	65.302
LAG_01326	murA1	1E+06	1E+06	1266	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	140	20	15.798	4.3	97.8	311.963	44.566
LAG_01327	NA	1E+06	1E+06	720	hypothetical protein	120	19	26.389	14.3	90.6	470.172	74.444
LAG_01328	NA	1E+06	1E+06	2094	putative ABC transporter ATP-binding protein	452	50	23.878	0.4	99.4	608.934	67.36
LAG_01329	NA	1E+06	1E+06	1734	putative ABC transporter ATP-binding protein	278	31	17.878	0.2	90.7	452.276	50.434
LAG_01330	fieF_1	1E+06	1E+06	1215	Ferrous-iron efflux pump FieF	161	14	11.523	0.3	86.1	373.816	32.506
LAG_01331	zitR_2	1E+06	1E+06	459	Transcriptional regulator ZitR	45	4	8.715	19.8	78.2	276.572	24.584
LAG_01332	tetA_2	1E+06	1E+06	1194	Tetracycline resistance protein, class C	237	36	30.151	1.6	96.7	559.954	85.056
LAG_01333	folT	1E+06	1E+06	540	Folate transporter FolT	113	11	20.37	5.4	75.9	590.327	57.465
LAG_01334	pepN	1E+06	1E+06	2541	Aminopeptidase N	259	37	14.561	2.5	89.7	287.543	41.078
LAG_01335	NA	1E+06	1E+06	801	hypothetical protein	113	14	17.478	1.9	96.1	397.974	49.306
LAG_01336	NA	1E+06	1E+06	477	hypothetical protein	40	6	12.579	33.1	98.3	236.565	35.485
LAG_01337	tsaD	1E+06	1E+06	1020	tRNA N6-adenosine threonylcarbamoyltransferase	0	0	0			0	0

LAG_01338	rimI_1	1E+06	1E+06	435	Ribosomal-protein-alanine acetyltransferase	17	5	11.494	34	93.1	110.247	32.426
LAG_01339	rimI_2	1E+06	1E+06	567	N-alpha-acetyltransferase RimI	21	5	8.818	13.6	91.9	104.483	24.877
LAG_01340	tsaB	1E+06	1E+06	711	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB	0	0	0			0	0
LAG_01341	NA	1E+06	1E+06	306	hypothetical protein	3	1	3.268	6.5	6.5	27.657	9.219
LAG_01342	rnj1	1E+06	1E+06	1707	Ribonuclease J 1	0	0	0			0	0
LAG_01343	NA	1E+06	1E+06	462	hypothetical protein	159	15	32.468	2.6	97.2	970.875	91.592
LAG_01344	add	1E+06	1E+06	1050	Adenosine deaminase	268	33	31.429	10.3	99.6	720.035	88.661
LAG_01345	NA	1E+06	1E+06	798	hypothetical protein	118	20	25.063	2.4	96.6	417.145	70.703
LAG_01346	NA	1E+06	1E+06	2796	hypothetical protein	513	74	26.466	3.1	99.7	517.593	74.663
LAG_01347	NA	1E+06	1E+06	798	hypothetical protein	210	31	38.847	2.4	99.9	742.377	109.589
LAG_01348	NA	1E+06	1E+06	804	hypothetical protein	86	12	14.925	1.6	89.3	301.752	42.105
LAG_01349	NA	1E+06	1E+06	426	Protein SprT-like protein	117	11	25.822	44.4	92.3	774.791	72.844
LAG_01350	rps1	1E+06	1E+06	2133	30S ribosomal protein S1	218	34	15.94	0.3	98.6	288.319	44.967
LAG_01351	NA	1E+06	1E+06	612	Putative NAD(P)H nitroreductase	94	12	19.608	11.9	97.4	433.296	55.314
LAG_01352	rpsD	1E+06	1E+06	612	30S ribosomal protein S4	0	0	0			0	0
LAG_01353	steT_1	1E+06	1E+06	1356	Serine/threonine exchanger SteT	146	21	15.487	5.5	99.6	303.74	43.689
LAG_01354	NA	1E+06	1E+06	450	hypothetical protein	154	13	28.889	2.4	97.3	965.42	81.497
LAG_01355	yknY	1E+06	1E+06	486	putative ABC transporter ATP-binding protein YknY	103	14	28.807	5.1	88.3	597.873	81.264
LAG_01356	NA	1E+06	1E+06	2037	hypothetical protein	515	62	30.437	1.6	99.4	713.222	85.864
LAG_01357	NA	1E+06	1E+06	76	tRNA-Pro	0	0	0			0	0
LAG_01358	NA	1E+06	1E+06	74	tRNA-Arg	0	0	0			0	0
LAG_01359	ecfT	1E+06	1E+06	804	Energy-coupling factor transporter transmembrane protein EcfT	0	0	0			0	0
LAG_01360	ecfA2	1E+06	1E+06	846	Energy-coupling factor transporter ATP-binding protein EcfA2	0	0	0			0	0
LAG_01361	ecfA1	1E+06	1E+06	834	Energy-coupling factor transporter ATP-binding protein EcfA1	0	0	0			0	0
LAG_01362	NA	1E+06	1E+06	495	hypothetical protein	54	7	14.141	19	99.6	307.749	39.893
LAG_01363	nrdG	1E+06	1E+06	600	Anaerobic ribonucleoside-triphosphate reductase-activating protein	74	8	13.333	4.3	92	347.927	37.614
LAG_01364	ycaM	1E+06	1E+06	1446	Inner membrane transporter YcaM	189	25	17.289	15.5	99.8	368.724	48.773
LAG_01365	nrdD	1E+06	1E+06	2241	Anaerobic ribonucleoside-triphosphate reductase	139	23	10.263	0.4	95.1	174.977	28.953
LAG_01366	pncA	1E+06	1E+06	513	Nicotinamidase/pyrazinamidase	123	9	17.544	2.3	98.8	676.388	49.492
LAG_01367	steT_2	1E+06	1E+06	1362	Serine/threonine exchanger SteT	125	14	10.279	0.8	93	258.905	28.997
LAG_01368	NA	1E+06	1E+06	954	putative epimerase/dehydratase	76	12	12.579	1.4	87.7	224.736	35.485
LAG_01369	NA	1E+06	1E+06	1191	Putative pyridoxal phosphate-dependent acyltransferase	28	6	5.038	15	69.7	66.322	14.212
LAG_01370	tdcB	1E+06	1E+06	1008	L-threonine dehydratase catabolic TdcB	54	11	10.913	5	98.7	151.127	30.785
LAG_01371	ald1_2	1E+06	1E+06	1095	Alanine dehydrogenase 1	71	15	13.699	6.8	98.2	182.916	38.644
LAG_01372	yvgN_1	1E+06	1E+06	846	Glyoxal reductase	73	11	13.002	0.5	77.4	243.423	36.68
LAG_01373	luxS	1E+06	1E+06	480	S-ribosylhomocysteine lyase	24	4	8.333	0.8	93.8	141.052	23.509
LAG_01374	NA	1E+06	1E+06	150	hypothetical protein	3	1	6.667	72	72	56.421	18.807
LAG_01375	yhhX_1	1E+06	1E+06	1014	putative oxidoreductase YhhX	188	20	19.724	1.4	97.7	523.032	55.642
LAG_01376	opuBA	1E+06	1E+06	843	Choline transport ATP-binding protein OpuBA	51	12	14.235	1.2	88.8	170.668	40.157
LAG_01377	opuCB	1E+06	1E+06	1503	Carnitine transport permease protein OpuCB	336	43	28.609	1.4	91.3	630.65	80.708
LAG_01378	NA	1E+06	1E+06	1269	Putative thiazole biosynthetic enzyme	189	25	19.701	10.5	96.8	420.154	55.576
LAG_01379	NA	1E+06	1E+06	86	tRNA-Leu	9	2	23.256	48.8	98.8	295.224	65.605
LAG_01380	NA	1E+06	1E+06	204	hypothetical protein	60	7	34.314	10.3	90.7	829.716	96.8
LAG_01381	NA	1E+06	1E+06	1098	hypothetical protein	219	34	30.965	9.7	98.9	562.665	87.354
LAG_01382	NA	1E+06	1E+06	1035	hypothetical protein	519	60	57.971	0.7	99.8	1414.605	163.538
LAG_01383	NA	1E+06	1E+06	795	hypothetical protein	363	47	59.119	0.8	98.2	1288.095	166.778
LAG_01384	rlmI	1E+06	1E+06	1170	Ribosomal RNA large subunit methyltransferase I	539	58	49.573	0.9	99.1	1299.604	139.846
LAG_01385	pgk	1E+06	1E+06	1197	Phosphoglycerate kinase	5	1	0.835	99.8	99.8	11.784	2.357
LAG_01386	NA	1E+06	1E+06	468	hypothetical protein	72	8	17.094	17.1	99.1	434.005	48.223
LAG_01387	NA	1E+06	1E+06	89	tRNA-Leu	0	0	0			0	0
LAG_01388	NA	1E+06	1E+06	72	tRNA-Gly	0	0	0			0	0
LAG_01389	NA	1E+06	1E+06	73	tRNA-Thr	0	0	0			0	0
LAG_01390	NA	1E+06	1E+06	1986	hypothetical protein	563	61	30.715	2.3	99.5	799.719	86.648
LAG_01391	xly	1E+06	1E+06	2352	Xanthan lyase	529	67	28.486	1.5	97.2	634.493	80.361

LAG_01392	NA	1E+06	1E+06	609	hypothetical protein	278	26	42.693	0.3	98.5	1287.762	120.438
LAG_01393	ugl	1E+06	1E+06	1155	Unsaturated chondroitin disaccharide hydrolase	390	40	34.632	1.3	99.7	952.557	97.698
LAG_01394	bga	1E+06	1E+06	1788	Beta-galactosidase	317	36	20.134	0.8	99.4	500.15	56.799
LAG_01395	mngR_2	1E+06	1E+06	708	Mannosyl-D-glycerate transport/metabolism system repressor MngR	124	21	29.661	4.7	87.3	494.079	83.675
LAG_01396	manX_2	1E+06	1E+06	930	PTS system mannose-specific EIIAB component	64	12	12.903	3.1	83.1	194.136	36.4
LAG_01397	sorA_2	1E+06	1E+06	798	PTS system sorbose-specific EIIC component	98	13	16.291	28.3	93.9	346.443	45.957
LAG_01398	manZ_2	1E+06	1E+06	825	PTS system mannose-specific EIID component	45	9	10.909	0.1	87	153.875	30.775
LAG_01399	gno_1	1E+06	1E+06	810	Gluconate 5-dehydrogenase	59	10	12.346	10	98.9	205.483	34.828
LAG_01400	NA	1E+06	1E+06	837	hypothetical protein	139	17	20.311	6	99.5	468.487	57.297
LAG_01401	NA	1E+06	1E+06	1761	hypothetical protein	332	39	22.147	2.2	98.5	531.847	62.476
LAG_01402	kdgR	1E+06	1E+06	1008	HTH-type transcriptional regulator KdgR	103	13	12.897	17.8	95.8	288.26	36.382
LAG_01403	kduI1	1E+06	1E+06	846	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase 1	130	22	26.005	10.4	100	433.492	73.36
LAG_01404	gno_2	1E+06	1E+06	807	Gluconate 5-dehydrogenase	165	18	22.305	16	100	576.791	62.923
LAG_01405	kdgK	1E+06	1E+06	969	2-dehydro-3-deoxygluconokinase	160	18	18.576	0.4	65.8	465.805	52.403
LAG_01406	kdgA	1E+06	1E+06	642	KHG/KDPG aldolase	78	11	17.134	7.6	75.5	342.742	48.335
LAG_01407	NA	1E+06	1E+06	138	hypothetical protein	64	5	36.232	12.3	91.3	1308.305	102.211
LAG_01408	NA	1E+06	1E+06	651	hypothetical protein	89	14	21.505	1.4	95.9	385.671	60.667
LAG_01409	NA	1E+06	1E+06	378	Putative esterase	91	8	21.164	9.8	92.9	679.138	59.704
LAG_01410	menC	1E+06	1E+06	1104	o-succinylbenzoate synthase	168	19	17.21	5.1	94.5	429.288	48.55
LAG_01411	menE	1E+06	1E+06	1353	2-succinylbenzoate--CoA ligase	162	17	12.565	8.5	98.4	337.773	35.445
LAG_01412	menB	1E+06	1E+06	843	1,4-dihydroxy-2-naphthoyl-CoA synthase	149	15	17.794	6	87.1	498.617	50.196
LAG_01413	menH_3	1E+06	1E+06	828	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	120	16	19.324	37	92.4	408.845	54.513
LAG_01414	menD	1E+06	1E+06	1647	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate synthase	154	21	12.75	2	94.3	263.776	35.969
LAG_01415	pchA	1E+06	1E+06	1137	Salicylate biosynthesis isochorismate synthase	114	18	15.831	1.8	78.8	282.848	44.66
LAG_01416	NA	1E+06	1E+06	570	hypothetical protein	45	6	10.526	40.7	78.9	222.713	29.695
LAG_01417	NA	1E+06	1E+06	1281	Cobalt-dependent inorganic pyrophosphatase	57	12	9.368	1.7	74.2	125.526	26.427
LAG_01418	nrnA	1E+06	1E+06	930	putative bifunctional oligoribonuclease and PAP phosphatase NrnA	14	2	2.151	0.1	3.7	42.467	6.067
LAG_01419	znuA_2	1E+06	1E+06	1572	High-affinity zinc uptake system binding-protein ZnuA	130	22	13.995	0.6	83.3	233.292	39.48
LAG_01420	ansA	1E+06	1E+06	966	L-asparaginase	68	12	12.422	0.1	99.6	198.582	35.044
LAG_01421	ycsE	1E+06	1E+06	1407	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YcsE	97	17	12.082	23.7	92.5	194.485	34.085
LAG_01422	NA	1E+06	1E+06	660	Phosphorylated carbohydrates phosphatase	6	1	1.515	99.1	99.1	25.646	4.274
LAG_01423	gdpP	1E+06	1E+06	1968	Cyclic-di-AMP phosphodiesterase GdpP	20	4	2.033	5.3	78.6	28.669	5.734
LAG_01424	rplI	1E+06	1E+06	453	50S ribosomal protein L9	0	0	0			0	0
LAG_01425	dnaC	1E+06	1E+06	1377	Replicative DNA helicase	0	0	0			0	0
LAG_01426	NA	1E+06	1E+06	264	hypothetical protein	0	0	0			0	0
LAG_01427	NA	1E+06	1E+06	774	hypothetical protein	12	2	2.584	28	95.5	43.737	7.289
LAG_01428	trmB	1E+06	1E+06	654	tRNA (guanine-N(7)-)-methyltransferase	71	9	13.761	30.1	78.1	306.259	38.822
LAG_01429	nrdR	1E+06	1E+06	450	Transcriptional repressor NrdR	55	2	4.444	11.8	94.7	344.793	12.538
LAG_01430	dnaB	1E+06	1E+06	1164	Replication initiation and membrane attachment protein	0	0	0			0	0
LAG_01431	dnaI	1E+06	1E+06	885	Primosomal protein DnaI	4	1	1.13	94.8	94.8	12.75	3.188
LAG_01432	nfrA2	1E+06	1E+06	717	FMN reductase [NAD(P)H]	135	19	26.499	0.6	93.7	531.157	74.755
LAG_01433	spkB	1E+06	1E+06	621	Serine/threonine-protein kinase B	112	20	32.206	0.6	99.2	508.785	90.855
LAG_01434	ulaC	1E+06	1E+06	1938	Ascorbate-specific PTS system EIIA component	596	71	36.636	1	98.7	867.562	103.351
LAG_01435	NA	1E+06	1E+06	300	hypothetical protein	144	19	63.333	0.7	99	1354.096	178.665
LAG_01436	ulaA	1E+06	1E+06	1368	Ascorbate-specific PTS system EIIC component	167	35	25.585	0.8	99.3	344.381	72.176
LAG_01437	tkt_1	1E+06	1E+06	2001	Transketolase	19	4	1.999	18.1	98.8	26.786	5.639
LAG_01438	NA	1E+06	1E+06	219	hypothetical protein	53	8	36.53	27.4	83.6	682.716	103.051
LAG_01439	noxE	1E+06	1E+06	1338	NADH oxidase	110	16	11.958	0.3	91.1	231.924	33.734
LAG_01440	NA	1E+06	1E+06	1452	hypothetical protein	224	39	26.86	1.8	95.5	435.201	75.772
LAG_01441	NA	1E+06	1E+06	675	hypothetical protein	254	26	38.519	5	90.2	1061.545	108.662
LAG_01442	NA	1E+06	1E+06	426	hypothetical protein	55	9	21.127	8.2	99.3	364.218	59.599
LAG_01443	NA	1E+06	1E+06	765	hypothetical protein	167	19	24.837	8.9	94.9	615.833	70.065
LAG_01444	NA	1E+06	1E+06	336	hypothetical protein	58	10	29.762	8.3	95.8	486.964	83.959
LAG_01445	NA	1E+06	1E+06	822	hypothetical protein	109	13	15.815	2.2	98.4	374.079	44.615

LAG_01446	NA	1E+06	1E+06	786	hypothetical protein	64	8	10.178	0.6	76.6	229.702	28.713
LAG_01447	NA	1E+06	1E+06	714	hypothetical protein	92	14	19.608	0.7	94.1	363.495	55.314
LAG_01448	NA	1E+06	1E+06	1131	hypothetical protein	298	39	34.483	3.3	99.7	743.296	97.277
LAG_01449	NA	1E+06	1E+06	1029	hypothetical protein	142	23	22.352	0.1	87.9	389.297	63.055
LAG_01450	NA	1E+06	1E+06	570	hypothetical protein	129	19	33.333	6.5	93.9	638.444	94.034
LAG_01451	NA	1E+06	1E+06	2028	hypothetical protein	267	34	16.765	0.3	99.8	371.408	47.295
LAG_01452	NA	1E+06	1E+06	1110	hypothetical protein	172	24	21.622	4.1	99.9	437.133	60.995
LAG_01453	NA	1E+06	1E+06	903	hypothetical protein	213	19	21.041	0.1	98.9	665.427	59.357
LAG_01454	NA	1E+06	1E+06	402	hypothetical protein	77	9	22.388	3	77.1	540.347	63.157
LAG_01455	rnj2	1E+06	1E+06	1737	Ribonuclease J 2	11	2	1.151	96.4	98.8	17.865	3.248
LAG_01456	ntpJ_1	1E+06	1E+06	1323	Potassium/sodium uptake protein NtpJ	159	20	15.117	11.3	100	339.036	42.646
LAG_01457	ktrA	1E+06	2E+06	654	Ktr system potassium uptake protein A	28	5	7.645	13.9	99.2	120.778	21.568
LAG_01458	ffh	2E+06	2E+06	1557	Signal recognition particle protein	16	1	0.642	96.9	96.9	28.989	1.812
LAG_01459	NA	2E+06	2E+06	1026	hypothetical protein	179	23	22.417	3.5	98.3	492.169	63.24
LAG_01460	der_1	2E+06	2E+06	1311	GTPase Der	0	0	0			0	0
LAG_01461	cidB	2E+06	2E+06	699	Holin-like protein CidB	135	21	30.043	5.9	99.1	544.835	84.752
LAG_01462	lrgA	2E+06	2E+06	396	Antiholin-like protein LrgA	100	10	25.253	4.8	99.5	712.382	71.238
LAG_01463	rimP	2E+06	2E+06	477	Ribosome maturation factor RimP	0	0	0			0	0
LAG_01464	nusA	2E+06	2E+06	1128	Transcription termination/antitermination protein NusA	0	0	0			0	0
LAG_01465	NA	2E+06	2E+06	321	hypothetical protein	0	0	0			0	0
LAG_01466	rplGA	2E+06	2E+06	306	putative ribosomal protein YlxQ	0	0	0			0	0
LAG_01467	infB	2E+06	2E+06	2718	Translation initiation factor IF-2	0	0	0			0	0
LAG_01468	rbfA	2E+06	2E+06	357	Ribosome-binding factor A	19	3	8.403	82.1	89.6	150.139	23.706
LAG_01469	zitB	2E+06	2E+06	933	Zinc transporter ZitB	298	40	42.872	2	89	901.038	120.945
LAG_01470	NA	2E+06	2E+06	180	hypothetical protein	34	9	50	15	98.9	532.862	141.052
LAG_01471	manA	2E+06	2E+06	957	Mannose-6-phosphate isomerase ManA	94	19	19.854	8.5	99.4	277.092	56.008
LAG_01472	NA	2E+06	2E+06	201	hypothetical protein	17	4	19.9	6	83.6	238.595	56.14
LAG_01473	sph	2E+06	2E+06	1764	Oleate hydratase	300	49	27.778	1.5	97.9	479.768	78.362
LAG_01474	NA	2E+06	2E+06	88	tRNA-Ser	7	2	22.727	34.1	93.2	224.4	64.114
LAG_01475	NA	2E+06	2E+06	75	tRNA-Arg	21	4	53.333	13.3	84	789.889	150.455
LAG_01476	iolW	2E+06	2E+06	996	scyllo-inositol 2-dehydrogenase (NADP(+))	66	12	12.048	15.7	95.4	186.936	33.988
LAG_01477	udk	2E+06	2E+06	624	Uridine kinase	39	6	9.615	47.8	98.4	176.315	27.125
LAG_01478	pta	2E+06	2E+06	981	Phosphate acetyltransferase	31	4	4.077	14.2	87.5	89.146	11.503
LAG_01479	NA	2E+06	2E+06	390	hypothetical protein	9	2	5.128	86.7	91.5	65.101	14.467
LAG_01480	rnc	2E+06	2E+06	696	Ribonuclease 3	10	1	1.437	71.4	71.4	40.532	4.053
LAG_01481	smc	2E+06	2E+06	3519	Chromosome partition protein Smc	145	24	6.82	3.4	95.8	116.24	19.24
LAG_01482	ltaS1	2E+06	2E+06	2208	Lipoteichoic acid synthase 1	43	8	3.623	88.4	99.1	54.939	10.221
LAG_01483	NA	2E+06	2E+06	423	hypothetical protein	23	4	9.456	46.8	79	153.39	26.676
LAG_01484	NA	2E+06	2E+06	1575	hypothetical protein	20	2	1.27	94.7	97.3	35.823	3.582
LAG_01485	NA	2E+06	2E+06	2094	hypothetical protein	16	4	1.91	95.5	99.4	21.555	5.389
LAG_01486	NA	2E+06	2E+06	1104	hypothetical protein	312	39	35.326	10	97	797.249	99.656
LAG_01487	NA	2E+06	2E+06	768	hypothetical protein	256	29	37.76	4	91.3	940.345	106.523
LAG_01488	NA	2E+06	2E+06	1326	hypothetical protein	315	39	29.412	0.5	95.6	670.155	82.972
LAG_01489	yidA_2	2E+06	2E+06	810	Sugar phosphatase YidA	39	7	8.642	28	63.5	135.828	24.379
LAG_01490	ftsY	2E+06	2E+06	1302	Signal recognition particle receptor FtsY	3	1	0.768	97	97	6.5	2.167
LAG_01491	prs	2E+06	2E+06	972	Ribose-phosphate pyrophosphokinase	4	1	1.029	96.9	96.9	11.609	2.902
LAG_01492	lrp	2E+06	2E+06	678	Leucine-rich protein	64	14	20.649	1.5	65.8	266.292	58.251
LAG_01493	leuS	2E+06	2E+06	2481	Leucine--tRNA ligase	0	0	0			0	0
LAG_01494	cpo	2E+06	2E+06	810	Non-heme chloroperoxidase	106	20	24.691	3.5	87.2	369.172	69.655
LAG_01495	NA	2E+06	2E+06	1170	hypothetical protein	313	45	38.462	0.9	98.1	754.687	108.501
LAG_01496	NA	2E+06	2E+06	354	hypothetical protein	68	8	22.599	6.5	91.2	541.893	63.752
LAG_01497	NA	2E+06	2E+06	1983	NADH dehydrogenase-like protein	639	51	25.719	2.8	99.5	909.047	72.553
LAG_01498	menA_3	2E+06	2E+06	1008	1,4-dihydroxy-2-naphthoate octaprenyltransferase	887	71	70.437	3.4	99.3	2482.398	198.704
LAG_01499	fcbA1	2E+06	2E+06	1533	4-chlorobenzoate--CoA ligase	503	65	42.401	1	98.8	925.623	119.613

LAG_01500	sdhB	2E+06	2E+06	672	L-serine dehydratase, beta chain	109	13	19.345	2.7	88.1	457.578	54.574
LAG_01501	sdhA	2E+06	2E+06	873	L-serine dehydratase, alpha chain	53	8	9.164	4.6	99.2	171.266	25.851
LAG_01502	copY	2E+06	2E+06	441	Transcriptional repressor CopY	32	5	11.338	8.2	81.9	204.701	31.985
LAG_01503	copZ	2E+06	2E+06	210	Copper chaperone CopZ	31	5	23.81	16.7	92.9	416.438	67.167
LAG_01504	copA	2E+06	2E+06	2088	putative copper-importing P-type ATPase A	289	53	25.383	0.9	98	390.459	71.607
LAG_01505	recQ	2E+06	2E+06	1779	ATP-dependent DNA helicase RecQ	385	64	35.975	2.5	99.6	610.51	101.487
LAG_01506	NA	2E+06	2E+06	951	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase	249	27	28.391	0.4	97.8	738.63	80.092
LAG_01507	gmuC_2	2E+06	2E+06	1371	PTS system oligo-beta-mannoside-specific EIIC component	295	48	35.011	0.4	99.1	607.006	98.767
LAG_01508	NA	2E+06	2E+06	519	hypothetical protein	59	4	7.707	25.2	40.1	320.696	21.742
LAG_01509	NA	2E+06	2E+06	1293	Putative dipeptidase	249	38	29.389	16.9	97.1	543.262	82.907
LAG_01510	yvoA_1	2E+06	2E+06	726	HTH-type transcriptional repressor YvoA	105	20	27.548	2.2	99.2	408.001	77.714
LAG_01511	NA	2E+06	2E+06	2595	hypothetical protein	506	62	23.892	6.3	97.6	550.074	67.4
LAG_01512	NA	2E+06	2E+06	780	hypothetical protein	43	9	11.538	3.8	94.2	155.519	32.55
LAG_01513	mnmA	2E+06	2E+06	1122	tRNA-specific 2-thiouridylase MnmA	0	0	0			0	0
LAG_01514	NA	2E+06	2E+06	528	hypothetical protein	69	9	17.045	4.4	83.3	368.658	48.086
LAG_01515	rpsA	2E+06	2E+06	1224	30S Ribosomal protein S1	0	0	0			0	0
LAG_01516	NA	2E+06	2E+06	381	hypothetical protein	35	7	18.373	10.5	95.5	259.15	51.83
LAG_01517	NA	2E+06	2E+06	1158	hypothetical protein	500	65	56.131	0.3	99.8	1218.063	158.348
LAG_01518	dexB	2E+06	2E+06	1629	Glucan 1,6-alpha-glucosidase	584	75	46.041	0.9	98.2	1011.347	129.882
LAG_01519	NA	2E+06	2E+06	906	6-phosphogluconate dehydrogenase, NAD(+)-dependent, decarboxylating	178	26	28.698	0.4	96.6	554.243	80.957
LAG_01520	xylB_2	2E+06	2E+06	1497	Xylulose kinase	281	34	22.712	6.4	98.5	529.533	64.072
LAG_01521	gntT	2E+06	2E+06	1353	High-affinity gluconate transporter	195	32	23.651	7.2	96.9	406.579	66.721
LAG_01522	nhaC	2E+06	2E+06	1416	Na(+)/H(+) antiporter NhaC	399	40	28.249	3.7	96.9	794.91	79.69
LAG_01523	pyrR	2E+06	2E+06	525	Bifunctional protein PyrR	93	10	19.048	6.1	70.7	499.726	53.734
LAG_01524	pyrP	2E+06	2E+06	1287	Uracil permease	160	23	17.871	7.1	90.9	350.711	50.415
LAG_01525	pyrB	2E+06	2E+06	924	Aspartate carbamoyltransferase	89	15	16.234	2.3	99.7	271.723	45.796
LAG_01526	carA	2E+06	2E+06	1065	Carbamoyl-phosphate synthase small chain	119	15	14.085	2.2	99.9	315.214	39.733
LAG_01527	bioY2	2E+06	2E+06	549	Biotin transporter BioY2	8	2	3.643	90.7	92.9	41.108	10.277
LAG_01528	spxA_13	2E+06	2E+06	396	Regulatory protein Spx	98	13	32.828	3.8	80.1	698.135	92.61
LAG_01529	NA	2E+06	2E+06	126	hypothetical protein	13	3	23.81	31.7	82.5	291.059	67.167
LAG_01530	NA	2E+06	2E+06	1683	hypothetical protein	458	38	22.579	1.7	98.6	767.697	63.695
LAG_01531	NA	2E+06	2E+06	579	hypothetical protein	116	14	24.18	3.6	95.7	565.181	68.212
LAG_01532	queA	2E+06	2E+06	1104	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	80	10	9.058	26.6	93.9	204.423	25.553
LAG_01533	NA	2E+06	2E+06	354	hypothetical protein	26	6	16.949	14.1	91	207.195	47.814
LAG_01534	NA	2E+06	2E+06	207	hypothetical protein	19	3	14.493	10.6	77.8	258.935	40.885
LAG_01535	tagH_3	2E+06	2E+06	1413	Teichoic acids export ATP-binding protein TagH	32	7	4.954	22.6	72.2	63.888	13.975
LAG_01536	tagG_3	2E+06	2E+06	810	Teichoic acid translocation permease protein TagG	13	4	4.938	18	88.3	45.276	13.931
LAG_01537	NA	2E+06	2E+06	2055	hypothetical protein	77	14	6.813	13.8	91.7	105.703	19.219
LAG_01538	tagD_2	2E+06	2E+06	426	Glycerol-3-phosphate cytidylyltransferase	20	3	7.042	7.3	89.7	132.443	19.866
LAG_01539	NA	2E+06	2E+06	435	hypothetical protein	81	9	20.69	2.3	92.6	525.296	58.366
LAG_01540	tarF_3	2E+06	2E+06	1185	Teichoic acid glycerol-phosphate transferase	107	16	13.502	2.6	99.1	254.726	38.09
LAG_01541	pucK	2E+06	2E+06	1302	Uric acid permease PucK	316	47	36.098	1.4	99.5	684.675	101.835
LAG_01542	xpt	2E+06	2E+06	594	Xanthine phosphoribosyltransferase	147	19	31.987	4.9	99.2	698.135	90.235
LAG_01543	rluB	2E+06	2E+06	717	Ribosomal large subunit pseudouridine synthase B	73	9	12.552	9.3	96	287.218	35.41
LAG_01544	scpB	2E+06	2E+06	579	Segregation and condensation protein B	101	16	27.634	16.4	91.4	492.097	77.956
LAG_01545	scpA	2E+06	2E+06	741	Segregation and condensation protein A	89	13	17.544	0.9	88.4	338.829	49.492
LAG_01546	ynbA	2E+06	2E+06	729	Tyrosine recombinase XerD-like protein	49	9	12.346	18.2	91.4	189.617	34.828
LAG_01547	ykuL	2E+06	2E+06	465	CBS domain-containing protein YkuL	36	4	8.602	21.9	99.4	218.403	24.267
LAG_01548	yfcE	2E+06	2E+06	510	Phosphodiesterase YfcE	52	5	9.804	4.5	88.8	287.635	27.657
LAG_01549	murI	2E+06	2E+06	1413	Glutamate racemase	35	6	4.246	64.7	99.9	69.877	11.979
LAG_01550	NA	2E+06	2E+06	240	hypothetical protein	0	0	0			0	0
LAG_01551	ilvE	2E+06	2E+06	1023	Branched-chain-amino-acid aminotransferase	145	19	18.573	5.3	100	399.853	52.395
LAG_01552	ykuT	2E+06	2E+06	747	putative MscS family protein YkuT	132	14	18.742	0.9	92.5	498.496	52.871
LAG_01553	rnhB	2E+06	2E+06	762	Ribonuclease HII	25	7	9.186	4.2	91.7	92.554	25.915

LAG_01554	rbgA	2E+06	2E+06	858	Ribosome biogenesis GTPase A	0	0	0			0	0
LAG_01555	NA	2E+06	2E+06	645	Putative 3-methyladenine DNA glycosylase	93	18	27.907	10.5	98.3	406.754	78.727
LAG_01556	ndx1	2E+06	2E+06	408	Diadenosine hexaphosphate hydrolase	75	11	26.961	7.1	91.7	518.572	76.057
LAG_01557	NA	2E+06	2E+06	492	hypothetical protein	85	12	24.39	1.8	99.4	487.374	68.806
LAG_01558	NA	2E+06	2E+06	672	hypothetical protein	119	15	22.321	0.3	82.6	499.558	62.97
LAG_01559	NA	2E+06	2E+06	1089	hypothetical protein	211	32	29.385	1.8	98.2	546.591	82.895
LAG_01560	dapE_2	2E+06	2E+06	1140	putative succinyl-diaminopimelate desuccinylase	164	26	22.807	1.6	97.6	405.833	64.339
LAG_01561	NA	2E+06	2E+06	492	hypothetical protein	73	12	24.39	12.6	99.8	418.568	68.806
LAG_01562	dinB_3	2E+06	2E+06	1452	DNA polymerase IV	177	28	19.284	7.3	99	343.886	54.4
LAG_01563	NA	2E+06	2E+06	183	hypothetical protein	66	5	27.322	15.3	95.1	1017.422	77.077
LAG_01564	NA	2E+06	2E+06	381	hypothetical protein	66	9	23.622	10.8	98.2	488.683	66.639
LAG_01565	psiE	2E+06	2E+06	399	Protein PsiE	37	8	20.05	29.1	99	261.6	56.562
LAG_01566	ppdK	2E+06	2E+06	2619	Pyruvate, phosphate dikinase	625	67	25.582	3	99.1	673.213	72.168
LAG_01567	ccpN	2E+06	2E+06	633	Transcriptional repressor CcpN	91	12	18.957	10.1	96.8	405.551	53.479
LAG_01568	yqfL	2E+06	2E+06	804	Putative pyruvate, phosphate dikinase regulatory protein	188	33	41.045	1.6	99	659.645	115.789
LAG_01569	NA	2E+06	2E+06	597	hypothetical protein	109	19	31.826	2.2	97.5	515.063	89.782
LAG_01570	NA	2E+06	2E+06	480	hypothetical protein	116	13	27.083	3.1	94.8	681.75	76.403
LAG_01571	NA	2E+06	2E+06	10074	hypothetical protein	1431	186	18.463	0	100	400.725	52.086
LAG_01572	asp3	2E+06	2E+06	444	Accessory Sec system protein Asp3	126	18	40.541	7.4	90.8	800.564	114.366
LAG_01573	asp2	2E+06	2E+06	1554	Accessory Sec system protein Asp2	355	54	34.749	1.9	100	644.445	98.028
LAG_01574	gtf1_1	2E+06	2E+06	1575	Glycosyltransferase Gtf1	551	63	40	0.7	98.7	986.914	112.841
LAG_01575	secY2	2E+06	2E+06	1248	Accessory Sec system protein translocase subunit SecY2	538	60	48.077	0.2	97.9	1216.119	135.627
LAG_01576	NA	2E+06	2E+06	180	hypothetical protein	81	10	55.556	5	94.4	1269.465	156.724
LAG_01577	gtf2	2E+06	2E+06	1347	Glycosyltransferase-stabilizing protein Gtf2	322	52	38.604	0.8	99.9	674.367	108.904
LAG_01578	gtf1_2	2E+06	2E+06	1503	Glycosyltransferase Gtf1	498	66	43.912	1.2	98.5	934.714	123.878
LAG_01579	wbbI	2E+06	2E+06	1029	Beta-1,6-galactofuranosyltransferase WbbI	238	38	36.929	0.9	99	652.484	104.178
LAG_01580	secA_2	2E+06	2E+06	2328	Protein translocase subunit SecA	514	73	31.357	1.1	99	622.857	88.46
LAG_01581	NA	2E+06	2E+06	435	Putative universal stress protein	121	19	43.678	8	100	784.701	123.218
LAG_01582	NA	2E+06	2E+06	429	Putative universal stress protein	74	15	34.965	1.6	95.1	486.612	98.638
LAG_01583	NA	2E+06	2E+06	156	hypothetical protein	20	3	19.231	58.3	91	361.671	54.251
LAG_01584	NA	2E+06	2E+06	438	hypothetical protein	138	20	45.662	0.9	96.8	888.819	128.814
LAG_01585	fieF_2	2E+06	2E+06	876	Ferrous-iron efflux pump FieF	339	45	51.37	5.3	99	1091.701	144.916
LAG_01586	NA	2E+06	2E+06	744	hypothetical protein	156	28	37.634	0.5	96.9	591.507	106.168
LAG_01587	NA	2E+06	2E+06	348	hypothetical protein	180	28	80.46	2	92.2	1459.155	226.98
LAG_01588	NA	2E+06	2E+06	348	hypothetical protein	70	10	28.736	1.1	92.8	567.449	81.064
LAG_01589	NA	2E+06	2E+06	1479	hypothetical protein	564	76	51.386	4.3	99.9	1075.769	144.962
LAG_01590	yagU	2E+06	2E+06	540	Inner membrane protein YagU	301	34	62.963	0.7	100	1572.465	177.621
LAG_01591	NA	2E+06	2E+06	159	hypothetical protein	52	7	44.025	2.5	98.1	922.602	124.196
LAG_01593	NA	2E+06	2E+06	750	hypothetical protein	117	21	28	6.5	98.1	440.081	78.989
LAG_01594	yxlF_2	2E+06	2E+06	888	putative ABC transporter ATP-binding protein YxlF	246	33	37.162	1.2	86.8	781.503	104.836
LAG_01595	NA	2E+06	2E+06	189	hypothetical protein	39	8	42.328	18	74.1	582.118	119.409
LAG_01596	NA	2E+06	2E+06	336	hypothetical protein	90	10	29.762	0.3	76.5	755.634	83.959
LAG_01597	phoP_2	2E+06	2E+06	699	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP	60	13	18.598	1	93.3	242.149	52.466
LAG_01598	phoR	2E+06	2E+06	1563	Alkaline phosphatase synthesis sensor protein PhoR	309	46	29.431	0.5	100	557.709	83.025
LAG_01599	yvoA_2	2E+06	2E+06	318	HTH-type transcriptional repressor YvoA	72	10	31.447	12.6	87.4	638.725	88.712
LAG_01600	yvoA_3	2E+06	2E+06	387	HTH-type transcriptional repressor YvoA	58	10	25.84	6.2	93.3	422.791	72.895
LAG_01601	tmpC_2	2E+06	2E+06	1053	Membrane lipoprotein TmpC	166	22	20.893	12.8	96	444.721	58.939
LAG_01602	cdd	2E+06	2E+06	393	Cytidine deaminase	13	3	7.634	13.7	79.4	93.317	21.535
LAG_01603	deoC1	2E+06	2E+06	663	Deoxyribose-phosphate aldolase 1	54	9	13.575	49.9	97.6	229.767	38.295
LAG_01604	NA	2E+06	2E+06	195	hypothetical protein	56	4	20.513	10.3	96.9	810.143	57.867
LAG_01605	pdp	2E+06	2E+06	1293	Pyrimidine-nucleoside phosphorylase	80	12	9.281	15.8	94.9	174.542	26.181
LAG_01606	rsmC	2E+06	2E+06	606	Ribosomal RNA small subunit methyltransferase C	42	9	14.851	6.3	77.6	195.517	41.897
LAG_01607	coaA	2E+06	2E+06	921	Pantothenate kinase	3	1	1.086	98.8	98.8	9.189	3.063
LAG_01608	guaA	2E+06	2E+06	1542	GMP synthase [glutamine-hydrolyzing]	39	7	4.54	0.6	88.1	71.349	12.806

LAG_01609	NA	2E+06	2E+06	297	hypothetical protein	27	5	16.835	27.6	60.6	256.458	47.492
LAG_01610	NA	2E+06	2E+06	426	Putative universal stress protein	60	7	16.432	11.3	87.1	397.329	46.355
LAG_01611	NA	2E+06	2E+06	594	hypothetical protein	178	26	43.771	5.9	98.8	845.36	123.48
LAG_01612	mhqA_3	2E+06	2E+06	1146	Putative ring-cleaving dioxygenase MhqA	225	32	27.923	4.5	96.1	553.868	78.772
LAG_01613	NA	2E+06	2E+06	804	hypothetical protein	208	26	32.338	4.4	92.2	729.82	91.227
LAG_01614	purK	2E+06	2E+06	1119	N5-carboxyaminoimidazole ribonucleotide synthase	328	45	40.214	1	97.8	826.898	113.446
LAG_01615	purE	2E+06	2E+06	486	N5-carboxyaminoimidazole ribonucleotide mutase	107	16	32.922	2.5	78.2	621.092	92.874
LAG_01616	purD	2E+06	2E+06	1233	Phosphoribosylamine--glycine ligase	262	29	23.52	16.2	99.5	599.441	66.35
LAG_01617	yfnB_2	2E+06	2E+06	693	Putative HAD-hydrolase YfnB	129	19	27.417	0.6	99	525.127	77.344
LAG_01618	treA	2E+06	2E+06	1611	Trehalose-6-phosphate hydrolase	158	26	16.139	4.2	99.9	276.675	45.529
LAG_01619	bglF_4	2E+06	2E+06	1545	PTS system beta-glucoside-specific EIIBCA component	200	32	20.712	1.1	94	365.182	58.429
LAG_01620	crr	2E+06	2E+06	486	PTS system glucose-specific EIIA component	57	6	12.346	7.4	97.3	330.862	34.828
LAG_01621	treR	2E+06	2E+06	717	HTH-type transcriptional regulator TreR	203	21	29.289	0.8	94.6	798.703	82.624
LAG_01622	purH	2E+06	2E+06	1551	Bifunctional purine biosynthesis protein PurH	360	37	23.856	0.6	94.5	654.785	67.297
LAG_01623	purN	2E+06	2E+06	543	Phosphoribosylglycinamide formyltransferase	168	26	47.882	7	97.6	872.806	135.077
LAG_01624	purM	2E+06	2E+06	1014	Phosphoribosylformylglycinamidine cyclo-ligase	270	22	21.696	1.4	91.6	751.163	61.206
LAG_01625	purF	2E+06	2E+06	1416	Amidophosphoribosyltransferase	220	30	21.186	1.3	98.4	438.296	59.768
LAG_01626	purL	2E+06	2E+06	2217	Phosphoribosylformylglycinamidine synthase subunit PurL	495	47	21.2	0.4	98.2	629.865	59.805
LAG_01627	purQ	2E+06	2E+06	681	Phosphoribosylformylglycinamidine synthase subunit PurQ	173	20	29.369	0.9	95.6	716.65	82.85
LAG_01628	purS	2E+06	2E+06	243	Phosphoribosylformylglycinamidine synthase subunit PurS	63	7	28.807	4.9	84.8	731.379	81.264
LAG_01629	purC	2E+06	2E+06	717	Phosphoribosylaminoimidazole-succinocarboxamide synthase	74	13	18.131	18.3	96.1	291.153	51.148
LAG_01630	NA	2E+06	2E+06	426	hypothetical protein	117	20	46.948	3.1	86.4	774.791	132.443
LAG_01631	yafP	2E+06	2E+06	462	putative N-acetyltransferase YafP	110	18	38.961	6.5	78.4	671.675	109.91
LAG_01632	thyA	2E+06	2E+06	840	Thymidylate synthase	0	0	0			0	0
LAG_01633	ettA_2	2E+06	2E+06	1851	Energy-dependent translational throttle protein EttA	385	55	29.714	0.5	99.1	586.763	83.823
LAG_01634	NA	2E+06	2E+06	1845	hypothetical protein	472	70	37.94	4.1	99.3	721.695	107.031
LAG_01635	pepDA	2E+06	2E+06	1395	Dipeptidase A	211	25	17.921	2.8	88.8	426.694	50.556
LAG_01636	cca	2E+06	2E+06	1197	CCA-adding enzyme	0	0	0			0	0
LAG_01637	NA	2E+06	2E+06	1344	Putative dipeptidase	248	38	28.274	9.2	99.5	520.548	79.761
LAG_01638	NA	2E+06	2E+06	1527	hypothetical protein	427	60	39.293	4.1	96.7	788.855	110.846
LAG_01639	NA	2E+06	2E+06	843	DegV domain-containing protein	96	13	15.421	3.9	97.7	321.256	43.503
LAG_01640	NA	2E+06	2E+06	399	hypothetical protein	24	5	12.531	12	86	169.686	35.351
LAG_01641	gph_3	2E+06	2E+06	585	Phosphoglycolate phosphatase	88	11	18.803	4.1	90.8	424.361	53.045
LAG_01642	trmD	2E+06	2E+06	729	tRNA (guanine-N(1)-)-methyltransferase	0	0	0			0	0
LAG_01643	rimM	2E+06	2E+06	516	Ribosome maturation factor RimM	6	1	1.938	5.4	5.4	32.803	5.467
LAG_01644	yhdG_1	2E+06	2E+06	1398	putative amino acid permease YhdG	283	36	25.751	3.2	98.6	571.068	72.645
LAG_01645	NA	2E+06	2E+06	447	hypothetical protein	116	20	44.743	13.9	94.9	732.08	126.221
LAG_01646	NA	2E+06	2E+06	636	hypothetical protein	107	17	26.73	1.1	95.9	474.608	75.405
LAG_01647	ubiE	2E+06	2E+06	726	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	121	17	23.416	2.6	97.2	470.172	66.057
LAG_01648	NA	2E+06	2E+06	243	hypothetical protein	67	9	37.037	9.5	95.9	777.816	104.483
LAG_01649	ceo	2E+06	2E+06	939	N(5)-(carboxyethyl)ornithine synthase	130	21	22.364	1.8	94.5	390.558	63.09
LAG_01650	NA	2E+06	2E+06	240	hypothetical protein	96	9	37.5	17.9	90.4	1128.413	105.789
LAG_01651	NA	2E+06	2E+06	561	hypothetical protein	121	18	32.086	6.6	94.5	608.458	90.514
LAG_01652	NA	2E+06	2E+06	189	hypothetical protein	67	9	47.619	2.1	94.7	1000.049	134.335
LAG_01653	NA	2E+06	2E+06	558	Stress response regulator gls24	109	19	34.05	0.7	96.2	551.062	96.057
LAG_01654	zntB	2E+06	2E+06	948	Zinc transport protein ZntB	187	28	29.536	5	96.1	556.47	83.322
LAG_01655	ifcA	2E+06	2E+06	1503	Fumarate reductase flavoprotein subunit	310	36	23.952	0.1	99.8	581.85	67.57
LAG_01656	corC_2	2E+06	2E+06	1275	Magnesium and cobalt efflux protein CorC	467	61	47.843	0.5	99.5	1033.273	134.967
LAG_01657	NA	2E+06	2E+06	558	hypothetical protein	82	13	23.297	8.6	93.4	414.56	65.723
LAG_01658	padC	2E+06	2E+06	534	Phenolic acid decarboxylase PadC	177	24	44.944	5.2	97	935.062	126.788
LAG_01659	spxA_14	2E+06	2E+06	399	Regulatory protein Spx	125	20	50.125	6	74.7	883.782	141.405
LAG_01660	NA	2E+06	2E+06	240	hypothetical protein	19	5	20.833	8.8	91.2	223.332	58.772
LAG_01661	rpsP	2E+06	2E+06	273	30S ribosomal protein S16	0	0	0			0	0
LAG_01662	mvaA	2E+06	2E+06	1221	3-hydroxy-3-methylglutaryl-coenzyme A reductase	6	1	0.819	2.2	2.2	13.863	2.31

LAG_01663	thlA	2E+06	2E+06	1161	Acetyl-CoA acetyltransferase	7	1	0.861	0.7	0.7	17.009	2.43
LAG_01664	mvaS	2E+06	2E+06	1152	Hydroxymethylglutaryl-CoA synthase	0	0	0			0	0
LAG_01665	fabG_2	2E+06	2E+06	795	3-oxoacyl-[acyl-carrier-protein] reductase FabG	179	29	36.478	7.5	99.2	635.176	102.906
LAG_01666	gmuR_2	2E+06	2E+06	714	HTH-type transcriptional regulator GmuR	230	28	39.216	0.7	99	908.736	110.629
LAG_01667	NA	2E+06	2E+06	855	hypothetical protein	196	21	24.561	3.6	98.2	646.693	69.289
LAG_01668	yhhX_2	2E+06	2E+06	1050	putative oxidoreductase YhhX	329	30	28.571	5.4	93.1	883.924	80.601
LAG_01669	hadI	2E+06	2E+06	4260	2-hydroxyisocaproyl-CoA dehydratase activator	1180	160	37.559	0.3	99	781.413	105.954
LAG_01670	slmA	2E+06	2E+06	648	Nucleoid occlusion factor SlmA	298	38	58.642	0.2	98.1	1297.327	165.431
LAG_01671	glpK_2	2E+06	2E+06	1491	Glycerol kinase	643	64	42.924	1	88.3	1216.583	121.091
LAG_01672	nagB	2E+06	2E+06	708	Glucosamine-6-phosphate deaminase	26	5	7.062	24.9	77.8	103.597	19.923
LAG_01673	lytR_2	2E+06	2E+06	909	Transcriptional regulator LytR	35	8	8.801	6.2	86	108.621	24.828
LAG_01674	NA	2E+06	2E+06	891	hypothetical protein	27	6	6.734	2.2	85.9	85.486	18.997
LAG_01675	tagB	2E+06	2E+06	309	Teichoic acid glycerol-phosphate primase	16	2	6.472	84.1	97.7	146.073	18.259
LAG_01676	NA	2E+06	2E+06	75	tRNA-Val	0	0	0			0	0
LAG_01677	NA	2E+06	2E+06	81	tRNA-Tyr	0	0	0			0	0
LAG_01678	NA	2E+06	2E+06	73	tRNA-Trp	0	0	0			0	0
LAG_01679	NA	2E+06	2E+06	74	tRNA-His	0	0	0			0	0
LAG_01680	NA	2E+06	2E+06	72	tRNA-Gln	0	0	0			0	0
LAG_01681	NA	2E+06	2E+06	86	tRNA-Leu	0	0	0			0	0
LAG_01682	yoaB_2	2E+06	2E+06	2607	Calcium-transporting ATPase 1	589	77	29.536	1	99.5	637.357	83.322
LAG_01683	NA	2E+06	2E+06	477	hypothetical protein	95	12	25.157	5.9	81.3	561.841	70.969
LAG_01684	gap	2E+06	2E+06	1011	Glyceraldehyde-3-phosphate dehydrogenase	0	0	0			0	0
LAG_01685	NA	2E+06	2E+06	954	hypothetical protein	264	34	35.639	10.7	99.5	780.663	100.54
LAG_01686	NA	2E+06	2E+06	342	hypothetical protein	70	9	26.316	13.7	92.4	577.405	74.238
LAG_01687	recG	2E+06	2E+06	2082	ATP-dependent DNA helicase RecG	52	10	4.803	4.3	83.3	70.458	13.55
LAG_01688	NA	2E+06	2E+06	255	hypothetical protein	23	5	19.608	32.5	93.3	254.446	55.314
LAG_01689	mnmE	2E+06	2E+06	1365	tRNA modification GTPase MnmE	22	3	2.198	2.4	61.9	45.467	6.2
LAG_01690	rsuA_2	2E+06	2E+06	711	Ribosomal small subunit pseudouridine synthase A	54	7	9.845	44.6	95.5	214.256	27.774
LAG_01691	ybhF	2E+06	2E+06	717	putative ABC transporter ATP-binding protein YbhF	35	4	5.579	1.1	75	137.707	15.738
LAG_01692	rbbA	2E+06	2E+06	1095	Ribosome-associated ATPase	171	18	16.438	18.4	93.6	440.545	46.373
LAG_01693	rpiA	2E+06	2E+06	672	Ribose-5-phosphate isomerase A	74	10	14.881	3.3	96	310.65	41.98
LAG_01694	NA	2E+06	2E+06	453	hypothetical protein	10	3	6.623	0.2	40.2	62.274	18.682
LAG_01695	mreC	2E+06	2E+06	834	Cell shape-determining protein MreC	58	10	11.99	2.3	89.9	196.187	33.825
LAG_01696	NA	2E+06	2E+06	507	hypothetical protein	4	1	1.972	39.3	39.3	22.257	5.564
LAG_01697	NA	2E+06	2E+06	1371	Secreted 45 kDa protein	22	4	2.918	13.6	71.6	45.268	8.231
LAG_01698	NA	2E+06	2E+06	1230	Secreted 45 kDa protein	16	4	3.252	3.7	99.2	36.696	9.174
LAG_01699	dnaJ	2E+06	2E+06	1131	Chaperone protein DnaJ	23	5	4.421	45	99.6	57.368	12.471
LAG_01700	ppaX	2E+06	2E+06	528	Pyrophosphatase PpaX	60	13	24.621	2.1	95.3	320.572	69.457
LAG_01701	zwf	2E+06	2E+06	1488	Glucose-6-phosphate 1-dehydrogenase	4	1	0.672	98.6	98.6	7.583	1.896
LAG_01702	NA	2E+06	2E+06	180	hypothetical protein	12	3	16.667	11.1	50.6	188.069	47.017
LAG_01703	NA	2E+06	2E+06	819	hypothetical protein	177	19	23.199	7.2	96.7	609.674	65.445
LAG_01704	NA	2E+06	2E+06	369	hypothetical protein	238	12	32.52	1.1	90.5	1819.528	91.741
LAG_01705	NA	2E+06	2E+06	85	tRNA-Leu	0	0	0			0	0
LAG_01706	NA	2E+06	2E+06	207	hypothetical protein	15	3	14.493	10.1	92.3	204.423	40.885
LAG_01707	glxR	2E+06	2E+06	885	2-hydroxy-3-oxopropionate reductase	157	17	19.209	5.6	94.2	500.455	54.189
LAG_01708	argS	2E+06	2E+06	1689	Arginine--tRNA ligase	4	1	0.592	20.2	20.2	6.681	1.67
LAG_01709	argR_2	2E+06	2E+06	447	Arginine repressor	0	0	0			0	0
LAG_01710	NA	2E+06	2E+06	342	hypothetical protein	32	7	20.468	0.3	93	263.956	57.74
LAG_01711	mutS	2E+06	2E+06	2508	DNA mismatch repair protein MutS	168	17	6.778	1.9	99.9	188.969	19.122
LAG_01712	NA	2E+06	2E+06	666	hypothetical protein	16	5	7.508	19.1	95	67.773	21.179
LAG_01713	mutL	2E+06	2E+06	1887	DNA mismatch repair protein MutL	172	17	9.009	2.2	97.2	257.137	25.415
LAG_01714	ykoT	2E+06	2E+06	963	putative glycosyltransferase YkoT	0	0	0			0	0
LAG_01715	ruvA	2E+06	2E+06	591	Holliday junction ATP-dependent DNA helicase RuvA	64	10	16.92	1.4	97.8	305.493	47.733
LAG_01716	ruvB	2E+06	2E+06	999	Holliday junction ATP-dependent DNA helicase RuvB	17	5	5.005	0.5	97.6	48.006	14.119

LAG_01717	yfkJ	2E+06	2E+06	372	Low molecular weight protein-tyrosine-phosphatase YfkJ	28	3	8.065	27.4	89.2	212.336	22.75
LAG_01718	glnR	2E+06	2E+06	366	HTH-type transcriptional regulator GlnR	14	3	8.197	1.1	35.5	107.908	23.123
LAG_01719	glnA	2E+06	2E+06	1341	Glutamine synthetase	31	6	4.474	31.2	84.7	65.214	12.622
LAG_01720	NA	2E+06	2E+06	432	hypothetical protein	100	7	16.204	8.8	94.9	653.017	45.711
LAG_01721	NA	2E+06	2E+06	270	hypothetical protein	31	3	11.111	12.6	49.6	323.896	31.345
LAG_01722	NA	2E+06	2E+06	267	hypothetical protein	13	4	14.981	19.1	73.4	137.354	42.263
LAG_01723	NA	2E+06	2E+06	294	hypothetical protein	42	7	23.81	4.1	87.1	403.005	67.167
LAG_01724	msrC	2E+06	2E+06	480	Free methionine-R-sulfoxide reductase	21	4	8.333	0.8	53.3	123.42	23.509
LAG_01725	NA	2E+06	2E+06	621	hypothetical protein	48	8	12.882	10.5	99.4	218.051	36.342
LAG_01726	dnaX_2	2E+06	2E+06	1659	DNA polymerase III subunit tau	5	1	0.603	99.3	99.3	8.502	1.7
LAG_01727	lysP_2	2E+06	2E+06	1464	Lysine-specific permease	154	19	12.978	1.3	85.9	296.748	36.612
LAG_01728	NA	2E+06	2E+06	213	hypothetical protein	3	1	4.695	17.8	17.8	39.733	13.244
LAG_01729	rpsF	2E+06	2E+06	294	30S ribosomal protein S6	0	0	0			0	0
LAG_01730	ssb	2E+06	2E+06	495	Single-stranded DNA-binding protein	0	0	0			0	0
LAG_01731	rpsR	2E+06	2E+06	246	30S ribosomal protein S18	10	2	8.13	85	97.6	114.676	22.935
LAG_01732	cpdA_3	2E+06	2E+06	768	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	78	12	15.625	17.7	83.9	286.511	44.079
LAG_01733	NA	2E+06	2E+06	309	hypothetical protein	0	0	0			0	0
LAG_01734	hexR_3	2E+06	2E+06	849	HTH-type transcriptional regulator HexR	126	15	17.668	3.2	85.4	418.669	49.842
LAG_01735	recX	2E+06	2E+06	834	Regulatory protein RecX	65	12	14.388	8	95.2	219.865	40.59
LAG_01736	ydhP	2E+06	2E+06	1182	Inner membrane transport protein YdhP	105	18	15.228	3.5	92.6	250.599	42.96
LAG_01737	ytbE	2E+06	2E+06	819	putative oxidoreductase YtbE	132	5	6.105	34.9	77.9	454.672	17.222
LAG_01738	ytcD	2E+06	2E+06	366	putative HTH-type transcriptional regulator YtcD	23	4	10.929	30.3	62.3	177.278	30.831
LAG_01739	fosB	2E+06	2E+06	393	Metallothiol transferase FosB	33	3	7.634	27	83	236.881	21.535
LAG_01740	rlmCD_2	2E+06	2E+06	1506	23S rRNA (uracil-C(5))-methyltransferase RlmCD	77	13	8.632	2.5	99.5	144.236	24.352
LAG_01741	NA	2E+06	2E+06	510	hypothetical protein	31	4	7.843	6.3	63.3	171.475	22.126
LAG_01742	NA	2E+06	2E+06	255	hypothetical protein	50	3	11.765	38.4	76.9	553.144	33.189
LAG_01743	NA	2E+06	2E+06	249	hypothetical protein	29	4	16.064	44.2	77.1	328.554	45.318
LAG_01744	NA	2E+06	2E+06	615	hypothetical protein	25	6	9.756	16.4	83.9	114.676	27.522
LAG_01745	valS	2E+06	2E+06	2643	Valine--tRNA ligase	0	0	0			0	0
LAG_01746	pgi	2E+06	2E+06	1347	Glucose-6-phosphate isomerase	4	1	0.742	98	98	8.377	2.094
LAG_01747	rsmD	2E+06	2E+06	582	Ribosomal RNA small subunit methyltransferase D	29	8	13.746	5.2	90.4	140.567	38.777
LAG_01748	coaD	2E+06	2E+06	498	Phosphopantetheine adenylyltransferase	13	2	4.016	94.6	95.8	73.641	11.329
LAG_01749	lon	2E+06	2E+06	1044	Lon protease	149	16	15.326	9.8	100	402.619	43.234
LAG_01750	adhE	2E+06	2E+06	2694	Aldehyde-alcohol dehydrogenase	145	23	8.537	4.9	88	151.837	24.085
LAG_01751	pgl	2E+06	2E+06	1041	6-phosphogluconolactonase	0	0	0			0	0
LAG_01752	rpsB	2E+06	2E+06	774	30S ribosomal protein S2	0	0	0			0	0
LAG_01753	tsf	2E+06	2E+06	1029	Elongation factor Ts	0	0	0			0	0
LAG_01754	ezrA	2E+06	2E+06	1731	Septation ring formation regulator EzrA	61	5	2.889	4.4	99.5	99.413	8.149
LAG_01755	der_2	2E+06	2E+06	1128	GTPase Der	0	0	0			0	0
LAG_01756	hflX	2E+06	2E+06	1236	GTPase HflX	114	17	13.754	4.4	100	260.192	38.801
LAG_01757	yhbY	2E+06	2E+06	309	RNA-binding protein YhbY	9	1	3.236	91.6	91.6	82.166	9.13
LAG_01758	nadD_2	2E+06	2E+06	594	putative nicotinate-nucleotide adenylyltransferase	31	6	10.101	3.7	97.3	147.226	28.495
LAG_01759	NA	2E+06	2E+06	594	hypothetical protein	12	3	5.051	37.7	98.8	56.991	14.248
LAG_01760	rsfS	2E+06	2E+06	360	Ribosomal silencing factor RsfS	78	9	25	8.6	96.4	611.224	70.526
LAG_01761	NA	2E+06	2E+06	732	Glycine/sarcosine N-methyltransferase	69	9	12.295	5.5	65.6	265.917	34.685
LAG_01762	NA	2E+06	2E+06	1086	hypothetical protein	4	1	0.921	96.6	96.6	10.391	2.598
LAG_01763	NA	2E+06	2E+06	714	putative transcriptional regulatory protein	21	2	2.801	65.3	66.8	82.972	7.902
LAG_01764	NA	2E+06	2E+06	531	hypothetical protein	233	27	50.847	4.3	93	1237.855	143.442
LAG_01765	NA	2E+06	2E+06	981	hypothetical protein	331	46	46.891	0.4	93.8	951.847	132.281
LAG_01766	catE	2E+06	2E+06	837	Catechol-2,3-dioxygenase	312	36	43.011	3.3	98.8	1051.568	121.335
LAG_01767	menG	2E+06	2E+06	732	Demethylmenaquinone methyltransferase	135	19	25.956	0.4	96.3	520.273	73.224
LAG_01768	eno	2E+06	2E+06	1302	Enolase	0	0	0			0	0
LAG_01769	NA	2E+06	2E+06	486	hypothetical protein	150	16	32.922	8.4	95.5	870.689	92.874
LAG_01770	rplT	2E+06	2E+06	360	50S ribosomal protein L20	0	0	0			0	0

LAG_01771	rpmI	2E+06	2E+06	201	50S ribosomal protein L35	0	0	0			0	0
LAG_01772	infC	2E+06	2E+06	495	Translation initiation factor IF-3	0	0	0			0	0
LAG_01773	strH	2E+06	2E+06	1161	Beta-N-acetylhexosaminidase	73	8	6.891	12.9	94.7	177.378	19.439
LAG_01774	hflK	2E+06	2E+06	894	Modulator of FtsH protease HflK	28	5	5.593	36.2	64.4	88.355	15.778
LAG_01775	galT_2	2E+06	2E+06	669	Galactose-1-phosphate uridylyltransferase	31	7	10.463	4.3	83	130.721	29.518
LAG_01776	miaA	2E+06	2E+06	894	tRNA dimethylallyltransferase	77	15	16.779	4.4	94.7	242.975	47.333
LAG_01777	pdaC	2E+06	2E+06	1422	Peptidoglycan-N-acetylmuramic acid deacetylase PdaC	239	32	22.504	1.3	98.8	474.14	63.483
LAG_01778	NA	2E+06	2E+06	180	hypothetical protein	9	3	16.667	10.6	80.6	141.052	47.017
LAG_01779	NA	2E+06	2E+06	171	hypothetical protein	7	2	11.696	32.7	66.1	115.481	32.995
LAG_01780	NA	2E+06	2E+06	273	hypothetical protein	35	6	21.978	12.5	98.2	361.671	62.001
LAG_01781	NA	2E+06	2E+06	360	hypothetical protein	22	3	8.333	55.3	78.1	172.396	23.509
LAG_01782	NA	2E+06	2E+06	327	hypothetical protein	78	8	24.465	1.8	85.3	672.907	69.016
LAG_01783	pyrDA	2E+06	2E+06	933	Dihydroorotate dehydrogenase A (fumarate)	84	18	19.293	10.7	71.4	253.984	54.425
LAG_01784	fhuC	2E+06	2E+06	735	Iron(3+)-hydroxamate import ATP-binding protein FhuC	144	17	23.129	4.8	99	552.692	65.248
LAG_01785	mntB	2E+06	2E+06	855	Manganese transport system membrane protein MntB	232	21	24.561	1.2	95.7	765.473	69.289
LAG_01786	mntA	2E+06	2E+06	930	Manganese-binding lipoprotein MntA	227	24	25.806	0.6	98	688.575	72.801
LAG_01787	gnd	2E+06	2E+06	1422	6-phosphogluconate dehydrogenase, decarboxylating	42	8	5.626	6.4	95.6	83.322	15.871
LAG_01788	NA	2E+06	2E+06	600	hypothetical protein	38	8	13.333	45.5	93.3	178.665	37.614
LAG_01789	NA	2E+06	2E+06	426	hypothetical protein	94	10	23.474	12	61.5	622.482	66.221
LAG_01790	NA	2E+06	2E+06	354	hypothetical protein	71	8	22.599	14.1	85.6	565.801	63.752
LAG_01791	lgt	2E+06	2E+06	786	Prolipoprotein diacylglyceryl transferase	160	14	17.812	0.8	98.7	574.256	50.247
LAG_01792	hprK	2E+06	2E+06	924	HPr kinase/phosphorylase	7	1	1.082	0.4	0.4	21.371	3.053
LAG_01793	NA	2E+06	2E+06	414	hypothetical protein	13	3	7.246	25.1	83.1	88.583	20.442
LAG_01794	NA	2E+06	2E+06	90	hypothetical protein	27	5	55.556	21.1	92.2	846.31	156.724
LAG_01795	NA	2E+06	2E+06	456	hypothetical protein	0	0	0			0	0
LAG_01796	NA	2E+06	2E+06	903	hypothetical protein	185	19	21.041	0.7	93.7	577.953	59.357
LAG_01797	map	2E+06	2E+06	858	Methionine aminopeptidase 1	5	1	1.166	1.9	1.9	16.44	3.288
LAG_01798	NA	2E+06	2E+06	444	Flavodoxin	50	8	18.018	0.9	92.3	317.684	50.829
LAG_01799	rlmB	2E+06	2E+06	729	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	122	22	30.178	3.2	91.9	472.107	85.134
LAG_01800	acyP	2E+06	2E+06	276	Acylphosphatase	7	2	7.246	64.5	68.1	71.548	20.442
LAG_01801	NA	2E+06	2E+06	612	hypothetical protein	23	5	8.17	20.1	67.6	106.019	23.048
LAG_01802	glyA	2E+06	2E+06	1242	Serine hydroxymethyltransferase	103	17	13.688	0.4	98.6	233.95	38.613
LAG_01803	NA	2E+06	2E+06	603	Putative threonylcarbamoyl-AMP synthase	8	2	3.317	3.2	6	37.427	9.357
LAG_01804	yvbK	2E+06	2E+06	429	putative N-acetyltransferase YvbK	13	2	4.662	19.6	94.9	85.486	13.152
LAG_01805	prmC_2	2E+06	2E+06	813	Release factor glutamine methyltransferase	42	6	7.38	45	59.4	145.736	20.819
LAG_01806	NA	2E+06	2E+06	537	hypothetical protein	70	10	18.622	37.4	88.1	367.733	52.533
LAG_01807	prfA	2E+06	2E+06	1074	Peptide chain release factor 1	9	2	1.862	95	98.9	23.64	5.253
LAG_01808	tdk	2E+06	2E+06	603	Thymidine kinase	61	8	13.267	4.8	90.5	285.378	37.427
LAG_01809	xerD_2	2E+06	2E+06	1200	Tyrosine recombinase XerD	148	24	20	2.3	99	347.927	56.421
LAG_01810	NA	2E+06	2E+06	186	hypothetical protein	47	9	48.387	14.5	99.5	712.842	136.502
LAG_01811	NA	2E+06	2E+06	219	hypothetical protein	29	4	18.265	10.5	72.6	373.562	51.526
LAG_01812	NA	2E+06	2E+06	249	hypothetical protein	56	6	24.096	0.8	98	634.449	67.977
LAG_01813	NA	2E+06	2E+06	510	hypothetical protein	88	12	23.529	2.4	77.5	486.767	66.377
LAG_01814	NA	2E+06	2E+06	249	hypothetical protein	14	3	12.048	12	67.1	158.612	33.988
LAG_01815	inlJ_3	2E+06	2E+06	2220	Internalin-J	522	73	32.883	1.1	99.6	663.324	92.764
LAG_01816	NA	2E+06	2E+06	501	hypothetical protein	64	12	23.952	11.8	97.8	360.372	67.57
LAG_01817	NA	2E+06	2E+06	1053	hypothetical protein	197	24	22.792	7.9	78.9	527.772	64.297
LAG_01818	NA	2E+06	2E+06	1794	hypothetical protein	770	83	46.265	0.3	99.8	1210.812	130.516
LAG_01819	NA	2E+06	2E+06	2496	hypothetical protein	584	97	38.862	0.9	99.2	660.05	109.632
LAG_01820	NA	2E+06	2E+06	393	hypothetical protein	100	16	40.712	28.5	98.7	717.82	114.851
LAG_01821	NA	2E+06	2E+06	222	hypothetical protein	133	13	58.559	18	95.5	1690.079	165.196
LAG_01822	NA	2E+06	2E+06	1236	hypothetical protein	305	47	38.026	2.6	98.8	696.129	107.272
LAG_01823	inlJ_4	2E+06	2E+06	2226	Internalin-J	816	88	39.533	1.8	99	1034.126	111.523
LAG_01824	NA	2E+06	2E+06	2796	hypothetical protein	650	86	30.758	0.9	99.1	655.82	86.77

LAG_01825	NA	2E+06	2E+06	1014	hypothetical protein	217	34	33.531	1.2	92.6	603.712	94.591
LAG_01826	NA	2E+06	2E+06	312	hypothetical protein	32	7	22.436	8.7	78.8	289.337	63.292
LAG_01827	NA	2E+06	2E+06	153	hypothetical protein	21	3	19.608	7.2	68	387.201	55.314
LAG_01828	inlJ_5	2E+06	2E+06	1281	Internalin-J	462	52	40.593	1.2	100	1017.422	114.515
LAG_01829	NA	2E+06	2E+06	303	hypothetical protein	125	13	42.904	1.3	94.7	1163.793	121.034
LAG_01830	NA	2E+06	2E+06	1149	hypothetical protein	249	34	29.591	2.6	99.5	611.347	83.477
LAG_01831	xre	2E+06	2E+06	498	HTH-type transcriptional regulator Xre	207	26	52.209	4	93.4	1172.598	147.283
LAG_01832	ftsK_2	2E+06	2E+06	1683	DNA translocase FtsK	287	44	26.144	1	98.9	481.068	73.753
LAG_01833	NA	2E+06	2E+06	480	hypothetical protein	113	16	33.333	1.9	99.6	664.118	94.034
LAG_01834	NA	2E+06	2E+06	300	hypothetical protein	39	4	13.333	39	98.3	366.734	37.614
LAG_01835	NA	2E+06	2E+06	225	hypothetical protein	76	7	31.111	0.9	66.7	952.882	87.765
LAG_01836	NA	2E+06	2E+06	366	hypothetical protein	24	4	10.929	81.7	93.2	184.986	30.831
LAG_01837	NA	2E+06	2E+06	951	hypothetical protein	397	56	58.885	1.9	98.5	1177.655	166.118
LAG_01838	NA	2E+06	2E+06	354	hypothetical protein	277	31	87.571	1.4	80.5	2207.419	247.04
LAG_01839	macB_2	2E+06	2E+06	1998	Macrolide export ATP-binding/permease protein MacB	854	107	53.554	0.2	96.8	1205.787	151.076
LAG_01840	yvgN_2	2E+06	2E+06	867	Glyoxal reductase	316	36	41.522	2.4	97.8	1028.197	117.136
LAG_01841	adhR	2E+06	2E+06	420	HTH-type transcriptional regulator AdhR	170	28	66.667	0.7	99.8	1141.847	188.069
LAG_01842	NA	2E+06	2E+06	1047	hypothetical protein	455	65	62.082	1.1	97.9	1225.951	175.136
LAG_01843	ntpJ_2	2E+06	2E+06	1338	Potassium/sodium uptake protein NtpJ	395	47	35.127	0.1	98.5	832.816	99.095
LAG_01844	spxA_15	2E+06	2E+06	378	Regulatory protein Spx	171	24	63.492	4.5	94.4	1276.182	179.113
LAG_01845	NA	2E+06	2E+06	195	hypothetical protein	88	13	66.667	12.3	98.5	1273.082	188.069
LAG_01846	NA	2E+06	2E+06	189	hypothetical protein	71	11	58.201	2.6	97.4	1059.753	164.187
LAG_01847	NA	2E+06	2E+06	74	tRNA-Met	15	3	40.541	4.1	24.3	571.831	114.366
LAG_01848	NA	2E+06	2E+06	153	hypothetical protein	46	7	45.752	34.6	98	848.154	129.067
LAG_01849	spxA_16	2E+06	2E+06	210	Regulatory protein Spx	41	5	23.81	30.5	95.2	550.773	67.167
LAG_01850	cspLA_1	2E+06	2E+06	201	Cold shock-like protein CspLA	16	2	9.95	13.4	93.5	224.56	28.07
LAG_01851	NA	2E+06	2E+06	303	hypothetical protein	104	14	46.205	10.2	95.7	968.276	130.345
LAG_01852	NA	2E+06	2E+06	339	hypothetical protein	115	15	44.248	7.4	92.3	956.988	124.824
LAG_01853	NA	2E+06	2E+06	74	tRNA-Met	13	2	27.027	20.3	37.8	495.587	76.244
LAG_01854	cspLA_2	2E+06	2E+06	201	Cold shock-like protein CspLA	20	3	14.925	15.9	34.3	280.7	42.105
LAG_01855	NA	2E+06	2E+06	837	hypothetical protein	304	42	50.179	0.7	93.8	1024.605	141.557
LAG_01856	NA	2E+06	2E+06	462	hypothetical protein	230	28	60.606	2.4	98.9	1404.411	170.972
LAG_01857	tadA_2	2E+06	2E+06	492	tRNA-specific adenosine deaminase	7	2	4.065	8.9	70.5	40.137	11.468
LAG_01858	rbn	2E+06	2E+06	735	Ribonuclease BN	86	7	9.524	1.5	79.5	330.08	26.867
LAG_01859	NA	2E+06	2E+06	672	hypothetical protein	62	14	20.833	6.7	96.3	260.274	58.772
LAG_01860	NA	2E+06	2E+06	1476	hypothetical protein	500	67	45.393	2.3	100	955.635	128.055
LAG_01861	spxA_17	2E+06	2E+06	351	Regulatory protein Spx	91	12	34.188	2.3	90	731.379	96.446
LAG_01862	NA	2E+06	2E+06	1476	hypothetical protein	513	71	48.103	0.6	92.8	980.481	135.7
LAG_01863	NA	2E+06	2E+06	2265	hypothetical protein	686	77	33.996	1.8	99.3	854.406	95.903
LAG_01864	NA	2E+06	2E+06	717	hypothetical protein	113	15	20.921	1.3	97.5	444.598	59.017
LAG_01865	NA	2E+06	2E+06	288	hypothetical protein	32	8	27.778	6.2	77.1	313.448	78.362
LAG_01866	NA	2E+06	2E+06	486	hypothetical protein	125	16	32.922	0.4	94.4	725.574	92.874
LAG_01867	NA	2E+06	2E+06	1200	hypothetical protein	133	19	15.833	5.2	94.1	312.665	44.666
LAG_01868	NA	2E+06	2E+06	426	hypothetical protein	60	11	25.822	5.2	91.3	397.329	72.844
LAG_01869	macB_3	2E+06	2E+06	1986	Macrolide export ATP-binding/permease protein MacB	348	38	19.134	0.1	96.9	494.32	53.977
LAG_01870	yusO	2E+06	2E+06	642	putative HTH-type transcriptional regulator YusO	16	4	6.231	60.3	99.7	70.306	17.577
LAG_01871	NA	2E+06	2E+06	1719	putative ABC transporter ATP-binding protein	304	42	24.433	0.8	99.7	498.891	68.926
LAG_01872	cydD	2E+06	2E+06	1707	ATP-binding/permease protein CydD	253	36	21.09	0.6	95.9	418.115	59.495
LAG_01873	cydB	2E+06	2E+06	996	Cytochrome bd-I ubiquinol oxidase subunit 2	93	11	11.044	3.5	78.2	263.41	31.156
LAG_01874	cydA	2E+06	2E+06	1449	Cytochrome bd ubiquinol oxidase subunit 1	142	18	12.422	11	87.9	276.457	35.044
LAG_01875	apu	2E+06	2E+06	1818	Amylopullulanase	186	32	17.602	0.3	92.3	288.621	49.655
LAG_01876	glgP	2E+06	2E+06	2403	Glycogen phosphorylase	173	35	14.565	6.7	95.3	203.096	41.089
LAG_01877	glgA	2E+06	2E+06	1437	Glycogen synthase	118	20	13.918	6.9	98.6	231.651	39.263
LAG_01878	glgD	2E+06	2E+06	1146	Glycogen biosynthesis protein GlgD	192	23	20.07	2.4	94.8	472.634	56.618

LAG_01879	glgC	2E+06	2E+06	1143	Glucose-1-phosphate adenylyltransferase	151	21	18.373	5.7	98.8	372.682	51.83
LAG_01880	nusB	2E+06	2E+06	975	N utilization substance protein B	13	3	3.077	1.8	98.2	37.614	8.68
LAG_01881	NA	2E+06	2E+06	402	hypothetical protein	0	0	0			0	0
LAG_01882	efp	2E+06	2E+06	558	Elongation factor P	0	0	0			0	0
LAG_01883	ypdF	2E+06	2E+06	1050	Aminopeptidase YpdF	130	20	19.048	2.1	95.1	349.271	53.734
LAG_01884	gph_4	2E+06	2E+06	654	Phosphoglycolate phosphatase	130	16	24.465	1.7	94.6	560.756	69.016
LAG_01885	fba_2	2E+06	2E+06	858	Fructose-bisphosphate aldolase	82	13	15.152	5.9	91.6	269.609	42.743
LAG_01886	lacC_2	2E+06	2E+06	930	Tagatose-6-phosphate kinase	94	13	13.978	1	97.5	285.137	39.434
LAG_01887	agaS	2E+06	2E+06	1152	Putative tagatose-6-phosphate ketose/aldose isomerase	146	14	12.153	9.1	97.8	357.527	34.283
LAG_01888	NA	2E+06	2E+06	648	Phosphorylated carbohydrates phosphatase	73	16	24.691	5.6	96	317.802	69.655
LAG_01889	fruA_3	2E+06	2E+06	1929	PTS system fructose-specific EIIABC component	230	34	17.626	3.3	99.4	336.36	49.723
LAG_01890	pfkB	2E+06	2E+06	933	ATP-dependent 6-phosphofructokinase isozyme 2	140	16	17.149	27.2	88.6	423.306	48.378
LAG_01891	ybbH_3	2E+06	2E+06	750	putative HTH-type transcriptional regulator YbbH	105	17	22.667	2.7	100	394.945	63.943
LAG_01892	manZ_3	2E+06	2E+06	840	PTS system mannose-specific EIID component	144	21	25	12.3	97.6	483.606	70.526
LAG_01893	agaC	2E+06	2E+06	810	N-acetylgalactosamine permease IIC component 1	74	14	17.284	14.8	86.9	257.724	48.759
LAG_01894	manX_3	2E+06	2E+06	477	PTS system mannose-specific EIIAB component	74	14	29.35	1.9	86.6	437.645	82.798
LAG_01895	NA	2E+06	2E+06	276	hypothetical protein	42	8	28.986	2.5	92.4	429.288	81.769
LAG_01896	manX_4	2E+06	2E+06	423	PTS system mannose-specific EIIAB component	80	12	28.369	0.9	87.9	533.529	80.029
LAG_01897	nagA_2	2E+06	2E+06	1149	N-acetylglucosamine-6-phosphate deacetylase	230	29	25.239	0.4	99.3	564.698	71.201
LAG_01898	hexR_4	2E+06	2E+06	753	HTH-type transcriptional regulator HexR	112	21	27.888	3.1	95.2	419.596	78.674
LAG_01899	fbp	2E+06	2E+06	1923	Fructose-1,6-bisphosphatase class 3	395	57	29.641	0.6	98.4	579.463	83.619
LAG_01900	uvrA_2	2E+06	2E+06	2820	UvrABC system protein A	107	18	6.383	0.1	94.6	107.039	18.007
LAG_01901	NA	2E+06	2E+06	300	hypothetical protein	35	5	16.667	5.7	44.7	329.121	47.017
LAG_01902	NA	2E+06	2E+06	327	hypothetical protein	66	11	33.639	3.4	80.1	569.383	94.897
LAG_01903	yceM	2E+06	2E+06	921	Putative oxidoreductase YceM	172	23	24.973	11.1	99.7	526.838	70.449
LAG_01904	thiN	2E+06	2E+06	618	Thiamine pyrophosphokinase	0	0	0			0	0
LAG_01905	NA	2E+06	2E+06	348	hypothetical protein	5	1	2.874	74.7	74.7	40.532	8.106
LAG_01906	asnS	2E+06	2E+06	1338	Asparagine--tRNA ligase	0	0	0			0	0
LAG_01907	NA	2E+06	2E+06	330	hypothetical protein	13	3	9.091	5.5	93.3	111.132	25.646
LAG_01908	NA	2E+06	2E+06	1194	Aspartate aminotransferase	59	10	8.375	0.9	99.6	139.398	23.627
LAG_01909	NA	2E+06	2E+06	444	hypothetical protein	8	1	2.252	56.1	56.1	50.829	6.354
LAG_01910	dinG	2E+06	2E+06	2355	putative ATP-dependent helicase DinG	123	19	8.068	12.3	90.8	147.341	22.76
LAG_01911	NA	2E+06	2E+06	438	Putative universal stress protein	66	12	27.397	0.9	89.7	425.087	77.289
LAG_01912	mprF	2E+06	2E+06	1692	Phosphatidylglycerol lysyltransferase	142	27	15.957	1.4	99.9	236.753	45.016
LAG_01913	NA	2E+06	2E+06	918	hypothetical protein	69	9	9.804	7.1	94.3	212.038	27.657
LAG_01914	NA	2E+06	2E+06	399	hypothetical protein	44	7	17.544	2.3	83.2	311.091	49.492
LAG_01915	NA	2E+06	2E+06	1656	hypothetical protein	394	56	33.816	0.7	100	671.188	95.397
LAG_01916	mnaA_1	2E+06	2E+06	1119	UDP-N-acetylglucosamine 2-epimerase	142	22	19.66	0.4	86.4	357.986	55.463
LAG_01917	NA	2E+06	2E+06	93	hypothetical protein	8	2	21.505	20.4	65.6	242.67	60.667
LAG_01918	NA	2E+06	2E+06	1299	Beta-monoglucosyldiacylglycerol synthase	262	41	31.563	1.1	97.2	568.984	89.04
LAG_01919	NA	2E+06	2E+06	3744	hypothetical protein	1169	141	37.66	2.2	100	880.82	106.241
LAG_01920	NA	2E+06	2E+06	1416	hypothetical protein	266	29	20.48	40.2	100	529.94	57.775
LAG_01921	aqpZ2	2E+06	2E+06	666	Aquaporin Z 2	98	10	15.015	1.8	95.2	415.107	42.358
LAG_01922	cna_2	2E+06	2E+06	1854	Collagen adhesin	231	32	17.26	0.6	99.9	351.488	48.691
LAG_01923	ybiV_2	2E+06	2E+06	789	Sugar phosphatase YbiV	237	25	31.686	0.6	99.5	847.383	89.386
LAG_01924	srrA_2	2E+06	2E+06	690	Transcriptional regulatory protein SrrA	83	16	23.188	0.1	95.5	339.342	65.415
LAG_01925	baeS	2E+06	2E+06	2088	Signal transduction histidine-protein kinase BaeS	397	62	29.693	1.6	99.3	536.375	83.766
LAG_01926	NA	2E+06	2E+06	204	hypothetical protein	10	3	14.706	17.2	37.7	138.286	41.486
LAG_01927	NA	2E+06	2E+06	564	hypothetical protein	122	15	26.596	3.2	100	610.224	75.027
LAG_01928	NA	2E+06	2E+06	1074	putative ABC transporter permease	196	33	30.726	3.7	98.3	514.826	86.68
LAG_01929	bceA	2E+06	2E+06	681	Bacitracin export ATP-binding protein BceA	153	18	26.432	3.2	98.1	633.801	74.565
LAG_01930	NA	2E+06	2E+06	1347	hypothetical protein	245	39	28.953	1.3	99.9	513.106	81.678
LAG_01931	icaA_2	2E+06	2E+06	2133	Poly-beta-1,6-N-acetyl-D-glucosamine synthase	550	59	27.661	1.6	95	727.411	78.031
LAG_01932	cph2	2E+06	2E+06	687	Phytochrome-like protein cph2	106	17	24.745	1.2	82.8	435.269	69.807

LAG_01933	NA	2E+06	2E+06	681	hypothetical protein	160	19	27.9	4.6	97.9	662.798	78.707
LAG_01934	yedQ	2E+06	2E+06	1140	putative diguanylate cyclase YedQ	341	45	39.474	2.5	99.6	843.835	111.357
LAG_01935	mnaA_2	2E+06	2E+06	1083	UDP-N-acetylglucosamine 2-epimerase	158	23	21.237	1.8	93.2	411.564	59.911
LAG_01936	kup	2E+06	2E+06	2019	Low affinity potassium transport system protein kup	286	49	24.269	0.2	98.2	399.611	68.465
LAG_01937	qorA	2E+06	2E+06	981	Quinone oxidoreductase 1	241	32	32.62	0.8	98.7	693.037	92.021
LAG_01938	NA	2E+06	2E+06	456	hypothetical protein	116	17	37.281	8.6	96.5	717.631	105.17
LAG_01939	NA	2E+06	2E+06	621	hypothetical protein	111	18	28.986	0.6	92.4	504.243	81.769
LAG_01940	NA	2E+06	2E+06	516	hypothetical protein	127	22	42.636	1.2	94	694.324	120.277
LAG_01941	marR	2E+06	2E+06	423	Multiple antibiotic resistance protein MarR	72	13	30.733	1.4	98.1	480.176	86.698
LAG_01942	yodC	2E+06	2E+06	639	Putative NAD(P)H nitroreductase YodC	140	20	31.299	4.5	85.4	618.067	88.295
LAG_01943	paiA	2E+06	2E+06	1212	Spermidine/spermine N(1)-acetyltransferase	469	60	49.505	1.5	99.8	1091.638	139.655
LAG_01944	NA	2E+06	2E+06	252	hypothetical protein	25	5	19.841	6.7	67.9	279.864	55.973
LAG_01945	NA	2E+06	2E+06	657	hypothetical protein	268	24	36.53	2.4	97.7	1150.741	103.051
LAG_01946	NA	2E+06	2E+06	567	hypothetical protein	224	25	44.092	2.1	96.8	1114.482	124.384
LAG_01947	NA	2E+06	2E+06	825	hypothetical protein	139	21	25.455	10.9	96.8	475.301	71.808
LAG_01948	gadC	2E+06	2E+06	1512	Glutamate/gamma-aminobutyrate antiporter	477	61	40.344	0.9	99.6	889.969	113.812
LAG_01949	gadB	2E+06	2E+06	1401	Glutamate decarboxylase	453	61	43.54	2.7	99.1	912.154	122.829
LAG_01950	patA_2	2E+06	2E+06	1164	Putative N-acetyl-LL-diaminopimelate aminotransferase	280	47	40.378	7.3	99.6	678.599	113.908
LAG_01951	lysA	2E+06	2E+06	1260	Diaminopimelate decarboxylase	314	40	31.746	1.3	99	703.019	89.557
LAG_01952	dapA	2E+06	2E+06	864	4-hydroxy-tetrahydrodipicolinate synthase	249	29	33.565	5.8	95.7	813.006	94.687
LAG_01953	dapB	2E+06	2E+06	711	4-hydroxy-tetrahydrodipicolinate reductase	178	22	30.942	0.1	96.5	706.25	87.289
LAG_01954	dapH	2E+06	2E+06	699	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	160	23	32.904	4.3	95.7	645.73	92.824
LAG_01955	asd	2E+06	2E+06	993	Aspartate-semialdehyde dehydrogenase	271	35	35.247	16.3	98.3	769.889	99.432
LAG_01956	yclM	2E+06	2E+06	1314	Aspartokinase 3	242	41	31.202	0.3	96.3	519.551	88.023
LAG_01957	NA	2E+06	2E+06	1134	N-acetyldiaminopimelate deacetylase	261	33	29.101	4	97.2	649.286	82.094
LAG_01958	NA	2E+06	2E+06	171	hypothetical protein	64	10	58.48	8.8	94.7	1055.825	164.973
LAG_01959	inlJ_6	2E+06	2E+06	1944	Internalin-J	668	89	45.782	5.6	99.7	969.368	129.152
LAG_01960	polC_2	2E+06	2E+06	4884	DNA polymerase III PolC-type	0	0	0			0	0
LAG_01961	NA	2E+06	2E+06	375	hypothetical protein	34	6	16	31.5	84.5	255.774	45.137
LAG_01962	proS	2E+06	2E+06	1851	Proline--tRNA ligase	0	0	0			0	0
LAG_01963	rasP	2E+06	2E+06	1248	Regulator of sigma-W protease RasP	57	4	3.205	42.8	70.9	128.845	9.042
LAG_01964	cdsA	2E+06	2E+06	795	Phosphatidate cytidylyltransferase	7	1	1.258	8.2	8.2	24.839	3.548
LAG_01965	uppS	2E+06	2E+06	738	Isoprenyl transferase	0	0	0			0	0
LAG_01966	NA	2E+06	2E+06	336	hypothetical protein	3	1	2.976	22.3	22.3	25.188	8.396
LAG_01967	NA	2E+06	2E+06	648	hypothetical protein	80	12	18.519	24.4	96.6	348.276	52.241
LAG_01968	rlmH	2E+06	2E+06	480	Ribosomal RNA large subunit methyltransferase H	84	15	31.25	1	62.5	493.681	88.157
LAG_01969	htrA	2E+06	2E+06	1218	Serine protease Do-like HtrA	129	18	14.778	4.8	92.5	298.779	41.69
LAG_01970	dgs	2E+06	2E+06	999	Processive diacylglycerol alpha-glucosyltransferase	3	1	1.001	96	96	8.472	2.824
LAG_01971	NA	2E+06	2E+06	1335	Alpha-monoglucosyldiacylglycerol synthase	56	7	5.243	17.9	99.6	118.335	14.792
LAG_01972	NA	2E+06	2E+06	225	hypothetical protein	32	4	17.778	0.9	56.9	401.214	50.152
LAG_01973	tmpC_3	2E+06	2E+06	1050	Membrane lipoprotein TmpC	265	39	37.143	1	98.3	711.975	104.781
LAG_01974	yfiC	2E+06	2E+06	750	tRNA1(Val) (adenine(37)-N6)-methyltransferase	235	38	50.667	0.7	100	883.924	142.932
LAG_01975	glgB	2E+06	2E+06	1944	1,4-alpha-glucan branching enzyme GlgB	870	72	37.037	0.2	98.7	1262.5	104.483
LAG_01976	tgt	2E+06	2E+06	1149	Queuine tRNA-ribosyltransferase	325	41	35.683	3.2	99.5	797.942	100.664
LAG_01977	NA	2E+06	2E+06	735	hypothetical protein	308	30	40.816	4.1	97.7	1182.147	115.144
LAG_01978	mdtG	2E+06	2E+06	1179	Multidrug resistance protein MdtG	410	55	46.65	5.1	97.4	981.021	131.6
LAG_01979	NA	2E+06	2E+06	210	hypothetical protein	95	15	71.429	1.4	94.3	1276.182	201.502
LAG_01980	polA	2E+06	2E+06	2616	DNA polymerase I	138	20	7.645	1.1	99.6	148.816	21.568
LAG_01981	NA	2E+06	2E+06	73	tRNA-Thr	0	0	0			0	0
LAG_01982	NA	2E+06	2E+06	72	tRNA-Gly	0	0	0			0	0
LAG_01983	NA	2E+06	2E+06	76	tRNA-Arg	0	0	0			0	0
LAG_01984	NA	2E+06	2E+06	76	tRNA-Pro	0	0	0			0	0
LAG_01985	NA	2E+06	2E+06	76	tRNA-Met	0	0	0			0	0
LAG_01986	NA	2E+06	2E+06	75	tRNA-Met	0	0	0			0	0

LAG_01987	NA	2E+06	2E+06	90	tRNA-Ser	0	0	0			0	0
LAG_01988	NA	2E+06	2E+06	75	tRNA-Phe	0	0	0			0	0
LAG_01989	NA	2E+06	2E+06	71	tRNA-Gly	0	0	0			0	0
LAG_01990	NA	2E+06	2E+06	76	tRNA-Ile	0	0	0			0	0
LAG_01991	NA	2E+06	2E+06	88	tRNA-Ser	0	0	0			0	0
LAG_01992	dnaG	2E+06	2E+06	1887	DNA primase	0	0	0			0	0
LAG_01993	sigA	2E+06	2E+06	1383	RNA polymerase sigma factor SigA	20	4	2.892	96.3	99.3	40.796	8.159
LAG_01994	clpE	2E+06	2E+06	2247	ATP-dependent Clp protease ATP-binding subunit ClpE	755	80	35.603	2	99	947.877	100.437
LAG_01995	NA	2E+06	2E+06	366	hypothetical protein	137	22	60.109	1.4	83.3	1055.961	169.57
LAG_01996	NA	2E+06	2E+06	246	hypothetical protein	130	14	56.911	1.2	100	1490.79	160.547
LAG_01997	def	2E+06	2E+06	627	Peptide deformylase	0	0	0			0	0
LAG_01998	rppH	2E+06	2E+06	456	RNA pyrophosphohydrolase	84	14	30.702	41.2	93.9	519.664	86.611
LAG_01999	uvrB	2E+06	2E+06	1989	UvrABC system protein B	135	22	11.061	0.4	96.5	191.473	31.203
LAG_02000	fabZ_2	2E+06	2E+06	459	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	0	0	0			0	0
LAG_02001	nanE	2E+06	2E+06	699	Putative N-acetylmannosamine-6-phosphate 2-epimerase	264	28	40.057	0.3	99.1	1065.455	113.003
LAG_02002	fabI	2E+06	2E+06	753	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	0	0	0			0	0
LAG_02003	NA	2E+06	2E+06	204	hypothetical protein	155	16	78.431	9.3	96.1	2143.432	221.258
LAG_02004	NA	2E+06	2E+06	1224	hypothetical protein	500	62	50.654	0.1	100	1152.383	142.895
LAG_02005	fnr_2	2E+06	2E+06	657	Anaerobic regulatory protein	309	35	53.272	3	88.7	1326.788	150.283
LAG_02006	misCB	2E+06	2E+06	993	Membrane protein insertase MisCB	64	11	11.078	0.5	99.7	181.819	31.25
LAG_02007	pgcA	2E+06	2E+06	1713	Phosphoglucomutase	0	0	0			0	0
LAG_02008	panT	2E+06	2E+06	582	Pantothenic acid transporter PanT	0	0	0			0	0
LAG_02009	coaBC_1	2E+06	2E+06	552	Coenzyme A biosynthesis bifunctional protein CoaBC	0	0	0			0	0
LAG_02010	coaBC_2	2E+06	2E+06	699	Coenzyme A biosynthesis bifunctional protein CoaBC	0	0	0			0	0
LAG_02011	NA	2E+06	2E+06	1290	hypothetical protein	240	31	24.031	0.2	99	524.843	67.792
LAG_02012	NA	2E+06	2E+06	180	putative tautomerase.1	45	11	61.111	6.1	95	705.258	172.396
LAG_02013	NA	2E+06	2E+06	1650	hypothetical protein	258	34	20.606	0.1	85.9	441.107	58.13
LAG_02014	NA	2E+06	2E+06	74	tRNA-Glu	0	0	0			0	0
LAG_02015	NA	2E+06	2E+06	73	tRNA-Asn	0	0	0			0	0
LAG_02016	NA	2E+06	2E+06	945	hypothetical protein	289	32	33.862	5.4	95	862.729	95.527
LAG_02017	NA	2E+06	2E+06	540	hypothetical protein	91	16	29.63	0.6	99.1	475.396	83.586
LAG_02018	glcU_2	2E+06	2E+06	897	Glucose uptake protein GlcU	419	42	46.823	1.2	99.9	1317.74	132.089
LAG_02019	yhdG_2	2E+06	2E+06	1389	putative amino acid permease YhdG	443	39	28.078	6	96.8	899.725	79.208
LAG_02020	dacA	2E+06	2E+06	1287	D-alanyl-D-alanine carboxypeptidase DacA	435	21	16.317	12.7	93	953.496	46.031
LAG_02021	immR_2	2E+06	2E+06	621	HTH-type transcriptional regulator ImmR	68	14	22.544	16.6	98.6	308.905	63.598
LAG_02022	rpsL	2E+06	2E+06	414	30S ribosomal protein S12	0	0	0			0	0
LAG_02023	rpsG	2E+06	2E+06	468	30S ribosomal protein S7	0	0	0			0	0
LAG_02024	NA	2E+06	2E+06	1941	hypothetical protein	197	28	14.426	0.4	96	286.318	40.695
LAG_02025	NA	2E+06	2E+06	372	hypothetical protein	46	4	10.753	33.3	81.7	348.837	30.334
LAG_02026	fus	2E+06	2E+06	2091	Elongation factor G	3	1	0.478	98.5	98.5	4.047	1.349
LAG_02027	purR	2E+06	2E+06	816	Pur operon repressor	150	15	18.382	2.6	77	518.572	51.857
LAG_02028	NA	2E+06	2E+06	489	hypothetical protein	119	13	26.585	13.1	89.6	686.509	74.997
LAG_02029	spsB	2E+06	2E+06	675	Signal peptidase IB	3	1	1.481	72	72	12.538	4.179
LAG_02030	rnhC	2E+06	2E+06	879	Ribonuclease HIII	10	3	3.413	6.8	86.1	32.094	9.628
LAG_02031	rplM	2E+06	2E+06	447	50S ribosomal protein L13	0	0	0			0	0
LAG_02032	rpsI	2E+06	2E+06	393	30S ribosomal protein S9	0	0	0			0	0
LAG_02033	NA	2E+06	2E+06	672	hypothetical protein	149	23	34.226	1.6	98.2	625.497	96.553
LAG_02034	clsA_2	2E+06	2E+06	1449	Major cardiolipin synthase ClsA	50	9	6.211	28.9	100	97.344	17.522
LAG_02035	NA	2E+06	2E+06	73	tRNA-Ala	0	0	0			0	0
LAG_02036	tarK	2E+06	2E+06	1134	Teichoic acid ribitol-phosphate primase	271	42	37.037	7.1	92.3	674.162	104.483
LAG_02037	NA	2E+06	2E+06	1398	hypothetical protein	93	13	9.299	28.7	76.4	187.665	26.233
LAG_02038	NA	2E+06	2E+06	909	hypothetical protein	23	4	4.4	1.9	62	71.379	12.414
LAG_02039	NA	2E+06	2E+06	75	tRNA-Ala	0	0	0			0	0
LAG_02040	NA	2E+06	2E+06	672	hypothetical protein	0	0	0			0	0

LAG_02041	NA	2E+06	2E+06	474	Calcium-transporting ATPase 1	0	0	0			0	0
LAG_02042	NA	2E+06	2E+06	198	hypothetical protein	0	0	0			0	0
LAG_02043	NA	2E+06	2E+06	75	tRNA-Val	0	0	0			0	0
LAG_02044	NA	2E+06	2E+06	73	tRNA-Asp	0	0	0			0	0
LAG_02045	NA	2E+06	2E+06	73	tRNA-Lys	0	0	0			0	0
LAG_02046	NA	2E+06	2E+06	82	tRNA-Leu	0	0	0			0	0
LAG_02047	NA	2E+06	2E+06	73	tRNA-Thr	0	0	0			0	0
LAG_02048	NA	2E+06	2E+06	72	tRNA-Gly	0	0	0			0	0
LAG_02049	lacG	2E+06	2E+06	339	6-phospho-beta-galactosidase	0	0	0			0	0
LAG_02050	lacF	2E+06	2E+06	312	PTS system lactose-specific EIIA component	0	0	0			0	0
LAG_02051	NA	2E+06	2E+06	903	hypothetical protein	0	0	0			0	0
LAG_02052	NA	2E+06	2E+06	150	hypothetical protein	0	0	0			0	0
LAG_02053	NA	2E+06	2E+06	210	hypothetical protein	24	4	19.048	60	80	322.404	53.734
LAG_02054	tkt_2	2E+06	2E+06	510	Transketolase	0	0	0			0	0
LAG_02055	NA	2E+06	2E+06	204	hypothetical protein	0	0	0			0	0
LAG_02056	sacX	2E+06	2E+06	657	Negative regulator of SacY activity	0	0	0			0	0
LAG_02057	NA	2E+06	2E+06	189	hypothetical protein	15	3	15.873	3.7	85.7	223.892	44.778
LAG_02058	NA	2E+06	2E+06	204	hypothetical protein	14	3	14.706	23	49.5	193.6	41.486
LAG_02059	NA	2E+06	2E+06	204	hypothetical protein	0	0	0			0	0
LAG_02060	NA	2E+06	2E+06	660	hypothetical protein	0	0	0			0	0
LAG_02061	bglH_6	2E+06	2E+06	1233	Aryl-phospho-beta-D-glucosidase BglH	0	0	0			0	0
LAG_02062	NA	2E+06	2E+06	633	hypothetical protein	0	0	0			0	0
LAG_02063	fba_3	2E+06	2E+06	564	Fructose-bisphosphate aldolase	0	0	0			0	0
LAG_02064	aroA_2	2E+06	2E+06	477	3-phosphoshikimate 1-carboxyvinyltransferase	0	0	0			0	0

Appendix 3

Table of annotations of each coding sequence for the PIMMS output pool of the *L. garvieae* 02106 genome used in this study

Locus	Gene	Start	Stop	CDS length	Product	Total number of insertions	Number of unique insertion positions	Unique insertions per1KbCDS (>=3)	First unique insertion centile	Last unique insertion centile %	Normalised Reads Mapped (NRM) score	Normalised Insertions Mapped (NIM) score
LAG_00001	parB	309	1097	789	Putative chromosome-partitioning protein ParB	27	4	5.07	7.7	95.9	113.953	16.882
LAG_00002	dnaA	1352	2710	1359	Chromosomal replication initiator protein DnaA	13	2	1.472	95.3	98.4	31.854	4.901
LAG_00003	dnaN	2874	4016	1143	DNA polymerase III subunit beta	0	0	0			0	0
LAG_00004	rexB	4060	7383	3324	ATP-dependent helicase/deoxyribonuclease subunit B	51	5	1.504	54.4	96.4	51.091	5.009
LAG_00005	addA	7376	10939	3564	ATP-dependent helicase/nuclease subunit A	0	0	0			0	0
LAG_00006	NA	10941	11144	204	hypothetical protein	0	0	0			0	0
LAG_00007	ychF	11260	12375	1116	Ribosome-binding ATPase YchF	24	5	4.48	34.9	87.5	71.612	14.919
LAG_00008	pth	12485	13057	573	Peptidyl-tRNA hydrolase	7	1	1.745	94.2	94.2	40.68	5.811
LAG_00009	mfd	13054	16539	3486	Transcription-repair-coupling factor	78	8	2.295	1.2	94.7	74.508	7.642
LAG_00010	hslR	16659	16931	273	Heat shock protein 15	0	0	0			0	0
LAG_00011	NA	16959	17330	372	hypothetical protein	35	3	8.065	76.9	97.6	313.302	26.854
LAG_00012	pnp_1	17327	17608	282	Polyribonucleotide nucleotidyltransferase	6	1	3.546	13.1	13.1	70.85	11.808
LAG_00013	hpaH	17605	19041	1437	Anthranilate 3-monooxygenase oxygenase component	86	6	4.175	4.4	58.9	199.287	13.904
LAG_00014	NA	19022	20323	1302	hypothetical protein	52	6	4.608	17.6	80.6	132.993	15.345
LAG_00015	tilS	20320	21573	1254	tRNA(Ile)-lysidine synthase	0	0	0			0	0
LAG_00016	hpt	21566	22105	540	Hypoxanthine-guanine phosphoribosyltransferase	0	0	0			0	0
LAG_00017	ftsH	22218	24263	2046	ATP-dependent zinc metalloprotease FtsH	0	0	0			0	0
LAG_00018	NA	24488	24561	74	tRNA-Glu	0	0	0			0	0
LAG_00019	NA	24566	24655	90	tRNA-Ser	0	0	0			0	0
LAG_00020	NA	24664	24739	76	tRNA-Met	0	0	0			0	0
LAG_00021	NA	24760	24834	75	tRNA-Phe	0	0	0			0	0
LAG_00022	NA	24837	24907	71	tRNA-Gly	0	0	0			0	0
LAG_00023	NA	24947	25020	74	tRNA-Ile	0	0	0			0	0
LAG_00024	NA	25140	25217	78	tRNA-Asn	6	1	12.821	88.5	88.5	256.15	42.692
LAG_00025	NA	26502	26825	324	hypothetical protein	109	8	24.691	4.6	98.5	1120.26	82.221
LAG_00026	NA	27385	27696	312	hypothetical protein	541	18	57.692	2.2	99	5774.044	192.112
LAG_00027	NA	28167	28535	369	hypothetical protein	274	5	13.55	28.2	89.2	2472.644	45.121
LAG_00028	NA	28532	29800	1269	hypothetical protein	369	20	15.76	5.5	89.2	968.283	52.481
LAG_00029	NA	30063	30458	396	hypothetical protein	396	15	37.879	3.3	93.9	3329.948	126.134
LAG_00030	NA	30857	32623	1767	hypothetical protein	256	35	19.808	1.3	85.1	482.437	65.958
LAG_00031	NA	32620	32751	132	hypothetical protein	22	4	30.303	9.8	82.6	554.991	100.908
LAG_00032	NA	32748	33077	330	hypothetical protein	37	5	15.152	6.7	85.2	373.358	50.454
LAG_00033	NA	33167	33436	270	hypothetical protein	49	4	14.815	28.5	88.9	604.324	49.333
LAG_00034	NA	33433	33585	153	hypothetical protein	26	2	13.072	25.5	52.9	565.873	43.529
LAG_00035	NA	33582	33734	153	hypothetical protein	0	0	0			0	0
LAG_00036	NA	33724	34011	288	hypothetical protein	112	7	24.306	6.9	84	1294.98	80.936
LAG_00037	NA	34008	34190	183	hypothetical protein	0	0	0			0	0
LAG_00038	NA	34190	34483	294	hypothetical protein	24	3	10.204	5.4	77.6	271.832	33.979
LAG_00039	NA	34600	34785	186	hypothetical protein	9	1	5.376	4.3	4.3	161.127	17.903
LAG_00040	NA	34867	35484	618	hypothetical protein	92	8	12.945	6.3	86.9	495.72	43.106
LAG_00041	NA	35630	35896	267	hypothetical protein	46	3	11.236	53.2	89.5	573.699	37.415
LAG_00042	NA	35939	36145	207	hypothetical protein	0	0	0			0	0
LAG_00043	NA	36413	36796	384	hypothetical protein	50	2	5.208	96.1	97.7	433.587	17.343
LAG_00044	NA	36808	37359	552	hypothetical protein	218	17	30.797	2.9	99.1	1315.088	102.553

LAG_00045	NA	37533	37772	240	hypothetical protein	363	14	58.333	6.7	92.1	5036.546	194.247
LAG_00046	NA	37857	39170	1314	hypothetical protein	672	25	19.026	15.7	99.2	1702.987	63.355
LAG_00047	NA	39187	39777	591	hypothetical protein	130	10	16.92	33.8	97	732.476	56.344
LAG_00048	NA	39807	40205	399	hypothetical protein	426	22	55.138	18.8	96	3555.283	183.606
LAG_00049	NA	40267	41121	855	hypothetical protein	735	29	33.918	0.1	98	2862.587	112.946
LAG_00050	Int-Tn_1	41576	42757	1182	Transposase from transposon Tn916	726	45	38.071	0.7	99.5	2045.298	126.775
LAG_00051	NA	43133	43206	74	tRNA-Lys	20	4	54.054	1.4	89.2	899.986	179.997
LAG_00052	recO	43356	44150	795	DNA repair protein RecO	0	0	0			0	0
LAG_00053	pdhD	44185	45606	1422	Dihydrolipoyl dehydrogenase	0	0	0			0	0
LAG_00054	pdhC	45630	47216	1587	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenas	23	3	1.89	6.2	32.7	48.26	6.295
LAG_00055	pdhB	47209	48189	981	Pyruvate dehydrogenase E1 component subunit beta	36	4	4.077	7.2	99.1	122.2	13.578
LAG_00056	pdhA	48192	49316	1125	Pyruvate dehydrogenase E1 component subunit alpha	3	1	0.889	59.7	59.7	8.88	2.96
LAG_00057	NA	49348	50343	996	Lipoate--protein ligase 1	34	6	6.024	4.1	29.8	113.673	20.06
LAG_00058	glpQ	50548	51318	771	Glycerophosphodiester phosphodiesterase	79	8	10.376	2.5	95.3	341.201	34.552
LAG_00059	NA	51330	51968	639	hypothetical protein	16	2	3.13	30.4	36.9	83.379	10.422
LAG_00060	trpS2	51986	53017	1032	Tryptophan--tRNA ligase 2	0	0	0			0	0
LAG_00061	osmC	53436	53876	441	Peroxiredoxin OsmC	152	12	27.211	0.7	98.9	1147.737	90.611
LAG_00062	mgtA	54232	56829	2598	Magnesium-transporting ATPase, P-type 1	193	22	8.468	0.8	98.1	247.375	28.198
LAG_00063	plsX	56865	57857	993	Phosphate acyltransferase	98	5	5.035	2.2	79.8	328.635	16.767
LAG_00064	ybiV_1	57972	58781	810	Sugar phosphatase YbiV	123	13	16.049	17.4	91	505.659	53.444
LAG_00065	ybiT_1	58857	60485	1629	putative ABC transporter ATP-binding protein YbiT	17	3	1.842	1.8	89.8	34.751	6.133
LAG_00066	NA	60768	61253	486	hypothetical protein	64	8	16.461	23.9	97.1	438.512	54.814
LAG_00067	tipA	61272	62009	738	HTH-type transcriptional activator TipA	90	13	17.615	2.3	96.1	406.091	58.658
LAG_00068	yueB	62110	64806	2697	ESX secretion system protein YueB	356	35	12.977	0.3	98.8	439.548	43.214
LAG_00069	NA	64853	65383	531	hypothetical protein	11	2	3.766	67.8	96.2	68.982	12.542
LAG_00070	NA	65611	66486	876	Penicillin acylase	118	8	9.132	3.1	93.5	448.555	30.41
LAG_00071	naiP	66740	67960	1221	Putative niacin/nicotinamide transporter NaiP	248	21	17.199	1	97.6	676.353	57.272
LAG_00072	Int-Tn_2	68238	69500	1263	Transposase from transposon Tn916	298	33	26.128	3.2	97.9	785.688	87.006
LAG_00073	NA	69588	69848	261	hypothetical protein	8	1	3.831	13.8	13.8	102.067	12.758
LAG_00074	repB	69850	70455	606	Replication protein RepB	136	13	21.452	2.6	99.2	747.315	71.435
LAG_00075	NA	70578	71159	582	hypothetical protein	357	19	32.646	15.3	99.8	2042.597	108.71
LAG_00076	NA	71156	72235	1080	hypothetical protein	603	35	32.407	0.6	64.4	1859.221	107.915
LAG_00077	NA	72237	72554	318	hypothetical protein	66	9	28.302	12.3	92.8	691.121	94.244
LAG_00078	NA	72766	73548	783	hypothetical protein	480	31	39.591	3.2	99	2041.347	131.837
LAG_00079	NA	73555	73908	354	hypothetical protein	228	14	39.548	10.7	100	2144.712	131.693
LAG_00080	dinB_1	74037	74639	603	DNA polymerase IV	59	9	14.925	1.3	98.5	325.816	49.701
LAG_00081	NA	74636	74815	180	hypothetical protein	58	8	44.444	19.4	85.6	1072.983	147.998
LAG_00082	NA	74958	76190	1233	hypothetical protein	818	68	55.15	0.2	97.9	2209.163	183.647
LAG_00083	NA	76387	76974	588	hypothetical protein	101	12	20.408	1.7	98	571.981	67.958
LAG_00084	pinR	77411	77719	309	Serine recombinase PinR	139	9	29.126	13.3	96.1	1497.938	96.989
LAG_00085	NA	78180	78473	294	hypothetical protein	186	14	47.619	16.3	99	2106.702	158.569
LAG_00086	NA	78836	79756	921	hypothetical protein	328	32	34.745	0.4	97.2	1185.91	115.699
LAG_00087	NA	79965	81119	1155	hypothetical protein	784	58	50.216	2.6	98.5	2260.328	167.218
LAG_00088	hhaIM	81138	82379	1242	Modification methylase HhaI	0	0	0			0	0
LAG_00089	rpmGA	83364	83513	150	50S ribosomal protein L33 1	81	2	13.333	7.3	35.3	1798.172	44.399
LAG_00090	rpmF	83544	83717	174	50S ribosomal protein L32	0	0	0			0	0
LAG_00091	zosA	84092	85885	1794	Zinc-transporting ATPase	50	5	2.787	14.5	55.2	92.808	9.281
LAG_00092	NA	85896	87164	1269	putative AAA domain-containing protein	38	4	3.152	57.8	90.9	99.715	10.496
LAG_00093	NA	87187	87660	474	L-methionine sulfoximine/L-methionine sulfone acetyltransferase	33	4	8.439	42.4	88.6	231.832	28.101
LAG_00094	NA	87797	88261	465	hypothetical protein	0	0	0			0	0
LAG_00095	prmA	88286	89239	954	Ribosomal protein L11 methyltransferase	69	9	9.434	30.4	90.9	240.845	31.415
LAG_00096	rsmE	89242	89997	756	Ribosomal RNA small subunit methyltransferase E	88	9	11.905	20.2	99.5	387.613	39.642
LAG_00097	relA	90122	92347	2226	Bifunctional (p)ppGpp synthase/hydrolase RelA	191	14	6.289	9.2	99.3	285.723	20.943
LAG_00098	dtd	92402	92851	450	D-aminoacyl-tRNA deacylase	30	4	8.889	0.9	92.9	221.997	29.6

LAG_00099	NA	92869	93480	612	D-ribitol-5-phosphate phosphatase	105	8	13.072	9.6	93.3	571.315	43.529
LAG_00100	plsC	93603	94223	621	1-acyl-sn-glycerol-3-phosphate acyltransferase	0	0	0			0	0
LAG_00101	secA_1	94323	96896	2574	Protein translocase subunit SecA	0	0	0			0	0
LAG_00102	aroF	96996	98024	1029	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive	194	20	19.436	0.6	75.9	627.804	64.722
LAG_00103	ptsH	98181	98447	267	Phosphocarrier protein HPr	0	0	0			0	0
LAG_00104	ptsI	98447	100174	1728	Phosphoenolpyruvate-protein phosphotransferase	0	0	0			0	0
LAG_00105	NA	100296	100595	300	Nucleoid-associated protein	58	6	20	1.7	95.3	643.79	66.599
LAG_00106	NA	100748	100833	86	tRNA-Leu	0	0	0			0	0
LAG_00107	menH_1	100917	101852	936	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	245	22	23.504	0.3	89.6	871.621	78.268
LAG_00108	NA	101911	102021	111	hypothetical protein	16	2	18.018	57.7	95.5	479.992	59.999
LAG_00109	rnpA	102222	102590	369	Ribonuclease P protein component	0	0	0			0	0
LAG_00110	misCA	102587	103402	816	Membrane protein insertase MisCA	0	0	0			0	0
LAG_00111	NA	103427	104338	912	hypothetical protein	0	0	0			0	0
LAG_00112	rpmH	104459	104593	135	50S ribosomal protein L34	0	0	0			0	0
LAG_00113	ydhF	104743	105654	912	Oxidoreductase YdhF	110	6	6.579	44	100	401.638	21.908
LAG_00114	NA	105844	106110	267	hypothetical protein	0	0	0			0	0
LAG_00115	yrrK	106110	106538	429	Putative pre-16S rRNA nuclease	6	1	2.331	96.7	96.7	46.573	7.762
LAG_00116	NA	106553	106876	324	hypothetical protein	7	1	3.086	4.3	4.3	71.943	10.278
LAG_00117	NA	107017	108624	1608	hypothetical protein	74	2	1.244	1.7	4.3	153.244	4.142
LAG_00118	codY	108761	109552	792	GTP-sensing transcriptional pleiotropic repressor CodY	3	1	1.263	77.4	77.4	12.613	4.204
LAG_00119	gatC	109698	110003	306	Glutamyl-tRNA(Gln) amidotransferase subunit C	0	0	0			0	0
LAG_00120	gatA	110003	111475	1473	Glutamyl-tRNA(Gln) amidotransferase subunit A	0	0	0			0	0
LAG_00121	gatB	111477	112910	1434	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	6	1	0.697	98.5	98.5	13.933	2.322
LAG_00122	mepA	112924	114279	1356	Multidrug export protein MepA	141	16	11.799	0.6	99.5	346.256	39.291
LAG_00123	cspC	114406	114603	198	Cold shock protein CspC	46	6	30.303	11.1	65.7	773.624	100.908
LAG_00124	NA	114715	115233	519	5-formyltetrahydrofolate cyclo-ligase	149	12	23.121	38.3	88.2	955.997	76.993
LAG_00125	gluP	115223	115915	693	Rhomboid protease GluP	92	11	15.873	7.2	95.8	442.071	52.856
LAG_00126	dut	115947	116399	453	Deoxyuridine 5'-triphosphate nucleotidohydrolase	127	16	35.32	4	95.8	933.562	117.614
LAG_00127	mggB	116489	117850	1362	Mannosylglucosyl-3-phosphoglycerate phosphatase	448	23	16.887	0.7	98	1095.313	56.233
LAG_00128	NA	117834	118436	603	hypothetical protein	86	9	14.925	22.2	53.2	474.918	49.701
LAG_00129	rlmN	118533	119603	1071	putative dual-specificity RNA methyltransferase RlmN	208	18	16.807	3.2	78.2	646.713	55.966
LAG_00130	arcA	119813	121042	1230	Arginine deiminase	122	6	4.878	16.7	93.3	330.288	16.244
LAG_00131	arcB	121169	122212	1044	Ornithine carbamoyltransferase, catabolic	51	8	7.663	10.1	99.7	162.67	25.517
LAG_00132	arcD1_1	122409	123872	1464	Arginine/ornithine antiporter ArcD1	154	13	8.88	1.6	94.6	350.281	29.569
LAG_00133	arcC1	123970	124920	951	Carbamate kinase 1	72	7	7.361	63.2	85.1	252.11	24.511
LAG_00134	proX	124972	125463	492	Prolyl-tRNA editing protein ProX	98	7	14.228	81.1	93.9	663.282	47.377
LAG_00135	vioD	125474	126604	1131	Capreomycidine synthase	177	16	14.147	0.2	96.3	521.132	47.108
LAG_00136	NA	126682	127293	612	Putative NAD(P)H nitroreductase	162	11	17.974	12.9	98.7	881.457	59.852
LAG_00137	hexs-b	127400	128380	981	Hexaprenyl-diphosphate synthase large subunit ((2E,6E)-farnesyl-diphosphate spec	52	7	7.136	2.5	96.4	176.511	23.761
LAG_00138	menA_1	128384	129286	903	1,4-dihydroxy-2-naphthoate octaprenyltransferase	330	16	17.719	0.4	96	1216.924	59.002
LAG_00139	feoB	129480	131585	2106	Fe(2+) transporter FeoB	4948	68	32.289	0.8	99.1	7823.638	107.52
LAG_00140	NA	131598	132059	462	hypothetical protein	114	7	15.152	27.1	98.3	821.675	50.454
LAG_00141	NA	132232	133902	1671	hypothetical protein	25	5	2.992	56.1	93.3	49.82	9.964
LAG_00142	NA	133902	134270	369	hypothetical protein	0	0	0			0	0
LAG_00143	rpmB	134556	134750	195	50S ribosomal protein L28	35	3	15.385	47.2	80.5	597.683	51.23
LAG_00144	NA	134932	135582	651	hypothetical protein	0	0	0			0	0
LAG_00145	ctpE	135686	138004	2319	putative cation-transporting ATPase E	143	16	6.9	40	76.9	205.34	22.975
LAG_00146	rfbA	138156	139025	870	Glucose-1-phosphate thymidylyltransferase 1	0	0	0			0	0
LAG_00147	rfbC	139026	139622	597	putative dTDP-4-dehydrorhamnose 3,5-epimerase	0	0	0			0	0
LAG_00148	NA	139672	139881	210	hypothetical protein	39	2	9.524	57.1	77.1	618.419	31.714
LAG_00149	rmlB	139904	140947	1044	dTDP-glucose 4,6-dehydratase	0	0	0			0	0
LAG_00150	rmlD_1	140963	141859	897	dTDP-4-dehydrorhamnose reductase	6	2	2.23	92.1	96.8	22.274	7.425
LAG_00151	NA	141970	143121	1152	hypothetical protein	0	0	0			0	0
LAG_00152	epsE	143143	144084	942	Putative glycosyltransferase EpsE	0	0	0			0	0

LAG_00153	tagG_1	144081	144890	810	Teichoic acid translocation permease protein TagG	0	0	0			0	0
LAG_00154	tagH_1	144901	146061	1161	Teichoic acids export ATP-binding protein TagH	0	0	0			0	0
LAG_00155	pssM	146058	146948	891	Exopolysaccharide glucosyl ketal-pyruvate-transferase	0	0	0			0	0
LAG_00156	NA	146959	148293	1335	hypothetical protein	0	0	0			0	0
LAG_00157	epsJ	148312	151245	2934	putative glycosyltransferase EpsJ	0	0	0			0	0
LAG_00158	pglJ	151329	152570	1242	N-acetylgalactosamine-N, N'-diacetylbacillosaminyl-diphospho-undecaprenol 4-alph	0	0	0			0	0
LAG_00159	NA	152567	153442	876	hypothetical protein	0	0	0			0	0
LAG_00160	ppm1	153445	154176	732	Polyprenol monophosphomannose synthase	0	0	0			0	0
LAG_00161	NA	154176	154535	360	hypothetical protein	0	0	0			0	0
LAG_00162	NA	154593	155390	798	hypothetical protein	0	0	0			0	0
LAG_00163	epsH	155427	156413	987	Putative glycosyltransferase EpsH	0	0	0			0	0
LAG_00164	cpsY	156415	157422	1008	Exopolysaccharide phosphotransferase CpsY	0	0	0			0	0
LAG_00165	rfbX	157499	158908	1410	Putative O-antigen transporter	0	0	0			0	0
LAG_00166	NA	158983	160356	1374	hypothetical protein	3	1	0.728	72.3	72.3	7.271	2.424
LAG_00167	NA	160361	162148	1788	hypothetical protein	28	4	2.237	48.3	72.1	52.147	7.45
LAG_00168	ancA	162569	164170	1602	Cellulosome-anchoring protein	128	11	6.866	1.5	89.9	266.063	22.865
LAG_00169	guaB	164339	165820	1482	Inosine-5'-monophosphate dehydrogenase	11	2	1.35	96.4	99.2	24.716	4.494
LAG_00170	rpsU	165946	166122	177	30S ribosomal protein S21	0	0	0			0	0
LAG_00171	comGA	166308	167252	945	ComG operon protein 1	235	16	16.931	13.9	93.2	828.082	56.38
LAG_00172	NA	167191	168210	1020	hypothetical protein	189	21	20.588	0.4	90.2	617.02	68.558
LAG_00173	pulG	168229	168534	306	Type II secretion system protein G	114	11	35.948	4.2	94.4	1240.569	119.704
LAG_00174	NA	168786	169190	405	hypothetical protein	152	13	32.099	2	91.9	1249.758	106.887
LAG_00175	NA	169171	169611	441	hypothetical protein	235	18	40.816	2.5	94.6	1774.462	135.916
LAG_00176	znuA_1	169843	170688	846	High-affinity zinc uptake system binding-protein ZnuA	155	17	20.095	0.8	99.5	610.097	66.914
LAG_00177	NA	170759	171643	885	putative RNA pseudouridine synthase	241	22	24.859	1.2	97.1	906.799	82.778
LAG_00178	pbpF_1	171719	174007	2289	Penicillin-binding protein 1F	67	6	2.621	39.4	92.2	97.469	8.729
LAG_00179	oatA	174176	176011	1836	O-acetyltransferase OatA	279	16	8.715	12.5	93.8	506.021	29.019
LAG_00180	NA	176208	176405	198	hypothetical protein	0	0	0			0	0
LAG_00181	nusG	176514	177074	561	Transcription termination/antitermination protein NusG	0	0	0			0	0
LAG_00182	yeeO	177121	178398	1278	putative FMN/FAD exporter YeeO	339	26	20.344	2.9	89.1	883.296	67.745
LAG_00183	mscL	178436	178816	381	Large-conductance mechanosensitive channel	66	7	18.373	3.7	84.3	576.841	61.18
LAG_00184	rpsJ	179142	179450	309	30S ribosomal protein S10	0	0	0			0	0
LAG_00185	rplC	179465	180088	624	50S ribosomal protein L3	0	0	0			0	0
LAG_00186	rplD	180111	180737	627	50S ribosomal protein L4	0	0	0			0	0
LAG_00187	rplW	180737	181033	297	50S ribosomal protein L23	0	0	0			0	0
LAG_00188	rplB	181049	181882	834	50S ribosomal protein L2	0	0	0			0	0
LAG_00189	rpsS	182096	182374	279	30S ribosomal protein S19	0	0	0			0	0
LAG_00190	rplV	182390	182737	348	50S ribosomal protein L22	0	0	0			0	0
LAG_00191	rpsC	182750	183403	654	30S ribosomal protein S3	0	0	0			0	0
LAG_00192	rplP	183407	183823	417	50S ribosomal protein L16	0	0	0			0	0
LAG_00193	rpmC	183820	184029	210	50S ribosomal protein L29	0	0	0			0	0
LAG_00194	rpsQ	184048	184308	261	30S ribosomal protein S17	0	0	0			0	0
LAG_00195	rplN	184330	184698	369	50S ribosomal protein L14	0	0	0			0	0
LAG_00196	rplX	184856	185161	306	50S ribosomal protein L24	0	0	0			0	0
LAG_00197	rplE	185181	185723	543	50S ribosomal protein L5	0	0	0			0	0
LAG_00198	rpsZ	185743	185928	186	30S ribosomal protein S14 type Z	0	0	0			0	0
LAG_00199	NA	186154	187758	1605	hypothetical protein	438	40	24.922	4.9	100	908.733	82.989
LAG_00200	spxA_1	188109	188510	402	Regulatory protein Spx	246	13	32.338	3.2	90.5	2037.729	107.685
LAG_00201	ldhB	188611	189564	954	L-lactate dehydrogenase 2	223	26	27.254	0.4	97.2	778.384	90.753
LAG_00202	rmlD_2	189561	190427	867	dTDP-4-dehydrorhamnose reductase	174	16	18.454	2.2	97.5	668.294	61.452
LAG_00203	NA	190428	190538	111	hypothetical protein	9	1	9.009	18	18	269.996	30
LAG_00204	rpsH	190761	191159	399	30S ribosomal protein S8	0	0	0			0	0
LAG_00205	rplF	191247	191783	537	50S ribosomal protein L6	0	0	0			0	0
LAG_00206	rplR	191926	192273	348	50S ribosomal protein L18	0	0	0			0	0

LAG_00207	rpsE	192294	192788	495	30S ribosomal protein S5	0	0	0			0	0
LAG_00208	rpmD	192799	192981	183	50S ribosomal protein L30	0	0	0			0	0
LAG_00209	tmpC_1	193119	194168	1050	Membrane lipoprotein TmpC	218	12	11.429	7.5	78.5	691.361	38.057
LAG_00210	rplO	194370	194822	453	50S ribosomal protein L15	0	0	0			0	0
LAG_00211	secY	194893	196209	1317	Protein translocase subunit SecY	0	0	0			0	0
LAG_00212	adk	196361	197008	648	Adenylate kinase	19	1	1.543	100	100	97.637	5.139
LAG_00213	znuB	197057	197866	810	High-affinity zinc uptake system membrane protein ZnuB	21	2	2.469	95.2	96.5	86.332	8.222
LAG_00214	znuC	197859	198581	723	High-affinity zinc uptake system ATP-binding protein ZnuC	0	0	0			0	0
LAG_00215	zitR_1	198603	199046	444	Transcriptional regulator ZitR	19	4	9.009	34	63.7	142.498	30
LAG_00216	infA	199248	199466	219	Translation initiation factor IF-1	0	0	0			0	0
LAG_00217	rpsM	199653	200018	366	30S ribosomal protein S13	0	0	0			0	0
LAG_00218	rpsK	200036	200419	384	30S ribosomal protein S11	0	0	0			0	0
LAG_00219	rpoA	200471	201409	939	DNA-directed RNA polymerase subunit alpha	0	0	0			0	0
LAG_00220	rplQ	201425	201805	381	50S ribosomal protein L17	0	0	0			0	0
LAG_00221	ctc	202195	203679	1485	S-layer protein	566	54	36.364	11.6	99.3	1269.192	121.089
LAG_00222	NA	203689	204141	453	hypothetical protein	463	18	39.735	0.9	98.5	3403.457	132.316
LAG_00223	NA	204389	204461	73	tRNA-Thr	5	1	13.699	32.9	32.9	228.079	45.616
LAG_00224	radA	204794	206011	1218	DNA repair protein RadA	191	22	18.062	6.7	98.5	522.184	60.147
LAG_00225	yacL	206143	207219	1077	putative PIN and TRAM-domain containing protein YacL	21	5	4.643	26.6	82.6	64.929	15.459
LAG_00226	NA	207242	207871	630	hypothetical protein	108	12	19.048	2.9	93.2	570.848	63.428
LAG_00227	ald	208058	209179	1122	Alanine dehydrogenase	207	24	21.39	5	100	614.349	71.229
LAG_00228	NA	209210	209704	495	hypothetical protein	186	9	18.182	2.2	98.8	1251.253	60.545
LAG_00229	gltX	209850	211289	1440	Glutamate--tRNA ligase	0	0	0			0	0
LAG_00230	adh	211316	212269	954	Alcohol dehydrogenase	160	18	18.868	7.7	98.7	558.482	62.829
LAG_00231	NA	212518	218886	6369	hypothetical protein	1025	84	13.189	0	98	535.908	43.918
LAG_00232	pepX	218959	221256	2298	Xaa-Pro dipeptidyl-peptidase	423	38	16.536	0.7	99.5	612.954	55.064
LAG_00233	NA	221433	221639	207	hypothetical protein	29	5	24.155	17.4	75.4	466.514	80.434
LAG_00234	fnr_1	221983	222645	663	Anaerobic regulatory protein	74	10	15.083	2.9	65.3	371.668	50.225
LAG_00235	gla	222894	223763	870	Glycerol facilitator-aquaporin gla	42	5	5.747	1.1	29.5	160.756	19.138
LAG_00236	metQ	224306	225157	852	putative D-methionine-binding lipoprotein MetQ	365	28	32.864	2.3	99.4	1426.562	109.435
LAG_00237	metN	225179	226255	1077	Methionine import ATP-binding protein MetN	307	24	22.284	1.5	100	949.205	74.205
LAG_00238	metP	226256	226951	696	Methionine import system permease protein MetP	135	10	14.368	21.4	91.1	645.895	47.844
LAG_00239	pepV_1	226972	228393	1422	Beta-Ala-Xaa dipeptidase	231	22	15.471	1.1	97.9	540.941	51.518
LAG_00240	NA	228492	228779	288	hypothetical protein	36	4	13.889	10.4	96.5	416.243	46.249
LAG_00241	hcaR	228951	229856	906	Hca operon transcriptional activator HcaR	108	10	11.038	22.5	94.6	396.947	36.754
LAG_00242	gpmA_1	229954	230655	702	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	0	0	0			0	0
LAG_00243	penA	230782	232938	2157	Penicillin-binding protein 2B	4	1	0.464	99.3	99.3	6.175	1.544
LAG_00244	NA	232976	233908	933	hypothetical protein	113	16	17.149	3.1	98.1	403.306	57.105
LAG_00245	cysL	234067	234909	843	HTH-type transcriptional regulator CysL	170	17	20.166	4.4	95.4	671.52	67.152
LAG_00246	NA	234872	235789	918	Monoacylglycerol lipase	215	17	18.519	2.7	95.3	779.89	61.666
LAG_00247	recR	236057	236659	603	Recombination protein RecR	0	0	0			0	0
LAG_00248	ddl	236672	237721	1050	D-alanine--D-alanine ligase	13	1	0.952	96.1	96.1	41.228	3.171
LAG_00249	ricR	237961	238227	267	Copper-sensing transcriptional repressor RicR	77	5	18.727	16.9	96.3	960.322	62.359
LAG_00250	murF_1	238333	239664	1332	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	22	1	0.751	97.7	97.7	54.999	2.5
LAG_00251	oppA	239979	241652	1674	Oligopeptide-binding protein OppA	435	28	16.726	0.5	97.7	865.309	55.698
LAG_00252	oppB	241726	242643	918	Oligopeptide transport system permease protein OppB	171	16	17.429	0.2	98.9	620.284	58.038
LAG_00253	dppC	242659	243693	1035	Dipeptide transport system permease protein DppC	232	16	15.459	1.4	88.1	746.423	51.477
LAG_00254	oppD	243710	244771	1062	Oligopeptide transport ATP-binding protein OppD	93	12	11.299	16.3	90.4	291.606	37.627
LAG_00255	oppF	244771	245706	936	Oligopeptide transport ATP-binding protein OppF	144	18	19.231	2.1	92.8	512.3	64.037
LAG_00256	NA	245859	246302	444	hypothetical protein	22	4	9.009	71.6	92.1	164.997	30
LAG_00257	prfC	246410	247981	1572	Peptide chain release factor 3	85	14	8.906	10.9	97.7	180.054	29.656
LAG_00258	ltaS	248139	250742	2604	Lipoteichoic acid synthase	550	50	19.201	3.8	97.1	703.33	63.939
LAG_00259	cshA	250964	252583	1620	ATP-dependent RNA helicase CshA	33	6	3.704	34	95.1	67.832	12.333
LAG_00260	sipW	253310	254470	1161	Signal peptidase I W	164	13	11.197	29.1	88.5	470.38	37.286

LAG_00261	NA	254445	255509	1065	hypothetical protein	179	18	16.901	6.9	96.2	559.681	56.281
LAG_00262	NA	255611	256633	1023	hypothetical protein	160	13	12.708	0.7	99	520.813	42.316
LAG_00263	cna_1	256672	259734	3063	Collagen adhesin	215	25	8.162	2.8	94	233.738	27.179
LAG_00264	era	260748	261659	912	GTPase Era	3	1	1.096	24.1	24.1	10.954	3.651
LAG_00265	mutM	261850	262674	825	Formamidopyrimidine-DNA glycosylase	81	7	8.485	9.8	86.3	326.94	28.254
LAG_00266	recA	262775	263926	1152	Protein RecA	24	2	1.736	95.9	99.6	69.374	5.781
LAG_00267	cycA	263963	265327	1365	D-serine/D-alanine/glycine transporter	257	28	20.513	5.4	98.4	626.957	68.307
LAG_00268	NA	265532	265906	375	hypothetical protein	30	5	13.333	13.6	90.1	266.396	44.399
LAG_00269	NA	265890	266246	357	hypothetical protein	26	6	16.807	0.3	90.2	242.517	55.966
LAG_00270	NA	266304	266822	519	hypothetical protein	235	21	40.462	3.7	94.8	1507.78	134.738
LAG_00271	yjbK	266952	267515	564	Putative triphosphatase YjbK	167	11	19.504	13.3	88.1	985.995	64.946
LAG_00272	yjbM	267866	268546	681	GTP pyrophosphokinase YjbM	41	2	2.937	87.1	93.2	200.481	9.78
LAG_00273	nadK	268533	269345	813	NAD kinase	6	1	1.23	98.6	98.6	24.575	4.096
LAG_00274	rluD_1	269558	270439	882	Ribosomal large subunit pseudouridine synthase D	296	20	22.676	3.2	99.7	1117.534	75.509
LAG_00275	NA	270966	271724	759	Putative peptidyl-prolyl cis-trans isomerase	289	21	27.668	0.8	81.8	1267.925	92.133
LAG_00276	lysP_1	271944	273479	1536	Lysine-specific permease	194	25	16.276	0.8	98.7	420.579	54.198
LAG_00277	artP	273492	274295	804	Arginine-binding extracellular protein ArtP	194	23	28.607	4.6	98.3	803.495	95.26
LAG_00278	nfr2	274352	274948	597	NADH-dependent flavin reductase subunit 2	0	0	0			0	0
LAG_00279	apbE_1	274941	275900	960	FAD:protein FMN transferase	23	6	6.25	17.3	96.8	79.78	20.812
LAG_00280	NA	275920	277518	1599	hypothetical protein	427	31	19.387	0.9	99.8	889.236	64.558
LAG_00281	lysS	277614	279101	1488	Lysine--tRNA ligase	0	0	0			0	0
LAG_00282	NA	279520	281358	1839	hypothetical protein	261	25	13.594	5.1	97.9	472.603	45.268
LAG_00283	NA	281373	281861	489	hypothetical protein	80	12	24.54	12.9	99.4	544.777	81.717
LAG_00284	NA	281883	282671	789	hypothetical protein	132	10	12.674	4.2	88.5	557.102	42.205
LAG_00285	kdgT	283022	284029	1008	2-keto-3-deoxygluconate permease	323	25	24.802	0.7	97.9	1067.037	82.588
LAG_00286	thiI	284119	285339	1221	putative tRNA sulfurtransferase	101	10	8.19	31.6	99.2	275.45	27.272
LAG_00287	ribZ_1	285405	286832	1428	Riboflavin transporter RibZ	246	38	26.611	2.4	96	573.646	88.612
LAG_00288	nhaK_1	286853	288943	2091	Sodium, potassium, lithium and rubidium/H(+) antiporter	452	31	14.825	0	92.6	719.817	49.368
LAG_00289	NA	289022	289489	468	hypothetical protein	111	9	19.231	7.5	98.3	789.795	64.037
LAG_00290	tyrS	289614	290873	1260	Tyrosine--tRNA ligase	0	0	0			0	0
LAG_00291	pbpF_2	291010	293433	2424	Penicillin-binding protein 1F	199	24	9.901	4.6	94.1	273.374	32.97
LAG_00292	ogt_1	293512	294021	510	Methylated-DNA--protein-cysteine methyltransferase	20	3	5.882	3.3	96.3	130.586	19.588
LAG_00293	ogt_2	294011	294415	405	Methylated-DNA--protein-cysteine methyltransferase, constitutive	28	5	12.346	32.1	88.6	230.219	41.11
LAG_00294	NA	294432	295115	684	hypothetical protein	82	9	13.158	0.4	89.5	399.204	43.815
LAG_00295	pepA	295226	296293	1068	Glutamyl aminopeptidase	145	13	12.172	0.1	99.7	452.1	40.533
LAG_00296	NA	296494	296781	288	hypothetical protein	0	0	0			0	0
LAG_00297	ytpP	296778	297098	321	Thioredoxin-like protein YtpP	10	1	3.115	93.5	93.5	103.737	10.374
LAG_00298	pheT_1	297100	297723	624	Phenylalanine--tRNA ligase beta subunit	116	13	20.833	0.6	99.4	619.029	69.374
LAG_00299	ssbA	297793	298182	390	Single-stranded DNA-binding protein A	80	9	23.077	5.9	95.4	683.066	76.845
LAG_00300	NA	298239	298769	531	hypothetical protein	93	8	15.066	0.6	64.6	583.211	50.169
LAG_00301	groS	298887	299168	282	10 kDa chaperonin	0	0	0			0	0
LAG_00302	groL	299198	300823	1626	60 kDa chaperonin	7	1	0.615	97.9	97.9	14.336	2.048
LAG_00303	yycJ	300873	301685	813	Putative metallo-hydrolase YycJ	130	15	18.45	2	100	532.464	61.438
LAG_00304	walK_1	301682	303100	1419	Sensor histidine kinase WalK	279	30	21.142	5.8	94.1	654.725	70.401
LAG_00305	walR_1	303093	303794	702	Transcriptional regulatory protein WalR	0	0	0			0	0
LAG_00306	tmk	304005	304634	630	Thymidylate kinase	0	0	0			0	0
LAG_00307	dnaX_1	304660	305523	864	DNA polymerase III subunit gamma/tau	0	0	0			0	0
LAG_00308	NA	305536	306309	774	hypothetical protein	76	8	10.336	4.3	94.3	326.972	34.418
LAG_00309	yabA	306334	306675	342	Initiation-control protein YabA	0	0	0			0	0
LAG_00310	rsmI	306672	307538	867	Ribosomal RNA small subunit methyltransferase I	87	12	13.841	22	96	334.147	46.089
LAG_00311	tcyK	307668	308510	843	L-cystine-binding protein TcyK	90	12	14.235	2.7	98.9	355.51	47.401
LAG_00312	NA	308530	308718	189	hypothetical protein	64	8	42.328	4.2	96.8	1127.601	140.95
LAG_00313	galK_1	308883	309815	933	Galactokinase	3	1	1.072	95.6	95.6	10.707	3.569
LAG_00314	teaD	309963	310376	414	TRAP-T-associated universal stress protein TeaD	34	4	9.662	28.7	41.8	273.474	32.173

LAG_00315	thrB	310559	311506	948	Homoserine kinase	0	0	0			0	0
LAG_00316	NA	311478	312434	957	Phosphomevalonate kinase	0	0	0			0	0
LAG_00317	fni	312427	313482	1056	Isopentenyl-diphosphate delta-isomerase	0	0	0			0	0
LAG_00318	sodA	313535	314143	609	Superoxide dismutase [Mn]	51	6	9.852	88	98.9	278.863	32.807
LAG_00319	cshB	314263	315603	1341	DEAD-box ATP-dependent RNA helicase CshB	51	7	5.22	35.6	98.7	126.642	17.382
LAG_00320	NA	315603	316187	585	hypothetical protein	276	23	39.316	0.9	100	1571.052	130.921
LAG_00321	glvR	316207	316947	741	HTH-type transcriptional regulator GlvR	338	27	36.437	1.8	94.7	1518.924	121.334
LAG_00322	licB_1	317162	317488	327	Lichenan-specific phosphotransferase enzyme IIB component	57	12	36.697	2.8	79.5	580.45	122.2
LAG_00323	licC_1	317513	318853	1341	Lichenan permease IIC component	602	44	32.811	0.1	99.8	1494.876	109.26
LAG_00324	bglA	319054	320556	1503	Aryl-phospho-beta-D-glucosidase BglA	285	28	18.629	11.8	98.1	631.427	62.035
LAG_00325	bglC	320556	321992	1437	Aryl-phospho-beta-D-glucosidase BglC	621	28	19.485	1	98.3	1439.038	64.884
LAG_00326	licB_2	322084	322404	321	Lichenan-specific phosphotransferase enzyme IIB component	53	9	28.037	2.8	89.4	549.804	93.363
LAG_00327	licA	322439	322771	333	Lichenan-specific phosphotransferase enzyme IIA component	47	8	24.024	57.1	99.1	469.993	79.999
LAG_00328	NA	322913	322983	71	tRNA-Cys	0	0	0			0	0
LAG_00329	NA	323427	324494	1068	hypothetical protein	499	21	19.663	1	99.7	1555.846	65.477
LAG_00330	lmrA	324631	326376	1746	Multidrug resistance ABC transporter ATP-binding and permease protein	435	33	18.9	2.6	91.5	829.626	62.937
LAG_00331	ponA_1	326419	328560	2142	Penicillin-binding protein 1A/1B	307	30	14.006	0.5	99.9	477.261	46.638
LAG_00332	NA	328560	329681	1122	hypothetical protein	266	22	19.608	2.7	98.7	789.453	65.293
LAG_00333	ligA	329785	331752	1968	DNA ligase	0	0	0			0	0
LAG_00334	dagK_1	331749	332753	1005	Diacylglycerol kinase	71	7	6.965	24.4	83.1	235.25	23.194
LAG_00335	NA	333064	334809	1746	hypothetical protein	191	26	14.891	5.6	99.9	364.273	49.587
LAG_00336	sugC	334952	336088	1137	Trehalose import ATP-binding protein SugC	108	11	9.675	17.2	94.5	316.301	32.216
LAG_00337	por	336349	339996	3648	Pyruvate synthase	368	40	10.965	1.9	95.4	335.916	36.513
LAG_00338	cdaA	340111	340938	828	Cyclic di-AMP synthase CdaA	0	0	0			0	0
LAG_00339	cdaR	340938	341891	954	CdaA regulatory protein CdaR	0	0	0			0	0
LAG_00340	glmM	341922	343283	1362	Phosphoglucosamine mutase	5	1	0.734	99.3	99.3	12.224	2.445
LAG_00341	tsaE	343477	343932	456	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	0	0	0			0	0
LAG_00342	mshD	343929	344444	516	Mycothiol acetyltransferase	47	5	9.69	18.4	87.4	303.309	32.267
LAG_00343	brpA	344568	345914	1347	Biofilm regulatory protein A	248	12	8.909	70.8	94.4	613.086	29.665
LAG_00344	NA	345977	346052	76	tRNA-Arg	0	0	0			0	0
LAG_00345	NA	346209	346799	591	hypothetical protein	293	28	47.377	2.7	84.3	1650.888	157.764
LAG_00346	NA	346811	347155	345	hypothetical protein	0	0	0			0	0
LAG_00347	NA	347436	347642	207	hypothetical protein	8	2	9.662	16.4	36.7	128.694	32.173
LAG_00348	NA	347654	347869	216	hypothetical protein	35	3	13.889	49.1	85.6	539.575	46.249
LAG_00349	truA	348095	348829	735	tRNA pseudouridine synthase A	4	1	1.361	83	83	18.122	4.531
LAG_00350	pdxK	348822	349655	834	Pyridoxine/pyridoxal/pyridoxamine kinase	0	0	0			0	0
LAG_00351	hmpT	349652	350134	483	Thiamine precursor transporter HmpT	32	6	12.422	6	72.3	220.618	41.366
LAG_00352	NA	350115	350657	543	hypothetical protein	18	4	7.366	67.2	93.6	110.385	24.53
LAG_00353	pyrG	351142	352746	1605	CTP synthase	3	1	0.623	99.4	99.4	6.224	2.075
LAG_00354	maa	352852	353469	618	Maltose O-acetyltransferase	153	19	30.744	2.3	95	824.405	102.377
LAG_00355	NA	353506	353682	177	hypothetical protein	16	2	11.299	19.8	94.4	301.012	37.627
LAG_00356	dnaE	353789	356905	3117	DNA polymerase III subunit alpha	12	1	0.321	99.3	99.3	12.82	1.068
LAG_00357	NA	356915	357568	654	hypothetical protein	55	8	12.232	17.7	98.6	280.041	40.733
LAG_00358	NA	357736	358572	837	DegV domain-containing protein	45	8	9.558	24.1	98.4	179.029	31.827
LAG_00359	lipC	358565	359389	825	Spore germination lipase LipC	132	14	16.97	4.5	87.9	532.792	56.508
LAG_00360	NA	359379	359963	585	hypothetical protein	63	4	6.838	59	80.2	358.61	22.769
LAG_00361	hup	360081	360356	276	DNA-binding protein HU	0	0	0			0	0
LAG_00362	iscS_1	360573	361745	1173	Cysteine desulfurase IscS	116	16	13.64	7.9	85.8	329.304	45.421
LAG_00363	cysK	361856	362776	921	Cysteine synthase	166	20	21.716	0.3	87.2	600.186	72.312
LAG_00364	NA	362961	363890	930	Autolysin	100	5	5.376	49.6	84.8	358.059	17.903
LAG_00365	NA	363993	364619	627	putative metallo-hydrolase	67	11	17.544	6.2	99.5	355.832	58.42
LAG_00366	ponA_2	364623	366710	2088	Penicillin-binding protein 1A	73	11	5.268	9.1	82.7	116.421	17.543
LAG_00367	recU	366742	367392	651	Holliday junction resolvase RecU	0	0	0			0	0
LAG_00368	NA	367665	368192	528	hypothetical protein	57	4	7.576	16.5	80.3	359.483	25.227

LAG_00369	spxA_2	368329	368721	393	Regulatory protein Spx	4	1	2.545	88.3	88.3	33.893	8.473
LAG_00370	NA	368745	369026	282	hypothetical protein	15	2	7.092	60.3	75.2	177.125	23.617
LAG_00371	suhB	368992	369780	789	Fructose-1, 6-bisphosphatase/inositol-1-monophosphatase	103	9	11.407	10.6	99.6	434.708	37.984
LAG_00372	murAA	369853	371136	1284	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	86	5	3.894	34.3	98.4	223.034	12.967
LAG_00373	NA	371129	371314	186	hypothetical protein	10	3	16.129	16.1	97.8	179.029	53.709
LAG_00374	tig	371468	372751	1284	Trigger factor	0	0	0			0	0
LAG_00375	NA	372908	373240	333	HTH-type transcriptional regulator	132	11	33.033	6.3	93.1	1319.979	109.998
LAG_00376	hchA_1	373237	373914	678	Molecular chaperone Hsp31 and glyoxalase 3	111	12	17.699	16.7	76.8	545.168	58.937
LAG_00377	NA	373914	374834	921	hypothetical protein	239	21	22.801	0.2	99.3	864.123	75.927
LAG_00378	yjjG	374932	375621	690	Pyrimidine 5'-nucleotidase YjjG	124	16	23.188	0.1	95.4	598.425	77.216
LAG_00379	NA	375673	375744	72	tRNA-Arg	3	1	13.889	87.5	87.5	138.748	46.249
LAG_00380	rnz	375931	376863	933	Ribonuclease Z	0	0	0			0	0
LAG_00381	ephD	376844	377491	648	putative oxidoreductase EphD	65	6	9.259	22.7	90.6	334.023	30.833
LAG_00382	recJ	377524	379758	2235	Single-stranded-DNA-specific exonuclease RecJ	67	8	3.579	1.2	98	99.824	11.919
LAG_00383	apt	379748	380260	513	Adenine phosphoribosyltransferase	7	2	3.899	17.3	18.5	45.438	12.982
LAG_00384	rpoE	380386	380946	561	putative DNA-directed RNA polymerase subunit delta	0	0	0			0	0
LAG_00385	mltG	381052	382767	1716	Endolytic murein transglycosylase	52	6	3.497	58.6	88.2	100.908	11.643
LAG_00386	greA	382792	383265	474	Transcription elongation factor GreA	0	0	0			0	0
LAG_00387	ctsR	383385	383837	453	Transcriptional regulator CtsR	8	2	4.415	6.2	36.2	58.807	14.702
LAG_00388	clpC	383827	386277	2451	ATP-dependent Clp protease ATP-binding subunit ClpC	173	25	10.2	5.8	86.7	235.039	33.965
LAG_00389	hpf_1	386400	386957	558	Ribosome hibernation promotion factor	102	6	10.753	21.1	60.6	608.7	35.806
LAG_00390	pflB	387205	389538	2334	Formate acetyltransferase	340	34	14.567	5.7	99	485.082	48.508
LAG_00391	coaE	389777	390382	606	Dephospho-CoA kinase	6	1	1.65	97.9	97.9	32.97	5.495
LAG_00392	yjhB	390429	391619	1191	Putative metabolite transport protein YjhB	186	24	20.151	1.3	99	520.042	67.102
LAG_00393	ftsW	391895	393118	1224	putative peptidoglycan glycosyltransferase FtsW	25	3	2.451	95.8	99.2	68.014	8.162
LAG_00394	cfiB	393551	396970	3420	2-oxoglutarate carboxylase small subunit	726	66	19.298	0.1	88.7	706.884	64.262
LAG_00395	clpP	397016	397615	600	ATP-dependent Clp protease proteolytic subunit	6	2	3.333	81.2	88.2	33.299	11.1
LAG_00396	NA	397795	398172	378	hypothetical protein	58	7	18.519	6.9	97.4	510.944	61.666
LAG_00397	NA	398232	398762	531	hypothetical protein	36	4	7.533	52.9	63.1	225.759	25.084
LAG_00398	spxA_3	398924	399322	399	Regulatory protein Spx	11	1	2.506	93.5	93.5	91.803	8.346
LAG_00399	dtd3	399458	400231	774	D-aminoacyl-tRNA deacylase	39	8	10.336	1.4	95.3	167.788	34.418
LAG_00400	rnmV	400228	400773	546	Ribonuclease M5	71	8	14.652	6.4	97.3	433.015	48.79
LAG_00401	drrA	400770	401696	927	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA	167	17	18.339	1.8	95.9	599.894	61.067
LAG_00402	yadH	401689	402459	771	Inner membrane transport permease YadH	184	19	24.643	7.1	88.8	794.696	82.061
LAG_00403	rbsR_1	402520	403488	969	Ribose operon repressor	131	19	19.608	3.1	94.3	450.179	65.293
LAG_00404	scrB	403488	404903	1416	Sucrose-6-phosphate hydrolase	82	11	7.768	18.6	99.2	192.836	25.868
LAG_00405	treP	405086	407023	1938	PTS system trehalose-specific EIIBC component	394	33	17.028	4.4	98.9	676.986	56.702
LAG_00406	gmuE	407046	407915	870	Putative fructokinase	122	10	11.494	2.3	98	466.958	38.275
LAG_00407	rsmA	408033	408980	948	Ribosomal RNA small subunit methyltransferase A	6	1	1.055	21.7	21.7	21.076	3.513
LAG_00408	NA	408981	409562	582	hypothetical protein	80	6	10.309	27.7	96.2	457.725	34.329
LAG_00409	NA	409660	410106	447	Acetyltransferase	11	3	6.711	8.1	29.3	81.945	22.349
LAG_00410	tqsA	410216	411337	1122	AI-2 transport protein TqsA	110	17	15.152	3	98.4	326.465	50.454
LAG_00411	corC_1	411383	412711	1329	Magnesium and cobalt efflux protein CorC	167	16	12.039	2.9	84.1	418.436	40.09
LAG_00412	bmr3	412824	414284	1461	Multidrug resistance protein 3	226	28	19.165	0.5	71.5	515.105	63.818
LAG_00413	pflA	414351	415145	795	Pyruvate formate-lyase 1-activating enzyme	76	10	12.579	6.8	87.7	318.335	41.886
LAG_00414	ppaC	415291	416235	945	putative manganese-dependent inorganic pyrophosphatase	6	1	1.058	95.9	95.9	21.143	3.524
LAG_00415	NA	416235	416999	765	hypothetical protein	133	12	15.686	0.5	90.5	578.932	52.234
LAG_00416	pepT	417002	418243	1242	Peptidase T	246	23	18.519	5	97.7	659.555	61.666
LAG_00417	yjeM_1	418583	420184	1602	Inner membrane transporter YjeM	180	15	9.363	4.4	95.5	374.151	31.179
LAG_00418	murE	420245	421696	1452	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L- lysine ligase	0	0	0			0	0
LAG_00419	NA	421890	422768	879	hypothetical protein	281	20	22.753	19.5	98.6	1064.523	75.767
LAG_00420	NA	423049	423384	336	hypothetical protein	49	4	11.905	8.3	77.4	485.617	39.642
LAG_00421	NA	423381	423548	168	hypothetical protein	64	4	23.81	44	76.2	1268.552	79.284
LAG_00422	NA	423557	424111	555	hypothetical protein	127	13	23.423	2.3	67.9	761.988	77.999

LAG_00423	murJ	424225	425943	1719	Lipid II flippase MurJ	0	0	0			0	0
LAG_00424	pepO	426039	427922	1884	Neutral endopeptidase	117	13	6.9	11.5	89.3	206.796	22.977
LAG_00425	NA	427916	428227	312	DNA base-flipping protein	3	1	3.205	25	25	32.019	10.673
LAG_00426	rpoB	428511	432101	3591	DNA-directed RNA polymerase subunit beta	0	0	0			0	0
LAG_00427	rpoC	432421	436068	3648	DNA-directed RNA polymerase subunit beta'	0	0	0			0	0
LAG_00428	ytlR	436161	437069	909	Putative lipid kinase YtlR	320	31	34.103	1.7	100	1172.259	113.563
LAG_00429	mecA	437316	437999	684	Adapter protein MecA	32	2	2.924	57.6	63.7	155.787	9.737
LAG_00430	tagO	438003	439259	1257	putative undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase	13	3	2.387	89.2	97.9	34.439	7.947
LAG_00431	NA	439337	440107	771	putative ABC transporter ATP-binding protein	91	9	11.673	10.2	92.1	393.029	38.871
LAG_00432	sufB_1	440179	441435	1257	FeS cluster assembly protein SufB	72	9	7.16	5.6	97.6	190.737	23.842
LAG_00433	sufS	441435	442646	1212	Cysteine desulfurase SufS	26	3	2.475	1.1	72.9	71.435	8.242
LAG_00434	iscU	442671	443126	456	Iron-sulfur cluster assembly scaffold protein IscU	24	4	8.772	22.1	68.9	175.26	29.21
LAG_00435	sufB_2	443151	444548	1398	FeS cluster assembly protein SufB	141	20	14.306	14.4	92.8	335.853	47.639
LAG_00436	NA	444845	445489	645	hypothetical protein	255	22	34.109	4.2	99.7	1316.491	113.58
LAG_00437	ybiT_2	445636	447192	1557	putative ABC transporter ATP-binding protein YbiT	277	38	24.406	0.3	99.7	592.418	81.27
LAG_00438	ybiR	447358	448533	1176	Inner membrane protein YbiR	401	31	26.361	0.2	99.7	1135.467	87.779
LAG_00439	comEA	448591	449235	645	ComE operon protein 1	160	15	23.256	4.3	100	826.034	77.441
LAG_00440	comEC	449255	451465	2211	ComE operon protein 3	731	68	30.755	4.3	99.1	1100.946	102.414
LAG_00441	axe1-6A	451620	452396	777	Carbohydrate acetyl esterase/feruloyl esterase	171	18	23.166	5.4	92	732.846	77.142
LAG_00442	atpE	452592	452807	216	ATP synthase subunit c	0	0	0			0	0
LAG_00443	atpB	452862	453575	714	ATP synthase subunit a	0	0	0			0	0
LAG_00444	atpF	453589	454095	507	ATP synthase subunit b	0	0	0			0	0
LAG_00445	atpH	454110	454637	528	ATP synthase subunit delta	0	0	0			0	0
LAG_00446	atpA	454703	456211	1509	ATP synthase subunit alpha	0	0	0			0	0
LAG_00447	atpG	456223	457104	882	ATP synthase gamma chain	0	0	0			0	0
LAG_00448	atpD	457164	458573	1410	ATP synthase subunit beta	4	1	0.709	3.4	3.4	9.447	2.362
LAG_00449	atpC	458591	459016	426	ATP synthase epsilon chain	18	4	9.39	87.1	99.8	140.702	31.267
LAG_00450	NA	459203	459874	672	hypothetical protein	371	24	35.714	6.2	87.8	1838.409	118.927
LAG_00451	NA	459906	460727	822	hypothetical protein	251	27	32.847	0.9	99	1016.809	109.378
LAG_00452	NA	460816	461733	918	L-2-hydroxyisocaproate dehydrogenase	232	19	20.697	2.5	97.3	841.555	68.92
LAG_00453	gpmA_2	461847	462551	705	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	55	3	4.255	0.6	45.4	259.783	14.17
LAG_00454	vanYB	462535	463320	786	D-alanyl-D-alanine carboxypeptidase	28	7	8.906	24.6	92.5	118.624	29.656
LAG_00455	NA	463352	463756	405	hypothetical protein	71	9	22.222	10.6	70.9	583.769	73.999
LAG_00456	hrcA	463895	464932	1038	Heat-inducible transcription repressor HrcA	0	0	0			0	0
LAG_00457	grpE	464966	465508	543	Protein GrpE	0	0	0			0	0
LAG_00458	dnaK	465586	467412	1827	Chaperone protein DnaK	0	0	0			0	0
LAG_00459	spxA_4	467561	467959	399	Regulatory protein Spx	3	1	2.506	46.9	46.9	25.037	8.346
LAG_00460	glcR	468137	468838	702	HTH-type transcriptional repressor GlcR	49	6	8.547	7.1	47	232.432	28.461
LAG_00461	lacC_1	468835	469761	927	Tagatose-6-phosphate kinase	10	1	1.079	98.3	98.3	35.922	3.592
LAG_00462	fruA_1	469776	471680	1905	PTS system fructose-specific EIIABC component	210	23	12.073	10.4	99.6	367.081	40.204
LAG_00463	rpmE2	471792	472034	243	50S ribosomal protein L31 type B	8	1	4.115	93.4	93.4	109.628	13.703
LAG_00464	NA	472251	472802	552	hypothetical protein	0	0	0			0	0
LAG_00465	arlR_1	472904	473599	696	Response regulator ArlR	4	1	1.437	100	100	19.138	4.784
LAG_00466	arlS_1	473687	475177	1491	Signal transduction histidine-protein kinase ArlS	32	5	3.353	15.4	97.6	71.468	11.167
LAG_00467	glnP	475573	477144	1572	Glutamine transport system permease protein GlnP	342	43	27.354	0.6	93.4	724.454	91.086
LAG_00468	artM_1	477145	477882	738	Arginine transport ATP-binding protein ArtM	140	16	21.68	11.7	94.9	631.697	72.194
LAG_00469	murD	478022	479383	1362	UDP-N-acetylmuramoylalanine--D-glutamate ligase	0	0	0			0	0
LAG_00470	murG	479385	480479	1095	UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecapr	0	0	0			0	0
LAG_00471	divIB	480479	481516	1038	Cell division protein DivIB	9	2	1.927	88.2	98	28.872	6.416
LAG_00472	artM_2	481612	482349	738	Arginine transport ATP-binding protein ArtM	5	1	1.355	44.2	44.2	22.561	4.512
LAG_00473	tcyB	482363	484507	2145	L-cystine transport system permease protein TcyB	12	1	0.466	32.2	32.2	18.629	1.552
LAG_00474	NA	484746	485402	657	putative membrane protein	24	5	7.61	3.8	60.7	121.642	25.342
LAG_00475	aroE	485476	486342	867	Shikimate dehydrogenase (NADP(+))	66	8	9.227	13.4	97.3	253.491	30.726

LAG_00476	aroB	486326	487387	1062	3-dehydroquinate synthase	39	4	3.766	21.6	88.9	122.286	12.542
LAG_00477	NA	487384	487497	114	hypothetical protein	3	1	8.772	93.9	93.9	87.63	29.21
LAG_00478	NA	487816	488742	927	hypothetical protein	37	5	5.394	31.6	88.5	132.911	17.961
LAG_00479	NA	488749	489339	591	hypothetical protein	219	11	18.613	20.1	89	1233.94	61.979
LAG_00480	aroC	489341	490510	1170	Chorismate synthase	52	9	7.692	31.4	99.1	147.998	25.615
LAG_00481	NA	490644	490994	351	hypothetical protein	28	4	11.396	26.2	78.9	265.637	37.948
LAG_00482	yxdL	491022	491810	789	ABC transporter ATP-binding protein YxdL	192	14	17.744	5.1	95.1	810.33	59.087
LAG_00483	bceB	491803	493776	1974	Bacitracin export permease protein BceB	466	47	23.81	0.2	88	786.097	79.284
LAG_00484	NA	493777	493995	219	hypothetical protein	0	0	0			0	0
LAG_00485	graR	494105	494761	657	Response regulator protein GraR	121	15	22.831	0.6	96.7	613.278	76.026
LAG_00486	graS	494748	495638	891	Sensor histidine kinase GraS	132	17	19.08	0.4	76	493.326	63.534
LAG_00487	NA	495628	496185	558	hypothetical protein	140	13	23.297	6.1	99.8	835.471	77.579
LAG_00488	aroA_1	496305	497615	1311	3-phosphoshikimate 1-carboxyvinyltransferase	264	22	16.781	1.5	97.3	670.562	55.88
LAG_00489	aroK	497606	498091	486	Shikimate kinase	172	13	26.749	16.9	87.9	1178.5	89.073
LAG_00490	pspB_1	498088	498684	597	Putative phosphoserine phosphatase 2	4	1	1.675	4.4	4.4	22.311	5.578
LAG_00491	recD2	498681	501122	2442	ATP-dependent RecD-like DNA helicase	83	11	4.505	3.2	99.4	113.18	15
LAG_00492	NA	501169	501378	210	hypothetical protein	45	6	28.571	19.5	90	713.56	95.141
LAG_00493	rny_1	501809	502318	510	Ribonuclease Y	92	5	9.804	6.9	90.6	600.696	32.647
LAG_00494	rpsT	502469	502702	234	30S ribosomal protein S20	29	5	21.368	40.2	98.7	412.686	71.153
LAG_00495	NA	502938	503597	660	hypothetical protein	112	11	16.667	31.5	99.4	565.082	55.499
LAG_00496	ung	503594	504253	660	Uracil-DNA glycosylase	153	15	22.727	4.2	95.9	771.942	75.681
LAG_00497	ybhL	504357	505061	705	Inner membrane protein YbhL	191	17	24.113	22.6	94.5	902.156	80.297
LAG_00498	yitU	505118	505942	825	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YitU	80	10	12.121	0.6	98.3	322.904	40.363
LAG_00499	pbuO	506306	507727	1422	Guanine/hypoxanthine permease PbuO	193	16	11.252	1.3	78.8	451.955	37.468
LAG_00500	NA	507805	508905	1101	hypothetical protein	74	11	9.991	3.5	94.4	223.811	33.269
LAG_00501	coiA	508981	509985	1005	Competence protein CoiA	172	18	17.91	0.4	94.7	569.902	59.641
LAG_00502	pepF1	509969	511774	1806	Oligoendopeptidase F, plasmid	158	21	11.628	9.6	80.1	291.324	38.72
LAG_00503	prmC_1	511774	512457	684	Release factor glutamine methyltransferase	16	3	4.386	26.9	96.6	77.894	14.605
LAG_00504	prsA	512555	513463	909	Foldase protein PrsA	59	6	6.601	36.5	91.9	216.135	21.98
LAG_00505	alaS	513713	516331	2619	Alanine--tRNA ligase	14	2	0.764	97.8	99.4	17.8	2.543
LAG_00506	rpiR_1	516671	517462	792	HTH-type transcriptional regulator RpiR	233	16	20.202	5.1	79.8	979.644	67.272
LAG_00507	glpF_1	517480	517737	258	putative glycerol uptake facilitator protein	123	7	27.132	6.2	65.9	1587.533	90.347
LAG_00508	pspB_2	517846	518403	558	Putative phosphoserine phosphatase 2	66	10	17.921	37.5	98	393.865	59.676
LAG_00509	bglH_1	518707	520140	1434	Aryl-phospho-beta-D-glucosidase BglH	315	29	20.223	1	96.9	731.474	67.342
LAG_00510	smpB	520208	520675	468	SsrA-binding protein	0	0	0			0	0
LAG_00511	pstS1_1	520856	521749	894	Phosphate-binding protein PstS 1	255	25	27.964	3.9	98.2	949.817	93.119
LAG_00512	pstS1_2	521979	522830	852	Phosphate-binding protein PstS 1	0	0	0			0	0
LAG_00513	pstC	522845	523768	924	Phosphate transport system permease protein PstC	0	0	0			0	0
LAG_00514	pstA2	523768	524655	888	Phosphate transport system permease protein PstA 2	0	0	0			0	0
LAG_00515	pstB3_1	524674	525477	804	Phosphate import ATP-binding protein PstB 3	0	0	0			0	0
LAG_00516	pstB3_2	525491	526252	762	Phosphate import ATP-binding protein PstB 3	0	0	0			0	0
LAG_00517	phoU	526308	526961	654	Phosphate-specific transport system accessory protein PhoU	0	0	0			0	0
LAG_00518	serS	526992	528263	1272	Serine--tRNA ligase	4	1	0.786	99.1	99.1	10.472	2.618
LAG_00519	NA	528605	529282	678	hypothetical protein	139	11	16.224	4.9	82	682.688	54.026
LAG_00520	NA	529353	529733	381	hypothetical protein	10	2	5.249	78.2	89.2	87.4	17.48
LAG_00521	manZ_1	529839	530936	1098	PTS system mannose-specific EIID component	88	9	8.197	5.9	83.8	266.881	27.295
LAG_00522	sorA_1	530959	531762	804	PTS system sorbose-specific EIIC component	3	1	1.244	8.8	8.8	12.425	4.142
LAG_00523	manX_1	531793	532782	990	PTS system mannose-specific EIIAB component	9	2	2.02	69.8	74	30.272	6.727
LAG_00524	NA	533284	533793	510	hypothetical protein	0	0	0			0	0
LAG_00525	cmk	533823	534485	663	Cytidylate kinase	10	2	3.017	95.3	97.4	50.225	10.045
LAG_00526	NA	534559	535083	525	hypothetical protein	88	7	13.333	7.4	85.9	558.163	44.399
LAG_00527	NA	535209	536255	1047	hypothetical protein	243	19	18.147	9.9	97.4	772.853	60.429
LAG_00528	NA	536308	536577	270	hypothetical protein	30	5	18.519	27.8	67.8	369.994	61.666
LAG_00529	msrA2	536637	537179	543	Peptide methionine sulfoxide reductase MsrA 2	79	12	22.099	4.4	91.3	484.468	73.59

LAG_00530	Int-Tn_3	537349	538530	1182	Transposase from transposon Tn916	154	18	15.228	0.1	95.1	433.851	50.71
LAG_00531	NA	538623	539030	408	hypothetical protein	60	9	22.059	3.7	99.3	489.698	73.455
LAG_00532	NA	539152	539334	183	hypothetical protein	42	4	21.858	39.3	88.5	764.25	72.786
LAG_00533	NA	539415	539522	108	hypothetical protein	0	0	0			0	0
LAG_00534	NA	539522	539872	351	hypothetical protein	7	2	5.698	15.4	29.3	66.409	18.974
LAG_00535	NA	539919	540167	249	hypothetical protein	55	5	20.08	20.1	97.2	735.531	66.866
LAG_00536	NA	540453	540866	414	hypothetical protein	52	8	19.324	20.8	91.5	418.254	64.347
LAG_00537	NA	540992	541276	285	hypothetical protein	35	5	17.544	4.6	56.8	408.941	58.42
LAG_00538	NA	541463	542017	555	hypothetical protein	62	7	12.613	31.9	82.2	371.994	41.999
LAG_00539	immR_1	542027	542410	384	HTH-type transcriptional regulator ImmR	0	0	0			0	0
LAG_00540	NA	542681	542887	207	hypothetical protein	6	1	4.831	71.5	71.5	96.52	16.087
LAG_00541	NA	542930	543205	276	hypothetical protein	0	0	0			0	0
LAG_00542	NA	543290	543472	183	hypothetical protein	16	2	10.929	6.6	12	291.143	36.393
LAG_00543	NA	543469	543744	276	hypothetical protein	0	0	0			0	0
LAG_00544	NA	543746	543997	252	hypothetical protein	22	4	15.873	27	65.5	290.71	52.856
LAG_00545	NA	543981	544250	270	hypothetical protein	5	1	3.704	99.3	99.3	61.666	12.333
LAG_00546	NA	544344	544673	330	hypothetical protein	57	7	21.212	32.1	95.8	575.173	70.635
LAG_00547	NA	544670	546379	1710	hypothetical protein	137	19	11.111	8	94.3	266.785	36.999
LAG_00548	NA	546986	548083	1098	hypothetical protein	157	20	18.215	3.6	93.4	476.14	60.655
LAG_00549	NA	548486	548737	252	hypothetical protein	104	11	43.651	3.6	98	1374.264	145.355
LAG_00550	NA	549152	549484	333	hypothetical protein	65	10	30.03	4.5	69.4	649.99	99.998
LAG_00551	qacC	549985	550314	330	Quaternary ammonium compound-resistance protein QacC	91	10	30.303	41.5	97	918.258	100.908
LAG_00552	NA	550508	550831	324	hypothetical protein	24	3	9.259	21.9	88.9	246.663	30.833
LAG_00553	NA	550969	553128	2160	hypothetical protein	210	25	11.574	0	98.8	323.745	38.541
LAG_00554	NA	553128	553829	702	hypothetical protein	76	11	15.67	2.1	81.9	360.507	52.179
LAG_00555	mccF	554356	555327	972	Microcin C7 self-immunity protein MccF	243	23	23.663	0.5	97.3	832.487	78.795
LAG_00556	msrR	555525	556895	1371	Regulatory protein MsrR	182	22	16.047	2.8	99.1	442.05	53.435
LAG_00557	malG	556936	557790	855	Maltose transport system permease protein MalG	115	14	16.374	12	95.4	447.888	54.525
LAG_00558	malF	557792	559141	1350	Maltose transport system permease protein MalF	220	31	22.963	1	93.6	542.658	76.465
LAG_00559	malX_1	559213	560448	1236	Maltose/maltodextrin-binding protein	215	26	21.036	1.6	97.3	579.239	70.047
LAG_00560	bbmA	560702	562456	1755	Intracellular maltogenic amylase	224	27	15.385	2.1	99.8	425.019	51.23
LAG_00561	malL	562709	564316	1608	Oligo-1,6-glucosidase	163	21	13.06	7.3	99.7	337.551	43.488
LAG_00562	malP	564341	566605	2265	Maltose phosphorylase	166	14	6.181	0.6	84.5	244.049	20.582
LAG_00563	pgmB	566598	567263	666	Beta-phosphoglucomutase	75	7	10.511	30.9	83.9	374.994	34.999
LAG_00564	malR	567290	568270	981	HTH-type transcriptional regulator MalR	17	5	5.097	1.1	95	57.706	16.972
LAG_00565	arlR_2	568440	569117	678	Response regulator ArlR	32	6	8.85	30.4	79.4	157.166	29.469
LAG_00566	arlS_2	569153	570535	1383	Signal transduction histidine-protein kinase ArlS	245	30	21.692	8.4	99.3	589.904	72.233
LAG_00567	dxs	570599	572341	1743	1-deoxy-D-xylulose-5-phosphate synthase	134	24	13.769	4.8	96.5	256.003	45.851
LAG_00568	yusV	572909	573691	783	putative siderophore transport system ATP-binding protein YusV	56	8	10.217	17.1	94	238.157	34.022
LAG_00569	yfhA_1	573681	574631	951	putative siderophore transport system permease protein YfhA	43	7	7.361	0.6	84.8	150.565	24.511
LAG_00570	feuC	574628	575566	939	Iron-uptake system permease protein FeuC	76	12	12.78	3.9	90.2	269.517	42.555
LAG_00571	fhuD	575578	576519	942	Iron(3+)-hydroxamate-binding protein FhuD	86	8	8.493	7.2	98.1	304.008	28.28
LAG_00572	hpr	576821	577396	576	HTH-type transcriptional regulator Hpr	3	1	1.736	32.8	32.8	17.343	5.781
LAG_00573	fabH	577396	578373	978	3-oxoacyl-[acyl-carrier-protein] synthase 3	0	0	0			0	0
LAG_00574	acpP	578461	578682	222	Acyl carrier protein	0	0	0			0	0
LAG_00575	fabD	578781	579704	924	Malonyl CoA-acyl carrier protein transacylase	0	0	0			0	0
LAG_00576	fabG_1	579783	580514	732	3-oxoacyl-[acyl-carrier-protein] reductase FabG	0	0	0			0	0
LAG_00577	fabF	580572	581789	1218	3-oxoacyl-[acyl-carrier-protein] synthase 2	0	0	0			0	0
LAG_00578	accB	581882	582355	474	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	0	0	0			0	0
LAG_00579	fabZ_1	582369	582803	435	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	0	0	0			0	0
LAG_00580	accC	582999	584363	1365	Biotin carboxylase	15	2	1.465	96.6	99.7	36.593	4.879
LAG_00581	csbB	584946	585881	936	Putative glycosyltransferase CsbB	247	23	24.573	8.2	99.3	878.736	81.826
LAG_00582	accD	586195	587061	867	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	0	0	0			0	0
LAG_00583	accA	587054	587809	756	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	3	1	1.323	98.3	98.3	13.214	4.405

LAG_00584	NA	587872	588114	243	hypothetical protein	34	4	16.461	3.7	70.4	465.919	54.814
LAG_00585	spxA_5	588258	588608	351	Regulatory protein Spx	9	2	5.698	57.5	85.8	85.383	18.974
LAG_00586	exoA	588639	589499	861	Exodeoxyribonuclease	66	10	11.614	1.5	89.4	255.257	38.675
LAG_00587	metG	589729	591717	1989	Methionine--tRNA ligase	0	0	0			0	0
LAG_00588	sdh	591750	592595	846	Serine 3-dehydrogenase	204	20	23.641	10.2	98.8	802.966	78.722
LAG_00589	NA	592738	592977	240	hypothetical protein	39	4	16.667	12.1	43.3	541.117	55.499
LAG_00590	bacC	592970	593689	720	Dihydroanticapsin 7-dehydrogenase	112	13	18.056	15.3	98.8	517.992	60.124
LAG_00591	queT	593807	594364	558	Queuosine precursor transporter QueT	155	18	32.258	9.5	100	924.986	107.418
LAG_00592	yidA_1	594419	595204	786	Sugar phosphatase YidA	105	14	17.812	1.3	97.7	444.84	59.312
LAG_00593	NA	595356	596138	783	hypothetical protein	111	12	15.326	2.9	94.6	472.062	51.034
LAG_00594	NA	596257	596682	426	Putative universal stress protein	17	2	4.695	80.8	90.6	132.885	15.634
LAG_00595	ftsK_1	596810	599173	2364	DNA translocase FtsK	0	0	0			0	0
LAG_00596	NA	599170	600171	1002	hypothetical protein	0	0	0			0	0
LAG_00597	gpsB	600284	600673	390	Cell cycle protein GpsB	0	0	0			0	0
LAG_00598	rlmL	601130	602287	1158	Ribosomal RNA large subunit methyltransferase K/L	161	17	14.68	4.6	96.9	462.972	48.885
LAG_00599	mapZ	602309	604153	1845	Mid-cell-anchored protein Z	234	23	12.466	8.7	100	422.335	41.512
LAG_00600	murR	604208	604951	744	HTH-type transcriptional regulator MurR	128	18	24.194	7.1	94.5	572.894	80.563
LAG_00601	NA	605091	606005	915	6-phosphogluconate dehydrogenase, NAD(+)-dependent, decarboxylating	267	31	33.88	2.1	94.9	971.69	112.818
LAG_00602	bglF_1	606012	607898	1887	PTS system beta-glucoside-specific EIIBCA component	378	48	25.437	2	97.8	667.048	84.705
LAG_00603	bglH_2	607888	609324	1437	Aryl-phospho-beta-D-glucosidase BglH	271	31	21.573	0.8	98.7	627.986	71.836
LAG_00604	xylB_1	609369	610868	1500	Xylulose kinase	335	36	24	0.3	99.3	743.688	79.919
LAG_00605	arsC	610941	611333	393	Glutaredoxin arsenate reductase	76	12	30.534	18.3	89.8	643.959	101.678
LAG_00606	pepQ	611376	612461	1086	Xaa-Pro dipeptidase	79	13	11.971	1.6	98.3	242.234	39.861
LAG_00607	ccpA	612664	613659	996	Catabolite control protein A	3	1	1.004	51.1	51.1	10.03	3.343
LAG_00608	cspL	613864	614064	201	Cold shock protein 2	0	0	0			0	0
LAG_00609	NA	614236	614309	74	tRNA-Met	0	0	0			0	0
LAG_00610	aroD	614427	615116	690	3-dehydroquinate dehydratase	88	7	10.145	3.2	88.7	424.689	33.782
LAG_00611	purB	615228	616523	1296	Adenylosuccinate lyase	8	1	0.772	43.2	43.2	20.555	2.569
LAG_00612	hlyU	616665	616988	324	Transcriptional activator HlyU	16	4	12.346	48.8	98.5	164.442	41.11
LAG_00613	cadA	617001	619034	2034	Cadmium, zinc and cobalt-transporting ATPase	405	44	21.632	0.2	98	663.043	72.034
LAG_00614	NA	619105	619911	807	hypothetical protein	209	25	30.979	1	99.8	862.403	103.158
LAG_00615	uvrC	620049	621827	1779	UvrABC system protein C	118	10	5.621	7.9	80.2	220.873	18.718
LAG_00616	NA	621941	622288	348	hypothetical protein	47	8	22.989	2.3	96.6	449.734	76.551
LAG_00617	mutY	622391	623464	1074	Adenine DNA glycosylase	88	16	14.898	50.9	93.5	272.845	49.608
LAG_00618	pepV_2	623575	624981	1407	Beta-Ala-Xaa dipeptidase	71	13	9.24	2.8	99.4	168.036	30.767
LAG_00619	NA	625224	626285	1062	hypothetical protein	304	36	33.898	1.4	98.3	953.205	112.88
LAG_00620	murQ	626282	627172	891	N-acetylmuramic acid 6-phosphate etherase	229	22	24.691	1.1	98.1	855.845	82.221
LAG_00621	NA	627196	629121	1926	PTS system EIIBC component	432	36	18.692	5.8	99.5	746.904	62.242
LAG_00622	acpS	629226	629588	363	Holo-[acyl-carrier-protein] synthase	6	1	2.755	98.9	98.9	55.04	9.173
LAG_00623	alr	629611	630723	1113	Alanine racemase	0	0	0			0	0
LAG_00624	spxA_6	630866	631297	432	Regulatory protein Spx	92	12	27.778	3.2	94	709.156	92.499
LAG_00625	pnuC	631411	632118	708	Nicotinamide riboside transporter PnuC	95	11	15.537	16.8	90.7	446.815	51.736
LAG_00626	sugE	632163	632483	321	Quaternary ammonium compound-resistance protein SugE	26	5	15.576	4.7	95.3	269.715	51.868
LAG_00627	NA	632972	633685	714	hypothetical protein	103	13	18.207	0.6	91.5	480.371	60.629
LAG_00628	folD	633769	634638	870	Bifunctional protein FolD protein	33	5	5.747	39	83.7	126.308	19.138
LAG_00629	xseA	634713	635966	1254	Exodeoxyribonuclease 7 large subunit	3	1	0.797	23.8	23.8	7.966	2.655
LAG_00630	xseB	635976	636200	225	Exodeoxyribonuclease 7 small subunit	0	0	0			0	0
LAG_00631	garK	636307	637362	1056	Glycerate 2-kinase	69	7	6.629	17.3	78.3	217.582	22.074
LAG_00632	NA	637475	637651	177	hypothetical protein	37	4	22.599	18.6	100	696.091	75.253
LAG_00633	NA	637777	638628	852	Farnesyl diphosphate synthase	60	11	12.911	15	82.7	234.503	42.992
LAG_00634	tlyA	638625	639434	810	Hemolysin A	24	3	3.704	27.8	63	98.665	12.333
LAG_00635	argR_1	639431	639877	447	Arginine repressor	13	3	6.711	34	49.4	96.844	22.349
LAG_00636	recN	639889	641553	1665	DNA repair protein RecN	209	20	12.012	16.8	93.6	417.993	39.999
LAG_00637	NA	641561	642520	960	hypothetical protein	81	9	9.375	0.2	76.4	280.964	31.218

LAG_00638	femA	642578	643795	1218	Aminoacyltransferase FemA	0	0	0			0	0
LAG_00639	femB	643795	644841	1047	Aminoacyltransferase FemB	0	0	0			0	0
LAG_00640	yumC	644941	645921	981	Ferredoxin--NADP reductase 2	0	0	0			0	0
LAG_00641	NA	645982	646536	555	hypothetical protein	21	4	7.207	2.9	56.9	125.998	24
LAG_00642	mutS2	646542	648878	2337	Endonuclease MutS2	131	17	7.274	19	93.8	186.659	24.223
LAG_00643	trxA	648965	649279	315	Thioredoxin	9	1	3.175	94	94	95.141	10.571
LAG_00644	NA	649475	649678	204	hypothetical protein	0	0	0			0	0
LAG_00645	NA	649768	649839	72	tRNA-Gln	0	0	0			0	0
LAG_00646	femX	649900	651069	1170	Lipid II:glycine glycyltransferase	0	0	0			0	0
LAG_00647	rsmH	651159	652130	972	Ribosomal RNA small subunit methyltransferase H	0	0	0			0	0
LAG_00648	ftsL	652163	652543	381	Cell division protein FtsL	0	0	0			0	0
LAG_00649	pbpX_1	652540	654834	2295	Penicillin-binding protein 2x	0	0	0			0	0
LAG_00650	mraY	654922	655914	993	Phospho-N-acetylmuramoyl-pentapeptide- transferase	3	1	1.007	99.9	99.9	10.06	3.353
LAG_00651	ywaC	656139	656792	654	GTP pyrophosphokinase YwaC	251	24	36.697	0.6	97.7	1278.008	122.2
LAG_00652	phoP_1	656792	657187	396	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP	220	7	17.677	2.3	93.7	1849.971	58.863
LAG_00653	cssS	657197	658582	1386	Sensor histidine kinase CssS	462	40	28.86	0.6	96.8	1109.983	96.102
LAG_00654	rplS	658676	659026	351	50S ribosomal protein L19	0	0	0			0	0
LAG_00655	NA	659219	659344	126	hypothetical protein	31	5	39.683	43.7	97.6	819.273	132.141
LAG_00656	NA	659489	659725	237	hypothetical protein	4	1	4.219	94.9	94.9	56.202	14.05
LAG_00657	NA	659941	660513	573	hypothetical protein	259	27	47.12	4.7	97.7	1505.16	156.909
LAG_00658	nlhH	660778	661731	954	Carboxylesterase NlhH	272	26	27.254	1	98.8	949.419	90.753
LAG_00659	ybbH_1	661886	662614	729	putative HTH-type transcriptional regulator YbbH	209	26	35.665	4.8	95.1	954.676	118.764
LAG_00660	malX_2	662720	664771	2052	PTS system maltose-specific EIICB component	484	48	23.392	5.7	98.7	785.426	77.894
LAG_00661	patB	664821	665990	1170	Cystathionine beta-lyase PatB	262	31	26.496	9.8	96.7	745.681	88.229
LAG_00662	NA	666035	666565	531	hypothetical protein	111	16	30.132	4.1	92.5	696.091	100.337
LAG_00663	mrp	666754	667092	339	Iron-sulfur cluster carrier protein	57	9	26.549	9.7	95	559.903	88.406
LAG_00664	NA	667158	667775	618	hypothetical protein	205	13	21.036	0.6	98.1	1104.594	70.047
LAG_00665	liaS	667772	668752	981	Sensor histidine kinase LiaS	91	11	11.213	0.4	98.8	308.894	37.339
LAG_00666	vraR	668770	669405	636	Response regulator protein VraR	90	10	15.723	41.2	97.5	471.219	52.358
LAG_00667	NA	669486	670289	804	Putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	49	6	7.463	13.7	96.9	202.945	24.85
LAG_00668	NA	670351	670941	591	Putative bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	63	9	15.228	0.8	69.9	354.969	50.71
LAG_00669	yugI	670943	671338	396	General stress protein 13	29	6	15.152	14.1	97.2	243.86	50.454
LAG_00670	ydjZ	671356	671961	606	TVP38/TMEM64 family inner membrane protein YdjZ	50	9	14.851	2.3	84.8	274.748	49.455
LAG_00671	rodA	672066	673379	1314	Peptidoglycan glycosyltransferase RodA	36	5	3.805	90.4	99.7	91.231	12.671
LAG_00672	NA	673523	673954	432	hypothetical protein	162	15	34.722	3.9	100	1248.73	115.623
LAG_00673	NA	674127	675347	1221	Secreted 45 kDa protein	137	19	15.561	0.5	91.7	373.631	51.817
LAG_00674	lptB	675498	676397	900	Lipopolysaccharide export system ATP-binding protein LptB	337	22	24.444	6.2	85.1	1246.88	81.399
LAG_00675	NA	676390	677658	1269	hypothetical protein	247	33	26.005	4.3	97.5	648.146	86.594
LAG_00676	spxA_7	677701	678135	435	Regulatory protein Spx	103	15	34.483	5.5	99.1	788.47	114.826
LAG_00677	carB	678720	681905	3186	Carbamoyl-phosphate synthase large chain	485	57	17.891	2.3	99.7	506.913	59.575
LAG_00678	rluE	681996	682529	534	Ribosomal large subunit pseudouridine synthase E	131	9	16.854	8.1	62	816.897	56.123
LAG_00679	NA	682557	683354	798	hypothetical protein	179	19	23.81	0.6	97.2	746.943	79.284
LAG_00680	NA	683351	684451	1101	hypothetical protein	184	23	20.89	1.9	99.7	556.504	69.563
LAG_00681	NA	684473	685702	1230	hypothetical protein	161	14	11.382	1.7	100	435.871	37.902
LAG_00682	pyrK	686134	686919	786	Dihydroorotate dehydrogenase B (NAD(+)), electron transfer subunit	12	4	5.089	5.3	90.5	50.839	16.946
LAG_00683	pyrDB	686919	687854	936	Dihydroorotate dehydrogenase B (NAD(+)), catalytic subunit	107	17	18.162	5.3	96.9	380.667	60.48
LAG_00684	pyrF	687847	688566	720	Orotidine 5'-phosphate decarboxylase	161	21	29.167	1.2	95.8	744.613	97.123
LAG_00685	rsmG	688599	689312	714	Ribosomal RNA small subunit methyltransferase G	99	5	7.003	1	74.6	461.715	23.319
LAG_00686	hepT	689312	690271	960	Heptaprenyl diphosphate synthase component 2	213	14	14.583	1.5	96.2	738.832	48.562
LAG_00687	NA	690262	690792	531	hypothetical protein	301	15	28.249	21.5	83.1	1887.598	94.066
LAG_00688	NA	690789	691184	396	hypothetical protein	544	18	45.455	18.2	94.7	4574.474	151.361
LAG_00689	gtaB	691287	692213	927	UTP--glucose-1-phosphate uridylyltransferase	0	0	0			0	0
LAG_00690	gpsA	692237	693256	1020	Glycerol-3-phosphate dehydrogenase [NAD(P)+]	0	0	0			0	0
LAG_00691	guaD	693476	693958	483	Guanine deaminase	9	2	4.141	17.6	26.5	62.049	13.789

LAG_00692	speG	693978	694475	498	Spermidine N(1)-acetyltransferase	112	17	34.137	3.6	73.3	748.904	113.673
LAG_00693	NA	694489	694977	489	hypothetical protein	43	6	12.27	11.5	98.6	292.818	40.858
LAG_00694	kcsA	695008	695343	336	pH-gated potassium channel KcsA	126	7	20.833	10.7	72.6	1248.73	69.374
LAG_00695	cfa	695406	696599	1194	Cyclopropane-fatty-acyl-phospholipid synthase	164	18	15.075	1.1	85.7	457.38	50.2
LAG_00696	NA	696798	697151	354	hypothetical protein	19	4	11.299	71.8	94.4	178.726	37.627
LAG_00697	NA	697184	697483	300	hypothetical protein	25	6	20	25	91.3	277.496	66.599
LAG_00698	NA	697531	697899	369	hypothetical protein	19	3	8.13	24.7	94	171.461	27.073
LAG_00699	NA	698059	698343	285	hypothetical protein	69	8	28.07	7	98.6	806.198	93.472
LAG_00700	NA	698391	698759	369	hypothetical protein	67	4	10.84	16.8	54.7	604.625	36.097
LAG_00701	NA	698814	699206	393	hypothetical protein	60	8	20.356	0.8	57.5	508.389	67.785
LAG_00702	NA	699306	699950	645	hypothetical protein	145	11	17.054	1.9	85.4	748.593	56.79
LAG_00703	NA	700473	700661	189	hypothetical protein	103	8	42.328	12.2	83.6	1814.734	140.95
LAG_00704	NA	700912	701490	579	hypothetical protein	91	12	20.725	11.2	99.7	523.36	69.014
LAG_00705	NA	701500	702672	1173	TelA-like protein	119	16	13.64	2.6	69.5	337.821	45.421
LAG_00706	nagA_1	702768	703919	1152	N-acetylglucosamine-6-phosphate deacetylase	36	6	5.208	2.3	98.4	104.061	17.343
LAG_00707	pfkA	704164	705192	1029	ATP-dependent 6-phosphofructokinase	0	0	0			0	0
LAG_00708	pyk	705302	706810	1509	Pyruvate kinase	0	0	0			0	0
LAG_00709	ldhA	707037	708014	978	L-lactate dehydrogenase 1	29	5	5.112	19.5	89.1	98.741	17.024
LAG_00710	NA	708119	709165	1047	hypothetical protein	297	29	27.698	11	99.5	944.598	92.234
LAG_00711	NA	709575	710528	954	hypothetical protein	154	16	16.771	9	85.1	537.539	55.848
LAG_00712	NA	710528	711598	1071	hypothetical protein	175	18	16.807	15.9	99.3	544.109	55.966
LAG_00713	xylG	711582	713111	1530	Xylose import ATP-binding protein XylG	112	18	11.765	13.3	98.8	243.761	39.176
LAG_00714	NA	713394	715019	1626	hypothetical protein	54	10	6.15	33.6	87.9	110.589	20.479
LAG_00715	queG	715123	716178	1056	Epoxyqueuosine reductase	77	8	7.576	4.7	95.2	242.809	25.227
LAG_00716	prfB	716230	717327	1098	Peptide chain release factor 2	0	0	0			0	0
LAG_00717	ftsE	717537	718229	693	Cell division ATP-binding protein FtsE	0	0	0			0	0
LAG_00718	ftsX	718222	719157	936	Cell division protein FtsX	0	0	0			0	0
LAG_00719	nrdF2	719257	720243	987	Ribonucleoside-diphosphate reductase subunit beta nrdF2	0	0	0			0	0
LAG_00720	nrdE1	720258	722426	2169	Ribonucleoside-diphosphate reductase subunit alpha 1	0	0	0			0	0
LAG_00721	NA	722480	722899	420	Putative NrdI-like protein	0	0	0			0	0
LAG_00722	nrdH	722896	723114	219	Glutaredoxin-like protein NrdH	0	0	0			0	0
LAG_00723	plsY	723223	723861	639	Glycerol-3-phosphate acyltransferase	0	0	0			0	0
LAG_00724	parE	724091	726028	1938	DNA topoisomerase 4 subunit B	0	0	0			0	0
LAG_00725	polC_1	726073	726894	822	DNA polymerase III PolC-type	25	4	4.866	80.5	87.3	101.276	16.204
LAG_00726	NA	726897	727358	462	Acetyltransferase	9	2	4.329	53.7	62.8	64.869	14.415
LAG_00727	parC	727404	729887	2484	DNA topoisomerase 4 subunit A	0	0	0			0	0
LAG_00728	gyrA	729900	732518	2619	DNA gyrase subunit A	30	4	1.527	2.2	98.9	38.144	5.086
LAG_00729	apbE_2	732520	733590	1071	FAD:protein FMN transferase	1460	47	43.884	0.3	97.8	4539.425	146.132
LAG_00730	NA	733602	734333	732	hypothetical protein	77	7	9.563	17.1	100	350.281	31.844
LAG_00731	NA	734384	735151	768	hypothetical protein	210	21	27.344	12.1	85.4	910.533	91.053
LAG_00732	natA_1	735164	736030	867	ABC transporter ATP-binding protein NatA	121	18	20.761	1.3	94	464.733	69.134
LAG_00733	pcrA	736241	738535	2295	ATP-dependent DNA helicase PcrA	29	7	3.05	20.6	99.6	42.078	10.157
LAG_00734	tag	738539	739105	567	DNA-3-methyladenine glycosylase 1	141	18	31.746	2.1	91.9	828.082	105.713
LAG_00735	NA	739303	740559	1257	hypothetical protein	210	26	20.684	0.2	98.8	556.316	68.877
LAG_00736	NA	740648	741100	453	hypothetical protein	42	7	15.453	31.3	93.6	308.737	51.456
LAG_00737	truB	741227	742132	906	tRNA pseudouridine synthase B	68	9	9.934	11.8	98.6	249.93	33.079
LAG_00738	ribF	742134	743045	912	Riboflavin biosynthesis protein RibF	12	1	1.096	92.1	92.1	43.815	3.651
LAG_00739	tpiA	743180	743938	759	Triosephosphate isomerase	13	2	2.635	95.1	99.5	57.035	8.775
LAG_00740	asD	744009	745601	1593	Bifunctional aspartate aminotransferase and L-aspartate beta-decarboxylase	421	39	24.482	0.4	98.9	880.043	81.524
LAG_00741	NA	745759	746346	588	hypothetical protein	76	7	11.905	11.4	94	430.401	39.642
LAG_00742	hemN	746391	747515	1125	Oxygen-independent coproporphyrinogen-III oxidase-like protein	194	20	17.778	18.7	98.4	574.231	59.199
LAG_00743	NA	747565	748392	828	hypothetical protein	36	9	10.87	0.1	80.3	144.78	36.195
LAG_00744	endA	748501	749394	894	DNA-entry nuclease	325	29	32.438	0.4	96.9	1210.552	108.018
LAG_00745	lytG	749481	750119	639	Exo-glucosaminidase LytG	98	12	18.779	5.5	69.2	510.696	62.534

LAG_00746	NA	750250	750942	693	hypothetical protein	125	13	18.759	0.6	99	600.64	62.467
LAG_00747	strB1	751344	752327	984	Inosamine-phosphate amidinotransferase 1	226	24	24.39	6	99.3	764.805	81.218
LAG_00748	gph_1	752381	752980	600	Phosphoglycolate phosphatase	119	13	21.667	0.8	100	660.44	72.149
LAG_00749	NA	752992	753726	735	hypothetical protein	122	18	24.49	0.4	93.2	552.726	81.55
LAG_00750	gyrB	753888	755846	1959	DNA gyrase subunit B	0	0	0			0	0
LAG_00751	xerD_1	755932	757056	1125	Tyrosine recombinase XerD	538	39	34.667	0.6	100	1592.455	115.438
LAG_00752	NA	757187	757765	579	hypothetical protein	306	18	31.088	1.6	93.8	1759.869	103.522
LAG_00753	NA	757818	758408	591	hypothetical protein	242	15	25.381	14	95.6	1363.532	84.516
LAG_00754	NA	758420	758773	354	hypothetical protein	0	0	0			0	0
LAG_00755	NA	759067	759861	795	hypothetical protein	125	19	23.899	5.2	99.6	523.577	79.584
LAG_00756	NA	760016	760246	231	hypothetical protein	46	4	17.316	11.7	89.6	663.107	57.661
LAG_00757	NA	760259	760510	252	hypothetical protein	38	5	19.841	20.6	71.8	502.135	66.07
LAG_00758	NA	760527	760676	150	hypothetical protein	27	3	20	4.7	94	599.391	66.599
LAG_00759	NA	760893	761669	777	hypothetical protein	29	6	7.722	43.2	89.8	124.284	25.714
LAG_00760	NA	761670	762635	966	hypothetical protein	100	11	11.387	7.3	86.5	344.715	37.919
LAG_00761	NA	762868	763194	327	hypothetical protein	74	7	21.407	0.9	91.7	753.566	71.283
LAG_00762	NA	763194	763979	786	hypothetical protein	202	27	34.351	2	96.6	855.788	114.388
LAG_00763	NA	763963	764247	285	hypothetical protein	151	7	24.561	11.2	87.7	1764.288	81.788
LAG_00764	NA	764244	764648	405	hypothetical protein	88	10	24.691	5.7	74.8	723.544	82.221
LAG_00765	NA	764755	765036	282	hypothetical protein	116	8	28.369	7.8	88.7	1369.766	94.467
LAG_00766	NA	765141	765530	390	hypothetical protein	160	12	30.769	3.3	97.7	1366.132	102.46
LAG_00767	spxA_8	765648	766046	399	Regulatory protein Spx	294	20	50.125	13	95.7	2453.646	166.915
LAG_00768	NA	766237	766638	402	hypothetical protein	149	13	32.338	9	99.8	1234.234	107.685
LAG_00769	NA	766936	768066	1131	hypothetical protein	436	45	39.788	8.8	99.6	1283.693	132.491
LAG_00770	NA	768286	768918	633	hypothetical protein	246	18	28.436	1.6	98.1	1294.103	94.69
LAG_00771	NA	769003	769078	76	tRNA-Arg	9	1	13.158	56.6	56.6	394.336	43.815
LAG_00772	NA	769203	769751	549	hypothetical protein	163	18	32.787	4.6	99.3	988.673	109.179
LAG_00773	NA	769963	770454	492	hypothetical protein	230	20	40.65	7.1	96.1	1556.683	135.364
LAG_00774	NA	770444	771727	1284	hypothetical protein	740	55	42.835	0.8	100	1919.129	142.638
LAG_00775	NA	771729	773324	1596	hypothetical protein	595	59	36.967	2.8	97.4	1241.428	123.1
LAG_00776	NA	773308	774198	891	hypothetical protein	108	14	15.713	1.9	98.9	403.63	52.322
LAG_00777	NA	774341	774910	570	hypothetical protein	312	25	43.86	11.4	97.9	1822.708	146.05
LAG_00778	NA	774921	775787	867	hypothetical protein	425	26	29.988	1.6	77.7	1632.327	99.86
LAG_00779	cgkA	775865	776323	459	Kappa-carrageenase	78	16	34.858	10	96.3	565.873	116.077
LAG_00780	NA	776336	776680	345	hypothetical protein	247	21	60.87	1.4	96.5	2384.05	202.692
LAG_00781	NA	776677	776952	276	hypothetical protein	111	10	36.232	0.7	63	1339.218	120.65
LAG_00782	NA	776952	777302	351	hypothetical protein	61	5	14.245	16.5	94.9	578.709	47.435
LAG_00783	NA	777299	777661	363	hypothetical protein	76	11	30.303	0.3	90.4	697.179	100.908
LAG_00784	NA	777672	778319	648	hypothetical protein	427	33	50.926	3.2	100	2194.271	169.581
LAG_00785	NA	778389	778832	444	hypothetical protein	259	22	49.55	3.2	97.7	1942.47	164.997
LAG_00786	NA	778877	779158	282	hypothetical protein	79	5	17.73	12.1	31.6	932.858	59.042
LAG_00787	NA	779158	781857	2700	hypothetical protein	1064	91	33.704	0.1	99.5	1312.246	112.232
LAG_00788	NA	781858	782703	846	hypothetical protein	306	29	34.279	0.8	98.6	1204.449	114.147
LAG_00789	NA	782700	784802	2103	hypothetical protein	846	74	35.188	9	99	1339.58	117.174
LAG_00790	NA	784792	786135	1344	hypothetical protein	514	44	32.738	0.8	94.1	1273.507	109.016
LAG_00791	NA	786176	786538	363	hypothetical protein	207	10	27.548	9.4	92.3	1898.896	91.734
LAG_00792	sle1	786522	787646	1125	N-acetylmuramoyl-L-alanine amidase sle1	569	55	48.889	0.8	100	1684.214	162.797
LAG_00793	NA	787721	788407	687	hypothetical protein	211	33	48.035	1.9	100	1022.735	159.954
LAG_00794	NA	788645	789109	465	hypothetical protein	116	11	23.656	22.8	98.9	830.697	78.773
LAG_00795	NA	789113	789919	807	hypothetical protein	112	17	21.066	17.2	99.1	462.149	70.148
LAG_00796	NA	790827	790949	123	hypothetical protein	109	9	73.171	15.4	100	2950.929	243.655
LAG_00797	pspB_3	791063	791659	597	Putative phosphoserine phosphatase 2	327	31	51.926	4.9	99.3	1823.941	172.912
LAG_00798	NA	791985	793511	1527	hypothetical protein	362	35	22.921	0.7	94.3	789.418	76.325
LAG_00799	NA	794046	794495	450	hypothetical protein	109	7	15.556	18.4	98.2	806.587	51.799

LAG_00800	emrB_1	794492	796018	1527	Multidrug export protein EmrB	390	38	24.885	1.4	99.2	850.478	82.867
LAG_00801	NA	796018	796734	717	hypothetical protein	95	12	16.736	1	88	441.206	55.731
LAG_00802	niaX	796933	797478	546	Niacin transporter NiaX	108	6	10.989	7.3	97.6	658.671	36.593
LAG_00803	rpiR_2	797554	798312	759	HTH-type transcriptional regulator RpiR	114	16	21.08	2.6	88.7	500.15	70.197
LAG_00804	ribZ_2	798476	799870	1395	Riboflavin transporter RibZ	138	22	15.771	7.2	89.1	329.414	52.515
LAG_00805	deoB	799952	801187	1236	Phosphopentomutase	32	8	6.472	13	91.2	86.212	21.553
LAG_00806	NA	801224	801460	237	hypothetical protein	45	4	16.878	9.7	60.3	632.269	56.202
LAG_00807	NA	801400	801489	90	hypothetical protein	7	1	11.111	66.7	66.7	258.996	36.999
LAG_00808	punA	801480	802295	816	Purine nucleoside phosphorylase 1	35	5	6.127	2.7	90.6	142.829	20.404
LAG_00809	deoD	802379	803077	699	Purine nucleoside phosphorylase DeoD-type	31	4	5.722	14.9	86	147.68	19.055
LAG_00810	fhs1	803207	804877	1671	Formate--tetrahydrofolate ligase 1	143	19	11.37	0.2	97	284.969	37.863
LAG_00811	NA	804891	805301	411	hypothetical protein	26	2	4.866	75.4	85.6	210.654	16.204
LAG_00812	yxeM_1	805468	806325	858	putative amino-acid-binding protein YxeM	6	2	2.331	14.5	41.8	23.286	7.762
LAG_00813	yxeN	806468	807355	888	putative amino-acid permease protein YxeN	0	0	0			0	0
LAG_00814	tcyC	807352	808113	762	L-cystine import ATP-binding protein TcyC	6	1	1.312	94.4	94.4	26.22	4.37
LAG_00815	NA	808106	808333	228	hypothetical protein	56	3	13.158	3.1	89.9	817.882	43.815
LAG_00816	trxB	808404	809324	921	Thioredoxin reductase	0	0	0			0	0
LAG_00817	secG	809438	809686	249	putative protein-export membrane protein SecG	0	0	0			0	0
LAG_00818	NA	809910	810371	462	hypothetical protein	234	25	54.113	8.9	81.4	1686.597	180.192
LAG_00819	mhqD	810692	811303	612	Putative hydrolase MhqD	131	21	34.314	14.5	99.5	712.783	114.263
LAG_00820	mhqA_1	811381	812550	1170	Putative ring-cleaving dioxygenase MhqA	238	30	25.641	3.3	96.8	677.374	85.383
LAG_00821	srrA_1	812597	813286	690	Transcriptional regulatory protein SrrA	166	23	33.333	2.6	89	801.118	110.998
LAG_00822	walK_2	813296	814762	1467	Sensor protein kinase WalK	674	54	36.81	2	97.3	1529.915	122.575
LAG_00823	NA	814876	815826	951	hypothetical protein	286	33	34.7	4.4	98	1001.435	115.55
LAG_00824	yjeM_2	815993	817522	1530	Inner membrane transporter YjeM	428	45	29.412	0.9	98.9	931.515	97.94
LAG_00825	NA	817679	817879	201	hypothetical protein	39	6	29.851	15.9	85.6	646.109	99.401
LAG_00826	NA	817929	818171	243	hypothetical protein	91	8	32.922	4.5	98.4	1247.018	109.628
LAG_00827	NA	818416	819045	630	hypothetical protein	246	17	26.984	3.7	93.7	1300.265	89.856
LAG_00828	rnr_1	819303	821738	2436	Ribonuclease R	568	57	23.399	0.4	96.8	776.441	77.917
LAG_00829	yecD	821763	822347	585	Isochorismatase family protein YecD	89	11	18.803	3.9	95.9	506.607	62.614
LAG_00830	NA	822697	824808	2112	hypothetical protein	653	76	35.985	0.2	99.9	1029.572	119.828
LAG_00831	NA	824898	825218	321	hypothetical protein	36	7	21.807	28	72	373.452	72.616
LAG_00832	tagH_2	825534	827078	1545	Teichoic acids export ATP-binding protein TagH	253	33	21.359	4.8	99.3	545.292	71.125
LAG_00833	tagG_2	827103	827915	813	Teichoic acid translocation permease protein TagG	334	33	40.59	0.9	99.5	1368.023	135.164
LAG_00834	tagF	828018	830378	2361	Teichoic acid poly(glycerol phosphate) polymerase	741	78	33.037	1.5	97.9	1045.104	110.011
LAG_00835	NA	830382	831404	1023	hypothetical protein	237	23	22.483	6.3	98.5	771.454	74.867
LAG_00836	tagD_1	831397	831831	435	Glycerol-3-phosphate cytidylyltransferase	56	8	18.391	5.7	95.4	428.683	61.24
LAG_00837	NA	831828	832250	423	hypothetical protein	109	9	21.277	2.1	95.5	858.072	70.85
LAG_00838	tarF_1	832271	833470	1200	Teichoic acid poly(glycerol phosphate) polymerase	212	24	20	0.2	97.6	588.291	66.599
LAG_00839	lytR_1	833515	834459	945	Transcriptional regulator LytR	131	14	14.815	2.3	100	461.612	49.333
LAG_00840	NA	834505	834879	375	hypothetical protein	63	6	16	1.9	76.5	559.431	53.279
LAG_00841	inlJ_1	834839	836902	2064	Internalin-J	389	38	18.411	2.7	90	627.592	61.307
LAG_00842	trmL	836977	837480	504	tRNA (cytidine(34)-2'-O)-methyltransferase	59	8	15.873	27.2	95.2	389.815	52.856
LAG_00843	dhfR	837969	838484	516	Dihydrofolate reductase	0	0	0			0	0
LAG_00844	clpX	838686	839924	1239	ATP-dependent Clp protease ATP-binding subunit ClpX	22	3	2.421	3.1	98.9	59.127	8.063
LAG_00845	engB	840105	840692	588	putative GTP-binding protein EngB	0	0	0			0	0
LAG_00846	folB	840676	841032	357	Dihydroneopterin aldolase	31	5	14.006	15.4	85.2	289.155	46.638
LAG_00847	folE	841089	842138	1050	GTP cyclohydrolase 1	37	7	6.667	2.2	95.9	117.341	22.2
LAG_00848	folP	842140	843213	1074	Dihydropteroate synthase	78	11	10.242	4.3	65	241.84	34.106
LAG_00849	folQ	843213	843707	495	putative DHNTP pyrophosphohydrolase	50	6	12.121	43	93.9	336.358	40.363
LAG_00850	fpgS	843704	844990	1287	Folylpolyglutamate synthase	106	2	1.554	95.7	99	274.261	5.175
LAG_00851	NA	845028	845666	639	Deoxyguanosine kinase	30	4	6.26	36	80.1	156.336	20.845
LAG_00852	glmS	845819	847636	1818	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]	0	0	0			0	0
LAG_00853	NA	847740	848423	684	hypothetical protein	154	15	21.93	1.6	99.3	749.725	73.025

LAG_00854	menH_2	848489	849418	930	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	171	15	16.129	8.3	94.1	612.281	53.709
LAG_00855	NA	849707	850570	864	hypothetical protein	120	19	21.991	4.1	95.6	462.493	73.228
LAG_00856	NA	850893	852626	1734	Fimbrial subunit type 1	531	56	32.295	7.5	98.7	1019.725	107.542
LAG_00857	NA	852760	856446	3687	hypothetical protein	1512	131	35.53	0.4	96.3	1365.577	118.314
LAG_00858	NA	856448	857080	633	hypothetical protein	146	21	33.175	10.3	93.7	768.045	110.472
LAG_00859	NA	857208	859004	1797	hypothetical protein	372	44	24.485	2.6	99.6	689.338	81.535
LAG_00860	spxA_9	859095	859424	330	Regulatory protein Spx	101	10	30.303	18.5	93.6	1019.166	100.908
LAG_00861	rex	859485	860138	654	Redox-sensing transcriptional repressor Rex	13	2	3.058	60.6	93.7	66.192	10.183
LAG_00862	gltC	860291	861184	894	HTH-type transcriptional regulator GltC	181	22	24.609	20.1	98	674.184	81.945
LAG_00863	mleA	861348	862970	1623	Malolactic enzyme	313	38	23.413	0.4	99.3	642.19	77.966
LAG_00864	citS	862988	864265	1278	Citrate-sodium symporter	208	30	23.474	1	98.1	541.963	78.168
LAG_00865	NA	864246	864422	177	hypothetical protein	41	7	39.548	6.2	96	771.344	131.693
LAG_00866	NA	864612	865466	855	hypothetical protein	244	28	32.749	0.5	93.8	950.301	109.051
LAG_00867	msrB	865608	866051	444	Peptide methionine sulfoxide reductase MsrB	45	6	13.514	0.9	46.2	337.495	44.999
LAG_00868	dkgB	866187	867026	840	2,5-diketo-D-gluconic acid reductase B	109	12	14.286	20.1	62	432.1	47.571
LAG_00869	NA	867208	867375	168	hypothetical protein	22	4	23.81	4.2	92.3	436.065	79.284
LAG_00870	dnaD	867437	868111	675	DNA replication protein DnaD	0	0	0			0	0
LAG_00871	nth	868089	868757	669	Endonuclease III	56	9	13.453	1.3	91	278.74	44.798
LAG_00872	trmK	868750	869427	678	tRNA (adenine(22)-N(1))-methyltransferase	38	6	8.85	43.2	93.2	186.634	29.469
LAG_00873	NA	869424	870194	771	GTP cyclohydrolase 1 type 2	92	11	14.267	10.8	94.7	397.348	47.509
LAG_00874	cof	870358	871122	765	HMP-PP phosphatase	136	15	19.608	1.7	97.8	591.991	65.293
LAG_00875	rlmCD_1	871165	872535	1371	23S rRNA (uracil-C(5))-methyltransferase RlmCD	188	23	16.776	5.1	98.7	456.623	55.863
LAG_00876	NA	872532	874262	1731	hypothetical protein	362	45	25.997	1	93.1	696.384	86.567
LAG_00877	ycgJ_1	874960	875577	618	putative methyltransferase YcgJ	10	3	4.854	7.8	59.5	53.883	16.165
LAG_00878	NA	875693	876874	1182	hypothetical protein	28	4	3.384	46	64.3	78.882	11.269
LAG_00879	lapB	876874	878115	1242	Lipopolysaccharide assembly protein B	38	10	8.052	17.1	93.1	101.882	26.811
LAG_00880	alsS	878315	879982	1668	Acetolactate synthase	229	22	13.189	8.7	88.8	457.169	43.92
LAG_00881	yddE	880125	880925	801	putative isomerase YddE	148	18	22.472	2.6	80.3	615.271	74.83
LAG_00882	NA	880986	882224	1239	Secreted 45 kDa protein	255	27	21.792	6.4	94.7	685.34	72.565
LAG_00883	NA	882590	883318	729	hypothetical protein	142	19	26.063	5.1	94.4	648.632	86.789
LAG_00884	gbpA	883353	884015	663	GlcNAc-binding protein A	149	17	25.641	1.4	81.9	748.359	85.383
LAG_00885	chiD	884047	885528	1482	Chitinase D	279	38	25.641	3.8	99.9	626.893	85.383
LAG_00886	crtK-2	885812	886297	486	Tryptophan-rich protein TspO	134	14	28.807	25.5	84.6	918.134	95.924
LAG_00887	NA	886385	887209	825	hypothetical protein	220	26	31.515	0.7	99.4	887.986	104.944
LAG_00888	spxA_10	887541	887777	237	Regulatory protein Spx	137	13	54.852	3.8	92	1924.907	182.655
LAG_00889	NA	887910	888551	642	hypothetical protein	140	24	37.383	9.3	99.8	726.157	124.484
LAG_00890	dosC	888564	889709	1146	Diguanylate cyclase DosC	372	34	29.668	0.7	97.6	1080.925	98.794
LAG_00891	nagE	890006	891973	1968	PTS system N-acetylglucosamine-specific EIICBA component	268	35	17.785	2.6	96.4	453.469	59.222
LAG_00892	copB	892133	894169	2037	Copper-exporting P-type ATPase B	208	25	12.273	8.7	95.4	340.024	40.868
LAG_00893	NA	894194	894643	450	hypothetical protein	115	10	22.222	8	86.7	850.987	73.999
LAG_00894	NA	894804	895130	327	hypothetical protein	46	7	21.407	20.8	87.5	468.433	71.283
LAG_00895	NA	895123	895743	621	hypothetical protein	268	21	33.816	8.9	93.4	1437.079	112.607
LAG_00896	NA	895740	896618	879	hypothetical protein	134	15	17.065	1.3	97.2	507.637	56.825
LAG_00897	uppP	896632	897471	840	Undecaprenyl-diphosphatase	131	15	17.857	0.5	83.5	519.313	59.463
LAG_00898	NA	897579	898220	642	hypothetical protein	159	16	24.922	3	98	824.707	82.989
LAG_00899	acuR	898407	898979	573	Transcriptional regulator AcuR	0	0	0			0	0
LAG_00900	NA	898999	899358	360	hypothetical protein	7	1	2.778	95.6	95.6	64.749	9.25
LAG_00901	rclA	899360	900718	1359	putative pyridine nucleotide-disulfide oxidoreductase RclA	137	20	14.717	6.5	87.7	335.69	49.006
LAG_00902	metC	900846	902000	1155	Cystathionine beta-lyase	154	9	7.792	31.5	97.4	443.993	25.948
LAG_00903	NA	902110	902658	549	hypothetical protein	31	5	9.107	54.8	92	188.03	30.327
LAG_00904	NA	902659	902940	282	hypothetical protein	0	0	0			0	0
LAG_00905	NA	903007	904380	1374	hypothetical protein	274	30	21.834	4.5	99.4	664.051	72.706
LAG_00906	ahpC	904645	905208	564	Alkyl hydroperoxide reductase subunit C	141	12	21.277	3.9	64.2	832.487	70.85
LAG_00907	ahpF	905267	906796	1530	NADH dehydrogenase	176	27	17.647	10.3	98.4	383.053	58.764

LAG_00908	azoR	906961	907578	618	FMN-dependent NADH-azoreductase	79	15	24.272	2.1	96.8	425.673	80.824
LAG_00909	hpf_2	907689	908246	558	Ribosome hibernation promotion factor	67	8	14.337	0.9	98.6	399.832	47.741
LAG_00910	NA	908297	909133	837	hypothetical protein	122	19	22.7	3.5	87	485.369	75.59
LAG_00911	mngR_1	909358	909978	621	Mannosyl-D-glycerate transport/metabolism system repressor MngR	77	13	20.934	10.6	98.9	412.892	69.709
LAG_00912	opuAA	910183	911385	1203	Glycine betaine transport ATP-binding protein OpuAA	63	13	10.806	4.5	98.8	174.386	35.984
LAG_00913	gbuB	911378	913102	1725	Glycine betaine/carnitine transport permease protein GbuB	166	26	15.072	0.8	92.2	320.447	50.191
LAG_00914	aldC_1	913245	913943	699	Alpha-acetolactate decarboxylase	87	13	18.598	6.9	80.5	414.457	61.93
LAG_00915	dprA	914030	914899	870	DNA processing protein DprA	114	16	18.391	3.3	72.9	436.338	61.24
LAG_00916	topA	915088	917238	2151	DNA topoisomerase 1	4	1	0.465	88.2	88.2	6.192	1.548
LAG_00917	trmFO	917287	918630	1344	Methylenetetrahydrofolate--tRNA-(uracil-5-)- methyltransferase TrmFO	58	9	6.696	29.3	87.2	143.703	22.299
LAG_00918	NA	918704	918925	222	hypothetical protein	14	3	13.514	52.7	86.5	209.997	44.999
LAG_00919	xerS	918991	920052	1062	Tyrosine recombinase XerS	0	0	0			0	0
LAG_00920	NA	920833	921549	717	hypothetical protein	335	35	48.815	0.1	95.3	1555.833	162.55
LAG_00921	walR_2	921771	922448	678	Transcriptional regulatory protein WalR	259	32	47.198	1.8	97.1	1272.06	157.166
LAG_00922	srrB	922449	923348	900	Sensor protein SrrB	316	37	41.111	0.1	96.2	1169.182	136.898
LAG_00923	NA	923394	924170	777	hypothetical protein	239	34	43.758	0.8	99.7	1024.27	145.712
LAG_00924	yxlF_1	924172	925095	924	putative ABC transporter ATP-binding protein YxlF	508	52	56.277	1.3	98.7	1830.751	187.4
LAG_00925	NA	925563	926627	1065	hypothetical protein	271	43	40.376	1.8	98.9	847.339	134.449
LAG_00926	NA	927188	928240	1053	putative zinc-binding alcohol dehydrogenase	407	47	44.634	0.4	96.6	1287.074	148.63
LAG_00927	NA	928253	928636	384	hypothetical protein	329	23	59.896	4.2	99.2	2853.002	199.45
LAG_00928	NA	928847	929284	438	putative HTH-type transcriptional regulator	140	14	31.963	5.5	96.8	1064.367	106.437
LAG_00929	asnA	929473	930477	1005	Aspartate--ammonia ligase	398	48	47.761	4.1	98.5	1318.726	159.042
LAG_00930	yjaB_1	930669	931118	450	putative N-acetyltransferase YjaB	168	16	35.556	6.4	92.7	1243.181	118.398
LAG_00931	ctpF	931199	933841	2643	putative cation-transporting ATPase F	999	96	36.322	0.6	100	1258.652	120.952
LAG_00932	comR	934107	934679	573	HTH-type transcriptional repressor ComR	262	22	38.394	5.2	98.3	1522.594	127.851
LAG_00933	NA	934761	935426	666	Putative NAD(P)H nitroreductase	86	16	24.024	30.2	96.8	429.993	79.999
LAG_00934	NA	935596	938802	3207	hypothetical protein	1567	155	48.332	0.7	99.4	1627.075	160.942
LAG_00935	NA	938829	939518	690	hypothetical protein	342	45	65.217	0.9	96.5	1650.496	217.171
LAG_00936	NA	939515	939829	315	hypothetical protein	147	22	69.841	1.3	98.4	1553.976	232.568
LAG_00937	NA	939844	940098	255	hypothetical protein	144	12	47.059	14.5	98.4	1880.441	156.703
LAG_00938	NA	940134	940937	804	hypothetical protein	350	35	43.532	8.2	96.6	1449.604	144.96
LAG_00939	NA	940979	941800	822	hypothetical protein	282	35	42.579	1.9	97.1	1142.391	141.786
LAG_00940	NA	941885	944659	2775	hypothetical protein	1160	108	38.919	1.2	100	1391.978	129.598
LAG_00941	NA	945013	946302	1290	hypothetical protein	288	34	26.357	4.1	98.4	743.43	87.766
LAG_00942	dltC	946289	946531	243	D-alanine--poly(phosphoribitol) ligase subunit 2	91	9	37.037	7	98.8	1247.018	123.331
LAG_00943	patA_1	946559	947773	1215	Peptidoglycan O-acetyltransferase	485	49	40.329	0.6	100	1329.238	134.294
LAG_00944	dltA	947773	949275	1503	D-alanine--poly(phosphoribitol) ligase subunit 1	384	52	34.597	0.7	98.5	850.765	115.208
LAG_00945	NA	949475	950416	942	hypothetical protein	169	25	26.539	1.2	83	597.411	88.374
LAG_00946	proA	950578	951834	1257	Gamma-glutamyl phosphate reductase	344	42	33.413	0.6	97.1	911.298	111.263
LAG_00947	proB	951831	952655	825	Glutamate 5-kinase 1	219	25	30.303	1.5	96.5	883.95	100.908
LAG_00948	NA	952765	955704	2940	hypothetical protein	607	54	18.367	0.4	99.4	687.51	61.162
LAG_00949	NA	955730	956407	678	hypothetical protein	163	15	22.124	9.1	88.5	800.563	73.671
LAG_00950	NA	956426	957670	1245	hypothetical protein	471	46	36.948	1	99.1	1259.763	123.034
LAG_00951	NA	957701	959422	1722	hypothetical protein	297	38	22.067	2.1	100	574.329	73.483
LAG_00952	NA	959563	959904	342	hypothetical protein	158	16	46.784	2.9	99.7	1538.397	155.787
LAG_00953	thiE	960042	960680	639	Thiamine-phosphate synthase	164	25	39.124	3.3	99.8	854.635	130.28
LAG_00954	thiD	960673	961473	801	Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	220	33	41.199	1	98	914.592	137.189
LAG_00955	thiM	961470	962231	762	Hydroxyethylthiazole kinase	261	25	32.808	0.8	95	1140.573	109.25
LAG_00956	rsgA_1	962548	963633	1086	Small ribosomal subunit biogenesis GTPase RsgA	186	25	23.02	11	96.3	570.323	76.656
LAG_00957	glcU_1	963813	964700	888	putative glucose uptake protein GlcU	172	20	22.523	1.2	99.5	644.99	74.999
LAG_00958	rbsD	964726	965121	396	D-ribose pyranase	102	8	20.202	10.4	84.8	857.714	67.272
LAG_00959	rbsK/rbiA	965133	966041	909	Bifunctional ribokinase/ribose-5-phosphate isomerase A	107	14	15.402	3.2	65.2	391.974	51.286
LAG_00960	rbsR_2	966043	967044	1002	Ribose operon repressor	251	30	29.94	1.1	98.5	834.149	99.699
LAG_00961	garB	967178	968500	1323	Glutathione amide reductase	271	27	20.408	0.8	99.2	682.098	67.958

LAG_00962	NA	968578	968850	273	hypothetical protein	34	5	18.315	27.1	74.4	414.719	60.988
LAG_00963	NA	968872	969132	261	hypothetical protein	33	5	19.157	6.1	82	421.028	63.792
LAG_00964	pox5	969151	970944	1794	Pyruvate oxidase	291	33	18.395	4.3	99.7	540.142	61.253
LAG_00965	lldD	971145	972242	1098	L-lactate dehydrogenase	246	27	24.59	4.8	99.2	746.054	81.884
LAG_00966	spxA_11	972287	972682	396	Regulatory protein Spx	3	1	2.525	85.1	85.1	25.227	8.409
LAG_00967	emrB_2	973035	974393	1359	Multidrug export protein EmrB	292	37	27.226	0.4	99.4	715.485	90.661
LAG_00968	NA	974524	975150	627	hypothetical protein	68	8	12.759	1	99.5	361.143	42.487
LAG_00969	pspE	975217	975540	324	Thiosulfate sulfurtransferase PspE	53	9	27.778	9	87.7	544.714	92.499
LAG_00970	glpE_1	975540	975836	297	Thiosulfate sulfurtransferase GlpE	116	15	50.505	1.3	99.3	1300.586	168.179
LAG_00971	bglK_1	975944	976816	873	Beta-glucoside kinase	208	25	28.637	4.7	91.5	793.39	95.359
LAG_00972	gmuD_1	976816	978249	1434	6-phospho-beta-glucosidase GmuD	397	40	27.894	2.6	92.1	921.889	92.886
LAG_00973	NA	978371	979543	1173	Endo-beta-N-acetylglucosaminidase	477	44	37.511	12.5	98.7	1354.122	124.909
LAG_00974	NA	979579	980859	1281	hypothetical protein	240	34	26.542	0.2	99.5	623.878	88.383
LAG_00975	mngB_1	980876	983500	2625	Mannosylglycerate hydrolase	501	64	24.381	1.6	91.5	635.544	81.187
LAG_00976	gmuC_1	983531	984871	1341	PTS system oligo-beta-mannoside-specific EIIC component	330	35	26.1	1.6	100	819.45	86.911
LAG_00977	gmuR_1	985049	985762	714	HTH-type transcriptional regulator GmuR	42	7	9.804	24.4	98.2	195.879	32.647
LAG_00978	ideR	985911	986606	696	Iron-dependent repressor IdeR	34	8	11.494	3.3	97.6	162.67	38.275
LAG_00979	mntH	986678	988234	1557	Divalent metal cation transporter MntH	82	14	8.992	3.7	97.4	175.373	29.942
LAG_00980	NA	988270	988968	699	hypothetical protein	95	15	21.459	8.2	100	452.568	71.458
LAG_00981	NA	989064	989579	516	hypothetical protein	100	13	25.194	11.4	86.4	645.339	83.894
LAG_00982	nhaK_2	989710	991659	1950	Sodium, potassium, lithium and rubidium/H(+) antiporter	541	50	25.641	0.5	96.8	923.847	85.383
LAG_00983	ycgJ_2	991772	992503	732	putative methyltransferase YcgJ	266	23	31.421	0.1	98.6	1210.063	104.63
LAG_00984	NA	992632	993849	1218	hypothetical protein	163	20	16.42	2.4	99	445.633	54.679
LAG_00985	ndk	993959	994375	417	Nucleoside diphosphate kinase	96	12	28.777	3.6	89.2	766.607	95.826
LAG_00986	clpB	994517	997120	2604	Chaperone protein ClpB	299	40	15.361	1.8	99.5	382.356	51.151
LAG_00987	NA	997280	997909	630	hypothetical protein	166	25	39.683	1.7	99.8	877.415	132.141
LAG_00988	ywnA	997998	998438	441	Putative HTH-type transcriptional regulator YwnA	43	6	13.605	1.8	99.1	324.689	45.305
LAG_00989	NA	998584	999114	531	hypothetical protein	128	15	28.249	1.3	94.5	802.699	94.066
LAG_00990	tetA_1	999163	1000329	1167	Tetracycline resistance protein, class B	145	16	13.71	5.5	95	413.747	45.655
LAG_00991	gshAB	1000531	1002792	2262	Glutathione biosynthesis bifunctional protein GshAB	367	42	18.568	0.4	99.8	540.27	61.829
LAG_00992	NA	1002902	1003348	447	hypothetical protein	35	4	8.949	50.8	75.8	260.734	29.798
LAG_00993	yxeM_2	1003489	1004337	849	putative amino-acid-binding protein YxeM	125	15	17.668	4	81.2	490.275	58.833
LAG_00994	nylA	1004324	1005799	1476	6-aminohexanoate-cyclic-dimer hydrolase	148	22	14.905	11.5	97.9	333.897	49.633
LAG_00995	yjaB_2	1005836	1006255	420	putative N-acetyltransferase YjaB	183	20	47.619	3.3	95.2	1450.906	158.569
LAG_00996	NA	1006357	1006932	576	hypothetical protein	56	9	15.625	4.2	99.5	323.745	52.03
LAG_00997	NA	1006974	1007174	201	hypothetical protein	40	6	29.851	9	95	662.676	99.401
LAG_00998	mhqA_2	1007164	1008060	897	Putative ring-cleaving dioxygenase MhqA	167	19	21.182	1.6	96.1	619.957	70.534
LAG_00999	murK	1008205	1009098	894	N-acetylmuramic acid/N-acetylglucosamine kinase	191	30	33.557	0.6	98.1	711.432	111.743
LAG_01000	NA	1009108	1010196	1089	hypothetical protein	338	38	34.894	0.7	98.6	1033.538	116.197
LAG_01001	NA	1010215	1010550	336	hypothetical protein	94	14	41.667	0.9	100	931.593	138.748
LAG_01002	licC_2	1010605	1011912	1308	Lichenan permease IIC component	341	33	25.229	2.6	96.7	868.129	84.012
LAG_01003	NA	1012442	1013119	678	hypothetical protein	56	11	16.224	0.7	74.8	275.04	54.026
LAG_01004	NA	1013324	1014364	1041	hypothetical protein	409	37	35.543	7.2	99.3	1308.308	118.355
LAG_01005	NA	1014527	1015759	1233	hypothetical protein	155	27	21.898	6.1	92.9	418.607	72.919
LAG_01006	NA	1015857	1017362	1506	Fumarate reductase flavoprotein subunit	268	31	20.584	4.7	98.3	592.58	68.545
LAG_01007	NA	1017836	1018996	1161	hypothetical protein	122	15	12.92	9.6	99.9	349.917	43.023
LAG_01008	NA	1019114	1019449	336	hypothetical protein	103	10	29.762	3.3	100	1020.788	99.106
LAG_01009	uvrA_1	1019464	1021665	2202	UvrABC system protein A	492	67	30.427	0.9	89.5	744.021	101.32
LAG_01010	licT_1	1021942	1022805	864	Transcription antiterminator LicT	402	40	46.296	7.3	96.9	1549.351	154.164
LAG_01011	bglH_3	1022817	1024271	1455	Aryl-phospho-beta-D-glucosidase BglH	731	71	48.797	0.1	99	1672.984	162.492
LAG_01012	bglF_2	1024293	1026110	1818	PTS system beta-glucoside-specific EIIBCA component	1072	100	55.006	1.4	99.4	1963.534	183.165
LAG_01013	NA	1026433	1026780	348	hypothetical protein	119	18	51.724	1.1	94	1138.689	172.239
LAG_01014	NA	1026822	1027496	675	hypothetical protein	143	19	28.148	1.8	99.7	705.456	93.732
LAG_01015	rplL	1027696	1028061	366	50S ribosomal protein L7/L12	0	0	0			0	0

LAG_01016	rplJ	1028140	1028655	516	50S ribosomal protein L10	0	0	0			0	0
LAG_01017	ribU	1028950	1029534	585	Riboflavin transporter RibU	96	1	1.709	2.9	2.9	546.453	5.692
LAG_01018	nhaK_3	1029808	1031865	2058	Sodium, potassium, lithium and rubidium/H(+) antiporter	372	33	16.035	0.5	98.6	601.915	53.396
LAG_01019	NA	1031874	1032320	447	hypothetical protein	56	10	22.371	11.9	100	417.175	74.495
LAG_01020	NA	1032463	1033260	798	hypothetical protein	225	20	25.063	2.9	92.1	938.895	83.457
LAG_01021	icaA_1	1033264	1034598	1335	Poly-beta-1,6-N-acetyl-D-glucosamine synthase	235	30	22.472	9.3	98.8	586.171	74.83
LAG_01022	NA	1034588	1035118	531	hypothetical protein	63	11	20.716	0.6	39.4	395.079	68.982
LAG_01023	ycdT	1035237	1036379	1143	putative diguanylate cyclase YcdT	394	51	44.619	1.2	98.4	1147.856	148.58
LAG_01024	NA	1036593	1037429	837	hypothetical protein	164	27	32.258	8.4	100	652.463	107.418
LAG_01025	yhfK	1037453	1038121	669	putative sugar epimerase YhfK	109	12	17.937	9.6	95.4	542.548	59.73
LAG_01026	guaC	1038249	1039238	990	GMP reductase	249	33	33.333	1.1	94	837.532	110.998
LAG_01027	NA	1039411	1040046	636	hypothetical protein	90	12	18.868	6.4	86.2	471.219	62.829
LAG_01028	yutF	1040048	1040827	780	Acid sugar phosphatase	91	10	12.821	3.8	91.4	388.494	42.692
LAG_01029	NA	1040824	1041585	762	hypothetical protein	157	24	31.496	0.9	97.9	686.092	104.88
LAG_01030	tadA_1	1041702	1042142	441	tRNA-specific adenosine deaminase	87	9	20.408	5	93.7	656.928	67.958
LAG_01031	NA	1042144	1042479	336	hypothetical protein	41	5	14.881	5.7	49.1	406.333	49.553
LAG_01032	cdr	1042598	1044241	1644	Coenzyme A disulfide reductase	381	36	21.898	6	99.9	771.721	72.919
LAG_01033	ygaP	1044252	1044536	285	Inner membrane protein YgaP	70	8	28.07	27	75.8	817.882	93.472
LAG_01034	NA	1044706	1044843	138	hypothetical protein	11	2	14.493	2.9	61.6	265.431	48.26
LAG_01035	NA	1044846	1045052	207	hypothetical protein	77	7	33.816	6.8	82.6	1238.676	112.607
LAG_01036	licC_3	1045071	1046552	1482	Lichenan permease IIC component	298	29	19.568	0.9	97.3	669.585	65.161
LAG_01037	NA	1046599	1047696	1098	hypothetical protein	2330	34	30.965	3.3	98.8	7066.283	103.113
LAG_01038	licB_3	1047736	1048059	324	Lichenan-specific phosphotransferase enzyme IIB component	108	7	21.605	4.3	54.3	1109.983	71.943
LAG_01039	NA	1048350	1049357	1008	hypothetical protein	240	29	28.77	3.7	83.4	792.845	95.802
LAG_01040	NA	1049362	1049787	426	hypothetical protein	54	7	16.432	1.2	91.3	422.106	54.717
LAG_01041	pyrC	1049871	1051136	1266	Dihydroorotase	176	23	18.167	4.4	98.4	462.931	60.497
LAG_01042	pyrE	1051175	1051804	630	Orotate phosphoribosyltransferase	96	12	19.048	2.7	97.6	507.421	63.428
LAG_01043	yheS	1052028	1053932	1905	putative ABC transporter ATP-binding protein YheS	103	18	9.449	2.1	99.7	180.044	31.464
LAG_01044	ybbH_2	1054037	1054888	852	putative HTH-type transcriptional regulator YbbH	126	13	15.258	1.3	98.9	492.457	50.809
LAG_01045	bsaA	1054970	1055458	489	Glutathione peroxidase BsaA	43	8	16.36	1.8	76.5	292.818	54.478
LAG_01046	rsuA_1	1055534	1056238	705	Ribosomal small subunit pseudouridine synthase A	82	12	17.021	7.7	84.3	387.313	56.68
LAG_01047	NA	1056284	1057645	1362	Magnesium transporter MgtE	116	17	12.482	17.8	99.6	283.608	41.563
LAG_01048	NA	1057763	1057969	207	hypothetical protein	13	3	14.493	43.5	88.4	209.127	48.26
LAG_01049	yloB	1058043	1060799	2757	Calcium-transporting ATPase	566	64	23.214	1	99.5	683.624	77.3
LAG_01050	NA	1061179	1061760	582	hypothetical protein	3	1	1.718	68	68	17.165	5.722
LAG_01051	potD	1063147	1064214	1068	Spermidine/putrescine-binding periplasmic protein	524	35	32.772	1	99.4	1633.795	109.128
LAG_01052	ydcV	1064230	1065030	801	Inner membrane ABC transporter permease protein YdcV	189	24	29.963	0.7	89.5	785.718	99.774
LAG_01053	potB	1065030	1065824	795	Spermidine/putrescine transport system permease protein PotB	104	11	13.836	15.1	96.1	435.616	46.075
LAG_01054	potA	1065821	1067092	1272	Spermidine/putrescine import ATP-binding protein PotA	235	25	19.654	0.4	97.9	615.203	65.447
LAG_01055	yfnB_1	1067928	1068830	903	Putative HAD-hydrolase YfnB	95	12	13.289	6.1	74.5	350.327	44.252
LAG_01056	murB	1068843	1069751	909	UDP-N-acetylenolpyruvoylglucosamine reductase	0	0	0			0	0
LAG_01057	rluD_2	1069905	1070810	906	Ribosomal large subunit pseudouridine synthase D	9	2	2.208	7.5	45.9	33.079	7.351
LAG_01058	lspA	1070811	1071350	540	Lipoprotein signal peptidase	146	17	31.481	9.3	84.3	900.319	104.832
LAG_01059	dapE_1	1071403	1072617	1215	putative succinyl-diaminopimelate desuccinylase	247	24	19.753	10.1	97.9	676.952	65.777
LAG_01060	acpB	1072722	1074215	1494	Capsule synthesis positive regulator AcpB	442	31	20.75	1.9	96	985.165	69.095
LAG_01061	spxA_12	1074287	1074691	405	Regulatory protein Spx	69	11	27.16	1.2	52.1	567.324	90.443
LAG_01062	cpdA_1	1074793	1075671	879	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	175	18	20.478	0.8	90.1	662.959	68.19
LAG_01063	NA	1075738	1076079	342	hypothetical protein	25	4	11.696	6.1	93	243.417	38.947
LAG_01064	NA	1076076	1077824	1749	hypothetical protein	379	45	25.729	1	88.5	721.584	85.676
LAG_01065	yerB	1077952	1078980	1029	Putative lipoprotein YerB	57	9	8.746	1.8	94.2	184.458	29.125
LAG_01066	mtlD	1079076	1080227	1152	Mannitol-1-phosphate 5-dehydrogenase	115	16	13.889	2.7	68.4	332.417	46.249
LAG_01067	mtlF	1080337	1080768	432	Mannitol-specific phosphotransferase enzyme IIA component	165	10	23.148	1.6	98.8	1271.855	77.082
LAG_01068	mtlR	1080770	1082704	1935	Transcriptional regulator MtlR	218	29	14.987	0.7	99.3	375.157	49.906
LAG_01069	mtlA	1082729	1084558	1830	PTS system mannitol-specific EIICB component	510	53	28.962	0.2	99.9	928.018	96.441

LAG_01070	NA	1084942	1085364	423	hypothetical protein	112	14	33.097	2.1	97.2	881.688	110.211
LAG_01071	pcp	1085358	1085999	642	Pyrrolidone-carboxylate peptidase	38	6	9.346	18.1	65.7	197.1	31.121
LAG_01072	NA	1086018	1086950	933	hypothetical protein	141	18	19.293	6.6	85.1	503.24	64.243
LAG_01073	NA	1086954	1087628	675	hypothetical protein	100	15	22.222	7.1	91.4	493.326	73.999
LAG_01074	NA	1087801	1088214	414	Organic hydroperoxide resistance protein-like protein	35	6	14.493	55.6	92.5	281.517	48.26
LAG_01075	sarZ	1088324	1088764	441	HTH-type transcriptional regulator SarZ	85	13	29.478	7.5	98.9	641.827	98.162
LAG_01076	hchA_2	1088810	1089502	693	Molecular chaperone Hsp31 and glyoxalase 3	111	12	17.316	3.6	88.3	533.368	57.661
LAG_01077	NA	1089602	1089964	363	hypothetical protein	91	11	30.303	1.4	83.2	834.78	100.908
LAG_01078	ycnE	1089974	1090258	285	Putative monooxygenase YcnE	27	4	14.035	8.4	68.1	315.469	46.736
LAG_01079	NA	1090510	1091991	1482	hypothetical protein	314	32	21.592	0.9	99.4	705.536	71.902
LAG_01080	ytrE	1092006	1092677	672	ABC transporter ATP-binding protein YtrE	162	21	31.25	2.8	99.3	802.755	104.061
LAG_01081	inlA	1092732	1094492	1761	Internalin-A	411	52	29.529	0.6	99.1	777.177	98.329
LAG_01082	NA	1094868	1095701	834	hypothetical protein	327	34	40.767	10.2	98.2	1305.627	135.753
LAG_01083	lepA	1095995	1097818	1824	Elongation factor 4	37	7	3.838	0.9	81.1	67.548	12.779
LAG_01084	NA	1097949	1099436	1488	hypothetical protein	376	41	27.554	0.6	99.7	841.438	91.753
LAG_01085	NA	1099548	1101437	1890	hypothetical protein	271	33	17.46	2	95.7	477.469	58.142
LAG_01086	NA	1101434	1101757	324	hypothetical protein	31	6	18.519	10.5	86.4	318.606	61.666
LAG_01087	NA	1101741	1102775	1035	hypothetical protein	83	10	9.662	45.2	85.2	267.039	32.173
LAG_01088	NA	1102873	1103484	612	hypothetical protein	87	14	22.876	5.7	87.4	473.375	76.175
LAG_01089	aldC_2	1103690	1104370	681	Alpha-acetolactate decarboxylase	0	0	0			0	0
LAG_01090	NA	1104392	1105123	732	hypothetical protein	119	11	15.027	1.2	95.5	541.344	50.04
LAG_01091	murF_2	1105675	1107024	1350	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	0	0	0			0	0
LAG_01092	cobQ	1107024	1107815	792	Cobyric acid synthase	27	2	2.525	90.8	96.1	113.521	8.409
LAG_01093	NA	1107880	1109472	1593	hypothetical protein	177	30	18.832	2.6	95.9	369.994	62.711
LAG_01094	NA	1109753	1112410	2658	hypothetical protein	838	81	30.474	1.9	96.5	1049.848	101.477
LAG_01095	NA	1112415	1113116	702	putative ABC transporter ATP-binding protein	103	16	22.792	3.4	90.2	488.582	75.896
LAG_01096	nadE	1113230	1114054	825	NH(3)-dependent NAD(+) synthetase	0	0	0			0	0
LAG_01097	wecD	1114057	1114545	489	dTDP-fucosamine acetyltransferase	126	11	22.495	2.5	73.8	858.023	74.907
LAG_01098	pncB2	1114550	1116013	1464	Nicotinate phosphoribosyltransferase pncB2	10	1	0.683	2.6	2.6	22.746	2.275
LAG_01099	nadD_1	1116281	1116868	588	putative nicotinate-nucleotide adenylyltransferase	0	0	0			0	0
LAG_01100	rnr_2	1116880	1118880	2001	Ribonuclease R	6	1	0.5	0.8	0.8	9.985	1.664
LAG_01101	mnmC	1118965	1120077	1113	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC	96	12	10.782	2.1	92.8	287.219	35.902
LAG_01102	NA	1120162	1120686	525	hypothetical protein	149	17	32.381	1.1	96.4	945.071	107.827
LAG_01103	NA	1120815	1120982	168	hypothetical protein	0	0	0			0	0
LAG_01104	obg	1121001	1122314	1314	GTPase Obg	0	0	0			0	0
LAG_01105	sbcC	1122567	1125704	3138	Nuclease SbcCD subunit C	269	37	11.791	0.2	99.8	285.454	39.263
LAG_01106	sbcD	1125707	1126879	1173	Nuclease SbcCD subunit D	142	10	8.525	13.6	75.6	403.114	28.388
LAG_01107	yycN	1127066	1127527	462	putative N-acetyltransferase YycN	34	4	8.658	43.7	93.7	245.061	28.831
LAG_01108	menA_2	1127630	1128571	942	1,4-dihydroxy-2-naphthoate octaprenyltransferase	99	14	14.862	0.4	98.1	349.963	49.49
LAG_01109	yoaB_1	1128622	1131297	2676	Calcium-transporting ATPase 1	472	48	17.937	0.1	95.6	587.345	59.73
LAG_01110	NA	1131678	1132019	342	hypothetical protein	27	3	8.772	35.4	88	262.891	29.21
LAG_01111	bglK_2	1132081	1132965	885	Beta-glucoside kinase	112	11	12.429	35.8	98.6	421.417	41.389
LAG_01112	gmuD_2	1132955	1134334	1380	6-phospho-beta-glucosidase GmuD	252	27	19.565	5.1	87.8	608.077	65.151
LAG_01113	hexR_1	1134347	1135144	798	HTH-type transcriptional regulator HexR	95	16	20.05	14.8	99.2	396.422	66.766
LAG_01114	mngB_2	1135154	1137772	2619	Mannosylglycerate hydrolase	616	74	28.255	1	96.3	783.218	94.088
LAG_01115	manP	1137830	1138282	453	PTS system mannose-specific EIIBCA component	172	12	26.49	1.3	97.8	1264.351	88.211
LAG_01116	fruA_2	1138297	1139790	1494	PTS system fructose-specific EIIB'BC component	279	29	19.411	0.3	96.7	621.858	64.638
LAG_01117	glpF_2	1139985	1140722	738	Glycerol uptake facilitator protein	91	13	17.615	2	96.2	410.603	58.658
LAG_01118	glpO	1140774	1142603	1830	Alpha-glycerophosphate oxidase	212	34	18.579	0.6	86.1	385.764	61.868
LAG_01119	glpK_1	1142640	1144136	1497	Glycerol kinase	343	47	31.396	2	95.8	762.974	104.547
LAG_01120	NA	1144296	1145978	1683	hypothetical protein	299	37	21.985	1.8	90.4	591.595	73.207
LAG_01121	acpA	1146271	1147737	1467	Capsule synthesis positive regulator AcpA	432	47	32.038	10.6	97.9	980.598	106.685
LAG_01122	eriC	1147897	1149108	1212	Chloride/fluoride channel protein	330	29	23.927	4.1	96.7	906.669	79.677
LAG_01123	NA	1149285	1149524	240	hypothetical protein	8	1	4.167	5.8	5.8	110.998	13.875

LAG_01124	glyS	1149541	1151574	2034	Glycine--tRNA ligase beta subunit	0	0	0			0	0
LAG_01125	glyQ	1151574	1152542	969	Glycine--tRNA ligase alpha subunit	0	0	0			0	0
LAG_01126	focA	1152556	1153335	780	putative formate transporter 1	35	6	7.692	15.3	93.8	149.421	25.615
LAG_01127	aes	1153653	1154675	1023	Acetyl esterase	156	22	21.505	6.8	96.6	507.793	71.612
LAG_01128	NA	1154710	1155732	1023	hypothetical protein	177	19	18.573	3.6	99.2	576.149	61.847
LAG_01129	yigZ	1155745	1156368	624	IMPACT family member YigZ	213	29	46.474	11.5	96.2	1136.665	154.757
LAG_01130	comFA	1156423	1157679	1257	ComF operon protein 1	222	26	20.684	2	99.4	588.105	68.877
LAG_01131	NA	1157676	1158320	645	hypothetical protein	720	7	10.853	19.4	96.7	3717.151	36.139
LAG_01132	dgkA	1158323	1158784	462	Undecaprenol kinase	98	2	4.329	55.8	74.5	706.353	14.415
LAG_01133	ybeY	1158768	1159256	489	Endoribonuclease YbeY	7	1	2.045	4.9	4.9	47.668	6.81
LAG_01134	nudC	1159266	1159739	474	NADH pyrophosphatase	55	9	18.987	2.7	54.2	386.386	63.227
LAG_01135	NA	1159741	1160700	960	PhoH-like protein	161	15	15.625	0.6	98.4	558.46	52.03
LAG_01136	ald1_1	1160820	1161926	1107	Alanine dehydrogenase 1	125	21	18.97	0.5	97.9	376.01	63.17
LAG_01137	NA	1162236	1162517	282	hypothetical protein	43	7	24.823	0.7	98.6	507.758	82.658
LAG_01138	rpmA	1162678	1162962	285	50S ribosomal protein L27	0	0	0			0	0
LAG_01139	NA	1162955	1163299	345	hypothetical protein	0	0	0			0	0
LAG_01140	rplU	1163303	1163617	315	50S ribosomal protein L21	0	0	0			0	0
LAG_01141	dagK_2	1163867	1164775	909	Diacylglycerol kinase	113	15	16.502	2.5	80.1	413.954	54.95
LAG_01142	NA	1164866	1166044	1179	hypothetical protein	150	19	16.115	20.4	97.5	423.657	53.663
LAG_01143	NA	1166047	1166424	378	hypothetical protein	0	0	0			0	0
LAG_01144	NA	1166625	1167923	1299	hypothetical protein	141	12	9.238	17.8	69.2	361.449	30.762
LAG_01145	NA	1167944	1168756	813	Putative phosphatase	40	6	7.38	12.1	85.7	163.835	24.575
LAG_01146	NA	1168749	1169117	369	hypothetical protein	32	6	16.26	56.6	93.2	288.776	54.145
LAG_01147	moeZ	1169137	1170150	1014	putative adenylyltransferase/sulfurtransferase MoeZ	30	5	4.931	4.6	81.4	98.519	16.42
LAG_01148	NA	1170238	1170696	459	hypothetical protein	6	1	2.179	16.8	16.8	43.529	7.255
LAG_01149	NA	1170797	1171399	603	hypothetical protein	46	5	8.292	8.8	40.5	254.026	27.612
LAG_01150	cat3	1171591	1172235	645	Chloramphenicol acetyltransferase 3	90	11	17.054	16	89.1	464.644	56.79
LAG_01151	cpdA_2	1172309	1173187	879	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	103	16	18.203	1.9	76.7	390.199	60.613
LAG_01152	NA	1173260	1173790	531	hypothetical protein	10	2	3.766	92.1	100	62.711	12.542
LAG_01153	NA	1173813	1175453	1641	hypothetical protein	285	36	21.938	1	99.7	578.327	73.052
LAG_01154	natA_2	1175466	1176344	879	ABC transporter ATP-binding protein NatA	142	20	22.753	5	96.5	537.944	75.767
LAG_01155	bm3R1	1176478	1177044	567	HTH-type transcriptional repressor Bm3R1	116	13	22.928	7.8	95.9	681.259	76.348
LAG_01156	whiA	1177041	1177961	921	Putative sporulation transcription regulator WhiA	35	5	5.429	13.6	97.6	126.545	18.078
LAG_01157	NA	1177958	1178944	987	Putative gluconeogenesis factor	0	0	0			0	0
LAG_01158	yvcJ	1178941	1179831	891	Nucleotide-binding protein YvcJ	0	0	0			0	0
LAG_01159	clsA_1	1179879	1181324	1446	Major cardiolipin synthase ClsA	382	30	20.747	0.6	97.4	879.696	69.086
LAG_01160	ettA_1	1181633	1183126	1494	Energy-dependent translational throttle protein EttA	131	18	12.048	1.4	98.7	291.983	40.12
LAG_01161	NA	1183180	1183341	162	hypothetical protein	57	3	18.519	11.7	27.2	1171.648	61.666
LAG_01162	yvbW_1	1183621	1184955	1335	putative amino acid permease YvbW	341	34	25.468	0.8	97.2	850.571	84.808
LAG_01163	NA	1185433	1186242	810	Putative phosphatase	94	15	18.519	8.5	99.1	386.438	61.666
LAG_01164	ccpB	1186239	1187162	924	Catabolite control protein B	139	18	19.481	2.4	95.7	500.934	64.869
LAG_01165	NA	1187209	1187982	774	hypothetical protein	57	11	14.212	10.1	89.5	245.229	47.325
LAG_01166	NA	1187979	1189772	1794	DegV domain-containing protein	294	33	18.395	0.1	93.6	545.711	61.253
LAG_01167	NA	1189785	1190198	414	hypothetical protein	120	16	38.647	2.4	91.1	965.202	128.694
LAG_01168	NA	1190384	1191541	1158	hypothetical protein	243	26	22.453	4.9	92.6	698.771	74.766
LAG_01169	NA	1191576	1192088	513	Stress response regulator gls24	92	7	13.645	4.1	67.8	597.184	45.438
LAG_01170	NA	1192120	1192305	186	hypothetical protein	92	10	53.763	1.6	81.7	1647.071	179.029
LAG_01171	NA	1192317	1192874	558	hypothetical protein	102	6	10.753	3.9	86.4	608.7	35.806
LAG_01172	NA	1192907	1193149	243	hypothetical protein	3	1	4.115	53.1	53.1	41.11	13.703
LAG_01173	NA	1193354	1193899	546	hypothetical protein	27	6	10.989	11	93.2	164.668	36.593
LAG_01174	tarF_2	1193984	1194268	285	Teichoic acid glycerol-phosphate transferase	36	3	10.526	36.1	61.1	420.625	35.052
LAG_01175	mnmG	1194562	1196436	1875	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	0	0	0			0	0
LAG_01176	NA	1196591	1197139	549	hypothetical protein	4	1	1.821	44.8	44.8	24.262	6.065
LAG_01177	NA	1197282	1197653	372	hypothetical protein	23	3	8.065	7.3	39.8	205.884	26.854

LAG_01178	mrnC	1197739	1198140	402	Mini-ribonuclease 3	6	1	2.488	11.2	11.2	49.701	8.283
LAG_01179	cysS	1198133	1199485	1353	Cysteine--tRNA ligase	5	1	0.739	99.6	99.6	12.306	2.461
LAG_01180	cysE	1199469	1200074	606	Serine acetyltransferase	0	0	0			0	0
LAG_01181	pnp_2	1200132	1202411	2280	Polyribonucleotide nucleotidyltransferase	297	32	14.035	3.8	97.2	433.77	46.736
LAG_01182	fecE	1202765	1203541	777	Fe(3+) dicitrate transport ATP-binding protein FecE	22	4	5.148	51	86.5	94.284	17.143
LAG_01183	yfhA_2	1203543	1204517	975	putative siderophore transport system permease protein YfhA	102	11	11.282	3.4	83.6	348.364	37.569
LAG_01184	hmuT	1204540	1205481	942	Hemin-binding periplasmic protein HmuT	200	19	20.17	37.8	99.7	706.995	67.165
LAG_01185	prs2	1205912	1206877	966	Ribose-phosphate pyrophosphokinase 2	0	0	0			0	0
LAG_01186	NA	1207083	1207433	351	hypothetical protein	180	18	51.282	5.7	89.7	1707.666	170.767
LAG_01187	iscS_2	1207944	1209005	1062	Cysteine desulfurase IscS	22	3	2.825	95.6	99.5	68.982	9.407
LAG_01188	NA	1209009	1209353	345	hypothetical protein	44	6	17.391	1.2	88.4	424.689	57.912
LAG_01189	tuf	1209471	1210658	1188	Elongation factor Tu	0	0	0			0	0
LAG_01190	NA	1210840	1211022	183	hypothetical protein	163	5	27.322	10.4	41.5	2966.019	90.982
LAG_01191	NA	1211084	1211200	117	hypothetical protein	0	0	0			0	0
LAG_01192	ileS	1211259	1214045	2787	Isoleucine--tRNA ligase	0	0	0			0	0
LAG_01193	divIVA	1214506	1215357	852	Cell division protein DivIVA	0	0	0			0	0
LAG_01194	NA	1215384	1216181	798	hypothetical protein	80	8	10.025	35.5	83.3	333.829	33.383
LAG_01195	NA	1216178	1216423	246	hypothetical protein	9	1	4.065	53.3	53.3	121.827	13.536
LAG_01196	sepF	1216430	1217002	573	Cell division protein SepF	0	0	0			0	0
LAG_01197	NA	1217043	1217714	672	hypothetical protein	51	2	2.976	41.5	47.8	252.719	9.911
LAG_01198	ftsZ	1217714	1218988	1275	Cell division protein FtsZ	0	0	0			0	0
LAG_01199	ftsA	1219016	1220377	1362	Cell division protein FtsA	0	0	0			0	0
LAG_01200	NA	1220497	1221369	873	DegV domain-containing protein	31	5	5.727	2.5	100	118.246	19.072
LAG_01201	NA	1221380	1222108	729	Putative TrmH family tRNA/rRNA methyltransferase	21	5	6.859	50.9	98.6	95.924	22.839
LAG_01202	pepC	1222158	1223468	1311	Aminopeptidase C	113	13	9.916	17.8	97.2	287.021	33.02
LAG_01203	mtnN	1223544	1224224	681	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	0	0	0			0	0
LAG_01204	NA	1224319	1224597	279	hypothetical protein	0	0	0			0	0
LAG_01205	act	1224590	1225174	585	Methanol dehydrogenase activator	8	2	3.419	65.8	73	45.538	11.384
LAG_01206	glmU	1225207	1226583	1377	Bifunctional protein GlmU	0	0	0			0	0
LAG_01207	proC	1226741	1227532	792	Pyrroline-5-carboxylate reductase	0	0	0			0	0
LAG_01208	rpsO	1227676	1227945	270	30S ribosomal protein S15	3	1	3.704	99.3	99.3	36.999	12.333
LAG_01209	stkP	1228027	1229985	1959	Serine/threonine-protein kinase StkP	55	5	2.552	80.8	98.7	93.49	8.499
LAG_01210	NA	1229985	1230758	774	Putative protein phosphatase 2C-type	35	3	3.876	79.2	92.5	150.579	12.907
LAG_01211	rsmB	1230779	1232050	1272	Ribosomal RNA small subunit methyltransferase B	91	11	8.648	13.1	83.8	238.227	28.797
LAG_01212	fmt	1232040	1232969	930	Methionyl-tRNA formyltransferase	0	0	0			0	0
LAG_01213	NA	1233302	1233781	480	hypothetical protein	25	6	12.5	9	95.2	173.435	41.624
LAG_01214	yvdD	1233765	1234319	555	LOG family protein YvdD	27	4	7.207	19.5	96.8	161.997	24
LAG_01215	NA	1234316	1234972	657	Deoxyguanosine kinase	71	8	12.177	3.8	94.5	359.857	40.547
LAG_01216	priA	1235219	1237546	2328	Primosomal protein N'	0	0	0			0	0
LAG_01217	rpoZ	1237698	1238057	360	DNA-directed RNA polymerase subunit omega	0	0	0			0	0
LAG_01218	gmk	1238174	1238803	630	Guanylate kinase	0	0	0			0	0
LAG_01219	rny_2	1238956	1240572	1617	Ribonuclease Y	8	2	1.237	72.9	75.5	16.475	4.119
LAG_01220	metK	1240872	1242065	1194	S-adenosylmethionine synthase	0	0	0			0	0
LAG_01221	birA	1242211	1242960	750	Bifunctional ligase/repressor BirA	0	0	0			0	0
LAG_01222	NA	1243028	1243387	360	hypothetical protein	0	0	0			0	0
LAG_01223	NA	1243422	1243622	201	hypothetical protein	5	1	4.975	1	1	82.835	16.567
LAG_01224	NA	1243660	1244748	1089	hypothetical protein	5	1	0.918	99.7	99.7	15.289	3.058
LAG_01225	NA	1244899	1246494	1596	N-acetylmuramoyl-L-alanine amidase domain-containing protein	157	20	12.531	15.5	96.2	327.57	41.729
LAG_01226	ydjP	1246694	1247425	732	AB hydrolase superfamily protein YdjP	47	5	6.831	0.5	99.5	213.808	22.746
LAG_01227	bglH_4	1247440	1248876	1437	Aryl-phospho-beta-D-glucosidase BglH	324	35	24.356	0.4	99.4	750.802	81.105
LAG_01228	bglH_5	1248878	1250323	1446	Aryl-phospho-beta-D-glucosidase BglH	158	20	13.831	0.4	98.8	363.853	46.057
LAG_01229	bglF_3	1250338	1252263	1926	PTS system beta-glucoside-specific EIIBCA component	190	25	12.98	0.3	96.4	328.5	43.224
LAG_01230	licT_2	1252344	1253183	840	Transcription antiterminator LicT	127	9	10.714	2.3	68.5	503.456	35.678
LAG_01231	NA	1253374	1253865	492	hypothetical protein	46	8	16.26	1.4	91.9	311.337	54.145

LAG_01232	fba_1	1254133	1255029	897	Fructose-bisphosphate aldolase	0	0	0			0	0
LAG_01233	thrS	1255186	1257126	1941	Threonine--tRNA ligase	0	0	0			0	0
LAG_01234	NA	1257577	1268085	10509	hypothetical protein	617	77	7.327	1.8	99.3	195.507	24.399
LAG_01235	hemH	1268267	1269214	948	Ferrochelatase	207	15	15.823	24.6	98.4	727.109	52.689
LAG_01236	NA	1269407	1277182	7776	hypothetical protein	430	57	7.33	3.2	100	184.141	24.409
LAG_01237	NA	1277375	1277752	378	hypothetical protein	63	5	13.228	6.6	57.1	554.991	44.047
LAG_01238	NA	1277898	1278506	609	hypothetical protein	132	13	21.346	6.7	87	721.762	71.083
LAG_01239	upp	1278656	1279285	630	Uracil phosphoribosyltransferase	41	8	12.698	41.3	91.9	216.711	42.285
LAG_01240	napA	1279360	1280487	1128	Na(+)/H(+) antiporter	119	10	8.865	4.7	97.3	351.298	29.521
LAG_01241	NA	1280578	1281447	870	hypothetical protein	107	15	17.241	1.3	97.6	409.545	57.413
LAG_01242	yhaM	1281463	1282407	945	3'-5' exoribonuclease YhaM	103	10	10.582	2.5	89.7	362.947	35.238
LAG_01243	NA	1282409	1283695	1287	hypothetical protein	23	5	3.885	6.8	74.4	59.51	12.937
LAG_01244	rpe	1283692	1284351	660	Ribulose-phosphate 3-epimerase	0	0	0			0	0
LAG_01245	NA	1284360	1284566	207	hypothetical protein	30	2	9.662	17.4	95.2	482.601	32.173
LAG_01246	rsgA_2	1284538	1285419	882	Small ribosomal subunit biogenesis GTPase RsgA	7	1	1.134	96	96	26.428	3.775
LAG_01247	NA	1285599	1286093	495	hypothetical protein	11	3	6.061	46.3	63.8	73.999	20.182
LAG_01248	NA	1286108	1286314	207	hypothetical protein	57	5	24.155	16.4	79.2	916.942	80.434
LAG_01249	NA	1286429	1287202	774	hypothetical protein	25	6	7.752	5.2	99.5	107.556	25.814
LAG_01250	NA	1287226	1287420	195	hypothetical protein	3	1	5.128	70.3	70.3	51.23	17.077
LAG_01251	yocH	1287572	1288603	1032	Cell wall-binding protein YocH	146	10	9.69	14.7	91.4	471.097	32.267
LAG_01252	pheT_2	1288763	1291171	2409	Phenylalanine--tRNA ligase beta subunit	0	0	0			0	0
LAG_01253	pheS	1291220	1292260	1041	Phenylalanine--tRNA ligase alpha subunit	3	1	0.961	3.8	3.8	9.596	3.199
LAG_01254	NA	1292625	1292840	216	hypothetical protein	25	3	13.889	28.7	76.4	385.411	46.249
LAG_01255	purA	1292949	1294238	1290	Adenylosuccinate synthetase	21	2	1.55	57.1	60.3	54.208	5.163
LAG_01256	hslO	1294546	1295430	885	33 kDa chaperonin	49	9	10.169	4.7	88.2	184.37	33.864
LAG_01257	clcA	1295427	1296971	1545	H(+)/Cl(-) exchange transporter ClcA	114	12	7.767	2.3	81.9	245.705	25.864
LAG_01258	dus	1297059	1298054	996	putative tRNA-dihydrouridine synthase	45	5	5.02	16.8	100	150.449	16.717
LAG_01259	NA	1298121	1298363	243	hypothetical protein	39	4	16.461	1.6	72.8	534.436	54.814
LAG_01260	NA	1298403	1299284	882	hypothetical protein	104	11	12.472	30.3	94.2	392.647	41.53
LAG_01261	NA	1299407	1300270	864	hypothetical protein	154	11	12.731	0.8	91.6	593.532	42.395
LAG_01262	aspS	1300281	1302029	1749	Aspartate--tRNA ligase	0	0	0			0	0
LAG_01263	hisS	1302085	1303368	1284	Histidine--tRNA ligase	6	2	1.558	0.2	1.9	15.561	5.187
LAG_01264	pgsA	1303690	1304241	552	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	0	0	0			0	0
LAG_01265	NA	1304290	1305198	909	hypothetical protein	105	6	6.601	0.1	97.5	384.647	21.98
LAG_01266	albF	1305250	1306533	1284	Putative zinc protease AlbF	121	10	7.788	2.9	74.1	313.804	25.934
LAG_01267	albE	1306514	1307758	1245	Antilisterial bacteriocin subtilosin biosynthesis protein AlbE	131	15	12.048	4	99.7	350.38	40.12
LAG_01268	NA	1307892	1308254	363	hypothetical protein	3	1	2.755	1.1	1.1	27.52	9.173
LAG_01269	recF	1308257	1309351	1095	DNA replication and repair protein RecF	5	1	0.913	90.2	90.2	15.205	3.041
LAG_01270	NA	1309323	1309544	222	hypothetical protein	8	2	9.009	51.8	93.2	119.998	30
LAG_01271	arcD1_2	1309566	1311026	1461	Arginine/ornithine antiporter ArcD1	73	9	6.16	27.7	99.7	166.383	20.513
LAG_01272	galE	1311213	1312196	984	UDP-glucose 4-epimerase	0	0	0			0	0
LAG_01273	galT_1	1312268	1313746	1479	Galactose-1-phosphate uridylyltransferase	90	10	6.761	10.3	81.3	202.634	22.515
LAG_01274	galK_2	1313758	1314957	1200	Galactokinase	309	15	12.5	38.2	94.7	857.462	41.624
LAG_01275	galM	1314968	1315996	1029	Aldose 1-epimerase	41	8	7.775	0.8	90.7	132.68	25.889
LAG_01276	lacS	1316049	1317446	1398	Lactose permease	244	20	14.306	1.6	84.7	581.193	47.639
LAG_01277	hexR_2	1317700	1318437	738	HTH-type transcriptional regulator HexR	169	17	23.035	7.2	99.7	762.549	76.706
LAG_01278	nadR	1318448	1319320	873	Trifunctional NAD biosynthesis/regulator protein NadR	98	10	11.455	2.6	84.8	373.809	38.144
LAG_01279	ydcP_1	1319343	1320632	1290	putative protease YdcP	240	21	16.279	5.4	95.1	619.525	54.208
LAG_01280	NA	1320699	1321637	939	2-haloacrylate reductase	107	14	14.909	13.1	97.7	379.451	49.648
LAG_01281	ydcP_2	1321634	1322557	924	putative protease YdcP	154	14	15.152	0.8	79.1	554.991	50.454
LAG_01282	NA	1322730	1323008	279	hypothetical protein	7	2	7.168	13.6	72.4	83.547	23.871
LAG_01283	rlmA	1323052	1323873	822	23S rRNA (guanine(745)-N(1))-methyltransferase	173	17	20.681	22.6	96.1	700.828	68.868
LAG_01284	NA	1324103	1324729	627	CutC-like protein	14	3	4.785	77.8	84.5	74.353	15.933
LAG_01285	NA	1324753	1325778	1026	hypothetical protein	203	22	21.442	9.8	97.3	658.849	71.402

LAG_01286	ecsA	1325765	1326505	741	ABC-type transporter ATP-binding protein EcsA	206	23	31.039	0.5	99.2	925.735	103.359
LAG_01287	NA	1326649	1327494	846	hypothetical protein	254	24	28.369	0.4	90.5	999.772	94.467
LAG_01288	gph_2	1327548	1328189	642	Phosphoglycolate phosphatase	44	6	9.346	6.4	79	228.221	31.121
LAG_01289	inlJ_2	1328300	1330048	1749	Internalin-J	450	45	25.729	0.6	97.3	856.762	85.676
LAG_01290	NA	1330248	1330643	396	putative HIT-like protein	72	7	17.677	3.3	89.4	605.445	58.863
LAG_01291	NA	1330640	1330867	228	hypothetical protein	128	4	17.544	1.8	41.2	1869.444	58.42
LAG_01292	NA	1330872	1331228	357	hypothetical protein	14	2	5.602	7.8	19.6	130.586	18.655
LAG_01293	rplA	1331342	1332031	690	50S ribosomal protein L1	0	0	0			0	0
LAG_01294	rplK	1332121	1332600	480	50S ribosomal protein L11	0	0	0			0	0
LAG_01295	macB_1	1332673	1333302	630	Macrolide export ATP-binding/permease protein MacB	122	11	17.46	3.2	74.1	644.847	58.142
LAG_01296	NA	1333309	1335381	2073	hypothetical protein	437	58	27.979	2.1	99.2	701.972	93.168
LAG_01297	NA	1335388	1335786	399	hypothetical protein	90	4	10.025	39.8	90.2	751.116	33.383
LAG_01298	gloA	1336020	1336391	372	Lactoylglutathione lyase	39	3	8.065	57.3	90.9	349.107	26.854
LAG_01299	NA	1336409	1336624	216	hypothetical protein	27	3	13.889	13	53.7	416.243	46.249
LAG_01300	msrA	1336621	1337136	516	Peptide methionine sulfoxide reductase MsrA	60	11	21.318	14.1	96.5	387.203	70.987
LAG_01301	cvfB	1337276	1338136	861	Conserved virulence factor B	49	6	6.969	8.9	73.9	189.509	23.205
LAG_01302	frr	1338247	1338804	558	Ribosome-recycling factor	0	0	0			0	0
LAG_01303	pyrH	1338833	1339549	717	Uridylate kinase	0	0	0			0	0
LAG_01304	ackA_1	1339640	1340833	1194	Acetate kinase	85	11	9.213	12.6	98.4	237.057	30.678
LAG_01305	ackA_2	1340952	1342145	1194	Acetate kinase	22	4	3.35	63.5	81.2	61.356	11.156
LAG_01306	NA	1342230	1343165	936	hypothetical protein	3	1	1.068	69	69	10.673	3.558
LAG_01307	NA	1343211	1343441	231	hypothetical protein	0	0	0			0	0
LAG_01308	typA	1343516	1345357	1842	GTP-binding protein TypA/BipA	0	0	0			0	0
LAG_01309	NA	1345677	1345889	213	hypothetical protein	24	2	9.39	0.9	20.7	375.205	31.267
LAG_01310	glcK	1345882	1346847	966	Glucokinase	131	12	12.422	14.8	77.7	451.577	41.366
LAG_01311	glpE_2	1346867	1347247	381	Thiosulfate sulfurtransferase GlpE	0	0	0			0	0
LAG_01312	dps	1347286	1347732	447	DNA protection during starvation protein	0	0	0			0	0
LAG_01313	comC	1347843	1348493	651	Type 4 prepilin-like proteins leader peptide-processing enzyme	83	10	15.361	11.5	85.9	424.556	51.151
LAG_01314	dinB_2	1348447	1349544	1098	DNA polymerase IV	116	19	17.304	17	99.3	351.798	57.622
LAG_01315	murC	1349707	1351038	1332	UDP-N-acetylmuramate--L-alanine ligase	3	1	0.751	86.3	86.3	7.5	2.5
LAG_01316	NA	1351089	1351718	630	hypothetical protein	0	0	0			0	0
LAG_01317	rapA	1351853	1354963	3111	RNA polymerase-associated protein RapA	227	27	8.679	1.7	96.5	242.976	28.9
LAG_01318	yvbW_2	1355525	1356865	1341	putative amino acid permease YvbW	156	20	14.914	18.6	99.6	387.376	49.664
LAG_01319	pbpX_2	1356939	1357883	945	Putative penicillin-binding protein PbpX	36	6	6.349	44	97.6	126.855	21.143
LAG_01320	NA	1357880	1358656	777	hypothetical protein	29	5	6.435	1.4	95	124.284	21.428
LAG_01321	NA	1358734	1359522	789	hypothetical protein	104	10	12.674	0.3	44.2	438.928	42.205
LAG_01322	thiT	1359711	1360247	537	Thiamine transporter ThiT	79	8	14.898	27.9	100	489.881	49.608
LAG_01323	ybaK	1360260	1360739	480	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase YbaK	149	11	22.917	11.2	98.1	1033.671	76.311
LAG_01324	NA	1360848	1361204	357	hypothetical protein	116	8	22.409	2	93.8	1082	74.621
LAG_01325	NA	1361275	1361490	216	hypothetical protein	37	4	18.519	2.8	68.1	570.408	61.666
LAG_01326	murA1	1361539	1362804	1266	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	119	16	12.638	6.6	94.9	313.005	42.085
LAG_01327	NA	1363037	1363756	720	hypothetical protein	217	17	23.611	12.6	99.3	1003.609	78.624
LAG_01328	NA	1363860	1365953	2094	putative ABC transporter ATP-binding protein	441	35	16.714	0.2	98.6	701.293	55.658
LAG_01329	NA	1366006	1367739	1734	putative ABC transporter ATP-binding protein	351	35	20.185	0.2	92.6	674.055	67.213
LAG_01330	fieF_1	1368057	1369271	1215	Ferrous-iron efflux pump FieF	129	11	9.053	0.3	86.1	353.55	30.148
LAG_01331	zitR_2	1369273	1369731	459	Transcriptional regulator ZitR	93	6	13.072	43.4	87.4	674.695	43.529
LAG_01332	tetA_2	1369828	1371021	1194	Tetracycline resistance protein, class C	222	27	22.613	1.6	96.6	619.136	75.3
LAG_01333	folT	1371032	1371571	540	Folate transporter FolT	71	10	18.519	7.2	78.7	437.826	61.666
LAG_01334	pepN	1371870	1374410	2541	Aminopeptidase N	164	23	9.052	6	89.7	214.92	30.141
LAG_01335	NA	1374645	1375445	801	hypothetical protein	135	16	19.975	1.9	96.1	561.227	66.516
LAG_01336	NA	1375455	1375931	477	hypothetical protein	33	6	12.579	33.1	77.1	230.374	41.886
LAG_01337	tsaD	1375965	1376984	1020	tRNA N6-adenosine threonylcarbamoyltransferase	0	0	0			0	0
LAG_01338	rimI_1	1376986	1377420	435	Ribosomal-protein-alanine acetyltransferase	5	1	2.299	59.1	59.1	38.275	7.655
LAG_01339	rimI_2	1377410	1377976	567	N-alpha-acetyltransferase RimI	0	0	0			0	0

LAG_01340	tsaB	1377930	1378640	711	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB	0	0	0			0	0
LAG_01341	NA	1378974	1379279	306	hypothetical protein	0	0	0			0	0
LAG_01342	rnj1	1379382	1381088	1707	Ribonuclease J 1	38	1	0.586	98.9	98.9	74.129	1.951
LAG_01343	NA	1381207	1381668	462	hypothetical protein	118	11	23.81	5.4	97.2	850.506	79.284
LAG_01344	add	1381665	1382714	1050	Adenosine deaminase	94	13	12.381	4.2	99.6	298.11	41.228
LAG_01345	NA	1382896	1383693	798	hypothetical protein	163	20	25.063	10	96.6	680.177	83.457
LAG_01346	NA	1383683	1386478	2796	hypothetical protein	439	50	17.883	3.5	99.1	522.835	59.548
LAG_01347	NA	1386490	1387287	798	hypothetical protein	385	22	27.569	6.6	99.9	1606.554	91.803
LAG_01348	NA	1387302	1388105	804	hypothetical protein	123	12	14.925	1.6	89.3	509.432	49.701
LAG_01349	NA	1388205	1388630	426	Protein SprT-like protein	129	13	30.516	5.6	92.3	1008.365	101.618
LAG_01350	rps1	1388620	1390752	2133	30S ribosomal protein S1	178	29	13.596	0.3	98.6	277.886	45.274
LAG_01351	NA	1390849	1391460	612	Putative NAD(P)H nitroreductase	59	5	8.17	36.9	88.9	321.024	27.205
LAG_01352	rpsD	1391580	1392191	612	30S ribosomal protein S4	0	0	0			0	0
LAG_01353	steT_1	1392394	1393749	1356	Serine/threonine exchanger SteT	242	19	14.012	2.4	96.9	594.283	46.659
LAG_01354	NA	1394020	1394469	450	hypothetical protein	104	8	17.778	6.2	82	769.588	59.199
LAG_01355	yknY	1394583	1395068	486	putative ABC transporter ATP-binding protein YknY	133	11	22.634	5.1	90.7	911.282	75.369
LAG_01356	NA	1395246	1397282	2037	hypothetical protein	498	52	25.528	0.5	97.3	814.096	85.006
LAG_01357	NA	1397687	1397762	76	tRNA-Pro	0	0	0			0	0
LAG_01358	NA	1397816	1397889	74	tRNA-Arg	0	0	0			0	0
LAG_01359	ecfT	1398009	1398812	804	Energy-coupling factor transporter transmembrane protein EcfT	5	1	1.244	98.6	98.6	20.709	4.142
LAG_01360	ecfA2	1398814	1399659	846	Energy-coupling factor transporter ATP-binding protein EcfA2	0	0	0			0	0
LAG_01361	ecfA1	1399656	1400489	834	Energy-coupling factor transporter ATP-binding protein EcfA1	4	1	1.199	3.5	3.5	15.971	3.993
LAG_01362	NA	1400555	1401049	495	hypothetical protein	0	0	0			0	0
LAG_01363	nrdG	1401046	1401645	600	Anaerobic ribonucleoside-triphosphate reductase-activating protein	45	5	8.333	5.5	92	249.746	27.75
LAG_01364	ycaM	1401837	1403282	1446	Inner membrane transporter YcaM	116	19	13.14	2.1	98.9	267.133	43.755
LAG_01365	nrdD	1403494	1405734	2241	Anaerobic ribonucleoside-triphosphate reductase	130	14	6.247	0.4	90	193.17	20.803
LAG_01366	pncA	1405895	1406407	513	Nicotinamidase/pyrazinamidase	88	12	23.392	7.4	98.8	571.219	77.894
LAG_01367	steT_2	1406512	1407873	1362	Serine/threonine exchanger SteT	67	12	8.811	5.2	93	163.808	29.339
LAG_01368	NA	1408021	1408974	954	putative epimerase/dehydratase	71	9	9.434	36	87.7	247.826	31.415
LAG_01369	NA	1409041	1410231	1191	Putative pyridoxal phosphate-dependent acyltransferase	26	5	4.198	15	66.9	72.694	13.98
LAG_01370	tdcB	1410459	1411466	1008	L-threonine dehydratase catabolic TdcB	63	8	7.937	31.7	97.3	208.122	26.428
LAG_01371	ald1_2	1411491	1412585	1095	Alanine dehydrogenase 1	132	17	15.525	1.9	90	401.418	51.698
LAG_01372	yvgN_1	1412764	1413609	846	Glyoxal reductase	44	5	5.91	1.9	94.3	173.189	19.681
LAG_01373	luxS	1413729	1414208	480	S-ribosylhomocysteine lyase	26	2	4.167	61.7	93.8	180.372	13.875
LAG_01374	NA	1414223	1414372	150	hypothetical protein	0	0	0			0	0
LAG_01375	yhhX_1	1414369	1415382	1014	putative oxidoreductase YhhX	265	12	11.834	11.4	97.1	870.253	39.408
LAG_01376	opuBA	1415481	1416323	843	Choline transport ATP-binding protein OpuBA	102	11	13.049	1.2	88.1	402.912	43.451
LAG_01377	opuCB	1416316	1417818	1503	Carnitine transport permease protein OpuCB	295	26	17.299	1.4	91.3	653.583	57.604
LAG_01378	NA	1417915	1419183	1269	Putative thiazole biosynthetic enzyme	105	17	13.396	12.1	95.9	275.528	44.609
LAG_01379	NA	1419267	1419352	86	tRNA-Leu	3	1	11.628	48.8	48.8	116.161	38.72
LAG_01380	NA	1419624	1419827	204	hypothetical protein	64	10	49.02	12.7	95.6	1044.69	163.233
LAG_01381	NA	1420041	1421138	1098	hypothetical protein	211	23	20.947	1.1	98.9	639.908	69.753
LAG_01382	NA	1421396	1422430	1035	hypothetical protein	524	52	50.242	0.7	98.6	1685.887	167.302
LAG_01383	NA	1422465	1423259	795	hypothetical protein	301	30	37.736	5.2	99.6	1260.773	125.658
LAG_01384	rlmI	1423475	1424644	1170	Ribosomal RNA large subunit methyltransferase I	511	41	35.043	3.4	99.1	1454.362	116.69
LAG_01385	pgk	1424692	1425888	1197	Phosphoglycerate kinase	0	0	0			0	0
LAG_01386	NA	1425981	1426448	468	hypothetical protein	86	10	21.368	17.1	99.1	611.914	71.153
LAG_01387	NA	1426852	1426940	89	tRNA-Leu	0	0	0			0	0
LAG_01388	NA	1426978	1427049	72	tRNA-Gly	0	0	0			0	0
LAG_01389	NA	1427120	1427192	73	tRNA-Thr	0	0	0			0	0
LAG_01390	NA	1427412	1429397	1986	hypothetical protein	556	49	24.673	3.2	90.7	932.251	82.159
LAG_01391	xly	1429497	1431848	2352	Xanthan lyase	443	48	20.408	2.7	95.7	627.197	67.958
LAG_01392	NA	1431867	1432475	609	hypothetical protein	253	22	36.125	0.3	95.9	1383.377	120.294
LAG_01393	ugl	1432829	1433983	1155	Unsaturated chondroitin disaccharide hydrolase	232	22	19.048	14.5	99.7	668.873	63.428

LAG_01394	bga	1433993	1435780	1788	Beta-galactosidase	472	41	22.931	0.8	99.4	879.047	76.358
LAG_01395	mngR_2	1435806	1436513	708	Mannosyl-D-glycerate transport/metabolism system repressor MngR	56	13	18.362	24.6	72	263.386	61.143
LAG_01396	manX_2	1436742	1437671	930	PTS system mannose-specific EIIAB component	86	11	11.828	3.1	96.9	307.931	39.386
LAG_01397	sorA_2	1437673	1438470	798	PTS system sorbose-specific EIIC component	106	12	15.038	5.8	93.2	442.324	50.074
LAG_01398	manZ_2	1438463	1439287	825	PTS system mannose-specific EIID component	49	10	12.121	1	96.8	197.779	40.363
LAG_01399	gno_1	1439461	1440270	810	Gluconate 5-dehydrogenase	64	11	13.58	10	93	263.107	45.222
LAG_01400	NA	1440291	1441127	837	hypothetical protein	108	14	16.726	17.3	99.5	429.671	55.698
LAG_01401	NA	1441183	1442943	1761	hypothetical protein	378	31	17.604	4.1	98.5	714.776	58.619
LAG_01402	kdgR	1442989	1443996	1008	HTH-type transcriptional regulator KdgR	62	11	10.913	12.7	100	204.818	36.339
LAG_01403	kduI1	1444144	1444989	846	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase 1	113	17	20.095	0.4	81.1	444.78	66.914
LAG_01404	gno_2	1445021	1445827	807	Gluconate 5-dehydrogenase	119	12	14.87	0.2	100	491.033	49.516
LAG_01405	kdgK	1445858	1446826	969	2-dehydro-3-deoxygluconokinase	160	20	20.64	8.9	95.7	549.837	68.73
LAG_01406	kdgA	1446826	1447467	642	KHG/KDPG aldolase	75	8	12.461	3.3	95.3	389.013	41.495
LAG_01407	NA	1447507	1447644	138	hypothetical protein	0	0	0			0	0
LAG_01408	NA	1447915	1448565	651	hypothetical protein	181	12	18.433	4	95.9	925.838	61.382
LAG_01409	NA	1448558	1448935	378	Putative esterase	38	4	10.582	20.4	67.2	334.757	35.238
LAG_01410	menC	1448932	1450035	1104	o-succinylbenzoate synthase	52	7	6.341	44.5	89.3	156.845	21.114
LAG_01411	menE	1450025	1451377	1353	2-succinylbenzoate--CoA ligase	124	16	11.826	9.3	98.4	305.184	39.379
LAG_01412	menB	1451381	1452223	843	1,4-dihydroxy-2-naphthoyl-CoA synthase	135	12	14.235	6	87.1	533.266	47.401
LAG_01413	menH_3	1452254	1453081	828	2-succinyl-6-hydroxy-2, 4-cyclohexadiene-1-carboxylate synthase	43	9	10.87	3.6	88.2	172.932	36.195
LAG_01414	menD	1453071	1454717	1647	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate synthase	143	23	13.965	8.4	80.4	289.121	46.502
LAG_01415	pchA	1454720	1455856	1137	Salicylate biosynthesis isochorismate synthase	120	10	8.795	3.4	74.1	351.446	29.287
LAG_01416	NA	1455937	1456506	570	hypothetical protein	40	6	10.526	32.6	86.3	233.681	35.052
LAG_01417	NA	1456499	1457779	1281	Cobalt-dependent inorganic pyrophosphatase	69	12	9.368	2.7	92.2	179.365	31.194
LAG_01418	nrnA	1457791	1458720	930	putative bifunctional oligoribonuclease and PAP phosphatase NrnA	5	1	1.075	52.2	52.2	17.903	3.581
LAG_01419	znuA_2	1458893	1460464	1572	High-affinity zinc uptake system binding-protein ZnuA	158	21	13.359	1.6	99.6	334.689	44.484
LAG_01420	ansA	1460526	1461491	966	L-asparaginase	116	9	9.317	2.8	93.4	399.87	31.024
LAG_01421	ycsE	1461753	1463159	1407	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YcsE	51	9	6.397	43	89.5	120.702	21.3
LAG_01422	NA	1463277	1463936	660	Phosphorylated carbohydrates phosphatase	10	1	1.515	14.7	14.7	50.454	5.045
LAG_01423	gdpP	1463997	1465964	1968	Cyclic-di-AMP phosphodiesterase GdpP	0	0	0			0	0
LAG_01424	rplI	1465961	1466413	453	50S ribosomal protein L9	0	0	0			0	0
LAG_01425	dnaC	1466415	1467791	1377	Replicative DNA helicase	0	0	0			0	0
LAG_01426	NA	1467900	1468163	264	hypothetical protein	0	0	0			0	0
LAG_01427	NA	1468328	1469101	774	hypothetical protein	0	0	0			0	0
LAG_01428	trmB	1469162	1469815	654	tRNA (guanine-N(7)-)-methyltransferase	6	1	1.529	4.4	4.4	30.55	5.092
LAG_01429	nrdR	1469819	1470268	450	Transcriptional repressor NrdR	0	0	0			0	0
LAG_01430	dnaB	1470302	1471465	1164	Replication initiation and membrane attachment protein	0	0	0			0	0
LAG_01431	dnaI	1471468	1472352	885	Primosomal protein DnaI	0	0	0			0	0
LAG_01432	nfrA2	1472345	1473061	717	FMN reductase [NAD(P)H]	149	21	29.289	33.3	94.7	691.998	97.53
LAG_01433	spkB	1473058	1473678	621	Serine/threonine-protein kinase B	91	13	20.934	1.3	99.2	487.963	69.709
LAG_01434	ulaC	1473888	1475825	1938	Ascorbate-specific PTS system EIIA component	606	58	29.928	1	99.4	1041.253	99.658
LAG_01435	NA	1475827	1476126	300	hypothetical protein	28	5	16.667	0.7	99	310.795	55.499
LAG_01436	ulaA	1476178	1477545	1368	Ascorbate-specific PTS system EIIC component	219	19	13.889	3.9	99.3	533.084	46.249
LAG_01437	tkt_1	1477675	1479675	2001	Transketolase	4	1	0.5	99.2	99.2	6.657	1.664
LAG_01438	NA	1480008	1480226	219	hypothetical protein	44	5	22.831	27.4	83.6	669.031	76.026
LAG_01439	noxE	1480457	1481794	1338	NADH oxidase	70	12	8.969	0.1	91.1	174.213	29.865
LAG_01440	NA	1481950	1483401	1452	hypothetical protein	264	28	19.284	7.9	98.4	605.445	64.214
LAG_01441	NA	1483623	1484297	675	hypothetical protein	155	14	20.741	9.5	96.4	764.655	69.066
LAG_01442	NA	1484319	1484744	426	hypothetical protein	84	9	21.127	1.9	85	656.609	70.351
LAG_01443	NA	1484791	1485555	765	hypothetical protein	206	20	26.144	17.9	99	896.692	87.057
LAG_01444	NA	1485858	1486193	336	hypothetical protein	40	5	14.881	9.2	91.7	396.422	49.553
LAG_01445	NA	1486219	1487040	822	hypothetical protein	134	13	15.815	1.7	98.4	542.838	52.663
LAG_01446	NA	1487067	1487852	786	hypothetical protein	3	1	1.272	6.2	6.2	12.71	4.237
LAG_01447	NA	1487889	1488602	714	hypothetical protein	46	9	12.605	21.1	94.1	214.534	41.974

LAG_01448	NA	1488792	1489922	1131	hypothetical protein	103	13	11.494	3.3	99.7	303.258	38.275
LAG_01449	NA	1489986	1491014	1029	hypothetical protein	77	10	9.718	6.2	87.9	249.18	32.361
LAG_01450	NA	1491011	1491580	570	hypothetical protein	61	11	19.298	10.9	88.6	356.363	64.262
LAG_01451	NA	1491593	1493620	2028	hypothetical protein	345	36	17.751	0.3	99	566.485	59.112
LAG_01452	NA	1493636	1494745	1110	hypothetical protein	156	16	14.414	0.6	97.8	467.993	47.999
LAG_01453	NA	1494831	1495733	903	hypothetical protein	319	19	21.041	0.1	98.9	1176.36	70.065
LAG_01454	NA	1495758	1496159	402	hypothetical protein	19	2	4.975	66.4	77.1	157.386	16.567
LAG_01455	rnj2	1496279	1498015	1737	Ribonuclease J 2	0	0	0			0	0
LAG_01456	ntpJ_1	1498147	1499469	1323	Potassium/sodium uptake protein NtpJ	228	18	13.605	16.9	80.3	573.869	45.305
LAG_01457	ktrA	1499471	1500124	654	Ktr system potassium uptake protein A	31	5	7.645	13.9	99.2	157.842	25.458
LAG_01458	ffh	1500214	1501770	1557	Signal recognition particle protein	3	1	0.642	96.9	96.9	6.416	2.139
LAG_01459	NA	1501889	1502914	1026	hypothetical protein	62	11	10.721	2.4	85.5	201.225	35.701
LAG_01460	der_1	1503097	1504407	1311	GTPase Der	0	0	0			0	0
LAG_01461	cidB	1504473	1505171	699	Holin-like protein CidB	88	10	14.306	2.1	98.6	419.221	47.639
LAG_01462	lrgA	1505171	1505566	396	Antiholin-like protein LrgA	74	8	20.202	4.8	93.4	622.263	67.272
LAG_01463	rimP	1505798	1506274	477	Ribosome maturation factor RimP	0	0	0			0	0
LAG_01464	nusA	1506366	1507493	1128	Transcription termination/antitermination protein NusA	0	0	0			0	0
LAG_01465	NA	1507498	1507818	321	hypothetical protein	0	0	0			0	0
LAG_01466	rplGA	1507826	1508131	306	putative ribosomal protein YlxQ	0	0	0			0	0
LAG_01467	infB	1508150	1510867	2718	Translation initiation factor IF-2	0	0	0			0	0
LAG_01468	rbfA	1510910	1511266	357	Ribosome-binding factor A	37	4	11.204	82.1	97.2	345.121	37.31
LAG_01469	zitB	1511433	1512365	933	Zinc transporter ZitB	304	37	39.657	1	99.6	1084.999	132.056
LAG_01470	NA	1512429	1512608	180	hypothetical protein	13	2	11.111	17.2	92.2	240.496	36.999
LAG_01471	manA	1512781	1513737	957	Mannose-6-phosphate isomerase ManA	41	8	8.359	30.3	95.1	142.662	27.837
LAG_01472	NA	1514001	1514201	201	hypothetical protein	5	1	4.975	8	8	82.835	16.567
LAG_01473	sph	1514600	1516363	1764	Oleate hydratase	234	30	17.007	4.5	86.6	441.728	56.632
LAG_01474	NA	1516589	1516676	88	tRNA-Ser	18	3	34.091	5.7	81.8	681.126	113.521
LAG_01475	NA	1516742	1516816	75	tRNA-Arg	12	2	26.667	44	100	532.792	88.799
LAG_01476	iolW	1516849	1517844	996	scyllo-inositol 2-dehydrogenase (NADP(+))	45	5	5.02	22.3	95.4	150.449	16.717
LAG_01477	udk	1518091	1518714	624	Uridine kinase	14	2	3.205	5.1	11.9	74.71	10.673
LAG_01478	pta	1518872	1519852	981	Phosphate acetyltransferase	0	0	0			0	0
LAG_01479	NA	1520071	1520460	390	hypothetical protein	3	1	2.564	60.5	60.5	25.615	8.538
LAG_01480	rnc	1520564	1521259	696	Ribonuclease 3	0	0	0			0	0
LAG_01481	smc	1521249	1524767	3519	Chromosome partition protein Smc	22	5	1.421	24.6	75.7	20.818	4.731
LAG_01482	ltaS1	1524882	1527089	2208	Lipoteichoic acid synthase 1	85	5	2.264	88.4	97.1	128.191	7.541
LAG_01483	NA	1527096	1527518	423	hypothetical protein	0	0	0			0	0
LAG_01484	NA	1527472	1529046	1575	hypothetical protein	21	2	1.27	94.7	97.3	44.399	4.229
LAG_01485	NA	1529030	1531123	2094	hypothetical protein	9	2	0.955	95.5	97.5	14.312	3.18
LAG_01486	NA	1531116	1532219	1104	hypothetical protein	258	28	25.362	2.3	96.9	778.194	84.455
LAG_01487	NA	1532212	1532979	768	hypothetical protein	273	22	28.646	8.6	87.6	1183.692	95.389
LAG_01488	NA	1533397	1534722	1326	hypothetical protein	332	22	16.591	0.5	94.4	833.743	55.248
LAG_01489	yidA_2	1535045	1535854	810	Sugar phosphatase YidA	49	4	4.938	22.7	92.5	201.441	16.444
LAG_01490	ftsY	1535863	1537164	1302	Signal recognition particle receptor FtsY	0	0	0			0	0
LAG_01491	prs	1537327	1538298	972	Ribose-phosphate pyrophosphokinase	0	0	0			0	0
LAG_01492	lrp	1538333	1539010	678	Leucine-rich protein	91	12	17.699	12.5	89.7	446.94	58.937
LAG_01493	leuS	1539117	1541597	2481	Leucine--tRNA ligase	0	0	0			0	0
LAG_01494	cpo	1541751	1542560	810	Non-heme chloroperoxidase	170	13	16.049	3.5	94.8	698.878	53.444
LAG_01495	NA	1542574	1543743	1170	hypothetical protein	250	30	25.641	2.6	98.1	711.527	85.383
LAG_01496	NA	1543878	1544231	354	hypothetical protein	61	8	22.599	6.5	86.4	573.805	75.253
LAG_01497	NA	1544486	1546468	1983	NADH dehydrogenase-like protein	506	30	15.129	2.8	98.1	849.699	50.377
LAG_01498	menA_3	1546619	1547626	1008	1,4-dihydroxy-2-naphthoate octaprenyltransferase	1155	65	64.484	3.6	99.3	3815.565	214.729
LAG_01499	fcbA1	1547677	1549209	1533	4-chlorobenzoate--CoA ligase	519	52	33.92	8.2	98.2	1127.36	112.953
LAG_01500	sdhB	1549488	1550159	672	L-serine dehydratase, beta chain	56	9	13.393	2.1	77.7	277.496	44.598
LAG_01501	sdhA	1550169	1551041	873	L-serine dehydratase, alpha chain	34	6	6.873	4.6	77.8	129.689	22.886

LAG_01502	copY	1551185	1551625	441	Transcriptional repressor CopY	0	0	0			0	0
LAG_01503	copZ	1551641	1551850	210	Copper chaperone CopZ	59	10	47.619	16.7	92.9	935.557	158.569
LAG_01504	copA	1551924	1554011	2088	putative copper-importing P-type ATPase A	366	39	18.678	1.2	97.6	583.698	62.197
LAG_01505	recQ	1554088	1555866	1779	ATP-dependent DNA helicase RecQ	349	40	22.485	2.5	93.1	653.261	74.872
LAG_01506	NA	1555993	1556943	951	N(4)-(Beta-N-acetylglucosaminyl)-L-asparaginase	130	16	16.824	2	79.9	455.198	56.024
LAG_01507	gmuC_2	1556960	1558330	1371	PTS system oligo-beta-mannoside-specific EIIC component	224	34	24.799	0.5	98.8	544.062	82.581
LAG_01508	NA	1558340	1558858	519	hypothetical protein	39	5	9.634	1.3	94.6	250.227	32.08
LAG_01509	NA	1558887	1560179	1293	Putative dipeptidase	219	26	20.108	8.5	95.4	564.005	66.96
LAG_01510	yvoA_1	1560221	1560946	726	HTH-type transcriptional repressor YvoA	64	11	15.152	17.1	91.6	293.549	50.454
LAG_01511	NA	1560970	1563564	2595	hypothetical protein	362	34	13.102	4.5	99.3	464.525	43.629
LAG_01512	NA	1563610	1564389	780	hypothetical protein	25	4	5.128	11.4	81.2	106.729	17.077
LAG_01513	mnmA	1564553	1565674	1122	tRNA-specific 2-thiouridylase MnmA	0	0	0			0	0
LAG_01514	NA	1565773	1566300	528	hypothetical protein	59	8	15.152	4.4	83.3	372.096	50.454
LAG_01515	rpsA	1566493	1567716	1224	30S Ribosomal protein S1	0	0	0			0	0
LAG_01516	NA	1567984	1568364	381	hypothetical protein	16	3	7.874	10.5	95.5	139.84	26.22
LAG_01517	NA	1568758	1569915	1158	hypothetical protein	355	34	29.361	4	95.5	1020.839	97.77
LAG_01518	dexB	1570029	1571657	1629	Glucan 1,6-alpha-glucosidase	391	52	31.921	1.5	99.9	799.269	106.297
LAG_01519	NA	1571817	1572722	906	6-phosphogluconate dehydrogenase, NAD(+)-dependent, decarboxylating	65	11	12.141	12.7	96.6	238.904	40.43
LAG_01520	xylB_2	1572732	1574228	1497	Xylulose kinase	123	19	12.692	0.7	97.7	273.603	42.264
LAG_01521	gntT	1574245	1575597	1353	High-affinity gluconate transporter	275	30	22.173	4.5	86.3	676.819	73.835
LAG_01522	nhaC	1575635	1577050	1416	Na(+)/H(+) antiporter NhaC	197	27	19.068	0.8	97	463.277	63.495
LAG_01523	pyrR	1577681	1578205	525	Bifunctional protein PyrR	43	8	15.238	6.1	73.5	272.739	50.742
LAG_01524	pyrP	1578208	1579494	1287	Uracil permease	32	6	4.662	36	98.1	82.796	15.524
LAG_01525	pyrB	1579595	1580518	924	Aspartate carbamoyltransferase	73	9	9.74	28.6	93	263.08	32.435
LAG_01526	carA	1580542	1581606	1065	Carbamoyl-phosphate synthase small chain	129	16	15.023	2.2	98.5	403.346	50.027
LAG_01527	bioY2	1581718	1582266	549	Biotin transporter BioY2	11	2	3.643	90.7	98.4	66.72	12.131
LAG_01528	spxA_13	1582480	1582875	396	Regulatory protein Spx	90	9	22.727	2	85.6	756.806	75.681
LAG_01529	NA	1582903	1583028	126	hypothetical protein	3	1	7.937	12.7	12.7	79.284	26.428
LAG_01530	NA	1583211	1584893	1683	hypothetical protein	163	18	10.695	1	98.6	322.508	35.614
LAG_01531	NA	1584953	1585531	579	hypothetical protein	68	4	6.908	3.6	67.7	391.082	23.005
LAG_01532	queA	1585532	1586635	1104	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	62	8	7.246	34.7	72.6	187.008	24.13
LAG_01533	NA	1586846	1587199	354	hypothetical protein	23	2	5.65	79.1	91	216.353	18.813
LAG_01534	NA	1587331	1587537	207	hypothetical protein	5	1	4.831	10.6	10.6	80.434	16.087
LAG_01535	tagH_3	1587634	1589046	1413	Teichoic acids export ATP-binding protein TagH	32	4	2.831	43.8	93.8	75.413	9.427
LAG_01536	tagG_3	1589046	1589855	810	Teichoic acid translocation permease protein TagG	28	2	2.469	63.1	68.3	115.109	8.222
LAG_01537	NA	1589857	1591911	2055	hypothetical protein	108	5	2.433	14.3	91.7	175.005	8.102
LAG_01538	tagD_2	1591936	1592361	426	Glycerol-3-phosphate cytidylyltransferase	0	0	0			0	0
LAG_01539	NA	1592362	1592796	435	hypothetical protein	44	6	13.793	26.7	47.6	336.822	45.93
LAG_01540	tarF_3	1592813	1593997	1185	Teichoic acid glycerol-phosphate transferase	79	9	7.595	2.6	94.9	221.997	25.291
LAG_01541	pucK	1594317	1595618	1302	Uric acid permease PucK	261	37	28.418	6.1	99.5	667.524	94.63
LAG_01542	xpt	1595636	1596229	594	Xanthine phosphoribosyltransferase	93	12	20.202	4.9	91.6	521.355	67.272
LAG_01543	rluB	1596572	1597288	717	Ribosomal large subunit pseudouridine synthase B	67	8	11.158	28.7	95.1	311.167	37.154
LAG_01544	scpB	1597275	1597853	579	Segregation and condensation protein B	9	1	1.727	96.2	96.2	51.761	5.751
LAG_01545	scpA	1597837	1598577	741	Segregation and condensation protein A	15	2	2.699	24.6	30.2	67.408	8.988
LAG_01546	ynbA	1598574	1599302	729	Tyrosine recombinase XerD-like protein	28	6	8.23	12.5	96.6	127.899	27.407
LAG_01547	ykuL	1599259	1599723	465	CBS domain-containing protein YkuL	15	2	4.301	3.4	30.5	107.418	14.322
LAG_01548	yfcE	1599744	1600253	510	Phosphodiesterase YfcE	20	3	5.882	4.5	98.8	130.586	19.588
LAG_01549	murI	1600289	1601701	1413	Glutamate racemase	20	4	2.831	63	85.1	47.133	9.427
LAG_01550	NA	1601729	1601968	240	hypothetical protein	0	0	0			0	0
LAG_01551	ilvE	1602089	1603111	1023	Branched-chain-amino-acid aminotransferase	100	11	10.753	15.5	100	325.508	35.806
LAG_01552	ykuT	1603249	1603995	747	putative MscS family protein YkuT	70	9	12.048	0.9	80.2	312.043	40.12
LAG_01553	rnhB	1604015	1604776	762	Ribonuclease HII	54	6	7.874	63.3	86.6	235.981	26.22
LAG_01554	rbgA	1604763	1605620	858	Ribosome biogenesis GTPase A	0	0	0			0	0
LAG_01555	NA	1605886	1606530	645	Putative 3-methyladenine DNA glycosylase	73	9	13.953	12.4	95.3	376.878	46.464

LAG_01556	ndx1	1606698	1607105	408	Diadenosine hexaphosphate hydrolase	74	8	19.608	9.8	82.1	603.961	65.293
LAG_01557	NA	1607155	1607646	492	hypothetical protein	89	7	14.228	20.5	99.4	602.369	47.377
LAG_01558	NA	1607762	1608433	672	hypothetical protein	82	11	16.369	10.6	92.4	406.333	54.508
LAG_01559	NA	1608508	1609596	1089	hypothetical protein	98	15	13.774	7.6	98.1	299.665	45.867
LAG_01560	dapE_2	1609625	1610764	1140	putative succinyl-diaminopimelate desuccinylase	189	15	13.158	1.6	93.9	552.07	43.815
LAG_01561	NA	1610924	1611415	492	hypothetical protein	93	10	20.325	35.6	97.6	629.441	67.682
LAG_01562	dinB_3	1611639	1613090	1452	DNA polymerase IV	235	31	21.35	1.4	99	538.938	71.094
LAG_01563	NA	1613080	1613262	183	hypothetical protein	59	4	21.858	6	92.3	1073.59	72.786
LAG_01564	NA	1613274	1613654	381	hypothetical protein	18	4	10.499	68.2	95.8	157.32	34.96
LAG_01565	psiE	1613951	1614349	399	Protein PsiE	9	2	5.013	81	91.5	75.112	16.691
LAG_01566	ppdK	1614390	1617008	2619	Pyruvate, phosphate dikinase	298	32	12.218	1.4	97.5	378.894	40.687
LAG_01567	ccpN	1617209	1617841	633	Transcriptional repressor CcpN	64	7	11.058	19.7	96.8	336.677	36.824
LAG_01568	yqfL	1617851	1618654	804	Putative pyruvate, phosphate dikinase regulatory protein	186	18	22.388	1.6	97	770.361	74.551
LAG_01569	NA	1618769	1619365	597	hypothetical protein	153	16	26.801	2.2	90.8	853.404	89.245
LAG_01570	NA	1619440	1619919	480	hypothetical protein	64	8	16.667	3.1	94.8	443.993	55.499
LAG_01571	NA	1620100	1630173	10074	hypothetical protein	1163	132	13.103	0	100	384.428	43.632
LAG_01572	asp3	1630208	1630651	444	Accessory Sec system protein Asp3	63	9	20.27	10.8	97.1	472.493	67.499
LAG_01573	asp2	1630641	1632194	1554	Accessory Sec system protein Asp2	365	48	30.888	1	99.5	782.131	102.856
LAG_01574	gtf1_1	1632187	1633761	1575	Glycosyltransferase Gtf1	235	32	20.317	5.5	93.6	496.849	67.656
LAG_01575	secY2	1633783	1635030	1248	Accessory Sec system protein translocase subunit SecY2	360	35	28.045	0.2	95.8	960.562	93.388
LAG_01576	NA	1635060	1635239	180	hypothetical protein	15	3	16.667	5	94.4	277.496	55.499
LAG_01577	gtf2	1635236	1636582	1347	Glycosyltransferase-stabilizing protein Gtf2	262	42	31.18	5.6	98.9	647.696	103.829
LAG_01578	gtf1_2	1636575	1638077	1503	Glycosyltransferase Gtf1	247	34	22.621	1.1	98.5	547.237	75.328
LAG_01579	wbbI	1638064	1639092	1029	Beta-1,6-galactofuranosyltransferase WbbI	188	25	24.295	14.6	98.4	608.387	80.903
LAG_01580	secA_2	1639112	1641439	2328	Protein translocase subunit SecA	293	38	16.323	15.7	93	419.104	54.355
LAG_01581	NA	1642087	1642521	435	Putative universal stress protein	220	12	27.586	0.5	100	1684.112	91.861
LAG_01582	NA	1642767	1643195	429	Putative universal stress protein	64	8	18.648	3.3	95.1	496.775	62.097
LAG_01583	NA	1643413	1643568	156	hypothetical protein	17	3	19.231	7.1	91	362.879	64.037
LAG_01584	NA	1643754	1644191	438	hypothetical protein	100	12	27.397	4.3	96.8	760.262	91.231
LAG_01585	fieF_2	1644624	1645499	876	Ferrous-iron efflux pump FieF	174	25	28.539	0.6	90.8	661.428	95.033
LAG_01586	NA	1645715	1646458	744	hypothetical protein	175	18	24.194	0.5	96.9	783.254	80.563
LAG_01587	NA	1646536	1646883	348	hypothetical protein	118	16	45.977	7.5	100	1129.12	153.101
LAG_01588	NA	1647000	1647347	348	hypothetical protein	23	7	20.115	18.7	63.8	220.083	66.982
LAG_01589	NA	1647823	1649301	1479	hypothetical protein	228	32	21.636	1.1	97.8	513.339	72.048
LAG_01590	yagU	1649472	1650011	540	Inner membrane protein YagU	494	31	57.407	0.7	93.9	3046.286	191.164
LAG_01591	NA	1650117	1650275	159	hypothetical protein	26	5	31.447	12.6	98.1	544.52	104.715
LAG_01593	NA	1650772	1651521	750	hypothetical protein	76	13	17.333	7.7	98.1	337.435	57.719
LAG_01594	yxlF_2	1651518	1652405	888	putative ABC transporter ATP-binding protein YxlF	79	13	14.64	1.2	80.3	296.245	48.749
LAG_01595	NA	1652398	1652586	189	hypothetical protein	32	5	26.455	18	96.3	563.801	88.094
LAG_01596	NA	1652611	1652946	336	hypothetical protein	17	4	11.905	0.3	67.6	168.48	39.642
LAG_01597	phoP_2	1653254	1653952	699	Alkaline phosphatase synthesis transcriptional regulatory protein PhoP	23	3	4.292	43.6	59.1	109.569	14.292
LAG_01598	phoR	1653939	1655501	1563	Alkaline phosphatase synthesis sensor protein PhoR	192	21	13.436	0.6	100	409.053	44.74
LAG_01599	yvoA_2	1655541	1655858	318	HTH-type transcriptional repressor YvoA	30	5	15.723	16	78.3	314.146	52.358
LAG_01600	yvoA_3	1655862	1656248	387	HTH-type transcriptional repressor YvoA	42	7	18.088	6.2	93.3	361.39	60.232
LAG_01601	tmpC_2	1656339	1657391	1053	Membrane lipoprotein TmpC	123	15	14.245	12.8	92	388.968	47.435
LAG_01602	cdd	1657563	1657955	393	Cytidine deaminase	8	2	5.089	13.7	24.4	67.785	16.946
LAG_01603	deoC1	1657942	1658604	663	Deoxyribose-phosphate aldolase 1	31	6	9.05	50.5	91.9	155.699	30.135
LAG_01604	NA	1658676	1658870	195	hypothetical protein	6	1	5.128	31.8	31.8	102.46	17.077
LAG_01605	pdp	1658870	1660162	1293	Pyrimidine-nucleoside phosphorylase	125	11	8.507	3	91.2	321.921	28.329
LAG_01606	rsmC	1660159	1660764	606	Ribosomal RNA small subunit methyltransferase C	10	3	4.95	9.6	77.6	54.95	16.485
LAG_01607	coaA	1660998	1661918	921	Pantothenate kinase	0	0	0			0	0
LAG_01608	guaA	1662035	1663576	1542	GMP synthase [glutamine-hydrolyzing]	0	0	0			0	0
LAG_01609	NA	1663845	1664141	297	hypothetical protein	25	6	20.202	11.1	75.8	280.299	67.272
LAG_01610	NA	1664276	1664701	426	Putative universal stress protein	10	3	7.042	5.9	33.1	78.168	23.45

LAG_01611	NA	1664835	1665428	594	hypothetical protein	183	20	33.67	5.9	96.8	1025.893	112.119
LAG_01612	mhqA_3	1665415	1666560	1146	Putative ring-cleaving dioxygenase MhqA	220	27	23.56	0.9	96.5	639.257	78.454
LAG_01613	NA	1666678	1667481	804	hypothetical protein	243	23	28.607	4.4	97.3	1006.439	95.26
LAG_01614	purK	1667503	1668621	1119	N5-carboxyaminoimidazole ribonucleotide synthase	322	28	25.022	1	93.8	958.216	83.323
LAG_01615	purE	1668744	1669229	486	N5-carboxyaminoimidazole ribonucleotide mutase	75	10	20.576	2.5	91.4	513.881	68.517
LAG_01616	purD	1669232	1670464	1233	Phosphoribosylamine--glycine ligase	106	13	10.543	19.6	97.7	286.273	35.109
LAG_01617	yfnB_2	1670568	1671260	693	Putative HAD-hydrolase YfnB	67	15	21.645	0.6	69.1	321.943	72.077
LAG_01618	treA	1671347	1672957	1611	Trehalose-6-phosphate hydrolase	6	2	1.241	40.3	60.9	12.402	4.134
LAG_01619	bglF_4	1672977	1674521	1545	PTS system beta-glucoside-specific EIIBCA component	118	19	12.298	10.9	90.4	254.326	40.951
LAG_01620	crr	1674534	1675019	486	PTS system glucose-specific EIIA component	23	6	12.346	43	96.9	157.59	41.11
LAG_01621	treR	1675149	1675865	717	HTH-type transcriptional regulator TreR	134	14	19.526	38.5	94.6	622.333	65.02
LAG_01622	purH	1675899	1677449	1551	Bifunctional purine biosynthesis protein PurH	155	19	12.25	1.5	93.7	332.78	40.792
LAG_01623	purN	1677490	1678032	543	Phosphoribosylglycinamide formyltransferase	85	14	25.783	8.5	76.2	521.263	85.855
LAG_01624	purM	1678029	1679042	1014	Phosphoribosylformylglycinamidine cyclo-ligase	157	15	14.793	20	91.6	515.584	49.26
LAG_01625	purF	1679035	1680450	1416	Amidophosphoribosyltransferase	117	22	15.537	1.3	98	275.144	51.736
LAG_01626	purL	1680435	1682651	2217	Phosphoribosylformylglycinamidine synthase subunit PurL	398	35	15.787	3.5	90.7	597.798	52.57
LAG_01627	purQ	1682648	1683328	681	Phosphoribosylformylglycinamidine synthase subunit PurQ	65	11	16.153	2.1	89.7	317.836	53.788
LAG_01628	purS	1683328	1683570	243	Phosphoribosylformylglycinamidine synthase subunit PurS	84	5	20.576	4.9	48.1	1151.093	68.517
LAG_01629	purC	1683626	1684342	717	Phosphoribosylaminoimidazole-succinocarboxamide synthase	86	12	16.736	21.5	99.9	399.408	55.731
LAG_01630	NA	1684447	1684872	426	hypothetical protein	72	10	23.474	9.6	76.1	562.808	78.168
LAG_01631	yafP	1684889	1685350	462	putative N-acetyltransferase YafP	119	9	19.481	48.1	87.4	857.714	64.869
LAG_01632	thyA	1685352	1686191	840	Thymidylate synthase	0	0	0			0	0
LAG_01633	ettA_2	1686339	1688189	1851	Energy-dependent translational throttle protein EttA	257	29	15.667	0.3	98.8	462.343	52.171
LAG_01634	NA	1688292	1690136	1845	hypothetical protein	343	38	20.596	4.1	95.7	619.063	68.584
LAG_01635	pepDA	1690309	1691703	1395	Dipeptidase A	81	12	8.602	18.4	88.8	193.352	28.645
LAG_01636	cca	1691700	1692896	1197	CCA-adding enzyme	0	0	0			0	0
LAG_01637	NA	1693086	1694429	1344	Putative dipeptidase	249	25	18.601	18.9	93	616.932	61.941
LAG_01638	NA	1694478	1696004	1527	hypothetical protein	278	35	22.921	11.2	94.8	606.238	76.325
LAG_01639	NA	1696232	1697074	843	DegV domain-containing protein	7	2	2.372	23.6	30.2	27.651	7.9
LAG_01640	NA	1697098	1697496	399	hypothetical protein	17	2	5.013	50.6	61.2	141.877	16.691
LAG_01641	gph_3	1697493	1698077	585	Phosphoglycolate phosphatase	132	7	11.966	53.7	97.9	751.373	39.846
LAG_01642	trmD	1698077	1698805	729	tRNA (guanine-N(1)-)-methyltransferase	0	0	0			0	0
LAG_01643	rimM	1698807	1699322	516	Ribosome maturation factor RimM	0	0	0			0	0
LAG_01644	yhdG_1	1699468	1700865	1398	putative amino acid permease YhdG	129	21	15.021	4	98.6	307.27	50.021
LAG_01645	NA	1701128	1701574	447	hypothetical protein	80	9	20.134	8.7	89.5	595.964	67.046
LAG_01646	NA	1701590	1702225	636	hypothetical protein	141	14	22.013	5.3	95.9	738.243	73.301
LAG_01647	ubiE	1702415	1703140	726	Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE	57	9	12.397	2.6	99.4	261.442	41.28
LAG_01648	NA	1703294	1703536	243	hypothetical protein	56	5	20.576	9.5	84.8	767.395	68.517
LAG_01649	ceo	1703680	1704618	939	N(5)-(carboxyethyl)ornithine synthase	91	10	10.65	6	94.5	322.711	35.463
LAG_01650	NA	1704896	1705135	240	hypothetical protein	34	6	25	0.4	90.4	471.743	83.249
LAG_01651	NA	1705169	1705729	561	hypothetical protein	48	6	10.695	23.9	94.5	284.915	35.614
LAG_01652	NA	1705739	1705927	189	hypothetical protein	39	7	37.037	2.1	74.6	687.132	123.331
LAG_01653	NA	1705949	1706506	558	Stress response regulator gls24	43	7	12.545	13.6	78.1	256.609	41.774
LAG_01654	zntB	1706621	1707568	948	Zinc transport protein ZntB	147	25	26.371	17.6	96.1	516.353	87.815
LAG_01655	ifcA	1707621	1709123	1503	Fumarate reductase flavoprotein subunit	138	25	16.633	21.8	99.8	305.744	55.388
LAG_01656	corC_2	1709299	1710573	1275	Magnesium and cobalt efflux protein CorC	217	28	21.961	0.5	98	566.744	73.128
LAG_01657	NA	1710747	1711304	558	hypothetical protein	153	21	37.634	8.6	97.8	913.05	125.321
LAG_01658	padC	1711442	1711975	534	Phenolic acid decarboxylase PadC	150	20	37.453	11.2	97	935.379	124.717
LAG_01659	spxA_14	1712094	1712492	399	Regulatory protein Spx	127	10	25.063	6	65.7	1059.908	83.457
LAG_01660	NA	1712690	1712929	240	hypothetical protein	4	1	4.167	8.8	8.8	55.499	13.875
LAG_01661	rpsP	1713006	1713278	273	30S ribosomal protein S16	0	0	0			0	0
LAG_01662	mvaA	1713437	1714657	1221	3-hydroxy-3-methylglutaryl-coenzyme A reductase	7	1	0.819	2.2	2.2	19.091	2.727
LAG_01663	thlA	1714688	1715848	1161	Acetyl-CoA acetyltransferase	0	0	0			0	0
LAG_01664	mvaS	1715953	1717104	1152	Hydroxymethylglutaryl-CoA synthase	3	1	0.868	99.1	99.1	8.672	2.891

LAG_01665	fabG_2	1717140	1717934	795	3-oxoacyl-[acyl-carrier-protein] reductase FabG	128	15	18.868	7.5	80.5	536.143	62.829
LAG_01666	gmuR_2	1718059	1718772	714	HTH-type transcriptional regulator GmuR	116	15	21.008	3.1	96.8	541	69.957
LAG_01667	NA	1718873	1719727	855	hypothetical protein	241	23	26.901	3.6	98.2	938.617	89.578
LAG_01668	yhhX_2	1719741	1720790	1050	putative oxidoreductase YhhX	311	30	28.571	5.4	93.1	986.299	95.141
LAG_01669	hadI	1720942	1725201	4260	2-hydroxyisocaproyl-CoA dehydratase activator	916	109	25.587	0.1	99	716.017	85.203
LAG_01670	slmA	1725417	1726064	648	Nucleoid occlusion factor SlmA	187	24	37.037	0.2	96.1	960.957	123.331
LAG_01671	glpK_2	1726168	1727658	1491	Glycerol kinase	319	30	20.121	1.1	83.5	712.444	67.001
LAG_01672	nagB	1727701	1728408	708	Glucosamine-6-phosphate deaminase	10	2	2.825	67.5	73.4	47.033	9.407
LAG_01673	lytR_2	1728552	1729460	909	Transcriptional regulator LytR	45	8	8.801	17.7	88	164.849	29.306
LAG_01674	NA	1729471	1730361	891	hypothetical protein	3	1	1.122	66	66	11.212	3.737
LAG_01675	tagB	1730358	1730666	309	Teichoic acid glycerol-phosphate primase	0	0	0			0	0
LAG_01676	NA	1730844	1730918	75	tRNA-Val	0	0	0			0	0
LAG_01677	NA	1730957	1731037	81	tRNA-Tyr	0	0	0			0	0
LAG_01678	NA	1731044	1731116	73	tRNA-Trp	0	0	0			0	0
LAG_01679	NA	1731127	1731200	74	tRNA-His	0	0	0			0	0
LAG_01680	NA	1731207	1731278	72	tRNA-Gln	0	0	0			0	0
LAG_01681	NA	1731308	1731393	86	tRNA-Leu	0	0	0			0	0
LAG_01682	yoaB_2	1731485	1734091	2607	Calcium-transporting ATPase 1	461	50	19.179	1	96.5	588.84	63.866
LAG_01683	NA	1734220	1734696	477	hypothetical protein	50	4	8.386	49.9	81.3	349.051	27.924
LAG_01684	gap	1734914	1735924	1011	Glyceraldehyde-3-phosphate dehydrogenase	0	0	0			0	0
LAG_01685	NA	1736065	1737018	954	hypothetical protein	250	20	20.964	0.4	96.2	872.628	69.81
LAG_01686	NA	1737061	1737402	342	hypothetical protein	110	6	17.544	8.8	98.5	1071.036	58.42
LAG_01687	recG	1737414	1739495	2082	ATP-dependent DNA helicase RecG	0	0	0			0	0
LAG_01688	NA	1739531	1739785	255	hypothetical protein	52	8	31.373	28.6	97.3	679.048	104.469
LAG_01689	mnmE	1739827	1741191	1365	tRNA modification GTPase MnmE	39	1	0.733	2.4	2.4	95.141	2.44
LAG_01690	rsuA_2	1741322	1742032	711	Ribosomal small subunit pseudouridine synthase A	16	1	1.406	95.5	95.5	74.936	4.683
LAG_01691	ybhF	1742035	1742751	717	putative ABC transporter ATP-binding protein YbhF	53	4	5.579	1.1	93.6	246.147	18.577
LAG_01692	rbbA	1742738	1743832	1095	Ribosome-associated ATPase	293	21	19.178	0.9	88.3	891.027	63.862
LAG_01693	rpiA	1743909	1744580	672	Ribose-5-phosphate isomerase A	3	1	1.488	98.5	98.5	14.866	4.955
LAG_01694	NA	1744605	1745057	453	hypothetical protein	10	2	4.415	23.8	88.3	73.509	14.702
LAG_01695	mreC	1745201	1746034	834	Cell shape-determining protein MreC	0	0	0			0	0
LAG_01696	NA	1746037	1746543	507	hypothetical protein	8	2	3.945	84	92.3	52.544	13.136
LAG_01697	NA	1746688	1748058	1371	Secreted 45 kDa protein	41	6	4.376	17.4	85.8	99.583	14.573
LAG_01698	NA	1748239	1749468	1230	Secreted 45 kDa protein	12	2	1.626	57.5	99.2	32.487	5.415
LAG_01699	dnaJ	1749678	1750808	1131	Chaperone protein DnaJ	12	2	1.768	67	70.7	35.331	5.889
LAG_01700	ppaX	1750880	1751407	528	Pyrophosphatase PpaX	21	1	1.894	95.3	95.3	132.441	6.307
LAG_01701	zwf	1751584	1753071	1488	Glucose-6-phosphate 1-dehydrogenase	0	0	0			0	0
LAG_01702	NA	1753095	1753274	180	hypothetical protein	44	3	16.667	11.1	50.6	813.987	55.499
LAG_01703	NA	1753411	1754229	819	hypothetical protein	234	17	20.757	1.7	97.6	951.414	69.12
LAG_01704	NA	1754226	1754594	369	hypothetical protein	124	12	32.52	1.1	78.6	1119.007	108.291
LAG_01705	NA	1754641	1754725	85	tRNA-Leu	0	0	0			0	0
LAG_01706	NA	1754777	1754983	207	hypothetical protein	15	2	9.662	72	92.3	241.301	32.173
LAG_01707	glxR	1754994	1755878	885	2-hydroxy-3-oxopropionate reductase	154	15	16.949	11.2	92	579.449	56.44
LAG_01708	argS	1755919	1757607	1689	Arginine--tRNA ligase	5	1	0.592	1.1	1.1	9.858	1.972
LAG_01709	argR_2	1757982	1758428	447	Arginine repressor	3	1	2.237	93.1	93.1	22.349	7.45
LAG_01710	NA	1758418	1758759	342	hypothetical protein	65	6	17.544	2.9	82.2	632.885	58.42
LAG_01711	mutS	1758869	1761376	2508	DNA mismatch repair protein MutS	248	19	7.576	2.8	99.9	329.277	25.227
LAG_01712	NA	1761446	1762111	666	hypothetical protein	40	4	6.006	79.4	97.4	199.997	20
LAG_01713	mutL	1762282	1764168	1887	DNA mismatch repair protein MutL	84	11	5.829	38.8	99.5	148.233	19.411
LAG_01714	ykoT	1764188	1765150	963	putative glycosyltransferase YkoT	0	0	0			0	0
LAG_01715	ruvA	1765150	1765740	591	Holliday junction ATP-dependent DNA helicase RuvA	40	4	6.768	54.5	95.8	225.377	22.538
LAG_01716	ruvB	1765778	1766776	999	Holliday junction ATP-dependent DNA helicase RuvB	11	1	1.001	97.6	97.6	36.666	3.333
LAG_01717	yfkJ	1766936	1767307	372	Low molecular weight protein-tyrosine-phosphatase YfkJ	10	2	5.376	59.9	71.2	89.515	17.903
LAG_01718	glnR	1767394	1767759	366	HTH-type transcriptional regulator GlnR	0	0	0			0	0

LAG_01719	glnA	1767816	1769156	1341	Glutamine synthetase	34	5	3.729	12.7	97.1	84.428	12.416
LAG_01720	NA	1769221	1769652	432	hypothetical protein	93	8	18.519	8.8	92.6	716.864	61.666
LAG_01721	NA	1769645	1769914	270	hypothetical protein	67	3	11.111	34.1	81.9	826.32	36.999
LAG_01722	NA	1770054	1770320	267	hypothetical protein	0	0	0			0	0
LAG_01723	NA	1770322	1770615	294	hypothetical protein	113	9	30.612	10.5	95.6	1279.878	101.937
LAG_01724	msrC	1770672	1771151	480	Free methionine-R-sulfoxide reductase	16	2	4.167	8.8	95.8	110.998	13.875
LAG_01725	NA	1771164	1771784	621	hypothetical protein	65	7	11.272	1.6	81.3	348.545	37.536
LAG_01726	dnaX_2	1771797	1773455	1659	DNA polymerase III subunit tau	0	0	0			0	0
LAG_01727	lysP_2	1773489	1774952	1464	Lysine-specific permease	109	11	7.514	24.9	86.7	247.926	25.02
LAG_01728	NA	1775419	1775631	213	hypothetical protein	6	1	4.695	1.9	1.9	93.801	15.634
LAG_01729	rpsF	1775817	1776110	294	30S ribosomal protein S6	0	0	0			0	0
LAG_01730	ssb	1776148	1776642	495	Single-stranded DNA-binding protein	0	0	0			0	0
LAG_01731	rpsR	1776762	1777007	246	30S ribosomal protein S18	16	1	4.065	85	85	216.582	13.536
LAG_01732	cpdA_3	1777116	1777883	768	3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA	74	6	7.812	40.5	76.4	320.854	26.015
LAG_01733	NA	1777917	1778225	309	hypothetical protein	3	1	3.236	27.8	27.8	32.33	10.777
LAG_01734	hexR_3	1778257	1779105	849	HTH-type transcriptional regulator HexR	95	9	10.601	16.8	85.4	372.609	35.3
LAG_01735	recX	1779188	1780021	834	Regulatory protein RecX	77	11	13.189	8	94.2	307.441	43.92
LAG_01736	ydhP	1780144	1781325	1182	Inner membrane transport protein YdhP	103	11	9.306	31	84	290.173	30.989
LAG_01737	ytbE	1781342	1782160	819	putative oxidoreductase YtbE	50	7	8.547	4.2	53.7	203.294	28.461
LAG_01738	ytcD	1782301	1782666	366	putative HTH-type transcriptional regulator YtcD	3	1	2.732	32	32	27.295	9.098
LAG_01739	fosB	1782694	1783086	393	Metallothiol transferase FosB	39	4	10.178	16.3	83	330.453	33.893
LAG_01740	rlmCD_2	1783187	1784692	1506	23S rRNA (uracil-C(5))-methyltransferase RlmCD	87	9	5.976	43.6	99.5	192.368	19.9
LAG_01741	NA	1784732	1785241	510	hypothetical protein	15	2	3.922	2.4	85.7	97.94	13.059
LAG_01742	NA	1785243	1785497	255	hypothetical protein	0	0	0			0	0
LAG_01743	NA	1785650	1785898	249	hypothetical protein	19	2	8.032	27.3	77.1	254.092	26.747
LAG_01744	NA	1786023	1786637	615	hypothetical protein	33	4	6.504	20.7	76.6	178.68	21.658
LAG_01745	valS	1786933	1789575	2643	Valine--tRNA ligase	0	0	0			0	0
LAG_01746	pgi	1789724	1791070	1347	Glucose-6-phosphate isomerase	0	0	0			0	0
LAG_01747	rsmD	1791126	1791707	582	Ribosomal RNA small subunit methyltransferase D	26	3	5.155	52.9	62.2	148.761	17.165
LAG_01748	coaD	1791697	1792194	498	Phosphopantetheine adenylyltransferase	40	2	4.016	87.3	95.8	267.466	13.373
LAG_01749	lon	1792184	1793227	1044	Lon protease	11	2	1.916	9	47.3	35.086	6.379
LAG_01750	adhE	1793259	1795952	2694	Aldehyde-alcohol dehydrogenase	114	14	5.197	1.2	73.9	140.911	17.305
LAG_01751	pgl	1796107	1797147	1041	6-phosphogluconolactonase	0	0	0			0	0
LAG_01752	rpsB	1797420	1798193	774	30S ribosomal protein S2	0	0	0			0	0
LAG_01753	tsf	1798270	1799298	1029	Elongation factor Ts	0	0	0			0	0
LAG_01754	ezrA	1799513	1801243	1731	Septation ring formation regulator EzrA	37	5	2.889	96.3	99.5	71.177	9.619
LAG_01755	der_2	1801369	1802496	1128	GTPase Der	0	0	0			0	0
LAG_01756	hflX	1802499	1803734	1236	GTPase HflX	20	4	3.236	58.3	94.8	53.883	10.777
LAG_01757	yhbY	1803749	1804057	309	RNA-binding protein YhbY	0	0	0			0	0
LAG_01758	nadD_2	1804061	1804654	594	putative nicotinate-nucleotide adenylyltransferase	13	2	3.367	18.5	25.6	72.878	11.212
LAG_01759	NA	1804647	1805240	594	hypothetical protein	41	3	5.051	37.7	50.3	229.845	16.818
LAG_01760	rsfS	1805267	1805626	360	Ribosomal silencing factor RsfS	24	3	8.333	15.6	28.6	221.997	27.75
LAG_01761	NA	1805627	1806358	732	Glycine/sarcosine N-methyltransferase	62	10	13.661	5.6	44.1	282.045	45.491
LAG_01762	NA	1806346	1807431	1086	hypothetical protein	12	3	2.762	57.6	66.4	36.795	9.199
LAG_01763	NA	1807471	1808184	714	putative transcriptional regulatory protein	0	0	0			0	0
LAG_01764	NA	1808968	1809498	531	hypothetical protein	198	18	33.898	4.3	84.7	1241.675	112.88
LAG_01765	NA	1809723	1810703	981	hypothetical protein	229	38	38.736	1.1	98.1	777.327	128.989
LAG_01766	catE	1810752	1811588	837	Catechol-2,3-dioxygenase	276	26	31.063	8.6	93.8	1098.047	103.439
LAG_01767	menG	1811711	1812442	732	Demethylmenaquinone methyltransferase	62	11	15.027	2.9	87.6	282.045	50.04
LAG_01768	eno	1812580	1813881	1302	Enolase	0	0	0			0	0
LAG_01769	NA	1814010	1814495	486	hypothetical protein	72	6	12.346	8.4	93.4	493.326	41.11
LAG_01770	rplT	1814557	1814916	360	50S ribosomal protein L20	0	0	0			0	0
LAG_01771	rpmI	1815171	1815371	201	50S ribosomal protein L35	0	0	0			0	0
LAG_01772	infC	1815401	1815895	495	Translation initiation factor IF-3	0	0	0			0	0

LAG_01773	strH	1816168	1817328	1161	Beta-N-acetylhexosaminidase	72	7	6.029	5.8	88.4	206.508	20.077
LAG_01774	hflK	1817423	1818316	894	Modulator of FtsH protease HflK	73	6	6.711	36.2	69.1	271.908	22.349
LAG_01775	galT_2	1818365	1819033	669	Galactose-1-phosphate uridylyltransferase	30	7	10.463	9.4	60.2	149.325	34.843
LAG_01776	miaA	1819023	1819916	894	tRNA dimethylallyltransferase	20	5	5.593	3.8	95	74.495	18.624
LAG_01777	pdaC	1820050	1821471	1422	Peptidoglycan-N-acetylmuramic acid deacetylase PdaC	202	20	14.065	1.3	98.8	473.031	46.835
LAG_01778	NA	1821659	1821838	180	hypothetical protein	15	2	11.111	32.8	56.1	277.496	36.999
LAG_01779	NA	1821871	1822041	171	hypothetical protein	0	0	0			0	0
LAG_01780	NA	1822082	1822354	273	hypothetical protein	9	2	7.326	2.2	15	109.779	24.395
LAG_01781	NA	1822356	1822715	360	hypothetical protein	13	2	5.556	66.4	78.1	120.248	18.5
LAG_01782	NA	1822715	1823041	327	hypothetical protein	13	3	9.174	26.3	47.1	132.383	30.55
LAG_01783	pyrDA	1823201	1824133	933	Dihydroorotate dehydrogenase A (fumarate)	46	8	8.574	6.2	71.4	164.177	28.553
LAG_01784	fhuC	1824490	1825224	735	Iron(3+)-hydroxamate import ATP-binding protein FhuC	64	13	17.687	4.8	95.6	289.955	58.897
LAG_01785	mntB	1825231	1826085	855	Manganese transport system membrane protein MntB	232	22	25.731	9.8	96.7	903.565	85.683
LAG_01786	mntA	1826082	1827011	930	Manganese-binding lipoprotein MntA	154	9	9.677	41.7	79.2	551.411	32.225
LAG_01787	gnd	1827451	1828872	1422	6-phosphogluconate dehydrogenase, decarboxylating	0	0	0			0	0
LAG_01788	NA	1828994	1829593	600	hypothetical protein	35	4	6.667	42.8	65.5	194.247	22.2
LAG_01789	NA	1829595	1830020	426	hypothetical protein	31	3	7.042	31.5	41.3	242.32	23.45
LAG_01790	NA	1830204	1830557	354	hypothetical protein	53	3	8.475	5.1	98.6	498.552	28.22
LAG_01791	lgt	1830691	1831476	786	Prolipoprotein diacylglyceryl transferase	129	7	8.906	0.8	99.6	546.518	29.656
LAG_01792	hprK	1831486	1832409	924	HPr kinase/phosphorylase	0	0	0			0	0
LAG_01793	NA	1832955	1833368	414	hypothetical protein	96	10	24.155	1	94.2	772.162	80.434
LAG_01794	NA	1833505	1833594	90	hypothetical protein	58	7	77.778	21.1	92.2	2145.966	258.996
LAG_01795	NA	1833662	1834117	456	hypothetical protein	0	0	0			0	0
LAG_01796	NA	1834158	1835060	903	hypothetical protein	271	20	22.148	0.7	96	999.353	73.753
LAG_01797	map	1835112	1835969	858	Methionine aminopeptidase 1	0	0	0			0	0
LAG_01798	NA	1836129	1836572	444	Flavodoxin	45	8	18.018	13.5	98.2	337.495	59.999
LAG_01799	rlmB	1836601	1837329	729	23S rRNA (guanosine-2'-O-)-methyltransferase RlmB	63	11	15.089	1.9	99.3	287.773	50.246
LAG_01800	acyP	1837391	1837666	276	Acylphosphatase	25	4	14.493	36.2	96.4	301.626	48.26
LAG_01801	NA	1837710	1838321	612	hypothetical protein	50	7	11.438	20.1	61.8	272.055	38.088
LAG_01802	glyA	1838487	1839728	1242	Serine hydroxymethyltransferase	75	7	5.636	0.4	98.9	201.084	18.768
LAG_01803	NA	1839843	1840445	603	Putative threonylcarbamoyl-AMP synthase	12	1	1.658	6	6	66.268	5.522
LAG_01804	yvbK	1840447	1840875	429	putative N-acetyltransferase YvbK	20	4	9.324	19.6	98.8	155.242	31.048
LAG_01805	prmC_2	1840876	1841688	813	Release factor glutamine methyltransferase	18	5	6.15	27.3	98	73.726	20.479
LAG_01806	NA	1841716	1842252	537	hypothetical protein	91	8	14.898	4.8	86	564.293	49.608
LAG_01807	prfA	1842252	1843325	1074	Peptide chain release factor 1	12	1	0.931	1	1	37.206	3.101
LAG_01808	tdk	1843350	1843952	603	Thymidine kinase	0	0	0			0	0
LAG_01809	xerD_2	1844099	1845298	1200	Tyrosine recombinase XerD	164	17	14.167	6.7	99	455.093	47.174
LAG_01810	NA	1845359	1845544	186	hypothetical protein	80	9	48.387	3.2	99.5	1432.236	161.127
LAG_01811	NA	1845656	1845874	219	hypothetical protein	28	3	13.699	10.5	89	425.747	45.616
LAG_01812	NA	1845889	1846137	249	hypothetical protein	66	5	20.08	0.8	98	882.637	66.866
LAG_01813	NA	1846149	1846658	510	hypothetical protein	120	11	21.569	8.8	72.9	783.517	71.822
LAG_01814	NA	1846675	1846923	249	hypothetical protein	18	4	16.064	17.7	83.9	240.719	53.493
LAG_01815	inlJ_3	1847016	1849235	2220	Internalin-J	641	65	29.279	1.4	99.9	961.485	97.498
LAG_01816	NA	1849438	1849938	501	hypothetical protein	160	14	27.944	18	95.8	1063.456	93.052
LAG_01817	NA	1849935	1850987	1053	hypothetical protein	171	17	16.144	13	65.7	540.761	53.76
LAG_01818	NA	1850962	1852755	1794	hypothetical protein	788	56	31.215	0.2	99	1462.653	103.945
LAG_01819	NA	1852767	1855262	2496	hypothetical protein	830	76	30.449	1.8	99.2	1107.314	101.393
LAG_01820	NA	1855246	1855638	393	hypothetical protein	129	10	25.445	30.3	93.1	1093.036	84.731
LAG_01821	NA	1855642	1855863	222	hypothetical protein	73	6	27.027	57.7	82	1094.983	89.999
LAG_01822	NA	1855902	1857137	1236	hypothetical protein	285	35	28.317	8.2	97.8	767.828	94.295
LAG_01823	inlJ_4	1857337	1859562	2226	Internalin-J	785	55	24.708	0.1	92.6	1174.308	82.276
LAG_01824	NA	1859936	1862731	2796	hypothetical protein	602	59	21.102	2.3	97.1	716.963	70.267
LAG_01825	NA	1862912	1863925	1014	hypothetical protein	302	31	30.572	15.4	96.4	991.76	101.803
LAG_01826	NA	1864139	1864450	312	hypothetical protein	68	8	25.641	1.3	92.3	725.758	85.383

LAG_01827	NA	1864529	1864681	153	hypothetical protein	3	1	6.536	10.5	10.5	65.293	21.764
LAG_01828	inlJ_5	1864879	1866159	1281	Internalin-J	490	31	24.2	1.2	97.4	1273.751	80.584
LAG_01829	NA	1866237	1866539	303	hypothetical protein	263	14	46.205	1.3	95	2890.351	153.859
LAG_01830	NA	1866572	1867720	1149	hypothetical protein	281	24	20.888	6.7	99.5	814.374	69.555
LAG_01831	xre	1867806	1868303	498	HTH-type transcriptional regulator Xre	130	14	28.112	8	97.8	869.264	93.613
LAG_01832	ftsK_2	1868685	1870367	1683	DNA translocase FtsK	293	37	21.985	0.2	87.1	579.724	73.207
LAG_01833	NA	1870374	1870853	480	hypothetical protein	42	9	18.75	1.9	96.2	291.37	62.437
LAG_01834	NA	1870869	1871168	300	hypothetical protein	48	6	20	3.3	98.3	532.792	66.599
LAG_01835	NA	1871866	1872090	225	hypothetical protein	166	11	48.889	0.9	92.9	2456.762	162.797
LAG_01836	NA	1873365	1873730	366	hypothetical protein	5	1	2.732	89.6	89.6	45.491	9.098
LAG_01837	NA	1873745	1874695	951	hypothetical protein	506	42	44.164	3.3	96.4	1771.77	147.064
LAG_01838	NA	1874885	1875238	354	hypothetical protein	238	17	48.023	1.4	78.8	2238.779	159.913
LAG_01839	macB_2	1875415	1877412	1998	Macrolide export ATP-binding/permease protein MacB	800	71	35.536	0.2	97.2	1333.312	118.331
LAG_01840	yvgN_2	1878083	1878949	867	Glyoxal reductase	267	23	26.528	2.7	96.2	1025.486	88.338
LAG_01841	adhR	1879028	1879447	420	HTH-type transcriptional regulator AdhR	156	13	30.952	12.9	99.3	1236.838	103.07
LAG_01842	NA	1880014	1881060	1047	hypothetical protein	387	44	42.025	1.8	96.7	1230.84	139.941
LAG_01843	ntpJ_2	1881111	1882448	1338	Potassium/sodium uptake protein NtpJ	505	42	31.39	0.1	98.5	1256.819	104.528
LAG_01844	spxA_15	1882675	1883052	378	Regulatory protein Spx	225	22	58.201	0.5	91.3	1982.112	193.806
LAG_01845	NA	1883206	1883400	195	hypothetical protein	58	11	56.41	10.3	93.8	990.446	187.843
LAG_01846	NA	1883505	1883693	189	hypothetical protein	94	10	52.91	2.6	92.1	1656.165	176.188
LAG_01847	NA	1883853	1883926	74	tRNA-Met	0	0	0			0	0
LAG_01848	NA	1884062	1884214	153	hypothetical protein	67	7	45.752	2.6	96.1	1458.212	152.351
LAG_01849	spxA_16	1884248	1884457	210	Regulatory protein Spx	50	3	14.286	35.7	77.1	792.845	47.571
LAG_01850	cspLA_1	1884695	1884895	201	Cold shock-like protein CspLA	7	1	4.975	93.5	93.5	115.968	16.567
LAG_01851	NA	1885100	1885402	303	hypothetical protein	80	8	26.403	22.1	91.4	879.194	87.919
LAG_01852	NA	1886203	1886541	339	hypothetical protein	133	12	35.398	2.4	93.5	1306.44	117.874
LAG_01853	NA	1886574	1886647	74	tRNA-Met	5	1	13.514	20.3	20.3	224.996	44.999
LAG_01854	cspLA_2	1886820	1887020	201	Cold shock-like protein CspLA	3	1	4.975	45.3	45.3	49.701	16.567
LAG_01855	NA	1887549	1888385	837	hypothetical protein	319	37	44.205	14.1	97.4	1269.12	147.202
LAG_01856	NA	1889008	1889469	462	hypothetical protein	379	30	64.935	4.3	97.8	2731.71	216.23
LAG_01857	tadA_2	1889548	1890039	492	tRNA-specific adenosine deaminase	0	0	0			0	0
LAG_01858	rbn	1890039	1890773	735	Ribonuclease BN	30	4	5.442	2.3	79.5	135.916	18.122
LAG_01859	NA	1890770	1891441	672	hypothetical protein	57	7	10.417	17.7	95.7	282.451	34.687
LAG_01860	NA	1892039	1893514	1476	hypothetical protein	401	43	29.133	1.1	97.2	904.681	97.011
LAG_01861	spxA_17	1894058	1894408	351	Regulatory protein Spx	122	12	34.188	2.3	90	1157.418	113.844
LAG_01862	NA	1894626	1896101	1476	hypothetical protein	333	41	27.778	0.6	99	751.269	92.499
LAG_01863	NA	1896217	1898481	2265	hypothetical protein	318	39	17.219	1.8	94.3	467.516	57.337
LAG_01864	NA	1898614	1899330	717	hypothetical protein	185	18	25.105	20.5	97.5	859.192	83.597
LAG_01865	NA	1899367	1899654	288	hypothetical protein	40	6	20.833	0.3	81.2	462.493	69.374
LAG_01866	NA	1900141	1900626	486	hypothetical protein	64	6	12.346	13.6	69.8	438.512	41.11
LAG_01867	NA	1900732	1901931	1200	hypothetical protein	88	12	10	0.9	96.7	244.196	33.299
LAG_01868	NA	1901962	1902387	426	hypothetical protein	124	7	16.432	5.2	50.5	969.281	54.717
LAG_01869	macB_3	1902777	1904762	1986	Macrolide export ATP-binding/permease protein MacB	255	30	15.106	10.6	99	427.561	50.301
LAG_01870	yusO	1904851	1905492	642	putative HTH-type transcriptional regulator YusO	13	1	1.558	85.8	85.8	67.429	5.187
LAG_01871	NA	1905591	1907309	1719	putative ABC transporter ATP-binding protein	84	12	6.981	1.7	93.5	162.72	23.246
LAG_01872	cydD	1907341	1909047	1707	ATP-binding/permease protein CydD	305	27	15.817	0.6	99.5	594.982	52.671
LAG_01873	cydB	1909193	1910188	996	Cytochrome bd-I ubiquinol oxidase subunit 2	19	4	4.016	3.5	98.2	63.523	13.373
LAG_01874	cydA	1910185	1911633	1449	Cytochrome bd ubiquinol oxidase subunit 1	137	10	6.901	15.3	75	314.84	22.981
LAG_01875	apu	1911841	1913658	1818	Amylopullulanase	121	15	8.251	2	72.9	221.63	27.475
LAG_01876	glgP	1913759	1916161	2403	Glycogen phosphorylase	221	29	12.068	3.4	97	306.25	40.187
LAG_01877	glgA	1916234	1917670	1437	Glycogen synthase	153	18	12.526	13.8	98.6	354.546	41.711
LAG_01878	glgD	1917721	1918866	1146	Glycogen biosynthesis protein GlgD	301	27	23.56	9	88	874.62	78.454
LAG_01879	glgC	1918856	1919998	1143	Glucose-1-phosphate adenylyltransferase	144	19	16.623	2	95.3	419.521	55.353
LAG_01880	nusB	1920482	1921456	975	N utilization substance protein B	0	0	0			0	0

LAG_01881	NA	1921449	1921850	402	hypothetical protein	0	0	0			0	0
LAG_01882	efp	1921938	1922495	558	Elongation factor P	0	0	0			0	0
LAG_01883	ypdF	1922652	1923701	1050	Aminopeptidase YpdF	142	17	16.19	1	87.7	450.336	53.913
LAG_01884	gph_4	1923814	1924467	654	Phosphoglycolate phosphatase	97	13	19.878	1.7	83.2	493.891	66.192
LAG_01885	fba_2	1925160	1926017	858	Fructose-bisphosphate aldolase	50	10	11.655	0.2	91.6	194.053	38.811
LAG_01886	lacC_2	1926042	1926971	930	Tagatose-6-phosphate kinase	94	16	17.204	2.9	99.6	336.575	57.289
LAG_01887	agaS	1926986	1928137	1152	Putative tagatose-6-phosphate ketose/aldose isomerase	193	12	10.417	19.7	98.4	557.882	34.687
LAG_01888	NA	1928292	1928939	648	Phosphorylated carbohydrates phosphatase	184	12	18.519	10.8	87.8	945.541	61.666
LAG_01889	fruA_3	1928941	1930869	1929	PTS system fructose-specific EIIABC component	180	19	9.85	0.6	99.4	310.726	32.799
LAG_01890	pfkB	1930879	1931811	933	ATP-dependent 6-phosphofructokinase isozyme 2	111	10	10.718	4.4	88.6	396.167	35.691
LAG_01891	ybbH_3	1931965	1932714	750	putative HTH-type transcriptional regulator YbbH	51	7	9.333	10.7	94.7	226.436	31.08
LAG_01892	manZ_3	1932754	1933593	840	PTS system mannose-specific EIID component	164	11	13.095	2.5	97.6	650.133	43.606
LAG_01893	agaC	1933583	1934392	810	N-acetylgalactosamine permease IIC component 1	69	7	8.642	2.1	98.6	283.662	28.777
LAG_01894	manX_3	1934545	1935021	477	PTS system mannose-specific EIIAB component	105	11	23.061	1.9	72.7	733.007	76.791
LAG_01895	NA	1935111	1935386	276	hypothetical protein	95	8	28.986	2.5	92.4	1146.178	96.52
LAG_01896	manX_4	1935387	1935809	423	PTS system mannose-specific EIIAB component	92	4	9.456	46.3	70	724.244	31.489
LAG_01897	nagA_2	1935951	1937099	1149	N-acetylglucosamine-6-phosphate deacetylase	83	17	14.795	0.4	97.5	240.545	49.268
LAG_01898	hexR_4	1937230	1937982	753	HTH-type transcriptional regulator HexR	105	16	21.248	0.9	95.2	464.335	70.756
LAG_01899	fbp	1938029	1939951	1923	Fructose-1,6-bisphosphatase class 3	506	41	21.321	0.8	98.1	876.211	70.997
LAG_01900	uvrA_2	1940108	1942927	2820	UvrABC system protein A	28	3	1.064	0.1	28.9	33.063	3.542
LAG_01901	NA	1943032	1943331	300	hypothetical protein	72	5	16.667	13.7	59.7	799.187	55.499
LAG_01902	NA	1943382	1943708	327	hypothetical protein	38	6	18.349	6.1	80.1	386.966	61.1
LAG_01903	yceM	1943728	1944648	921	Putative oxidoreductase YceM	228	18	19.544	6.5	99.7	824.352	65.08
LAG_01904	thiN	1944658	1945275	618	Thiamine pyrophosphokinase	0	0	0			0	0
LAG_01905	NA	1945272	1945619	348	hypothetical protein	9	2	5.747	85.1	97.1	86.119	19.138
LAG_01906	asnS	1945743	1947080	1338	Asparagine--tRNA ligase	0	0	0			0	0
LAG_01907	NA	1947101	1947430	330	hypothetical protein	11	2	6.061	78.8	91.5	110.998	20.182
LAG_01908	NA	1947420	1948613	1194	Aspartate aminotransferase	8	1	0.838	32.2	32.2	22.311	2.789
LAG_01909	NA	1948617	1949060	444	hypothetical protein	0	0	0			0	0
LAG_01910	dinG	1949243	1951597	2355	putative ATP-dependent helicase DinG	114	16	6.794	5.5	82.4	161.195	22.624
LAG_01911	NA	1951951	1952388	438	Putative universal stress protein	70	13	29.68	0.9	99.5	532.183	98.834
LAG_01912	mprF	1952458	1954149	1692	Phosphatidylglycerol lysyltransferase	196	32	18.913	1.4	99.9	385.739	62.978
LAG_01913	NA	1954191	1955108	918	hypothetical protein	53	9	9.804	7.1	94.3	192.252	32.647
LAG_01914	NA	1955294	1955692	399	hypothetical protein	40	4	10.025	35.6	83.2	333.829	33.383
LAG_01915	NA	1955913	1957568	1656	hypothetical protein	516	42	25.362	0.7	99	1037.592	84.455
LAG_01916	mnaA_1	1957744	1958862	1119	UDP-N-acetylglucosamine 2-epimerase	125	11	9.83	0.4	77.2	371.978	32.734
LAG_01917	NA	1958965	1959057	93	hypothetical protein	25	4	43.011	20.4	79.6	895.147	143.224
LAG_01918	NA	1959071	1960369	1299	Beta-monoglucosyldiacylglycerol synthase	262	26	20.015	1.1	93.9	671.629	66.65
LAG_01919	NA	1960438	1964181	3744	hypothetical protein	1231	104	27.778	8.1	99.8	1094.863	92.499
LAG_01920	NA	1964398	1965813	1416	hypothetical protein	134	21	14.831	2.7	98.2	315.122	49.385
LAG_01921	aqpZ2	1966065	1966730	666	Aquaporin Z 2	108	11	16.517	1.8	95.2	539.992	54.999
LAG_01922	cna_2	1966845	1968698	1854	Collagen adhesin	311	37	19.957	2.9	99.9	558.583	66.455
LAG_01923	ybiV_2	1968879	1969667	789	Sugar phosphatase YbiV	66	11	13.942	7.9	94.6	278.551	46.425
LAG_01924	srrA_2	1969816	1970505	690	Transcriptional regulatory protein SrrA	121	11	15.942	0.1	95.5	583.947	53.086
LAG_01925	baeS	1970483	1972570	2088	Signal transduction histidine-protein kinase BaeS	393	49	23.467	1.6	99.2	626.757	78.145
LAG_01926	NA	1972609	1972812	204	hypothetical protein	5	1	4.902	32.4	32.4	81.616	16.323
LAG_01927	NA	1973037	1973600	564	hypothetical protein	72	8	14.184	11.3	100	425.1	47.233
LAG_01928	NA	1973636	1974709	1074	putative ABC transporter permease	248	29	27.002	0.3	98.3	768.927	89.915
LAG_01929	bceA	1974712	1975392	681	Bacitracin export ATP-binding protein BceA	216	21	30.837	1.2	96	1056.195	102.686
LAG_01930	NA	1975440	1976786	1347	hypothetical protein	244	27	20.045	0.9	99.9	603.198	66.747
LAG_01931	icaA_2	1977102	1979234	2133	Poly-beta-1,6-N-acetyl-D-glucosamine synthase	460	39	18.284	2.8	97	718.132	60.885
LAG_01932	cph2	1979272	1979958	687	Phytochrome-like protein cph2	171	15	21.834	5.5	82.8	828.852	72.706
LAG_01933	NA	1980023	1980703	681	hypothetical protein	62	11	16.153	2.6	95.4	303.167	53.788
LAG_01934	yedQ	1980719	1981858	1140	putative diguanylate cyclase YedQ	324	28	24.561	3.2	99.6	946.406	81.788

LAG_01935	mnaA_2	1981882	1982964	1083	UDP-N-acetylglucosamine 2-epimerase	253	22	20.314	1.7	97	777.91	67.644
LAG_01936	kup	1983208	1985226	2019	Low affinity potassium transport system protein kup	188	25	12.382	12.9	96.3	310.069	41.233
LAG_01937	qorA	1985400	1986380	981	Quinone oxidoreductase 1	206	26	26.504	0.8	96.7	699.255	88.255
LAG_01938	NA	1986507	1986962	456	hypothetical protein	59	7	15.351	11.8	96.5	430.849	51.118
LAG_01939	NA	1986952	1987572	621	hypothetical protein	81	9	14.493	0.6	75	434.341	48.26
LAG_01940	NA	1987598	1988113	516	hypothetical protein	210	16	31.008	2.7	96.9	1355.211	103.254
LAG_01941	marR	1988261	1988683	423	Multiple antibiotic resistance protein MarR	68	11	26.005	11.8	98.1	535.311	86.594
LAG_01942	yodC	1988685	1989323	639	Putative NAD(P)H nitroreductase YodC	108	13	20.344	5.2	86.7	562.808	67.745
LAG_01943	paiA	1989377	1990588	1212	Spermidine/spermine N(1)-acetyltransferase	237	34	28.053	2	99.8	651.153	93.414
LAG_01944	NA	1990600	1990851	252	hypothetical protein	59	5	19.841	6.7	98.8	779.631	66.07
LAG_01945	NA	1991144	1991800	657	hypothetical protein	150	18	27.397	17.7	88.9	760.262	91.231
LAG_01946	NA	1991918	1992484	567	hypothetical protein	59	11	19.4	2.1	91	346.503	64.602
LAG_01947	NA	1992978	1993802	825	hypothetical protein	256	22	26.667	8.8	98.4	1033.293	88.799
LAG_01948	gadC	1993947	1995458	1512	Glutamate/gamma-aminobutyrate antiporter	291	35	23.148	0.9	91.6	640.883	77.082
LAG_01949	gadB	1995479	1996879	1401	Glutamate decarboxylase	402	50	35.689	2.5	99.8	955.488	118.842
LAG_01950	patA_2	1997033	1998196	1164	Putative N-acetyl-LL-diaminopimelate aminotransferase	340	37	31.787	0.7	99.9	972.665	105.849
LAG_01951	lysA	1999001	2000260	1260	Diaminopimelate decarboxylase	363	30	23.81	1.6	99.6	959.342	79.284
LAG_01952	dapA	2000476	2001339	864	4-hydroxy-tetrahydrodipicolinate synthase	267	25	28.935	0.5	96.6	1029.046	96.353
LAG_01953	dapB	2001339	2002049	711	4-hydroxy-tetrahydrodipicolinate reductase	166	11	15.471	4.6	96.5	777.456	51.518
LAG_01954	dapH	2002143	2002841	699	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	331	29	41.488	3.9	96.7	1576.842	138.152
LAG_01955	asd	2003007	2003999	993	Aspartate-semialdehyde dehydrogenase	155	24	24.169	6.7	98.1	519.78	80.482
LAG_01956	yclM	2003996	2005309	1314	Aspartokinase 3	211	27	20.548	5.1	96.7	534.718	68.424
LAG_01957	NA	2005333	2006466	1134	N-acetyldiaminopimelate deacetylase	231	23	20.282	1.8	95.1	678.323	67.539
LAG_01958	NA	2007821	2007991	171	hypothetical protein	92	5	29.24	11.7	79.5	1791.551	97.367
LAG_01959	inlJ_6	2008578	2010521	1944	Internalin-J	597	62	31.893	1.6	99.7	1022.623	106.202
LAG_01960	polC_2	2010875	2015758	4884	DNA polymerase III PolC-type	8	2	0.41	37.8	38.6	5.454	1.364
LAG_01961	NA	2015903	2016277	375	hypothetical protein	26	3	8	1.9	65.1	230.876	26.64
LAG_01962	proS	2016745	2018595	1851	Proline--tRNA ligase	0	0	0			0	0
LAG_01963	rasP	2018622	2019869	1248	Regulator of sigma-W protease RasP	5	1	0.801	46.2	46.2	13.341	2.668
LAG_01964	cdsA	2020046	2020840	795	Phosphatidate cytidylyltransferase	0	0	0			0	0
LAG_01965	uppS	2020837	2021574	738	Isoprenyl transferase	0	0	0			0	0
LAG_01966	NA	2021774	2022109	336	hypothetical protein	29	3	8.929	36.3	48.8	287.406	29.732
LAG_01967	NA	2022184	2022831	648	hypothetical protein	72	9	13.889	7.3	72.2	369.994	46.249
LAG_01968	rlmH	2022828	2023307	480	Ribosomal RNA large subunit methyltransferase H	121	12	25	1	99.4	839.424	83.249
LAG_01969	htrA	2023611	2024828	1218	Serine protease Do-like HtrA	105	13	10.673	4.8	98.4	287.064	35.541
LAG_01970	dgs	2024925	2025923	999	Processive diacylglycerol alpha-glucosyltransferase	0	0	0			0	0
LAG_01971	NA	2025936	2027270	1335	Alpha-monoglucosyldiacylglycerol synthase	19	4	2.996	87.4	99.6	47.393	9.977
LAG_01972	NA	2027321	2027545	225	hypothetical protein	23	3	13.333	56.9	91.1	340.395	44.399
LAG_01973	tmpC_3	2027574	2028623	1050	Membrane lipoprotein TmpC	222	24	22.857	1.4	97.6	704.046	76.113
LAG_01974	yfiC	2028782	2029531	750	tRNA1(Val) (adenine(37)-N6)-methyltransferase	182	23	30.667	2.4	100	808.067	102.118
LAG_01975	glgB	2029616	2031559	1944	1,4-alpha-glucan branching enzyme GlgB	599	47	24.177	0.5	99.9	1026.049	80.508
LAG_01976	tgt	2031690	2032838	1149	Queuine tRNA-ribosyltransferase	204	18	15.666	4	97.1	591.218	52.166
LAG_01977	NA	2032973	2033707	735	hypothetical protein	294	29	39.456	7.9	97.1	1331.979	131.386
LAG_01978	mdtG	2033718	2034896	1179	Multidrug resistance protein MdtG	418	45	38.168	4.5	97.4	1180.592	127.097
LAG_01979	NA	2035187	2035396	210	hypothetical protein	92	11	52.381	1.4	89.5	1458.834	174.426
LAG_01980	polA	2035447	2038062	2616	DNA polymerase I	38	3	1.147	1.1	78.4	48.371	3.819
LAG_01981	NA	2038398	2038470	73	tRNA-Thr	0	0	0			0	0
LAG_01982	NA	2038541	2038612	72	tRNA-Gly	0	0	0			0	0
LAG_01983	NA	2038629	2038704	76	tRNA-Arg	0	0	0			0	0
LAG_01984	NA	2038744	2038819	76	tRNA-Pro	0	0	0			0	0
LAG_01985	NA	2038846	2038921	76	tRNA-Met	0	0	0			0	0
LAG_01986	NA	2038936	2039010	75	tRNA-Met	0	0	0			0	0
LAG_01987	NA	2039016	2039105	90	tRNA-Ser	0	0	0			0	0
LAG_01988	NA	2039112	2039186	75	tRNA-Phe	0	0	0			0	0

LAG_01989	NA	2039189	2039259	71	tRNA-Gly	0	0	0			0	0
LAG_01990	NA	2039298	2039373	76	tRNA-Ile	0	0	0			0	0
LAG_01991	NA	2039411	2039498	88	tRNA-Ser	0	0	0			0	0
LAG_01992	dnaG	2039572	2041458	1887	DNA primase	0	0	0			0	0
LAG_01993	sigA	2041494	2042876	1383	RNA polymerase sigma factor SigA	16	1	0.723	96.5	96.5	38.524	2.408
LAG_01994	clpE	2043095	2045341	2247	ATP-dependent Clp protease ATP-binding subunit ClpE	232	26	11.571	4.9	88.5	343.813	38.531
LAG_01995	NA	2045619	2045984	366	hypothetical protein	206	18	49.18	1.4	89.6	1874.233	163.768
LAG_01996	NA	2046067	2046312	246	hypothetical protein	95	6	24.39	14.2	87.8	1285.955	81.218
LAG_01997	def	2046357	2046983	627	Peptide deformylase	0	0	0			0	0
LAG_01998	rppH	2047088	2047543	456	RNA pyrophosphohydrolase	35	6	13.158	7.9	84.6	255.588	43.815
LAG_01999	uvrB	2047540	2049528	1989	UvrABC system protein B	29	4	2.011	90	98.6	48.551	6.697
LAG_02000	fabZ_2	2049555	2050013	459	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	0	0	0			0	0
LAG_02001	nanE	2050291	2050989	699	Putative N-acetylmannosamine-6-phosphate 2-epimerase	208	23	32.904	0.3	99.1	990.886	109.569
LAG_02002	fabI	2051204	2051956	753	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	0	0	0			0	0
LAG_02003	NA	2052174	2052377	204	hypothetical protein	51	7	34.314	9.3	96.1	832.487	114.263
LAG_02004	NA	2052432	2053655	1224	hypothetical protein	414	48	39.216	2	100	1126.306	130.586
LAG_02005	fnr_2	2053664	2054320	657	Anaerobic regulatory protein	196	26	39.574	2.6	82.3	993.409	131.779
LAG_02006	misCB	2054420	2055412	993	Membrane protein insertase MisCB	36	5	5.035	0.5	99.7	120.723	16.767
LAG_02007	pgcA	2055581	2057293	1713	Phosphoglucomutase	3	1	0.584	99.2	99.2	5.832	1.944
LAG_02008	panT	2057452	2058033	582	Pantothenic acid transporter PanT	0	0	0			0	0
LAG_02009	coaBC_1	2058038	2058589	552	Coenzyme A biosynthesis bifunctional protein CoaBC	0	0	0			0	0
LAG_02010	coaBC_2	2058582	2059280	699	Coenzyme A biosynthesis bifunctional protein CoaBC	0	0	0			0	0
LAG_02011	NA	2059420	2060709	1290	hypothetical protein	278	27	20.93	1.5	98.5	717.617	69.697
LAG_02012	NA	2060759	2060938	180	putative tautomerase.1	39	6	33.333	6.1	78.3	721.489	110.998
LAG_02013	NA	2061254	2062903	1650	hypothetical protein	318	29	17.576	0.1	86.1	641.772	58.526
LAG_02014	NA	2063140	2063213	74	tRNA-Glu	0	0	0			0	0
LAG_02015	NA	2063251	2063323	73	tRNA-Asn	0	0	0			0	0
LAG_02016	NA	2063395	2064339	945	hypothetical protein	188	21	22.222	14.1	95	662.466	73.999
LAG_02017	NA	2064332	2064871	540	hypothetical protein	124	8	14.815	0.6	33.9	764.655	49.333
LAG_02018	glcU_2	2065153	2066049	897	Glucose uptake protein GlcU	429	32	35.674	9.4	98.9	1592.584	118.794
LAG_02019	yhdG_2	2066091	2067479	1389	putative amino acid permease YhdG	525	39	28.078	3.9	98.8	1258.62	93.497
LAG_02020	dacA	2067509	2068795	1287	D-alanyl-D-alanine carboxypeptidase DacA	525	16	12.432	12.7	96.3	1358.37	41.398
LAG_02021	immR_2	2069093	2069713	621	HTH-type transcriptional regulator ImmR	83	8	12.882	17.7	98.6	445.065	42.898
LAG_02022	rpsL	2070026	2070439	414	30S ribosomal protein S12	0	0	0			0	0
LAG_02023	rpsG	2070459	2070926	468	30S ribosomal protein S7	0	0	0			0	0
LAG_02024	NA	2071141	2073081	1941	hypothetical protein	270	23	11.85	2.6	91.6	463.208	39.458
LAG_02025	NA	2073074	2073445	372	hypothetical protein	42	2	5.376	33.3	44.6	375.962	17.903
LAG_02026	fus	2073615	2075705	2091	Elongation factor G	13	1	0.478	97.8	97.8	20.703	1.593
LAG_02027	purR	2075886	2076701	816	Pur operon repressor	199	17	20.833	5	73.3	812.083	69.374
LAG_02028	NA	2076688	2077176	489	hypothetical protein	113	9	18.405	19.2	89.6	769.497	61.287
LAG_02029	spsB	2077195	2077869	675	Signal peptidase IB	0	0	0			0	0
LAG_02030	rnhC	2077880	2078758	879	Ribonuclease HIII	0	0	0			0	0
LAG_02031	rplM	2078939	2079385	447	50S ribosomal protein L13	0	0	0			0	0
LAG_02032	rpsI	2079402	2079794	393	30S ribosomal protein S9	0	0	0			0	0
LAG_02033	NA	2080032	2080703	672	hypothetical protein	219	13	19.345	1.6	57.9	1085.206	64.419
LAG_02034	clsA_2	2080967	2082415	1449	Major cardiolipin synthase ClsA	226	20	13.803	5.4	100	519.371	45.962
LAG_02035	NA	2086083	2086155	73	tRNA-Ala	0	0	0			0	0
LAG_02036	tarK	2087973	2089106	1134	Teichoic acid ribitol-phosphate primase	120	19	16.755	15.2	88.4	352.375	55.793
LAG_02037	NA	2089885	2091282	1398	hypothetical protein	78	7	5.007	29	74	185.791	16.674
LAG_02038	NA	2091290	2092198	909	hypothetical protein	3	1	1.1	3	3	10.99	3.663
LAG_02039	NA	2092260	2092334	75	tRNA-Ala	0	0	0			0	0
LAG_02040	NA	2093206	2093877	672	hypothetical protein	0	0	0			0	0
LAG_02041	NA	2093927	2094400	474	Calcium-transporting ATPase 1	0	0	0			0	0
LAG_02042	NA	2094496	2094693	198	hypothetical protein	0	0	0			0	0

LAG_02043	NA	2094855	2094929	75	tRNA-Val	0	0	0			0	0
LAG_02044	NA	2094931	2095003	73	tRNA-Asp	0	0	0			0	0
LAG_02045	NA	2095042	2095114	73	tRNA-Lys	0	0	0			0	0
LAG_02046	NA	2095161	2095242	82	tRNA-Leu	0	0	0			0	0
LAG_02047	NA	2095254	2095326	73	tRNA-Thr	0	0	0			0	0
LAG_02048	NA	2095397	2095468	72	tRNA-Gly	0	0	0			0	0
LAG_02049	lacG	2095500	2095838	339	6-phospho-beta-galactosidase	0	0	0			0	0
LAG_02050	lacF	2095851	2096162	312	PTS system lactose-specific EIIA component	0	0	0			0	0
LAG_02051	NA	2096296	2097198	903	hypothetical protein	0	0	0			0	0
LAG_02052	NA	2097786	2097935	150	hypothetical protein	0	0	0			0	0
LAG_02053	NA	2098381	2098590	210	hypothetical protein	24	2	9.524	35.2	80	380.565	31.714
LAG_02054	tkt_2	2099060	2099569	510	Transketolase	0	0	0			0	0
LAG_02055	NA	2099727	2099930	204	hypothetical protein	0	0	0			0	0
LAG_02056	sacX	2100379	2101035	657	Negative regulator of SacY activity	0	0	0			0	0
LAG_02057	NA	2101072	2101260	189	hypothetical protein	3	1	5.291	3.7	3.7	52.856	17.619
LAG_02058	NA	2103041	2103244	204	hypothetical protein	11	2	9.804	19.6	49.5	179.556	32.647
LAG_02059	NA	2104140	2104343	204	hypothetical protein	0	0	0			0	0
LAG_02060	NA	2104318	2104977	660	hypothetical protein	0	0	0			0	0
LAG_02061	bglH_6	2104873	2106105	1233	Aryl-phospho-beta-D-glucosidase BglH	0	0	0			0	0
LAG_02062	NA	2106181	2106813	633	hypothetical protein	0	0	0			0	0
LAG_02063	fba_3	2106753	2107316	564	Fructose-bisphosphate aldolase	0	0	0			0	0
LAG_02064	aroA_2	2107277	2107753	477	3-phosphoshikimate 1-carboxyvinyltransferase	0	0	0			0	0