Norwegian University of Life Sciences
Faculty of Veterinary Medicine
Department of Paraclinical Sciences

Philosophiae Doctor (PhD)
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The effect of food chain stressors on *Listeria monocytogenes*

Effekten av stressfaktorer i matkjeden på *Listeria monocytogenes*

Kristin Sæbø Pettersen

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List of abbreviations

ALOA	Agar Listeria according to Ottaviani and Agosti
AMR	Antimicrobial resistance
CFU	Colony Forming Units
DNA	DeoxyriboNucleic Acid
LAB	Lactic Acid Bacteria
L. monocytogenes	*Listeria monocytogenes*
LOV	Light Oxygen Voltage receptor
mRNA	messenger RiboNucleic Acid
PFGE	Pulsed Field Gel Electrophoresis
qRT-PCR	quantitative Real-Time PCR method
RNA	RiboNucleic Acid
RNA seq	RiboNucleic Acid sequencing
ROS	Reactive Oxygen Species
rRNA	ribosomal RiboNucleic Acid
SigB (σ^B)	Sigma B
sigB	Gene coding for SigB
SNPs	Single Nucleotide Polymorphism
WGS	Whole Genome Sequencing

Summary

Listeria monocytogenes is the causative agent of food-borne listeriosis, a disease often transmitted by contaminated Ready-To-Eat (RTE) food. Immunosuppressed individuals, fetuses, and the elderly are at higher risk of developing a lethal form of listeriosis. Despite preventive actions taken against *L. monocytogenes* contamination of food, human listeriosis is still a food safety challenge. *L. monocytogenes* is a robust ubiquitous soil bacterium that is highly resistant to several stressors in the food chain, from farm to the human host. It is therefore difficult to eradicate it from raw food material and food processing environments. However, avoiding contamination and subsequent inhibiting growth of the bacterium in the food are important and highly prioritized preventive measures taken by the food industry. *L. monocytogenes'* ability to persist in the food environment and to cause severe disease makes it a costly foodborne pathogen to control both in the food industry and in the society. This PhD project has explored how *L. monocytogenes* copes with a selected set of stressors present in the food, in the environment and in the human host, focusing on the aim of increasing food safety.

As *L. monocytogenes* is not considered to be a heat resistant bacterium, its presence in heat-treated RTE food products is assumed to be due to recontamination after heat treatment. Subsequently, as the risk for listeriosis increases by the number of *L. monocytogenes* cells consumed, it is important to estimate the growth of *L. monocytogenes* in food products during storage as accurately as possible. *L. monocytogenes* challenge tests were performed with bacteria that were preadapted to the storage conditions of the respective food product, according to the European guidelines for conducting *L. monocytogenes* challenge tests. This approach is, however, likely to overestimate the growth potential of *L. monocytogenes* in foods compared to naturally contaminated food, where the bacteria have to recover from stress for a while before they start to grow. In paper I, we tested an alternative challenge test method where we simulated a contamination route from cleaned and disinfected food contact surfaces, and subsequently measured bacterial growth in two different RTE food products. This method resulted in significant, but contrasting effects on the growth potentials in the two different RTE food products tested. Also, stress exposure prior to inoculation of RTE food products challenged standardization of the inoculum concentration and we therefore concluded not to recommend the alternative challenge test method for estimation of *L. monocytogenes* growth.

Stress exposure in food products may influence the ability of *L. monocytogenes* to tackle subsequent stressors in the digestive system of the human host. NaCl represents a stressor which, at sufficiently high concentrations, reduce bacterial growth in food. High NaCl content is a frequently used food preservative, but for public health reasons the food industry is under pressure to reduce the NaCl content in their products. In paper II a standardized *in vitro* digestion (IVD) method was used to evaluate how reduced NaCl content in foods may influence the survival of *L. monocytogenes* outbreak strains through the human digestive system. Paper II concluded that reduction of the NaCl content from 5 to 0.5 % has the potential to cause significant changes in the bacterial survival fraction through the digestive system and that this effect is strain dependent.

Finally, in paper III, the response of *L. monocytogenes* to stress, imposed by low intensity broad-spectrum visible light exposure, was explored using phenotypical and global transcriptomic analyses. The results revealed that light exposure inhibited bacterial growth and caused major changes in the global gene expression pattern. The effect of light were both time- and temperature-dependent. These results highlight the importance of considering visible light as a significant environmental factor when designing experiments in the laboratory and when developing innovative strategies for inhibiting growth of *L. monocytogenes* as part of food safety management systems.

Sammendrag (summary in Norwegian)

L. monocytogenes er årsaken til matbåren listeriose, en sykdom som ofte er forårsaket av spiseklar mat (Ready-To-Eat, RTE) som er forurenset med *L. monocytogenes*. Individer med nedsatt immunforsvar, fostre og eldre har høyere risiko for å få listeriose med dødelig utfall. Til tross for forebyggende tiltak mot *L. monocytogenes* i mat, er listeriose hos mennesker fortsatt en utfordring for mattryggheten. *L. monocytogenes* er en robust bakterie som finnes nesten overalt og som er svært resistent mot mange stressfaktorer i matkjeden. Den er derfor vanskelig å eliminere fra råvarer og fra matproduskjonsmiljøer. Til tross for dette er det høyt prioritert av matindustrien å iverksette forebyggende tiltak for å redusere forurensning med *L. monocytogenes* og påfølgende vekst av denne bakterien i matproduktene. *L. monocytogenes* evne til å persistere i miljøet og dens evne til å forårsake alvorlig sykdom gjør at den er en kostbar matbåren bakterie for både matindustrien og for samfunnet. Med mål om å styrke mattryggheten har dette PhD prosjektet undersøkt hvordan *L. monocytogenes* håndterer ulike stressfaktorer som finnes i mat, i miljøet og i mennesket som vertsorganisme.

L. monocytogenes er ikke en varmeresistent bakterie og derfor antas det at tilstedeværelse av *L. monocytogenes* i varmebehandlede spiseklare produkter skyldes rekontaminering. Ettersom risikoen for Listeriose øker med økende antall *L. monocytogenes* celler som blir spist, er det viktig å kunne estimere veksten av *L. monocytogenes* under lagring av produktet så nøyaktig som mulig.

I henhold til de Europeiske retningslinjene for å utføre belastningsstudier med *L. monocytogenes* skal næringsmidlene som testes podes (inokuleres) med bakterier som er tilpasset miljøbetingelsene i det respektive matproduktet. Sammenliknet med naturlig forurensede produkter kan denne metoden overestimere bakterienes evne til å vokse i næringsmiddelprodukter ettersom de i utgangspunktet er stresset og trenger en tilpasningsperiode etter forurensningstidspunktet før de er i stand til å begynne å vokse. Dermed utsettes start-tidspunktet for vekst. I artikkel I ble det simulert en forurensningsvei fra vaskede og desinfiserte matkontaktflater til to ulike RTE produkter, noe som resulterte i signifikant endret, men motsatt effekt på vekst i produktene. I tillegg ble standardiseringen av inokulum-konsentrasjonen utfordret av stresseksponeringen av bakteriene før inokulering av RTE produktene. Studien konkluderte derfor med at den alternative belastningsstudie metoden ikke kunne anbefales for å estimere vekst av *L. monocytogenes*.

Stress-eksponering i matprodukter kan påvirke bakteriens evne til å håndtere påfølgende stress i fordøyelseskanalen etter at maten har blitt spist. Vanlig bordsalt (NaCl) representerer en stressfaktor som i tilstrekkelig høye konsentrasjoner kan redusere bakterievekst i mat. Høyt NaCl innhold er en hyppig brukt konserveringsmetode, men pga. helsemessige konsekvenser er matindustrien under press for å redusere saltinnholdet i mat. I artikkel II har vi benyttet en standardisert *in vitro* fordøyelsesmetode (IVD) for å evaluere hvordan redusert NaCl innhold i maten påvirker overlevelsen av *L. monocytogenes* utbruddsstammer i et humant fordøyelses-system. Artikkel II konkluderte med at reduksjon av NaCl fra 5 to 0.5 % kan forårsake signifikante endringer i bakterienes evne til å overleve gjennom fordøyelsessystemet og at denne effekten er stammeavhengig.

I det siste arbeidet har prosjektet undersøkt hvordan stress forårsaket av bredspektret synlig lys med lav intensitet påvirker vekst og global genekspresjon hos *L. monocytogenes.* Resultatene viste store endringer i vekst og genekspresjon og at denne effekten er både tid- og temperatur-avhengig. Disse resultatene aktualiserer synlig lys som en viktig miljøfaktor å ta hensyn til ved design av eksperimenter på laboratoriet og ved utvikling av nye strategier for bedre mattryggheten.

List of papers

Paper I

Sæbø Pettersen K, Aspholm M, Wasteson Y, Haugland Moen L, Skjerdal T. 2020. **The impact of disinfection stressed *Listeria monocytogenes* in challenge testing of foods.** Euroreference 4: 8-21. http://doi.org/10.5281/zenodo.3730766

Paper II

Sæbø Pettersen K, Skjerdal T, Wasteson Y, Lindbäck T, Vegarud G, Comi I, Aspholm M. 2019. **Survival of *Listeria monocytogenes* during *in vitro* gastrointestinal digestion after exposure to 5 and 0.5 % sodium chloride.** Food Microbiology 77: 78-84. https://doi.org/10.1016/j.fm.2018.08.010

Paper III

Sæbø Pettersen K, Sundaram AYM, Skjerdal T, Wasteson Y, Kijewski A, Lindbäck T, Aspholm M. 2019. **Exposure to broad-spectrum visible light causes major transcriptomic changes in *Listeria monocytogenes* EGDe.** Appl Environ Microbiol 85:e01462-19. https://doi .org/10.1128/AEM.01462-19.

Introduction

Listeria monocytogenes

Listeria monocytogenes was first described in 1926 after an outbreak causing disease among rabbits and guinea pigs [1]. The name arises from Joseph Lister (1827-1912, England), latin; monocytum (monocytes – one type of the immune cells) and greek: gennaio (produce) [2]. In the 1980s, the bacterium was recognized as a foodborne pathogen [3]. Today, several ready to eat (RTE) food products are known to be high risk products for transferring *L. monocytogenes* to humans.

L. monocytogenes is a Gram-positive, facultative anaerobic, none spore-forming bacterium. It is a small sized bacterium (0.4 by 1 to 1.5 µm) with 4-6 peritrichiously distributed flagella and is considered motile at 10 - 25 °C [4, 5]. Biochemically, it is characterized by being catalase positive (except for a few strains), oxidase negative and beta-hemolytic on blood agar [6].

The *Listeria* genus consists of twenty species: *L. aquatica, L. booriae, L. cornellensis, L. fleischmannii, L. floridensis, L. grandensis, L. grayi, L. innocua, L. ivanovii, L. marthii, L. monocytogenes, L. newyorkensis, L. riparia, L. rocourtiae, L. seeligeri, L. weihenstephanensis, L. welshimeri*, *L. costaricensis, L. goaensis* and *L. thailandensis* [7-10]. *L. monocytogenes, L. seeligeri, L. marthii, L. ivanovii, L. welshimeri,* and *L. innocua* clearly share some geno-and phenotypic characteristics and are categorized as the *Listeria sensu stricto* clade, while the remaining 11 species are referred to as the *Listeria sensu lato* clade. Within the *Listeria* genus, only *L. monocytogenes* is considered to be a significant human and animal pathogen, causing serious infections in humans and in a variety of other vertebrates, including birds and mammals [11]. However, *L. ivanovii* is also isolated from abortions, stillbirths, and neonatal septicaemias in sheep and cattle [4], and occasional human infections have been reported due to *L. ivanovii* and *L. seeligeri* [11]. Even though individual studies have made statistical indications of different *Listeria sensu stricto* species belonging to different environmental niches [12], it is not generally accepted that a clear statistical link of strain-dependent niche specialization exists [10]. However, new insight into potential niche-specialization is likely to come after increasing applications and implementation of whole genome sequencing (WGS) technology in outbreak investigations and surveillance activities.

Based on somatic and flagellar antigens, *L. monocytogenes* is categorized into 13 serotypes [6]. Serotyping by antigen-antibody agglutination is a time-consuming method, and the objectivity when interpreting the serotype is challenging. In 2005, the serotyping was therefore replaced by 5 genoserogroups determined by a more rapid method with higher objectivity; the PCR method.

This PCR method defines the genoserogroups as IIa (serotype 1/2a and 3a), IIb (serotype 1/2b and 3b), IIc (serotype 1/2c and 3c), IVb (serotype 4b, 4d and 4e) and L (other serotypes) [6]. Additionally, evolutionary aspects categorize *L. monocytogenes* serotypes in three linages according to their genotype and the presence of certain genes [13]. Among the serotypes, 1/2a, 1/2b and 4b account for more than 90 % of human and animal disease cases [4, 14-16]. In humans, serotype 4b is the most frequent clinical isolate in sporadic and outbreak cases, followed by 1/2a and 1/2b [17]. A meta-analysis of 12 previous studies concluded that 4b, 1/2a, and 1/2b were the most prevalent serotypes found in food and human samples which is in line with the general international trends of *L. monocytogenes* serotype distribution [18]. However, 1/2a, 1/2b and 1/2c are most frequently isolated from food, thereby suggesting that the pathogenic potential varies among serotypes as 4b is frequently isolated from human clinical cases [4]. In accordance with this assumption, mouse model studies suggested 4b to be more pathogenic and to have a distinct ability to replicate in monocytes/macrophages compared to serotype 1/2b and 3b [17, 19].

Disease is assumed to occur in a host-pathogen-environment interplay (Figure 1). The contribution of these three aspects are dynamic, complex and challenging to predict. Even though risk factors for listeriosis are defined, the complexity between and within each of these aspects challenges prediction of disease as they all depend upon each other. On the host side, healthy persons with normal immune status can tolerate high doses of *L. monocytogenes,* while immunosuppressed individuals, the elderly and fetuses may achieve invasive listeriosis from 10^2 -10^4 Colony Forming Units (CFU)/g [20]. On the pathogen side, different *L. monocytogenes* strains may have different virulence potential. Antimicrobial resistance (AMR) has been reported in *L. monocytogenes*, and different strains may have different susceptibility levels to antibiotics [21]. Finally, environmental conditions such as temperature, food product characteristics, distribution chains and storage time, may also affect the risk for human listeriosis. All environmental conditions may to a certain extent cause bacterial stress, affecting the ability of *L. monocytogenes* to grow and survive.

Closing the knowledge gaps on how stressors affect survival and the virulence potential of *L. monocytogenes* throughout the food chain, from farm to the human host, is important for optimizing food safety control. The work in this thesis highlights some of the stressors *L. monocytogenes* experiences in the environment, including its natural habitat, food plant facilities, food products and in the human host.

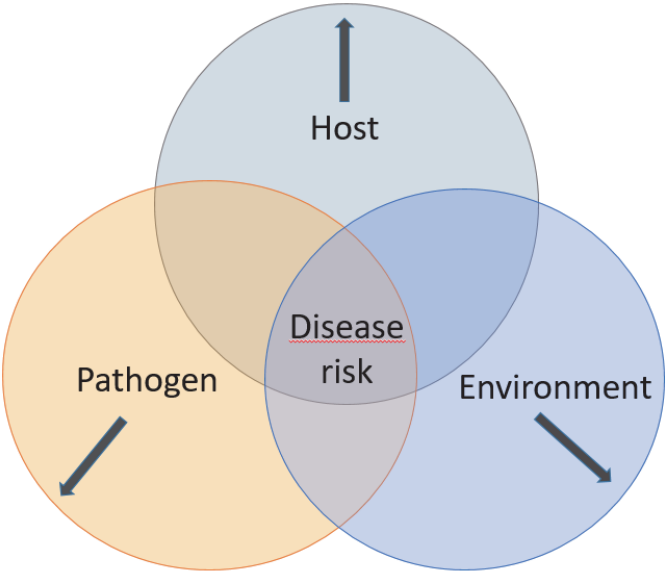


Figure 1. Illustration of the host-pathogen-environment triangle. Preventive actions for disease are illustrated by arrows pulling the circles apart to reduce the overlap illustrating disease risk. Illustrated by K. S. Pettersen, 2020.

Human listeriosis

Ethiology

In the 1970s, *L. monocytogenes* was recognized as a human pathogen. Today, the number of listeriosis cases per year is relatively low compared to infections caused by other foodborne pathogens [20]. Given the low reported incidence of listeriosis in a population, despite the ubiquitous nature and consequently frequent exposure to *L. monocytogenes*, dose-response models assume illnesses occur after exposure to high doses of this pathogen [22]. The European Food Safety Authority (EFSA) recently reported that the probability of a single CFU to cause illness may range 100 million times depending on variability in host susceptibility and the virulence of the infecting *L. monocytogenes* strain [23]. This suggests that also the consumer health status is important to consider in addition to the level and virulence of *L. monocytogenes* in the ingested food [23]. Both the invasive and the non-invasive form of listeriosis may occur in the general population (Figure 2). The invasive form of listeriosis is diagnosed by isolating *L. monocytogenes* from blood or cerebrospinal fluid, which are normally sterile, while the gastrointestinal and non-invasive form is diagnosed based on isolation of *L. monocytogenes* from feces. However, about 5 % of the human population is estimated to be healthy fecal carriers of *L. monocytogenes* [24, 25].

Healthy persons with normal immune status can tolerate high doses of *L. monocytogenes* and most likely only experience mild to severe gastro-enteritis. In contrast, if a pregnant woman is infected, transplacental infection usually proceed to the neonatal after a few days, while the mother does not necessarily experience any symptoms of disease. Fetal *L. monocytogenes* infections, are usually severe. The bacterium can cause spontaneous abortion, death in utero and premature birth. Generally, the lethality of invasive listeriosis is often high and immediate treatment with antibiotics is of critical importance to increase the survival rate. *L. monocytogenes* strains are usually sensitive to antibiotics, but some strains are reported to be resistant against commonly used antibiotics such as penicillin, ampicillin and gentamicin [21, 26]. In addition, *L. monocytogenes´* intracellular behavior and its ability to cross the blood-brain and blood-placental barriers may prevent antibiotics from reaching the infection site. The intracellular cell-to-cell spread of the bacterium also challenges the effect of the humoral immune response and eradication of the bacterium is, therefore highly dependent on the cellular immune response – the monocytes. A patient with listeriosis will often have an increased level of monocytes in the blood, called monocytosis. The pathophysiology of listeriosis is illustrated in Figure 2.

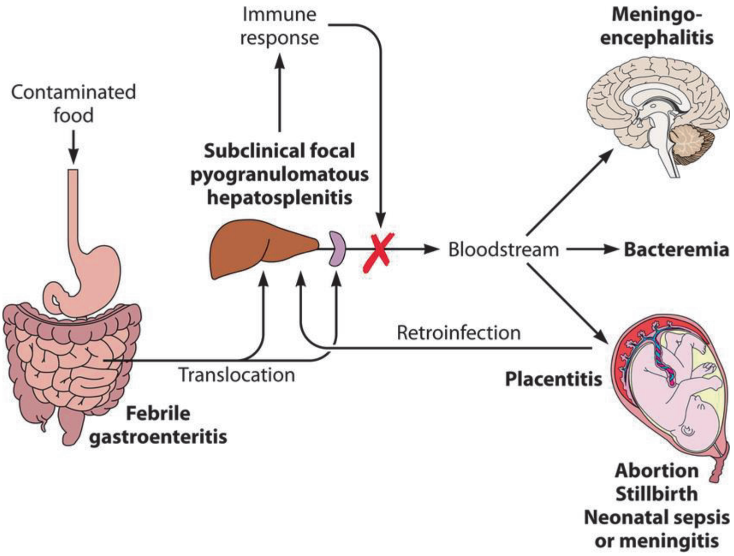


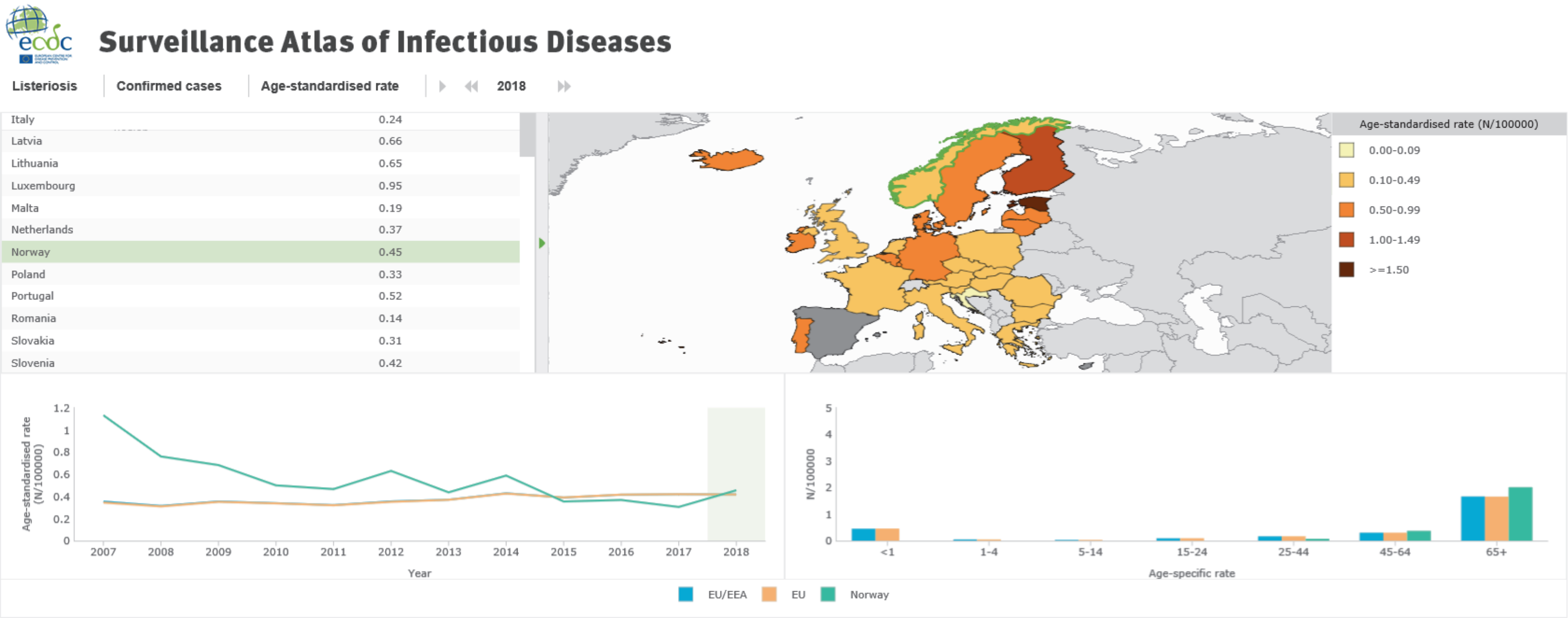
Figure 2. Pathophysiology of food-borne listeriosis [4, 27]. After passing through the oral, gastric and intestinal phase, *L. monocytogenes* crosses the intestinal epithelial barrier. The bacteria then translocate to the mesenteric lymph nodes before reaching the liver and spleen. Establishment of infectious pyogranulomatous foci (hepatosplenitis) will usually be cleared in persons without any predisposing conditions. Contrastingly, in persons within the risk-group, the T-cell mediated response is more likely to

fail clearing the hepatosplenitis and *L. monocytogenes* is more likely to be released into the blood stream (bacteremia). When released into the bloodstream, *L. monocytogenes* may pass the blood-brain or placental barriers and cause febrile bacteremia, infection of the brain and infection of the fetus, respectively. The text is reformulated in accordance with the reference [27] and with permission to reuse the figure, Copyright © 2017, American Society for Microbiology.

Epidemiology

Internationally

Among 31 pathogens listed in USA, the leading cause of death were non-typhoidal *Salmonella* spp. (28 %), *T. gondii* (24 %), *L. monocytogenes* (19 %) and norovirus (11 %), confirming the relatively high case mortality rate of *L. monocytogenes* [28]. The European Centre for Disease Control (ECDC) reported 2575 listeriosis cases in the EU/EES in 2018, resulting in an age-standardised incidence rate of 0.42/100 000 as shown in Figure 3 [29].



Italy	0.24
Latvia	0.66
Lithuania	0.65
Luxembourg	0.95
Malta	0.19
Netherlands	0.37
Norway	0.45
Poland	0.33
Portugal	0.52
Romania	0.14
Slovakia	0.31
Slovenia	0.42

Figure 3. Surveillance Atlas of Infectious Diseases from ECDC using data from 2018. The results must be interpreted carefully as the national surveillance systems differ between countries. Notification of listeriosis in humans is mandatory in most EU Member States, including Norway and Iceland, but is voluntary in Belgium, Luxembourg and the United Kingdom. Finally, the population coverage might differ between countries and the countries may also provide different types of data, ex case-based versus aggregate data. Copyright CDC with permission. The material is freely available on CDC webpages https://atlas.ecdc.europa.eu/public/index.aspx. The figure represent no endorsement for the conclusions in this thesis.

Listeriosis has the highest case fatality rate among all foodborne zoonotic diseases surveilled in the EU [30], and is therefore considered one of the most severe foodborne diseases. Despite improved control measurements since the 1990s, which have greatly reduced the prevalence of *L. monocytogenes* in many food products [22, 31], there is an increasing trend of invasive listeriosis cases reported within the EU. This could, at least partly, be explained by the fact that an increasing fraction of the European population is included in the high-risk group for listeriosis (children, elderly and immune-compromised persons). There is also an increasing trend of consuming RTE food, which is often the source of food borne listeriosis [32]. Since stool cultures for detection of *L. monocytogenes* are not taken routinely, *L. monocytogenes* may be a more common cause of febrile gastroenteritis than is currently recognized [33]. Grif et al, 2003 analysed faeces samples from three volunteers over a one-year period and found *L. monocytogenes* in 3.5 % of the samples. Based on this finding, they suggested that each person in the study was exposed to *L. monocytogenes* between 5 and 9 times per year [25].

Global trends of listeriosis outbreaks, sporadic cases and food recalls are changing [34]. Today's international trade and global movement of food products and ingredients, in combination with *L. monocytogenes´* ability to persist and multiply at hardy conditions, facilitate the spread of contaminated food across borders [34]. The modern large scale, sometimes highly complex, food industry and food trade systems increase the risk of massive recalls of contaminated food. In worst case scenarios, large batches of contaminated food are widespread and consumed. A South African outbreak caused by a contaminated meat product called "polony" lasting from 2017-2018, included 443 confirmed clinical cases and is considered as the largest listeriosis outbreak so far [35]. The size of this outbreak highlights the ability of food-borne pathogens to spread widely in the human population through the food market [34, 36]. In 2011, contaminated whole cantaloupe melons, all which originated from a single farm in the United States, caused a large outbreak. The outbreak included 147 cases and 33 patients died, resulting in the highest death rate in a foodborne outbreak in USA in more than 80 years [34, 37, 38].

In general, *L. monocytogenes* is assumed to cause sporadic cases of illness rather than large outbreaks. However, new highly discriminatory typing methods such as WGS reveals outbreaks which previously were considered as separate sporadic cases. Genomic methods has contributed to an epidemiological breakthrough in the *L. monocytogenes* outbreak investigation. Also, establishment of databases across country borders facilitate information sharing and increases the chance of detecting multinational outbreaks. Among 123 events reported in the ProMed database from 1996 to 2018, 17 % (21 of 123) outbreaks involved multiple countries. There is an increasing number of listeriosis outbreaks involving several countries; 17 outbreaks in the period

2008 – 2018 were multinational, compared to only 4 in the period 1996 to 2007 [34]. Development of both available databases and new methods for strain characterization are significant contributors for detecting national and international outbreaks of *L. monocytogenes*. Both these factors may be a reason for the increasing number of multinational structure outbreaks reported. Detecting strain-relatedness is highly relevant for track of sources and cluster analysis in foodborne outbreak investigations. Thus, the relatedness between two different strains and its certainty, is strongly dependent on the discriminatory level of the method applied. Today, a potentially powerful discriminatory method is represented by WGS. However, without a bacterial isolate, high discriminatory methods such as WGS cannot be applied and detection of the potential biological link fails. Detection of a biological link between the food source and the patients being ill from a foodborne disease is highly valued in foodborne outbreak investigations. Under optimal circumstances, both the biological and epidemiological link in the foodborne outbreak is detected.

In Norway

In Norway, the age-standardised incidence rate was 0.45/100 000 in 2018. This rate was thereby slightly above the European average of 0.42/100 000 [29]. Listeriosis cases in Norway are mainly sporadic, but outbreaks do occur. As mentioned, both cases are more easily detected after implementation of WGS: (1) In the period 2018-2019, 13 people got ill after consuming “rakfisk” (fermented fish product), (2) in 2013, 3 people got ill also after consuming “rakfisk”, (3) in 2007, 19 people got ill and 5 of them died, after consuming of organically produced camembert cheese from a small scale producer, (4) in 2005, 3 people got ill due to a contaminated slicer and (5) in 1992, eight people got ill after consuming heat treated RTE meat. In total, 17-30 listeriosis cases have been reported annually in Norway under the period 2011-2018 [2]. Among these, 15-27 cases are among individuals above 50 years of age. The number of registered listeriosis cases during pregnancy in Norway has been 0-2 cases per year (MSIS, a national reporting system for infectious human disease, 2011-2018). However, as abortion in early stage of pregnancy is often characterized by diffuse symptoms and there is often a lack of sampling, the number of cases during pregnancy might be higher.

More than 99% of human listeriosis cases results from consumption of *L. monocytogenes* contaminated food, particularly RTE food [26]. However, the long incubation time of up to three months makes the linkage between the patient strain and the food product responsible for the outbreak or sporadic case, difficult to find. When an outbreak occurs, the responsible food product is often already consumed or discarded, and it may be difficult for the patients to remember what they had eaten after so long time. This makes microbial and epidemiological investigations very challenging.

Socioeconomic impact

Foodborne illnesses affect the population at large by increasing healthcare costs, decreasing the quality and shorten the lifespan for sick individuals and by having an impact on the food industry. The invasive form of listeriosis, the subsequent severe clinical symptoms and the 20-30 % mortality rate makes *L. monocytogenes* a very costly foodborne pathogen for the society [39-41]. A cost-benefit analysis of the burden of listeriosis compared to the costs spent on preventive strategies estimated the annual cost of *L. monocytogenes* in the USA to be between US$ 2.3 and 22 billion, and the annual benefit of *Listeria* food safety measures to be between $0.01 and 2.4 billion [42].

An English study from 2001 to 2007 reported an increased risk for listeriosis in socioeconomically deprived areas compared to the more affluent ones [43]. This study also revealed increased likelihood for developing listeriosis for individuals purchasing food from small local food stores and convenience stores [43]. It also highlighted that increased life expectancy and rising food prices may cause food poverty (the inability to afford or have access to a healthy diet) to become an increasingly important driver for foodborne disease in the future [43].

L. monocytogenes in the food chain

The combination of *L. monocytogenes´* ubiquitous nature, its ability to adapt to a diverse set of stressors, survive under harsh conditions, and to grow at low temperatures are the main features making this pathogen a food safety concern along the whole food production chain (Figure 4) [44, 45].

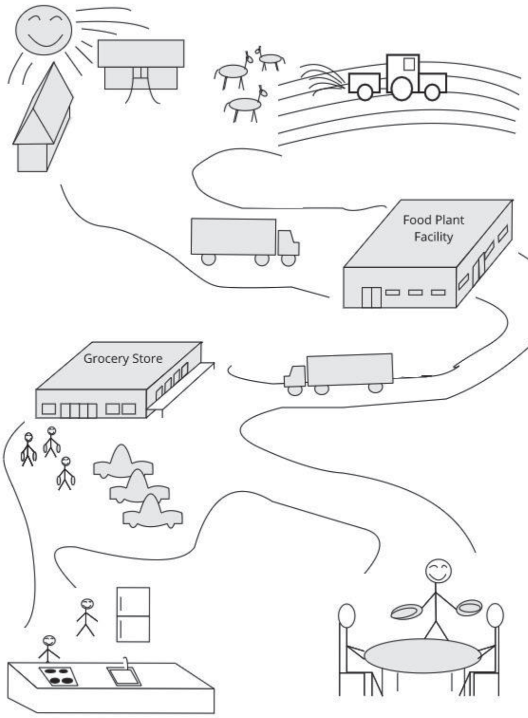


Figure 4. Illustration of the food production chain from farm to human host. Illustrated by K. S. Pettersen, 2020.

The first reported human foodborne outbreak of listeriosis was caused by contaminated coleslaw [3]. The coleslaw had been produced from cabbage harvested from fields fertilized with untreated sheep manure at a farm with a history of ovine listeriosis [3, 46]. *L. monocytogenes* is widely distributed in nature and its natural habitat as a saprophyte is thought to be decomposing plant matter. Listeriosis is also a well-known disease in food producing animals, especially in ruminants, and herd outbreaks are often associated with consumption of poor-quality silage contaminated with *L. monocytogenes* [4]. However, ruminants may also be healthy carriers of *L. monocytogenes* and even though *L. monocytogenes* survive very well as a saprophyte outside a mammalian host, farm animals may contribute to amplification and dispersal of *L. monocytogenes* in the rural environment via a continuous faecal-oral enrichment cycle [46]. Wild animals may also play a role for the life-cycle of *L. monocytogenes* in nature. In an ongoing project at the Norwegian Veterinary Institute, *L. monocytogenes* was isolated from faeces originating from clinically healthy deer in Norway (Taran Skjerdal, personal communication).

L. monocytogenes is able to colonize abiotic surfaces and may persist in food processing facilities for years [47]. Such persistent strains increase the risk for contamination of food products [47]. *L. monocytogenes* has the potential to grow and reach high concentrations in a wide spectrum of food products under different conditions such as anaerobic atmospheres, at high salt concentrations and in the presence of several traditionally used food preservatives [6, 48-50]. The diversity of food products and categories reported to be contaminated with *L. monocytogenes* is high [51]. Refrigerated RTE food products with a long shelf life, and in which *L. monocytogenes* is able to grow, are considered as high-risk products. Even though food products are heat treated along the production line, further industrial processing may pose a risk for re-contamination from food plant facilities or from additional ingredients. Also un-processed food products of animal or plant origin may pose a risk for listeriosis [46].

Despite the large variety of potential food vehicles for transmission of *L. monocytogenes*, there are some general factors defining a risk product; (1) high frequency of *L. monocytogenes* contamination in the specific food product, and/or (2) rapid growth of *L. monocytogenes* in the food product, and/or (3) long storage at refrigeration temperature and/or (4) often eaten by people within the high-risk group. On the other hand, heat treatment of food products, immediately before consumption, will significantly reduce the risk of foodborne listeriosis. A review of ProMed Reports from 1996 -2008 assembled a list of novel food products causing foodborne outbreaks or precautionary recalls due to *L. monocytogenes* contamination [51]. This list was long and included products such as fresh/frozen/ sliced fruit and vegetables, different sprouts, ice cream and caramel apples. The latter product was an excellent example of how complexity of the whole product must be considered when estimating the risk for food-borne disease. As the “toothpicker” penetrated the apple, mixing up the caramel with the apple juice, a new niche for growth of *L. monocytogenes* was provided. Therefore, sub-niches for growth must be considered when categorizing risk products based on general growth conditions (Table 1).

Parameter	**Lower growth limit**	**Fastest growth**	**Upper growth limit**
Temperature (°C)	-1.5	30 - 37	45
pH	4.2 - 4.3	7.0	9.4 - 9.5
A_w	0.93 (0.90 with glycerol)	0.99	> 0.99
Percent sodium chloride in water phase	< 0.5	0.7	12 – 16
Atmosphere	Facultative anaerobic (Able to grow both with and without oxygen)		

Table 1. Growth data based on research carried out primarily in lab media under otherwise optimal growth conditions. Modified by K. S. Pettersen, 2020, from table in "EURL Lm TECHNICAL GUIDANCE DOCUMENT for conducting shelf-life studies on *Listeria monocytogenes* in ready-to-eat foods, Version 3 – 6 June 2014" by ANSES [52]. The ranges may vary depending on the strain and the food matrix [52].

Legislation and growth estimates in food

Underestimation of the concentration of *L. monocytogenes* in a specific food product may lead to unacceptably high risk for the consumers while overestimation of growth may lead to unnecessary food waste. Therefore, growth estimation requirements are defined by international regulations. Estimation of growth is only needed if *L. monocytogenes* is able to grow in a specific food product, in accordance with data given in Table 1. If growth is defined as likely, it is essential to estimate the growth rate in order to predict the *L. monocytogenes* concentration by the time of consumption. Different hurdles are frequently used, separately or in combination, and at different concentrations to lower the growth rate and thereby reduce the *L. monocytogenes* concentration during the products' shelf life. Examples of such hurdles are: low pH, organic acids, nitrite, low water activity, background bacterial microbiota, modified atmosphere and cold temperature [53, 54]. These variables are therefore included in predictive models for estimating *L. monocytogenes* concentrations in food products. Predictive models may be beneficial tools in many contexts. However, the models do not include all variables. Thorough analytical characterization of the food product must be performed to generate good quality predictions. Thus, the use of models may be very costly. Challenge or durability studies may therefore be preferred alternatives (Figure 5). EU has approved all three approaches for *L. monocytogenes* growth estimations, and the method chosen is often dependent on the competence available, the product complexity, the economy and which type of samples that are available.

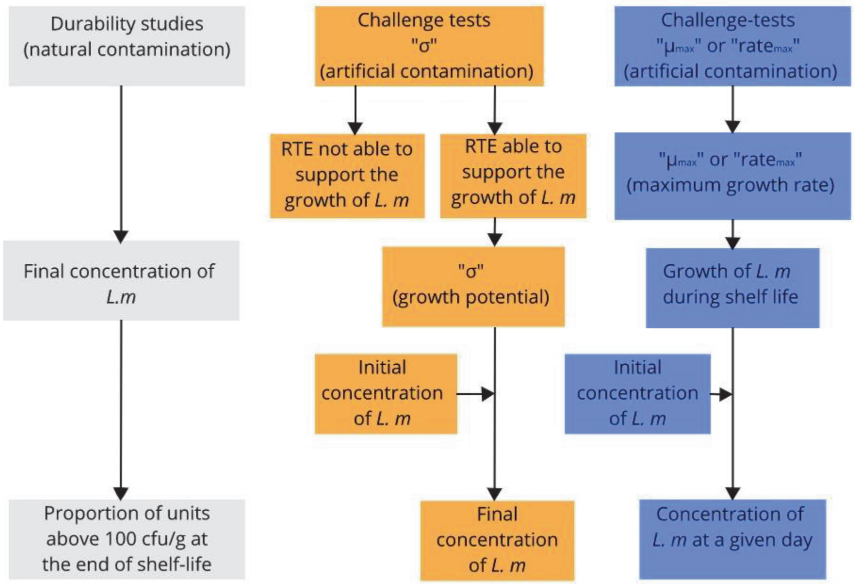


Figure 5. Microbiological procedures for determining the growth and growth rate of *L. monocytogenes* using challenge tests and durability studies. Modified by K. S. Pettersen, 2020, from Figure 1 in "EURL Lm TECHNICAL GUIDANCE DOCUMENT for conducting shelf-life studies on *Listeria monocytogenes* in ready-to-eat foods, Version 3 – 6 June 2014" by ANSES [52].

According to the European Food Law, the mandatory sampling and analysis regimes are different for food products that support growth of *L. monocytogenes* than for products that do not; for RTE foods able to support growth, and which are not intended for high risk groups such as infants or for medical purposes, two criteria are laid down: (1) a qualitative criterion requiring absence in 25 g before the food has left the immediate control of the food business operator (FBO) or (2) a quantitative criterion defining an upper limit of 100 CFU/g during the products' shelf-life) [55, 56]. The latter criterion is only valid if the FBO demonstrates, to the satisfaction of the competent authority, that the product will not exceed the limit of 100 CFU/g throughout the product' shelf-life. Food intended for vulnerable groups is often produced according to a zero-tolerance for *L. monocytogenes* in the products when entering the food market. It is the maximum limit of a 100 CFU/g food during shelf life, which is the background for performing challenge tests, durability studies and using predictive models for *L. monocytogenes* growth. Regardless of the method used, data needed to perform satisfying estimations of bacterial growth in food products, causes significant costs for the food industry.

A bacterial growth curve can be categorized into three growth phases; (1) the lag phase where the bacteria prepare for growth, (2) the exponential phase where the bacteria demonstrate maximum growth rate (µmax) and finally, (3) the stationary phase where the bacterial population reaches maximum concentration and the growth curve flattens out due to limited access to nutrients, accumulation of inhibitory metabolites, and lack of space. In the stationary phase, the replication rate is balanced out by the rate of death. After the stationary phase, there is a death or decline phase which ends by the survival phase. All three methods for *L. monocytogenes* growth estimation, tries to estimate the growth curve and the *L. monocytogenes* concentration at the likely time of food consumption.

In challenge tests, *L. monocytogenes* is added to food products experimentally before storage under realistic conditions. The European guidelines for conducting *L. monocytogenes* challenge testing were primarily developed to assess whether a specific food product supports growth of this bacterium or not [52]. However, several food production companies have used challenge studies to estimate the storage time until a 2 Log CFU/g increase in the concentration of *L. monocytogenes* is reached under reasonably foreseeable conditions. This period is often referred to as the "*Listeria* shelf life" [56, 57]. Even though the regulations clearly state which food safety criteria to fulfill, the applied approaches and evaluations may be challenging in practice. Therefore, needs for practical guidance resulted in an EU guideline for conducting *L. monocytogenes* challenge test studies. The first version was finalized in 2008 [52, 58], revised in 2014 [52], and an amendment was added in 2019 [59]. In the current PhD project, the 2014 version was used.

According to the European guidelines for challenge testing, the *L. monocytogenes* strains must be adapted to cold temperature prior to inoculation of the food in order to shorten the lag phase and to obtain maximum growth potential during the shelf life of the food product [52]. Consequently, these guidelines do not account for other stressors which may influence the physiological state of the inoculated strains. One such group of stressors is cleaning agents and chemical disinfectants, in particular alkali treatments, which are commonly used for disinfection of hard surfaces in food production facilities [60, 61]. Exposure to environmental stressors prior to food contamination may thus cause a discrepancy between naturally contaminated food samples and the traditionally performed challenge tests, which in turn may lead to non-optimal assessments and decisions. Álvarez-Ordóñez et al. (2015) points out in a review that comparing the European guidelines for challenge testing with any alternative methodology for growth estimations will be valuable [57]. In line with this idea, the current PhD project has explored an alternative method for performing challenge testing by simulating a contamination route including chloro-alkaline stress from a disinfectant frequently used in the food industry.

Influence of stressors on *L. monocytogenes*

Although remaining relatively small and simple in structure throughout their evolutionary history, prokaryotes exhibit an incredible diversity regarding their metabolism and physiology compared to eukaryotes. This is reflected by the wide range of habitats where prokaryotes can live [62]. Also, in contrast to multicellular organisms, individual cells of unicellular organisms are continuously exposed to a changing environment [62]. Sensing environmental changes followed by stress responses enables bacteria to survive and adapt to adverse and fluctuating conditions in their surroundings [62, 63] or to frame it “what does not kill them, can make them stronger” [64].

Even though *L. monocytogenes* is a well-studied organism, there are still unanswered questions related to how it senses stress, its physiology and pathogenesis [20, 65]. To optimize risk assessment and reduce human food-borne listeriosis, it is important to understand how a broader specter of environmental factors, both in the food chain and in the human host, influence growth and/or the virulence of *L. monocytogenes*. Optimization of risk assessment also has the potential to reduce food waste in the society and economic loss for the food industry.

In the food chain

To cause disease, foodborne pathogens must be able to handle a diverse set of environments present along the food production chain and overcome defence systems in the human host. Consequently, many foodborne pathogens can rapidly adapt to and survive in a large spectrum of harsh environments. This adaptability makes them difficult to eradicate from food production chains, although both tailor-made and targeted food safety strategies are being applied.

L. monocytogenes has an arsenal of regulatory factors facilitating its ubiquitous and pathogenic lifestyle [66]. Temperature, osmotic, oxidative and acidic stress are examples of stressors that are of importance both in its natural environment, in the food chain and when *L. monocytogenes* enters the mammalian host. As an example, - in the natural environment, osmotic stress arises due to water evaporation, while in the food or in the host, osmotic molecules such as NaCl will bind water causing the same type of stress.

L. monocytogenes is able to withstand a wide-range of stressors encountered in food and food processing conditions such as high/low temperatures, acidity, osmotic stress, bacteriocins, high hydrostatic pressure, UV light, pulsed electric fields and oxidative stress [67]. The review by Bucur et al further elaborate on these stressors: It is able to replicate between -0.4 and 45 °C. Mild heat treatment below 100 °C have the potential to increase food safety, but may also decrease the nutritional value and sensory properties of the food products. In milk, *L. monocytogenes* is capable of surviving heat treatment at 71.7 °C for 15 s, which is the short time treatment imposed for reducing microbial contamination by U.S Food and Drug Administration. However, the heat resistance is strain dependent, food matrix dependent, and may lead to bacterial stress hardening. Stress hardening refers to an increased ability of the pathogen to survive otherwise lethal conditions [68]. This is a phenomenon were the bacterium experiences one type of stress and become more resistant to subsequent stressors. Such stressors can be exemplified by NaCl or pretreatment with sublethal heat. Its psycrotolerance (tolerance to cold exposure) is the reason why we find this bacterium is able to survive and grow in refrigerated stored food products. *L. monocytogenes* tolerates cold by expression of cold shock proteins, uptake of cryoprotective compounds and by altering the fatty acid composition and structure of the membrane. Acidification of food products for preservation is widely applied by fermentation using nonpathogenic bacterial cultures. Beneficial bacteria which ferment food, produce weak acids, such as lactate and acetate. These organic acids preserve food by lowering the surrounding pH. However, *L. monocytogenes* displays adaptive acid tolerance and is capable of increasing its acid resistance if pre-exposed to acidic conditions, in both planktonic and surface attached culture. Bacteriocins are mostly active against Gram positive bacteria. They consist of antimicrobial peptides and are considered as safe and natural food additives for a wide range of foods. Bacteriocins are specific towards the targeted organism, and only nisin is approved as an *additive* in food. The inhibitory effect of bacteriocins on bacterial growth results from disturbance of peptidoglycan synthesis and by forming pores in the bacterial cell membrane. However, natural resistance against bacteriocins in *L. monocytogenes* is estimated to be between 1-8 % depending on the type of bacteriocin and *L. monocytogenes* strain. High hydrostatic pressure is used to kill both spoilage bacteria and food borne pathogens. The effect of hydrostatic pressure on *L. monocytogenes* is both strain and food matrix dependent. The growth phase also seems to impact the resistance towards hydrostatic pressure and the bacteria in the long-time survival phase seem to exhibit the strongest resistance.

When bacteria experience stress, they express sigma (σ) factor(s) that facilitate expression of genes involved in protection against the respective type of stress experienced [64, 69]. A σ factor is a bacterial transcription initiation factor that is needed for binding of the RNA polymerase (RNAP) to promoter sequences. There are many different σ factors; some are involved in transcription of housekeeping genes while others are involved in transcription of genes whose products are needed under certain environmental conditions and in response to stress [64]. Some σ factors can make the RNAP recognise hundreds of genes and thereby regulate very complex cellular responses [64].

L. monocytogenes has up to four alternative σ factors (σ^B, σ^C, σ^H, and σ^L) in addition to the housekeeping σ^A [70]. Among the alternative σ factors, σ^B has the largest regulon including more than 200 genes [70]. σ^B is the most studied stressosome regulator in *L. monocytogenes* and it has been shown to play a key role in responses against acidic-, osmotic-, arsenate-, oxidative-, and cold stress [70-72]. σ^B regulates transcription of several virulence and stress-associated genes including those that facilitate bacterial survival through the gastrointestinal system [73]. It is, therefore, of particular interest to explore the role of σ^B in the pathogenic lifestyle of *L. monocytogenes* and *sigB* gene deletion mutants are often included in laboratory experiments [64, 68, 74].

Persistent *L. monocytogenes* strains in food production environments confer a constant risk for contamination of the food products. Such strains are assumed to be continuously exposed to cleaning and disinfectant chemicals which reduce their physiological state. Their physiological state correlates with the length of the lag phase. If such strains contaminates food, bacterial cells in good physiological condition may start to grow at an earlier time point than those being in a physiologically reduced state, thereby affecting the maximum concentration of *L. monocytogenes* in the product during shelf life. Sub-lethal stress may also alter the ability of *L. monocytogenes* to withstand exposure to subsequent stressors it encounters in food products and in the human host [60, 75-78]. Sublethal alkaline treatment may increase the *L. monocytogenes* resistance against the lethal effect of heat [78], and thereby pose an increased risk for the presence of this bacterium in food products. However, free chlorine may, on the other hand, sensitize *L. monocytogenes* to heat [78]. Also, the alkaline stress-response of *L. monocytogenes* may be transient, as shown for *E.coli* [79, 80].

RTE foods can impose several different environmental stresses upon *L. monocytogenes*, such as anaerobic stress, osmotic stress (NaCl or sugars), organic acid stress (fermentation), acidic, alkali, heat and cold stress. Even though the food industry is under great pressure to reduce the NaCl content in RTE foods [81], NaCl is still a frequently used food preservative. Several studies have explored the inhibitory effect of NaCl on the growth of *L. monocytogenes* in food and found that it tolerates high levels of salt stress [49, 50, 82]. When the osmotic balance between the cytoplasm and the extracellular environment is challenged, the bacteria experience osmotic stress. In food, osmotic stress is often due to increased amount of sugar and/or salts, which determine the water activity. *L. monocytogenes* compensates mainly by osmolyte transport across the cytoplasmic membrane when exposed to hyper osmotic conditions, and potentially by mechanosensitive channels when exposed to hypo-osmotic conditions [67]. Some of the genes responsible for such osmotolerance are under regulation of σ^B, and a *sigB* mutant strain was therefore included when analyzing for the effect of reduced NaCl on *L. monocytogenes* survival through a digestion model in Paper II.

Certain conditions seem to preadapt the bacteria to the harsh environment in the digestive system and enhance their survival trough the upper gastrointestinal tract. Changes in oxygen availability influence the response to stressors encountered within the host, including changes in pH, osmolarity, and bile [68]. Pre-exposure to 0.3 M NaCl has increased bacterial survival 1000-times compared to naive cells, when subsequently exposed to lethal concentrations of bile [83]. Both intrinsic and extrinsic factors such as glutamate [84], carnitine, salt, acid [85], and hypoxia [86, 87] may lead to stress hardening. Exposure to such stressors may thus influence the number of *L. monocytogenes* cells surviving the passage through the acidic environment in the human stomach, and their subsequent ability to attach, invade and cause disease.

Stressful conditions present in the food production environment may also influence resistance of *L. monocytogenes* to clinically important antimicrobials [88]. Antimicrobial resistance (AMR) has been reported in isolates from food producing animals, food processing environments and food products [21, 26]. According to a systematic review of papers published in Persian and English journals until the 20th May 2019 and indexed in the Scientific Information Database, PubMed, Scopus and Google Scholar databases, *L. monocytogenes* resistance to commonly used antibiotics i.e. penicillin, ampicillin and gentamicin was 34.5 %, 26.4 %, 8.9 % in isolates from foods and food processing environments, 47.1 %, 29.5 %, 9.2 % in isolates from animal specimens and 56.8 %, 29.5%, 32.4% in human strains, respectively [21]. Allen and colleagues further suggested that food chain factors may influence *L. monocytogenes* AMR through (1) horizontal exchange of AMR genes, (2) induction of AMR-related stress responses through sub-lethal exposure to factors controlling microbial growth in food, and (3) recurring exposure to disinfectants in the food production environment [26].

The damaging effect of ultraviolet (UV) light on bacteria is well documented and has been applied for preventing and reducing bacterial contamination in many settings, including food safety. Pulsed field or continuous UV light is a more recent method applied for food surface decontamination. The UV light damages the DNA and has both a photophysical and photothermal effect on the bacteria. The efficacy of UV light treatment depends on the food product, distance and position relative to the light source, energy level, number of pulses and the bacterial concentration etc. Pulsed electric fields processing consists of short, highly intense pulses of electric fields applied to the product and is not limited to surface treatment. The inactivating effect on pathogens is due to irreversible damage to the cytoplasmic membrane. *L. monocytogenes* is more resistant to pulsed electric fields than *E. coli* and *Salmonella*, and it is recommended to combine this with additional stressors for food safety control [67].

Less is known about how light in the human visible wave spectrum (hereafter defined as visible light) affect the bacteria and how bacteria are able to sense and respond to visible light [89]. Sunlight contains a wide range of wavelengths which is constantly changing during time of the day and during different seasons [90]. Recently, it has been discovered that several non-phototrophic bacteria are capable of sensing visible light in order to adapt to light-induced stress which has a bactericidal or growth inhibitory effect on many types of bacteria [91, 92]. Exposure to natural sun-light has been shown to significantly limit the long-term survival of *L. monocytogenes* in sea-water [93]. Furthermore, light-exposure has been suggested to function as a signal for upcoming osmotic stress, caused by water evaporation under sunlight [94]. Another reason to detect visible light may be to avoid damage by solar UV radiation [91]. However, the inactivation of microbes by visible light is most effective within the blue light spectrum (405-410 nm) [95] which is more phototoxic than red light [96]. Further, the blue light spectrum is believed to have a photochemical toxic effect, rather than a photothermic toxic effect, especially if the agar is not colored [95]. Last, but not least, it has been suggested that the absence of visible light could signal to the bacterium that it has entered the dark environment inside a mammalian host [91, 97].

A possible mechanism for the bactericidal effect of visible light involves generation of reactive oxygen species (ROS) inside the bacterial cell [96] [98] and light-induced responses in chemotrophic bacteria include pigment formation, DNA repair, changes in motility and multicellular behavior such as formation of biofilms and fruiting bodies [97]. *L. monocytogenes* is recognized to have a light oxygen voltage (LOV) receptor for detecting blue light and it may also have a red-light receptor [91, 94]. In 2011, it was discovered that both blue and red light modulates σ^B-dependent transcription, flagellar motility and the ability of *L. monocytogenes* to invade cultured human cells [94]. One year later, the *L. monocytogenes* blue light receptor, which is homologous to the blue light receptor YtvA in *Bacillus subtilis*, was expressed recombinantly in *E. coli* [99]. Due to the unusual amino acid sequence of the *L. monocytogenes* LOV-STAS protein, encoded by the *lmo0799* gene, Chan and colleagues suggested that it exhibits altered spectral features and activation/deactivation kinetics compared to its homologue in *B. subtilis* [100]. These altered features could potentially expand its sensory capacity to also include other stressors such as cold stress in addition to blue light [99]. The *L. monocytogenes* blue light receptor (lmo0799) has been characterized as a flavin mononucleotide-containing protein and reported to be involved in the blue light-mediated inhibition of *L. monocytogenes* growth together with σ^B [98, 101]. Tiensuu and colleagues also reported that *L. monocytogenes* shows a cyclic and reversibly altered colony behavior in response to blue light, which resulted in opaque and translucent rings when the bacteria were grown on mobility agar plates [101]. Cell density has been suggested to influence light-dependent inhibition of *L. monocytogenes* growth [98]. Increased cell density may cause less light exposure per cell, thereby reducing the stress effect of light.

The responses in *L. monocytogenes* to visible light may therefore deserve attention not only as a separate factor but also in combination with other stressors that are applied as hurdles in food products to prevent bacterial growth.

In the human host

During the first steps in the infectious cycle, *L. monocytogenes* is exposed to pH 2 in the gastric environment, followed by elevated osmolarity (equivalent to 0.3 M NaCl) and bile in the upper small intestine [85]. These conditions are believed to function as important barriers which reduce the number of infective bacteria significantly. As reviewed by Horlbog and colleagues, *L. monocytogenes* is capable of surviving pH 2.5 for 2h, but the sensitivity to HCl is strain dependent [102]. Since the sensitivity in the digestion environment do not match the genetic cluster analyses, this strain-dependency may rely on mobile genetic elements, such as plasmids, transposons or insertion sequences. Mobile genetic elements are the likely causes when the phenotypic pattern of different strains refuse to align with any classification systems derived from the genome such as lineages or clonal complexes [102]. When *L. monocytogenes* is exposed to increased H+ levels, it can (1) reduce the H^+ ions through decarboxylation reactions, (2) export H^+ ions through pumps in the membrane and (3) repair damage from low pH by heat shock proteins etc. All these mechanisms can be encoded on mobile genetic elements [102].

Many different stressors, such as host defense mechanisms, impose oxidative stress upon the bacteria. During oxidative stress, molecular oxygen reacts with reduced flavoproteins, Fe-S proteins and cytochromes to be reduced to hydrogen peroxide (H_2O_2) or superoxide ($O_2^{\cdot-}$). Both H_2O_2 and $O_2^{\cdot-}$ have high redox potentials and are thereby strong oxidants. Reactive oxygen species (ROS) causes oxidative damage to carbohydrates, lipids and proteins, and bacteria have to rely on multiple mechanisms to protect themselves [103]. These mechanisms include detoxifying enzymes, small redox proteins, small molecules maintaining an intracellular reducing environment and production of scavengers such as glutathione and NADPH. The bacterial response to oxidative stress includes both reduction of the oxidants and repair of damage to proteins, DNA, RNA and lipids. When the ROS generation is higher than the ROS degeneration the cells experience oxidative stress.

Aims of the study

The aim of this thesis was to analyse how exposure to selected stressors present along the food production chain from farm to the human host, affects the risk for human listeriosis.

This aim was accomplished through the following objectives:

1. Analyse if *L. monocytogenes* growth potential in RTE food differs using a standard inoculum preadapted for immediate growth and an inoculum pre-exposed to chlorinated alkaline disinfectant-induced stress. (Paper I).
2. Explore how adaptation to different levels of NaCl stress in a growth medium influences *L. monocytogenes* survival in an *in vitro* human digestion (IVD) model. (Paper II).
3. Investigate whether exposure to broad spectrum visible light changes the phenotypic responses, global gene expression and the functional pathways in *L. monocytogenes.* (Paper III).

Summary of papers

Paper I. The impact of disinfection stressed *Listeria monocytogenes* in challenge testing of foods

The aim of Paper 1 was to explore how disinfectant-stressed *L. monocytogenes* cells grow in RTE foods. A disinfectant which is frequently used in the food industry was chosen for the study. The experiment was designed to simulate a contamination scenario including chlorinated alkaline disinfectant-induced stress and how it influences the lag-phase and growth potential of *L. monocytogenes* strains during growth in two different RTE food products. A comparison was made between the standard inoculum procedure, given by the European challenge test guidelines, and an inoculum pre-exposed to a chlorinated alkaline disinfectant. Standardization of the inoculum concentration was challenging for the stressed samples and resulted in varying inoculation levels, which may have impacted the final growth potential. Furthermore, exposure to the disinfectant caused contrasting effects upon the growth potential in the food products tested. Together, the results in Paper 1 indicate that inoculum preparation including chlorinated alkaline stress confers more uncertainty and a potential bias in the prediction of *L. monocytogenes* growth in food products.

Paper II. Survival of *L. monocytogenes* during *in vitro* gastrointestinal digestion after exposure to 5 or 0.5 % NaCl.

Due to public health issues, the food industry is under great pressure to reduce the NaCl content in their food products. NaCl is traditionally used as a preservative and taste additive to prevent growth of foodborne pathogens. *L. monocytogenes* is able to survive at high NaCl concentrations, but less is known about how sub-lethal NaCl-induced osmotic stress may affect its subsequent virulence potential. In Paper II, a recently developed human static *in vitro* digestion (IVD) model with international consensus was applied to analyze the survival ratio of *L. monocytogenes* in the gastric and intestinal phases after pre exposure to either 5 or 0.5 % NaCl. Strains from Scandinavian foodborne outbreaks of listeriosis, all related to NaCl containing foods, the EGDe reference isolate and an EGDe Δ*sigB* mutant was included in the study. The results suggest that a reduction of the NaCl content from 5 to 0.5 %, has the potential to cause a change in the relative survival ratio in an IVD model and that the effect is isolate, strain and σ^B dependent. All *L. monocytogenes* strains and isolates tested survived successfully passage through the IVD model and were subsequently able to invade cultured cells. The standardized IVD model was therefore considered as an applicable method for analyzing the behavior of *L. monocytogenes* in a simulated human host digestive environment.

Paper III. Exposure to broad-spectrum visible light causes major transcriptomic changes in the *L. monocytogenes* EGDe strain

Paper III explores how *L. monocytogenes* sense and adapt to environmental stress in the form of low intensity broad-spectrum visible light. This work explores how visible light influences both the global gene expression pattern and the growth phenotype of this bacterium. Phenotypic alterations on semisolid agar occurred during light exposure regardless of the presence of the blue light receptor or *sigB*, indicating that other regulatory pathways are involved in these changes. Global transcriptomic analyses revealed light-dependent altered expression of 2409 genes, belonging to 18 characterized functional pathways, involved in basic cellular energy-, stress, and motility. Downregulation of genes involved in the vitamin B12 metabolism suggests that *L. monocytogenes* downregulates endogenous photosensitizing compounds when adapting to visible light. Together, the results indicate that visible light alters the physiology and behavior of *L. monocytogenes* and that it is an important environmental variable to consider both when performing experiments in the lab and when developing novel strategies to control this pathogen in food production environments.

Discussion

Material and methodological considerations

Materials

Materials used in the PhD project consists of 19 different strains of *L. monocytogenes* shown in Table 2 and two different RTE food products.

Bacterial isolates

Before starting the laboratory experiments in Paper I, challenge tests for the private food industry in Norway had been performed. Therefore, the current study had exclusive access to *L. monocytogenes* strains isolated from relevant food sources (Table 2). All these strains were documented to be fast growing in food and relevant for challenge tests. The ANSES reference strain collection for *L. monocytogenes* challenge testing in food was established after the current study was initiated and therefore not used.

To analyze how stress from NaCl exposure influences the ability of *L. monocytogenes* to tolerate exposure to subsequent stress in the digestive tract of the human host (Paper II), we used Nordic outbreak strains, known to have survived through the food chain and having the potential to enter the host and cause disease. *L. monocytogenes* food isolates from outbreaks is challenging to get hold of due to the long incubation time relative to the often shorter shelf life of the food products. WGS performed during the Swedish outbreak revealed that the Patient 2 isolate compared to isolates from Patient 1 and from the food, differed by eight single nucleotide polymorphisms (SNPs). This was considered to be a minor difference [104] but both patient isolates were included in the experiment as the potential phenotypic consequences of the SNPs were unknown.

The strain collection used in paper III was kindly provided by Professor Jörgen Johansson at Umeå University and consisted of the laboratory strain EGDe, the Δ*lmo0799* mutant, the Δ *sigB* mutant, the trans complemented Δ*lmo0799* mutant strain using pMk4 as a plasmid backbone for trans-complementation, and the EGDe strain carrying the pMK4 plasmid. EGDe (serotype 1/2a) was the first *L. monocytogenes* isolated and it was collected from an infected laboratory animal by E.G.D. Murray [1]. This strain is still commonly used in laboratories today [105]. The complete genome of EGDe was determined in 2001 and was found to be 2.9 Mbp long with an average GC content of 39 % and to consist of 2853 predicted protein-coding genes [106, 107]. The EGDe strain and its mutant derivative strains have previously been included in studies which explored the effect of blue and red light on *L. monocytogenes* [101]. The copy number of a plasmid may affect the expression level of the gene of interest. The pMK4 shuttle vector is a medium-copy-number, replicative plasmid. As no phenotypically differences were observed between the wild type strain and the trans complemented Δ*lmo0799* mutant strain under the conditions tested, the pMk4 plasmid copy-number was assumed to be acceptable for use in the current study design. To test whether the response to visible light was valid for more strains than EGDe, we also tested the effect of broad-spectrum visible light on two of the food isolates from Paper I in the study (Table 2).

Isolate:	Reference:	Isolated from:	Serogroup:	Paper:
1	VI 59788 (Skjerdal *et al.*, 2010)	Unknown product	II c	I
2	VI 59789 (Skjerdal *et al.*, 2010)	RTE chicken	II a	I, III
3	VI 59790 (Skjerdal *et al.*, 2010)	RTE sliced deli meat	II a	I
4	VI 59791 (Skjerdal *et al.*, 2010)	RTE sliced deli meat	II a	I
5	VI 59792 (Skjerdal *et al.*, 2010)	Meat balls	II c	I, III
6	VI 59793 (Skjerdal *et al.*, 2010)	Wiener sausage	II c	I
7	NVH-FMN, Reference strain	Laboratory	IV b	I
8	Scott A, Reference strain	Laboratory	IV b	I
9	EGDe wild type (O'Donoghue et al., 2016)	Rabbit	IIa (I/2a)	II, III
10	EGDe + pMK4 (O'Donoghue et al., 2016)	Laboratory	IIa (I/2a)	III
11	EGDe *ΔsigB* (O'Donoghue et al., 2016)	Laboratory	IIa (I/2a)	II, III
12	EGDe Δlmo0799 +pMK4 (O'Donoghue et al., 2016)	Laboratory	IIa (I/2a)	II, III
13	EGDe Δlmo0799 + pMK4 – 0799 (O'Donoghue et al., 2016)	Laboratory	IIa (I/2a)	III
14	Outbreak, Norway (Johnsen et al., 2010)	Cheese brine	IIa (I/2a)	II
15	Outbreak, Denmark (Kvistholm Jensen et al., 2016)	Ready-to-eat spiced meat roll	IIb	II
16	Outbreak, Sweden* (Dahl et al., 2017)	Liver patê	IIa	II
17	Outbreak, Sweden* (Dahl et al., 2017)	Boiled medwurst	IIa	II
18	Outbreak, Sweden* (Dahl et al., 2017)	Patient 1	IIa	II
19	Outbreak, Sweden* (Dahl et al., 2017)	Patient 2	IIa	II

Table 2. Overview of strains used in the PhD project.

Food products

In general, RTE food products are highlighted as risk products for containing *L. monocytogenes*. If the food products have a relatively long shelf life, *L. monocytogenes* may reach the legal limit concentration of 100 CFU/g. The two model products used in Paper I are representative for red and white meat; sliced deli meat and chicken meat for RTE salads. They are both heat-treated products with a relatively long shelf life (18 and 35 days, respectively), and thereby considered as potential risk products. Due to intrinsic and extrinsic differences between these products, they were assumed to provide different and representable growth conditions for *L. monocytogenes* in RTE food. The food company kindly provided about 370 packages of chicken and almost 200 sliced deli meat packages. The package sizes of 200 and 100 g for RTE chicken and sliced deli meat, respectively, provided enough food matrix for necessary analyses. Furthermore, the use of commercially produced real food packages were used in the experimental design to mimic realistic scenarios. *L. monocytogenes* growth data and results from the challenge tests were shared with the respective food company, improving their knowledge about the *Listeria* shelf life in the tested products.

Laboratory methods

Challenge tests

Challenge tests are used as model experiments to estimate growth of *L. monocytogenes* in food products. In paper 1, *L. monocytogenes* was inoculated into the food products, and the bacterial concentration was analysed during storage. Analysis at the start and at the end of the storage period is an absolute minimum for estimation of the growth potential. However, if the maximum growth rate is to be calculated, then a minimum of nine timepoints for quantification are needed, as performed in Paper 1 [52].

The guidelines for challenge tests underline the use of realistic temperatures during storage considering different storage temperatures in the company, during distribution and retail, and in the consumer refrigerator. However, as the purpose of this study was to investigate the effect of the inoculation preparation, the studies were carried out at a fixed temperature (4 °C).

Preparation of the inoculum and the inoculum procedure during challenge testing

Titan Hypo is often used for disinfection of food production facilities. The producer of this disinfectant recommend 1 % concentration and 5 min exposure time. Initial experiments indicated survival after treatment with this time-concentration scenario when exposing *L. monocytogenes* in broth and this time-concentration combination was therefore included in the experimental design for stressing the inoculum. However, it was challenging to standardise the final inoculum concentration when exposing the bacteria to disinfectant-induced stress. In real life, it is assumed that *L. monocytogenes* persist in food plant facilities as biofilms. Bacteria in biofilms are hypothesized to withstand higher concentrations of disinfectants when grown planktonically in culture [108]. With respect to standardisation of the stressed inoculum concentration, including biofilm inoculation in the study would have introduced a great challenge and was therefore considered infeasible.

The experimental design required an approach to end the phase of stressing the inoculum after 5 min. To stop the biochemical stress caused by Titan Hypo, pilot studies were performed using Dey Engley and tenfold dilution with physiological saline water, respectively. However, the negative effect of transferring Dey Engley to the food product was considered higher than the negative effect of dilution in physiological saline water. Another option discussed was to add a centrifugation step to remove the disinfectant from the cells. However, centrifugation is not representative for a natural contamination route and was therefore not included in the experimental design. After the current study was performed, an ISO protocol for stressing of inoculum was published; Annex C in ISO 20976-1:2019-04 from 2019 describes different injury protocols leading to a loss of recoverability close to 1.5 log10, including hypochlorite stress.

The inoculum concentrations used in the current study ranged from 1 to 4.0 $\log_{10}$ CFU/g growth media. A significant impact of the inoculum concentration has been described in the literature by other research groups and both low and high inoculum concentrations may reduce the growth potential of *L. monocytogenes* in food [109-111]. If only a few cells contaminate a food product it is less likely that one of the cells is adapted and ready for immediate growth (single cell variation) compared to an inoculum containing a higher number of cells. On the other hand, if a high inoculum concentration is introduced, there may be only a limited growth interval before reaching stationary phase. Additionally, a background bacterial microbiome may compete within the same habitat suppressing *L. monocytogenes* growth through the Jameson effect [109]. The European guidelines recommend a contamination level of 100 CFU/g in the food, as a suitable compromise to the subsequent effects of a too high or a too low inoculum concentration.

Each inoculum cocktail was specially designed with strains considered relevant for the respective food product. Due to the different strain cocktails used in these two food products, the observed growth kinetic data for the two products had to be assessed separately and were deemed incomparable.

Quantitative and qualitative analysis of L. monocytogenes

It is important to verify that batches of food products to be used for challenge testing are not naturally contaminated with *L. monocytogenes*. Absence of naturally contamination with *L. monocytogenes* in the samples was confirmed by qualitative analysis at the beginning of each challenge test performed in Paper 1.

Total aerobic count, Lactic Acid Bacteria (LAB) and general analysis of food characteristics

As different intrinsic factors in the food products may cause a bias in the growth of *L. monocytogenes,* the presence of total aerobic count, Lactic Acid Bacteria (LAB) and other food characteristics, potentially influencing the *L. monocytognes* growth, were analyzed.

The background bacterial microbiome may inhibit growth of *L. monocytogenes* at a certain level by competing within the same bacterial niche or by secreting factors that inhibit growth of *L. monocytogenes*. For example, LAB inhibit *L. monocytogenes* growth by producing lactic acid that lowers the pH in the food matrixes [112].

Both RTE chicken and sliced deli meat are expected to consist of several different growth compartments which may represent niches with different growth conditions. However, methods for food product characterization and standard sample size for *L. monocytogenes* quantification demands sufficiently large quantities of the matrixes, thereby camouflaging differences between microscopic growth habitats.

Finally, for chemical characterization of the food product, it is important to use the concentration of NaCl etc. in the water phase of the product, as it is mainly components in the water phase that have the potential to influence bacterial growth. Also, organic acids must be considered in their un-dissociative state, as it is only in this state the organic acids are able to cross the bacterial cell membrane. Therefore, the preservative effect of the organic acids increases as pH decreases.

Exposure to NaCl prior to simulation of human digestion

It was decided to use Brain Heart Infusion (BHI) with either 5 or 0.5% NaCl and *L. monocytogenes* in pure culture to study the effect of NaCl on bacterial survival through the IVD model. A NaCl concentration of 0.5 % is normally used in laboratory growth media such as BHI. Meat products and dairy products are all NaCl-containing RTE food products often associated with *L. monocytogenes* contamination [113]. For example, typical salted Norwegian meat products often contain 5-8 % NaCl while cheeses often contain 1.5-2.5 % NaCl. The Norwegian high-risk product “rakfisk” contains 4.2 % NaCl. We therefore considered a tenfold difference in the interval between 0.5 and 5% NaCl concentration as realistic and appropriate for the experimental design.

Static in vitro *digestion*

The *in vitro* digestion method applied in the current study was static, in terms of reagents needed to be manually transferred to subsequent phases after entering the model (Figure 6).

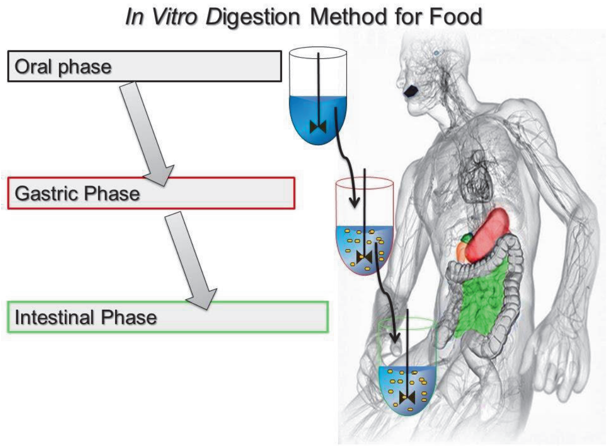


Figure 6. Graphical abstract of a static *In Vitro* Digestion (IVD) method for food [114], Published by The Royal Society of Chemistry. The method includes an oral, gastric and upper intestine phase and hold international consensus regarding standardised meal, enzyme-activity, electrolytes, bile, pH and time of digestion in each phase. The standardisation is based on available physiological data.

Given the low incidence of listeriosis in a population, despite the ubiquitous nature of the causative bacterium, dose-response models presume that illnesses result from exposure to high bacterial doses [22]. The initial concentration of *L. monocytogenes* before entering the IVD model in the current study was 8.2 Log_{10} CFU/g, which is considered a high concentration compared to what is normally detected in food. However, documentation of bacteria being able to adhere and invade epithelial cells after passing through the IVD model was considered essential for the experimental design, and as the bacteria entered the IVD model in pure BHI broth, unprotected by a food matrix, we decided to use a high initial bacterial concentration. The bacteria were grown in BHI and the culture was used as representative for a meal. BHI mainly contains protein, and as the oral phase contributes with mixing (for solid food) and amylase (for starch digestion), the oral phase was excluded. Other studies have demonstrated that *L. monocytogenes* strains survive in gastric phase at pH 2 for up to 90 min [115]. The time of gastric digestion for a liquid is reported to be between 5 and 45 min at 37 °C [116] and the time in this phase were therefore reduced compared to the standardised IVD method. As *L. monocytogenes* is known to tackle acid stress and low pH very well, the pH was reduced to 2 instead of 3. The shorter gastric phase exposure

(40 min) may have contributed to the lack of detectable strain-dependent differences in survival in this phase.

Pancreatin contains both lipase (for digestion of lipids) and trypsin (for digestion of proteins). In the current study BHI represented the food, which mainly contains proteins. The added pancreatin volume was therefore calculated according to the trypsin enzyme (protease) activity to make the model as physiologically relevant as possible. Bacteria contains both carbohydrates, proteins and lipids, and the secreted enzymes during digestion may potentially target not only the digested food, but also *L. monocytogenes* itself. Human digestion aspirates have been suggested to alter the expression of virulence genes and the virulence potential of this pathogen [117]. Also, the food matrix may impact *L. monocytogenes* ability to cause disease, directly by altering the physiology and behaviour of the bacterium [118] and indirectly by altering the gut microbiota [119]. Exchange of BHI with another food matrix could therefore alter the *L. monocytogenes* survival rates and results from the cell culture assay detected in the current study. Quantification of *L. monocytogenes* is not defined in the Nature protocol by Brodkorb, but was performed as described for probiotic bacteria; no neutralizing reagents were added and the samples were analysed immediately [120].

The intracellular cycle of *L. monocytogenes* starts with the epithelial cells in the intestine. A cell culture assay with an epithelial cell line was therefore included as a final step. As the digestive environment within the mammalian host is dark, the digestive experiment and cell culture assay were performed in darkness. Another significant factor during digestion is the anaerobic conditions, which we unfortunately were unable to include in the experimental design. Anaerobic conditions are suggested to alter the *L. monocytogenes* stress behaviour against several stressors [68], and should ideally be considered in digestive experiments. Both the pipetting for adding reagents and the sampling throughout the digestive assay used in this PhD project made application of anaerobic conditions difficult.

Survival in the gastro-intestinal tract is a key-event for dose-response models [121]. There are still large knowledge gaps concerning how different environmental, bacterial and host factors influence the ability of *L. monocytogenes* to survive through the digestive system and subsequently cause invasive listeriosis. *In vivo* digestion models are costly and may touch upon ethical issues. *In vitro* models, which simulate the human digestive system, are therefore widely used within food science [114]. However, the use of different non-standardized models provide inconsistent results and make comparisons of results across research groups and laboratories challenging. Therefore, the standardized method described by Minnekus et al (2014) was used in the current study [120].

Light exposure assays

To analyze how visible light as an environmental factor affect phenotypic behavior of the bacterium, we chose to use a light source representative for broad spectrum visible daylight (Figure 7). The selected Juwel Aquarium Discover Life light source (Day 24W T5; 9,000 K) are normally applied in aquariums for simulating daylight. However, as the light exposure was performed through plastic or glass, the UV spectrum from this light source was naturally excluded.

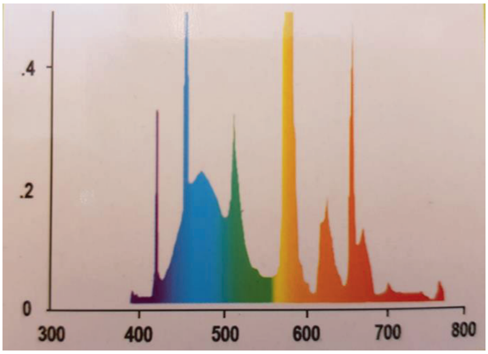


Figure 7. The light profile for Juwel Aquarium Discover Life light source (Day 24W T5; 9,000 K). Photo: K.S. Pettersen, 2020.

Measurements of light (µw/cm^2) were performed to calculate the relative difference between the red and blue wavelengths. Blue and red light had to be measured separately with specific instruments and their respective detectors (Figure 8).

Figure 8. Picture to the left: Red light Detector-model 247, serial number 77079, with the instrument 371 Optical Power Meter, United Detector Technology. Picture to the right showing the blue light instrument and detector: Solar Light Co, PMA2100, Detector; Blue Light Safety, Solar Light Co, Philadelphia, Pennsylvania, Serial number; 2894. Photo: K.S. Pettersen, 2016.

Because the shape of the detectors for blue and red light were different, light had to be measured through a small hole in aluminium foil to ensure measurement of equal amounts of light (Figure 9).

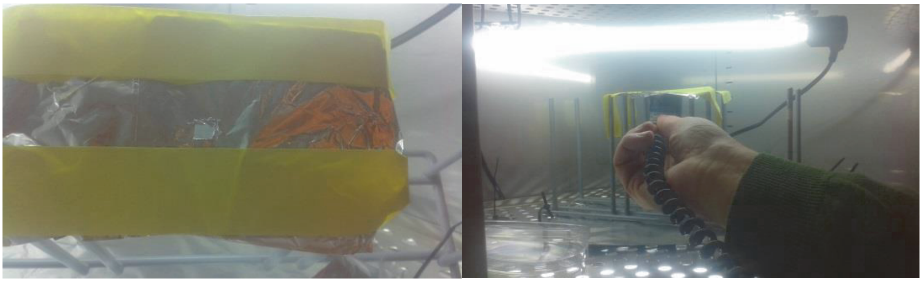


Figure 9. The picture to the left shows the 5×5 mm hole made for excluding all radiation coming from the sides when placing the detector just below the hole (picture to the right). Photo: K.S. Pettersen, 2016.

With the red-light detector we measured 173 µw/cm^2 and with the blue light detector we measured 68 µw/cm^2 which give a ratio of red to blue of 2.54. We had previously measured 0.25 – 0.27 Joule/ cm^2 for the blue light. When including the ratio of 2.54 ((0.25 – 0.27 Joule/cm^2)×2.54 = 0.635 – 0.686 Joule/cm^2), we gain knowledge about the spectrum present outside the blue area, and we thereby include the red area, which is relevant for *L. monocytogenes*.

The measurement of blue light was performed at the same distance as used for exposing the bacteria to broad-spectrum visible light. The light exposure changes by the distance from the light source, and it is therefore important to place the bacteria at the same distance from the light source in the experiments. There was no available detector that could measure the complete visible spectrum of wavelengths at the same time.

Under the conditions described above, the level of irradiation exposure ranged from 0.25 - 0.27 Joule/cm^2 across the petri dish radius (4.5 cm). This variation was considered acceptable, corresponding to an even spread of the light. The lamp was placed so that the short end was positioned at the incubator door side. That is probably why increasing µw/cm^2 was measured when the detector was moved deeper into the incubator. However, this effect ceased when the incubator door was closed, probably due to equal reflection of light from each of the four sides within the incubator.

L. monocytogenes *growth assays during light exposure*

To simulate scenarios at room temperature, laboratory conditions and in the human host, the bacteria were light exposed at both 20 and 37 °C. Furthermore, we found it interesting to investigate the phenotypic effect of visible light on *L. monocytogenes* at a typical food plant facility temperature (12 °C).

The bacteria were exposed to light for several days before macroscopic analysis, quantification by viable plate counts and optical density measurements. This is a different time-temperature scenario than used for transcriptomic analyses and was needed to allow observation of potential light-dependent phenotypic effects.

L. monocytogenes' response to light is described as instant, while the adaptation to darkness is slow. Control samples kept in strict darkness were considered as highly important for being able to assess the effect of light exposure. The dark condition was ensured by wrapping up the plates in double layers of aluminum foil. Both control and light exposed Petri dishes were sealed using Petri film, in order to ensure equal atmospheric conditions.

Stamping out agar from specific growth zones in agar plates for bacterial count is a previously used method to determine the bacterial growth density during growth [101]. However, the uncertainties due to microscopic accuracy of the manual stamping procedure was considered too high. Bacterial count was therefore performed by transferring all semisolid agar, plate by plate, to individual stomacher bags. Quantification was successively performed in the same way as done with typical food samples.

The plates were incubated at either 12, 20 or 37 °C for 7, 12 and 7 days, respectively, under continuous light exposure or in complete darkness. Different incubation times were used for the different temperatures to allow detection of potential phenotypical differences between light and dark-exposed samples.

Light exposure prior to RNA isolation was more challenging due to necessary pipetting and keeping the controls in complete darkness. The issue was solved by wrapping up both the cell culture flasks and the caps in aluminum foil and use caps with a filter area. Before light exposure, the aluminum foil was removed and immediately after light/dark exposure the Bacteria Protect Reagent (BPR) was added to snapshot the bacterial transcriptomic profile at that time. Pipetting of the BPR was performed by perforation of the filter area in the cap with the pipette tip. To cope with the challenge of isolating enough RNA, each preculture 1, representing one colony from the blood agar plates, was split into three technical replicates during the phase of preculture 2 and light exposure, and finally pooled again after adding the BPR. To ensure that the cells did not enter stationary growth phase, we aimed to harvest the cells in exponential and early stationary phase.

Preparation of RNA for sequencing

There are previous studies addressing the effect of visible light on gene expression of *L. monocytogenes*. Transcriptomics is the study of all RNA in one cell or a population of cells and provides precise measurement of gene expression and a full picture of the whole transcriptome [122].

To our knowledge, Paper III was the first study applying global transcriptomic analysis to explore the response and adaptation of *L. monocytogenes* to broad-spectrum visible light. Global transcriptomics was chosen in the current study as knowledge on regulatory mechanisms and genes involved in visible light responses in *L. monocytogenes* is limited. The global approach for analysing gene expression is instrumental for detecting broad coordinated trends, such as the response to broad spectrum visible light. Such trends cannot be discerned by more targeted assays using single gene expression analysis [123]. Furthermore, global transcriptomics data can be re-used for addressing additional research questions.

Both microarrays and RNASeq are frequently used transcriptomic techniques. Microarrays target known sequences and cannot be optimally applied for studying unknown or poorly characterized target sequences. With global transcriptomic analysis the sequences may either be assembled *de novo* or mapped against an already sequenced genome, as done with the EGDe strain in the current study. RNASeq can be used for both qualitative and quantitative analysis of any type of RNA, including messenger RNAs (mRNAs), microRNAs and small interfering RNAs [122]. RNAseq can also reveal expression and potential functions of previously unannotated genes [123]. A transcriptome analysis captures a snapshot in time of the total transcripts present in a cell, as applied for the given time-temp conditions in Paper III.

Global transcriptomics is still in its infancy when studying bacterial stress responses and is the least used omic-techniques [122]. Reasons for this are probably high costs and the need for special competence within bioinformatics. However, the omics techniques are rapidly developing, providing more cost-efficient sequencing. Today, RNA-Seq assays are more frequently used than microarrays.

When merging different omics-methods representing different layers in the central biological dogma, each layer has the potential to confirm the previous one and may thus provide an incredible insight into how a bacterium responds to the environment [41]. In the current study a proteomics dataset could have been applied to achieve such insight.

The resources available for the current study limited transcriptomic analysis to the use of only one strain. It was decided to use the EGDe strain as its genome is sequenced and well annotated. The statistical power increases significantly when including more biological replicates, rather than investing in increased sequencing depth [124]. The current study therefore decided to start with

7 biological replicates aiming for at least 5 usable ones to be implemented in the final gene expression analyses. Additionally, the light-dependent bacterial response was expected to be complex, possibly involving only slightly up/down regulated genes. Detection of genes expressed at a low level requires higher sequencing depth (increasing the likelihood of a cDNA fragment to be sequenced), which is in contrast to highly expressed genes. For DNA sequencing, coverage is a frequently used term. However, for RNAseq, read depth is typically used instead of coverage, defined by number of reads per sample. Sequencing depth is decided by number of samples divided by number of reads per lane (one lane gives you a fixed number of reads). If acceptable depth is not achieved in the first sequencing run, it is possible to increase the depth by a second sequencing run. The current study aimed for a depth of 15 million reads per sample. To avoid lane bias, all the samples were represented in each lane. High sequencing depth requires high sequencing capacity which is costly. One way to handle this dilemma is to perform ribosomal RNA (rRNA) depletion. rRNA makes up about 90 % of total RNA in a bacterial cell, and since we were interested in mRNA, this approach was considered beneficial. It is, however, challenging to evaluate the quality and level of mRNA in rRNA depleted samples as the RNA Integrity Number (RIN) values cannot be assessed when the rRNA peaks are removed from the bioanalyzer profile (RNA integrity is given a number between 1 - 10 calculated from the rRNA peaks). In rRNA depleted samples, only the mRNA tail, at the very end on the y-scale in the graphical bioanalyzer output, can be subjectively evaluated. An expert at the Norwegian Sequencing Centre evaluated the sample quality before cDNA library preparation and considered all 42 mRNA samples as acceptable for further processing.

Many steps are needed before finding the significantly differentially expressed genes (Figure 10).

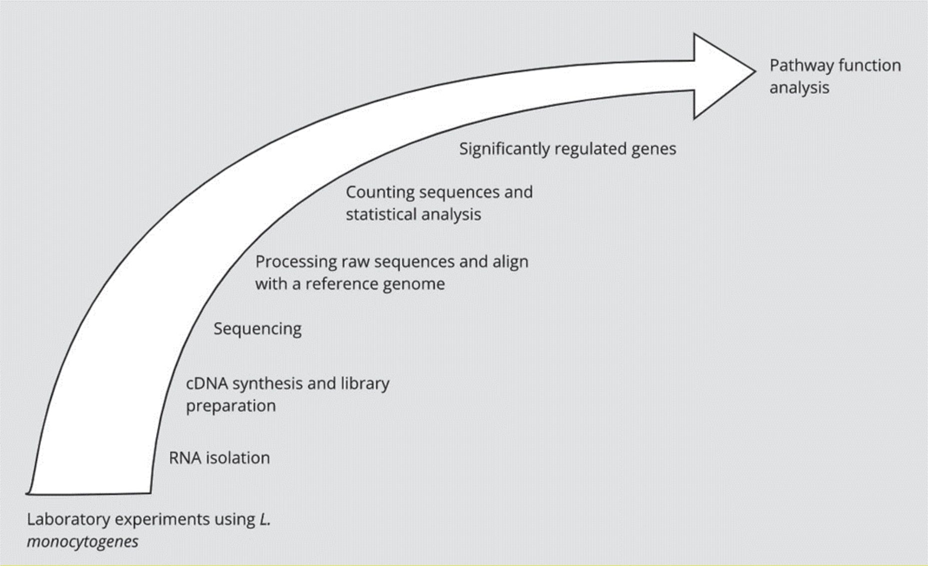


Figure 10. The process of finding expressed genes when exposing *L. monocytogenes* to visible light started out with laboratory experiments exposing the EDGe strain to broad spectrum visible light or darkness. After RNA isolation, cDNA synthesis and library preparation, the cDNA was sequenced. Finally, the sequences were quality checked, aligned with the EGDe reference genome and counted for calculation of gene expression. The gene expression files were further used for pathway function analysis. Illustrated by K.S. Pettersen, 2020.

Analysis of differentially expressed genes

After sequencing, processing, aligning to a reference genome, counting the sequences and performing statistical analysis, a list of differentially expressed genes is generated (Figure 10). In contrast to single gene expression analysis, baseline differences in gene expression do not exist in global transcriptomic analysis. In global transcriptomics, the gene-expression is calculated by normalizing the expression of all genes, including both treated and non-treated samples (controls), assuming no difference. Thereafter, the different groups and replicates are related to that general normalization level and analysed for significant changes in gene expression between treated (light exposed etc) and untreated (controls kept in darkness).

However, it is not unusual that some of the samples fail to pass the quality check along this process. One control sample from the 20 °C and 20 min condition in darkness, two samples from 20 °C 20 min in light, one sample from the 20 °C and 180 min in light and one sample at the 37 °C and 20 min in light were excluded from the further analysis due to low percentage of alignment (10.6 - 37.4 % feature count alignment). A low alignment percentage means that the sequenced sample does not match the reference genome. This may indicate that the sequenced material has been contaminated with other genetic material or that the preparation of the sample before sequencing was not satisfying resulting in poor sequence quality. In addition, due to outliers defined by the cluster dendrogram and Principal Component Analysis (PCA) during statistical analysis, two more samples were removed (one from the 20 °C and 20 min in darkness, and one from the 37 °C and 20 min in darkness). In principal component analysis a collection of points in three different dimensions are fitted to respective lines by minimizing the average squared distance. The points may then appear as clusters relating to factors in the experimental design, such as light exposure and/or temperature, used in the current study. Final calculation of differentially expressed genes was performed using samples which had a feature count alignment ranging from 71 - 83.4 %. As a minimum of five biological replicates were included for each condition, the analysis was considered to have good statistical power.

Functional pathway analysis

When ending up with 2,409 significantly regulated genes, it is not feasible to analyze the genes manually. There are several programs and tools to handle this process, which starts by first ensuring that you have the correct type of gene ID. The gene converter tool (DAVID Bioinformatics Resources 6.8, NIAID/NIH https://david.ncifcrf.gov/tools.jsp [125]) therefore converts your gene ID to the needed one for in-put to the functional pathway analysis. In our case, the Pathview program (https://pathview.uncc.edu/) required conversion to Entrez gene ID [126-128]. The Pathview program is based on the KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways and the level of expression can be graphically illustrated by different coloring of the genes involved in the respective pathways. Statistical analyses are performed to find significantly differentially regulated metabolic pathways. Thereafter, the specific genes within each pathway are highlighted. Additionally, for studies of specific genes, such as virulence or AMR genes, these genes can be imported to Pathview and visualized in context of a relevant functional pathway. The opening for functional pathway analysis is essential for analyzing global transcriptomic data; it is important to not narrow in too early due to the enormous amount of data generated. Too early narrowing will increase the risk of missing the “big picture”.

Congo red assays

Congo red is a histological dye, which binds to polysaccharides present in EPS and turns red at pH > 5.2. Congo red can be applied in the agar to visualize EPS production. The level of stress may impact the membrane permeability, and thereby the level of dye in the supernatant. However, since Tiensuu *et al.*, successfully visualized light-dependent EPS differences using Congo red [101], it was applied in the current study when analysing the effect of broad-spectrum visible light.

Motility test

Light-dependent motility assays have been performed by adding two microliters of bacterial culture to the centre of semisolid BHI agar plates, followed by measurements of the colony diameter after incubation [101]. However, the diameter of the colony may be affected by the number of bacteria as well as bacterial motility. Therefore, to get a more accurate measurement of bacterial motility, all bacteria in the colonies were quantified in addition to measuring the diameter of the colonies. The increased bacterial density in the colonies was then used as an indication of decreased bacterial motility. However, our measurements of the colony diameter did only include one measurement across each colony. Improved determination of colony areas could probably be achieved by measuring the diameter at two places of the colony, perpendicular to each other, and by subtracting the inoculum area size at the beginning of the growth experiment from the measured values, as described by Tiensuu et al (2013)[101]. In this PhD project, the measurements of the colony diameter for motility analysis was combined with an umbrella motility test.

Statistical methods

Both Microsoft Excel 2010 and STATA, version 14, are widely used and trusted software. In statistics, every conjecture concerning the unknown distribution F of a random variable X is called a statistical hypothesis [129]. The likelihood of mistakenly rejecting the null hypothesis is often set to 5 %, emphasizing a minor risk to draw wrong conclusions. A significance level of 5 % was also used in the current PhD project. A higher number of replicates will often increase the strength of the conclusions. However, this is not always possible for practical and economic reasons.

Multiple linear regression analysis is often used when analysing for factors having an impact on an outcome. This method was used to analyse the association between two or more independent variables and a single continuous dependent variable, such as factors affecting growth potential, accounting for batch, level of stress exposure of the inoculum and inoculum concentration in paper I. In order to end up with only significant predictors in the model, backward selection was chosen instead of forward selection. The forward method may produce so-called suppressor effects when predictors are only significant when another predictor is held constant. The backward method is therefore the generally preferred method. Linear regression analysis demands normal distribution of the residuals. Normal distribution can be confirmed by applying the Shapiro–Wilk test and this test was therefore used for testing normality of the predicted residuals in paper II. In paper I, potential outliers were evaluated by their residual and leverage values. The leverage is a measure of how unusual the X value of a point is, relative to the X observations as a whole. In Paper I, one of the outliers was removed due to the results from this analysis. However, being aware of the effect of the inoculum size on the growth potential, it may be discussed whether this point was a true outlier. Its residual value was 4.2 with a leverage of 0.8; it was therefore excluded from the regression model.

Linear regression analysis was also applied in Paper III to analyse if a bias due to different agar weight was present. *L. monocytogenes* growth data in Paper III was analysed by pairwise comparisons using two-tailed paired Student t-tests with significance levels of P <0.01 and P <0.05. The t-test is a statistical method to determine whether the mean difference between two sets of observations is zero. It has two competing hypotheses were the null-hypotheses assumes the true mean to be zero, and the alternative one assumes the mean to be different from zero. Since the direction of the alternative one could take both directions, a two-tailed approach was used.

Results

The *L. monocytogenes* genome consists of a relatively large portion of regulatory genes which facilitate rapid adaptation to different environments such as those encountered in the whole food chain and in the human or animal host.

In paper I, the phenotypic consequence of this adaptability was analysed. The first criterium for analysing growth of chlorinated alkaline stressed cells in paper 1, is that *L. monocytogenes* survives cleaning and disinfection of food plant facilities. The ability of *L. monocytogenes* to persist in different environmental niches, such as on stainless steel, in drains or in cracks in food plant facilities, increases the risk of foods being contaminated. However, the physiological condition of bacterial cells that survive cleaning, may affect their subsequent growth, as shown in paper 1, where the stressed inoculum showed significantly altered growth potential in both RTE chicken and sliced deli meat. The main reason for exploring the effect of stress exposure on subsequent growth in contaminated products is the importance of the *L. monocytogenes* growth potential and the consequences it has for food safety and the economy for food producers. The inoculum concentration in naturally contaminated food is reported to be low (approximately 1 CFU/g) [130] and, in the perspective of the relatively high infective dose, growth in food during storage is regarded as a critical step for the risk of listeriosis. The significantly reduced growth potential observed in RTE chicken matrix after pre-treatment with the disinfectant was in accordance with expectations. In contrast, the increased growth effect in RTE sliced deli meat was not expected. However, measurements of pH in the food products and the stressed inoculum revealed a possible explanation. For RTE sliced deli meat, the pH in the stressed inoculum may have provided a larger increase in pH between the food packages inoculated with stressed cells and the controls, than for the RTE chicken. As the pH in RTE chicken are already closer to the pH optimum for *L. monocytogenes*, this increase may have provided a benefit larger than the cost of stress by the disinfectant. Carry-over effects such as change in pH may also interfere with other components in the food, such as the inhibiting growth effect of organic acids. Carry-over effects may thereby result in additional growth compartments with unexpected and different growth conditions compared to the rest of the food product. A similar phenomenon appeared during the caramel-apple outbreak in USA where the interface between the caramel and the apple provided excellent, but unexpected growth conditions for *L. monocytogenes* [131].

In paper 1, only the inoculum which was exposed to 0.5 % disinfectant demonstrated growth above 0.5 $\log_{10}$ CFU/g in RTE sliced deli meat. This result suggests that pre-exposure of *L. monocytogenes* to disinfectant-induced stress may re-categorize food products defined by official regulations.

Both the inoculum concentration and the level of stress significantly affected the growth potential of *L. monocytogenes* during storage throughout the commercial shelf life, and also after prolonging the storage time by additional eight days for both food products. The effect of the inoculum concentration was as expected, due to the factors previously described in the section "Methodological considerations". Also, in addition to significance levels of ≤ 0.02 for the predictors, the models explained at least 76 % of the observed growth potentials after the commercial shelf life, making the linear regression model strong. The model then supports these assumptions of inoculum size and stress being highly relevant for the growth potential. For robust challenge study results, it is important to analyse the intrinsic and extrinsic food product conditions at start and at the end, standardise the inoculum procedure and to an acceptable level ensure that the inoculation procedure does not alter the original growth conditions compared to the non-inoculated product. The results indicated that the stressed inoculum did not fulfil any of these criteria. It was therefore recommended not to use the stressed inoculum.

After being able to survive through the food production line and when consumed by a human host, *L. monocytogenes* changes its physiology by changing from a saprophytic lifestyle to become a potential intracellular pathogen. If it survives through the gastrointestinal environment and invades the intestinal epithelium, it has successfully crossed the initial defence mechanisms against pathogens and entered the intracellular life cycle. If the bacteria hold a high virulence potential, the likelihood for severe listeriosis increases, especially in combination with a high number of bacteria enterring an immunosuppressed host (Figure 1). As the food industry strives to reduce the NaCl content in their products, and bacterial stress has been reported to affect survival through subsequent stress exposure, the tenfold reduction of NaCl in the bacterial growth environment may influence its survival through a human *in vitro* digestion model. No cross-protection between NaCl stress and the digestion barriers was observed when analysing all strains at each of the two NaCl concentration categories (5 and 0.5 %). However, strain by strain analysis revealed that the difference in survival in the *in vitro* digestion model, after a tenfold reduction of the NaCl concentration, was strain dependent; the EGDe strain showed reduced survival when the NaCl concentration increased, while one of the Swedish patient isolates demonstrated increased survival (no 1). This highlights the diversity between *L. monocytogenes* strains and the importance of including several strains before considering conclusions to be valid for *L. monocytogenes* in general.

In the human digestive tract, the bacteria are exposed to pH 2 in the gastric lumen and this acidic environment is often mentioned as the main host barrier for *L. monocytogenes*. Surprisingly, the reduced survival of the EGDe strain was more prominent in the intestinal than in the gastric phase when exposed to 5 % NaCl. The reduced survival could be due to sensitivity to bile, which was added to mimic the intestinal phase. For some of the strains, a significant difference in survival between 0.5 and 5 % NaCl exposed inoculums were only apparent when analysing survival in both the gastric and intestinal phase together. However, the reduced survival fraction of the EGDe Δ*sigB* strain compared to the EGDe background strain indicates the importance of a fully functional σ^B regulon for subsequent survival in the digestion model after exposure to 5 % NaCl. Again, the intestinal phase demonstrated the importance of a functional σ^B regulon to a larger extent than the gastric phase. When reducing the NaCl concentration in the growth media by tenfold, from 5 to 0.5 % NaCl, no strain-dependent difference in survival in the gastric phase was detected. Such difference was only detected in the intestinal phase which highlights the importance of the intestinal phase as a host barrier to *L. monocytogenes.*

Temperature and salt stress have been suggested to increase the sensitivity to light and visible light was therefore included as a stressor in the pilot studies preparing the experimental design for paper II [132, 133]. However, due to the methodological challenges described under the "Methodological consideration" section, the risk of causing bias between light and dark-exposed samples excluded light as a stressor in II. Instead, we only analysed the dark-exposed samples and the effect of a tenfold reduction in NaCl concentration.

In nature, light usually occurs in a broad spectrum of different wavelengths and the light emitted by the lam used in paper III contains a broad spectrum of wavelengths. In one of our initial experiments, we revealed the toxic and dose-dependent effect of light as shown in Figure 11.

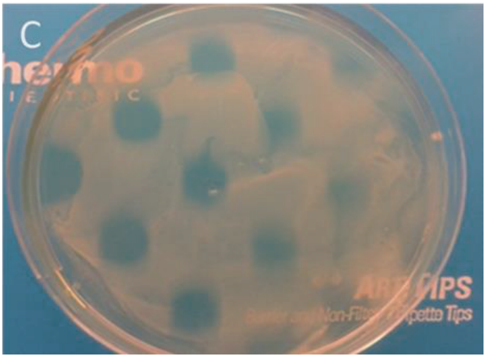


Figure 11. *L. monocytogenes* spread on a BHI agar plate and incubated under light exposure. The opaque areas represent reduced growth while the transparent zones represent no growth. The transparent zones

were exposed to light from both above and below, corresponding to the shelf pattern shown in Figure 12. While the opaque areas were only exposed to light from above. Photo: K.S. Pettersen, 2016.

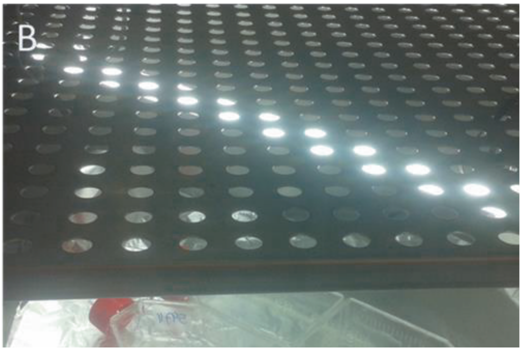


Figure 12. The shelf in the incubator, with the light source installed above and below. Photo: K.S. Pettersen, 2016.

Exposure to broad-spectrum visible light significantly inhibits growth of *L. monocytogenes* strain EGDe and alters its multicellular behaviour at both 20 and 37 °C. The colony diameter was also significantly reduced when growing on plates in the present visible light. However, the growth density was only significantly higher during light exposure at 37 °C compared to dark controls, which may indicate an alteration of aggregative behaviour of *L. monocytogenes. L. monocytogenes* is not generally assumed to exhibit flagellar motility at temperatures above 30 °C, and the observed increase in growth density at 37 °C was therefore unexpected. Bacteria have several strategies for avoiding, surviving and being able to grow in the presence of environmental stressors. The increased cellular density may protect the bacteria against light-induced damage, as the light will be absorbed more in outer cell layers compared to underlying layers. We also found that the growth inhibitory effect of light decreased when the cell-density increased in broth cultures, maybe as a result of less light reaching through to individual cells.

In the transcriptomic analysis, exposure to broad-spectrum visible light significantly altered transcription of 1336 - 1735 genes across the temperature-time conditions. Up-and down regulation among the significantly regulated genes were approximately 50/50 and in line with the results from the recent study by Dorey et al (2019) using blue light [134]. It has previously been suggested that absence of light function as a signal for pathogenic bacteria entering the human host [91]. If this is the case for *L. monocytogenes,* the presence of light signals an upcoming major change in environmental conditions which may explain why such a major shift in the transcriptomic landscape was detected in the current study.

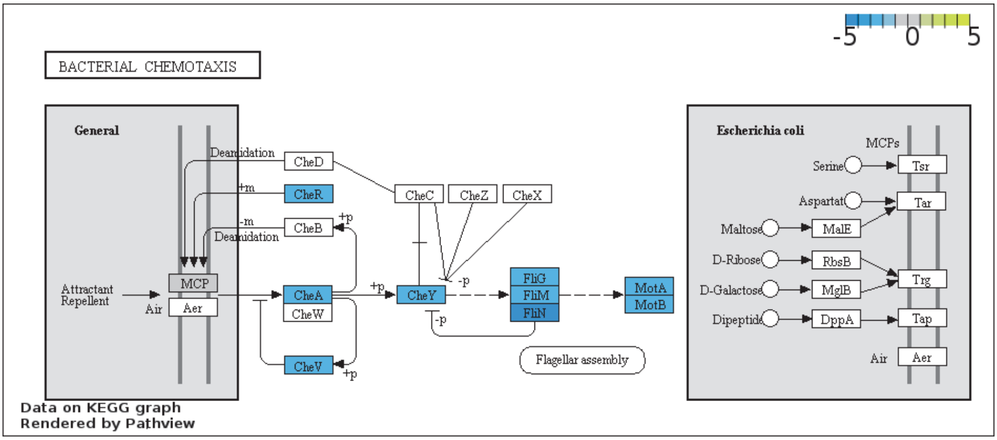
Dorey et al (2019) revealed alteration of only 10 gene-transcripts when exposing a Δ*sigB* mutant to blue light, suggesting the blue light response in *L. monocytogenes* to be almost entirely σ^B dependent [134]. However, this dependency did only appear at 30 °C, and not at 37 °C, indicating that the light-dependent σ^B pathway is of less relevance in the human host. This was supported by the current transcriptional data as *sigB* was only significantly regulated at 20 °C and not at 37 °C. However, several functional pathways in the current study were significantly regulated also at 37 °C, indicating that the light response may be activated through other routes than through the σ^B stressosome. Further, deletion mutants lacking σ^B or the blue light receptor did not show altered growth behaviour compared to the EGDe strain during light exposure on semi-solid agar. This was in contrast to the observations by Dorey et al (2019) at 37 °C, were a temperature-dependent difference in growth between the Δ*sigB* mutant strain and the wild type background appeared. However, Dorey et al., performed their growth studies in BHI broth with only blue light exposure, while the current study used semisolid BHI agar and a broad-spectrum visible light source which could explain the divergent results. Additionally, the current study performed growth studies over several days, while Dorey et al., designed a growth experiment that lasted for 6 h [134]. The light resistance observed in stationary phase compared to the exponential phase [134] may explain why the current study did not observe any difference in growth after several days.

The current results may indicate regulation of σ^B at additional levels than the transcriptional one or that additional response pathways to broad-spectrum visible light exposure, than through σ^B, might exist.

Alternative pathways for activation σ^B than through the blue light receptor have been suggested [93, 134]. One such alternative pathway could be a homologue to the red-light receptor described for *B. subtilis.* However, genes encoding the red-light receptor homologue were not found in the *L. monocytogenes* genome. Another light-responsive pathway could be through porphyrines and flavines, which are endogenous acceptors of optical radiation involved in photo inactivation of microbial cells. The large conjugated system in porphyrins absorb visible light strongly and during light exposure, they transitions to excited electronic states [135]. The excited porphyrins may then react directly with biological structures (type I reactions) or with molecular oxygen, generating excited singlet oxygen (type II reactions) [135].

Both direct damage to biological structures by excited porphyrins and damage by porphyrin-generated excited singlet oxygen, may take place in the bacterial cells during light exposure. Downregulation of endogenous photosensitizers may therefore be part of the cellular adaptation strategies to visible light. However, as no correlation between the concentration of endogenous porphyrins and the magnitude of light has been detected, it has been suggested that there could also be other factors, such as flavins, which determines the photosensitivity of microbial cells [95]. Flavins have been suggested to be light sensitizing chromophores but this has not yet been reliably confirmed experimentally [95].

The porphyrin pathway ends up reducing the cobalamin (vitamin B12) coenzyme. Vitamin B12 has been described as relevant for the bacterial response to visible light. However, no alteration growth was observed when adding vitamin B12 to the broth culture when *L. monocytogenes* was grown in the presence of broad-spectrum visible light in the current study. Further, superoxide dismutase (Lmo1439) and catalase (Lmo2785), both being important for protection against oxidative stress, were upregulated during exposure to broad-spectrum visible light at all temperature conditions tested. This may indicate that broad-spectrum visible light triggered intracellular ROS production. Also, after 180 min light exposure at 20 °C, the pentose phosphate pathway, producing NADPH, was upregulated. Production of NADPH is an important defence mechanism against ROS and may be a mechanism coming into play after a longer time of light exposure.



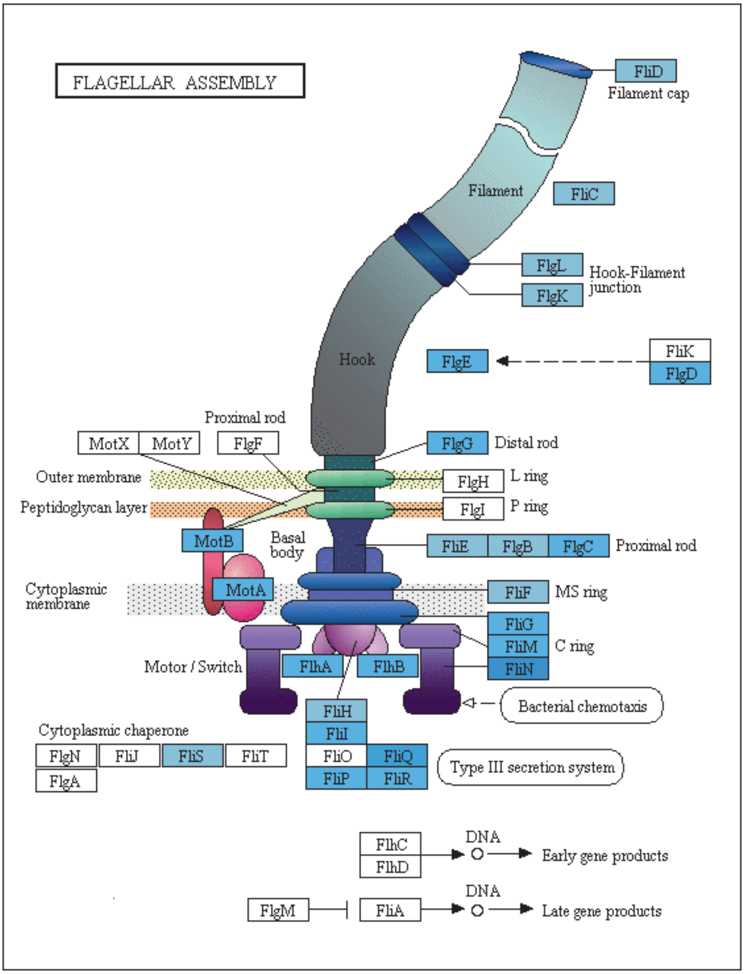


Figure 13, A and B. Significantly regulated genes in the Chemotaxis (lmo02030) (Figure 13 A) and Flagellar Assembly (lmo02040) (Figure 13 B) KEGG pathways. Data on KEGG graph is rendered by Pathview [126-128]. Blue coloured genes indicate downregulation after light exposure at 37 °C.

One of the most profound results from the transcriptomic analyses was the light-dependent downregulation of the flagellar assembly and chemotaxis genes at both 20 and 37 °C (Figure 13). Both the number of significantly regulated genes in these pathways and the altered level of transcripts, strongly indicated changes in the chemotaxis and flagella response at all temperature-time conditions tested. However, the level of downregulation during light exposure was primarily calculated relative to the same conditions in darkness. To be able to compare across temperatures, the absolute transcript levels were compared for each temperature-time condition, revealing that flagellar assembly genes were most transcribed in the dark-exposed samples at 20 °C, followed by light-exposed samples at 20 °C, controls at 37 °C and finally samples that were light exposed at 37 °C. *L. monocytogenes* has been reported to be mainly non-motile by the flagella at 37 °C, although this is a strain-dependent feature [136-139]. Finally, the transcriptomic results indicated that transcription regulation of MogR, which functions as a temperature-dependent swimming repressor of flagellar and chemotaxis genes [138, 140], appeared to be of less relevance for the light-induced effects on motility. To analyse the light-dependent gene-expression results on motility phenotypically, two food isolates (59792 and 59789, Table 2) and the EGDe strain were tested for motility in soft agar. All three strains showed the characteristic umbrella-shaped motility when incubated in darkness at 20 °C, reduced motility during light exposure, and no motility at 37 °C regardless of dark/light conditions. This highlights the importance of phenotypic testing of gene-expression results.

C-di-GMP is a small cellular second messenger molecule which is previously reported to induce the expression of an exopolysaccharide. Exopolysaccharide expression may, in turn, inhibit bacterial migration on semisolid agar, increase cellular aggregation, and confer enhanced tolerance to disinfectants and desiccation. The biochemical process behind cyclic di-GMP requires catalysation by diguanylate cyclase. In *L. monocytogenes dgcA* (lmo1911), *dgcB* (lmo1912), and *dgcC* (lmo2174) all encodes diguanylate cyclases [141]. The *dgcC* gene was consistently upregulated at all light-temperature conditions: *dgcB* was only upregulated after 20 min of light exposure at 20 °C, and *dgcA* was not upregulated at any of the conditions tested. Upregulation of *dgcC* may then have contributed to reduced motility during light exposure.

Both previous and the current study suggest that visible light-induced stress reduce flagella motility in *L. monocytogenes* [142]. Flagellar structures contribute to the virulence of multiple gastrointestinal pathogens either by making the bacteria motile, functioning as adhesins, or as secretion machineries for virulence factors [5]. In *L. monocytogenes*, the flagella have been described to be critical for biofilm formation under static hydrodynamic conditions [143] [144].

However, *L. monocytogenes* is also able to adhere to inert surfaces without involvement of flagella [145]. In *L. monocytogenes*, the flagella increases the epithelial cell invasion efficiency [5, 136]. Thus, it seems like it is the motility rather than the adhesive capacity of the flagella that plays a role in the invasion process as flagellated, but non-motile bacteria invade human epithelial cells with the same efficiency as non-flagellated and non-motile bacteria. O'Neil and colleagues further demonstrated in a mouse model that motile *L. monocytogenes* cells outcompeted non-motile derivative strains when colonizing the intestine after oral infection [5]. These results suggest that flagellum mediated motility increases the pathogenicity of *L. monocytogenes*, at least in the mouse model [5].

The *pssA-E* operon (lmo0527, lmo0531) has been linked to c-di-GMP-induced EPS biosynthesis in *L. monocytogenes* and could potentially contribute to the increased cell-wall thickness reported for *L. monocytogenes* during light exposure [141]. In the current study upregulation of *pssA-E* was detected at 20 °C, but did not result in increased EPS production according to the results from the Congo red assay. Contrastingly, at 37 °C, no transcriptional upregulation of *pssA-E* was detected, even though EPS production was observed regardless of light/dark-exposure at this temperature. This indicates that other regulatory mechanisms than *pssA-E* are involved in activating EPS production.

In *L. monocytogenes*, PrfA is the main regulator of virulence genes and plays an important role in mediating the *L. monocytogenes* transition from saprophyte to pathogen [146]. Thus, in the current study, PrfA was most upregulated after 20 min light exposure at 20 °C, before it decreased when analysed after additional 2 h. At 37 °C, the PrfA was significantly down-regulated after 20 min. The PrfA regulation is regulated both at a transcriptional level by binding to a cofactor, and at a translational level. Below 30 °C the ribosomal binding site is masked, whereas this structure melts at 37 °C and may be a key mechanism for rapid synthesis of already present PrfA trancripts when entering the host [6]. As PrfA is regulated at additional levels than the transcriptional one, the phenotypic consequence of the *prfA* upregulation is hard to predict from transcriptomic data. However, the results from the current study suggest that genes encoding the virulence factors Internalin A and Internalin B were upregulated under all light-temperature conditions tested. Internalin A and Internalin B are relevant for attachment to and invasion of eukaryotic cells [147]. These genes are previously shown to be regulated by other mechanisms than only via PrfA [148], and an intimate link beween PrfA and SigB has been suggested [146]. A previous global transcriptomic study has implicated σ^B regulation for bacterial survival in the intestine, while PrfA promotes bacterial replication in the blood [87]. Internalin A and B have also been shown to be involved in attachment of *L. monocytogenes* to abiotic surfaces [149]. As the *L. monocytogenes* seems to benefit from higher culture densities during light exposure, increased adhesiveness to surfaces could also function as a protective mechanism. As suggested for the gene responsible for actin-based intracellular motility (ActA) [101], this phenomenon could exemplify how classical virulence genes may be beneficial outside the host, thereby conserving virulence genes which may cause environmental dependent fitness costs.

The light-dependent response in *L. monocytogenes* seem complex according to the high number of light-dependent regulated genes and further mutational and phenotypic analyses are needed to confirm the role of individual factors in the bacterial response to broad-spectrum visible light. Recent techniques and methods are now being applied in several research groups for analyzing the effect of light in *L. monocytogenes*, and novel technologies are developing. This increases the likelihood for potentially applying antimicrobial effect of visible light in the food industry, both for surface decontamination and in food by coating food products with photosensitizing compounds [150-152].

Main conclusions

This PhD project revealed significant impact of stressors on the behaviour of *L. monocytogenes*, potentially having an impact on food safety.

Objective I

- Stress imposed by an alkali disinfection agent prior to inoculation of RTE food, significantly altered the growth of *L. monocytogenes* in RTE chicken and sliced deli meat. This may lead to other *L. monocytogenes* shelf life estimations than those imposed by performing traditional challenge tests in RTE chicken and sliced deli meat.
- Exposure of *L. monocytogenes* to chlorinated alkaline stress prior to inoculation of RTE chicken and sliced deli meat resulted in decreased growth potential in the RTE chicken and increased growth potential in the RTE sliced deli meat.
- An alternative challenge test protocol, including chlorinated alkaline stress of *L. onocytogenes* prior to inoculation of RTE food, is not recommended due to:
    - The potential carry-over of disinfection chemicals to the food product affecting the subsequent *L. monocytogenes* growth.
    - The challenge of standardizing the chlorinated alkaline stressed inoculum concentration and the subsequent significant impact of the inoculum concentration upon the growth potential.

Objective II

- A reduction of the NaCl content from 5 to 0.5 % in the growth media can alter the ability of *L. monocytogenes* to survive passage through a human IVD model.
- The NaCl-dependent survival in the human IVD model, may be strain-dependent.
- The intestinal phase demonstrated the importance of a functional σ^B regulon to a larger extent than the gastric phase in the IVD model.
- *L. monocytogenes* invaded epithelial cells after passage through the standardized human IVD model.
- The tenfold reduction in NaCl concentration increased the ability of *L. monocytogenes* to invade cultured cells after passage through the IVD model.

Objective III

- Exposure to broad-spectrum visible light induced major changes in the transcriptomic landscape of *L. monocytogenes*
- The effect of broad-spectrum visible light on *L. monocytogenes* is exposure time and temperature dependent.

- The effect of broad-spectrum visible light alters the phenotypic behaviour of *L. monocytogenes* during growth on semi-solid BHI plates.
- Exposure to broad-spectrum visible light conferred reduced bacterial growth and motility on semisolid BHI agar, which correlated well with the light-dependent reduction in transcription levels of flagellar and chemotaxis genes.

Future perspectives

- Further studies should be performed using single strains to determine the effect of stress imposed by disinfectants upon lag-phases and maximum growth rates of *L. monocytogenes* in food products.
- Further development for the internationally standardized IVD model should be prioritized to represent sub-populations in the listeriosis risk category. Individual physiological differences in gastric pH, pepsin content, gastric lipase levels, bile concentrations, level of proteolytic enzymes and transit time, should be considered and implemented.
- Further studies on general food-trends to include analysis of food matrix effects on the risk for listeriosis should be considered.
- *L. monocytogenes* outbreak investigations question the realistic infection dose for immunosuppressed individuals. More studies on the virulence potential of *L. monocytogenes* should be prioritized.
- The *L. monocytogenes* outbreak caused by contaminated caramel apples included listeriosis in healthy children between 5 - 15 years. This questions our understanding of the pathogenesis of listeriosis and the traditionally considered high risk groups. This should be elucidated.
- Further studies are required to elucidate whether light influences attachment of *L. monocytogenes* to abiotic and biotic surfaces, which would be relevant for food production environments.
- Despite major effort of *L. monocytogenes* to adapt to light, the inhibitory effect of light upon bacterial growth remains. This effect should be further explored in the context of finding new preventive actions for increasing food safety.
- Within food-omics, transcriptomic analysis may reveal potentially "food safety targets" in complex physiological pathways and thereby be a tool for developing novel technology to enhance food safety. The existing gene expression dataset should be used for generating new hypotheses for phenotypic testing.
- Additional -omics studies should be applied to explore the effect of light on *L. monocytogenes.* A proteomic dataset is highly relevant to add to the already consisting gene expression dataset to provide data closer to the phenotypic profile and perhaps reveal additional information on light dependent responses. Adding phosphoproteomics could also provide new information on light dependent signaling pathways.

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Scientific Papers I-III

Paper I

The impact of disinfection stressors on *Listeria monocytogenes* in challenge testing of foods

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Introduction

Listeria monocytogenes is a foodborne pathogen causing listeriosis (Schlech *et al.*, 1983; Cartwright *et al.*, 2013). The mortality rate can exceed 25% and listeriosis has the highest proportion of hospitalisation cases of all zoonotic diseases under EU surveillance (EFSA, 2017). *L. monocytogenes* infections are most commonly reported in people over 64 years old. The trend for an increase in foodborne listeriosis has been attributed to the rising proportion of older people, along with the higher consumption of ready-to-eat (RTE) food products (Cartwright *et al.*, 2013; EFSA, 2017; Rossi *et al.*, 2008).

According to the European Food Law (European Commission, 2005), the required sampling and analysis regimes are different for food products that support the growth of *L. monocytogenes* than for products that do not. Accordingly, European guidelines for conducting *L. monocytogenes* challenge tests were developed to determine whether a specific food product supports the growth of the bacterium (Beaufort *et al.*, 2014). Under these guidelines, *L. monocytogenes* should be acclimated to the temperature at which the experiment will be undertaken prior to inoculation of the food to shorten the lag phase during the challenge testing and to obtain maximum growth potential during the food's shelf life. These guidelines do not account for factors other than temperature influencing the physiological state of the inoculated strains.

L. monocytogenes contamination of RTE foods, heat-treated or not, usually occurs during food production, when the food is handled and/or is in contact with the production environment. Some *L. monocytogenes* strains can persist in food production facilities for years (Ferreira *et al.*, 2014) despite thorough cleaning and disinfection, conferring a continuous risk for contaminating production environments and food products. Persistent in-house strains are likely to be frequently exposed to washing agents and chemical disinfectants, particularly alkali treatments, which are frequently used to disinfect hard surfaces (Giotis *et al.*, 2010; Taormina and Beuchat, 2002b). The sub-lethal stress imposed by alkaline disinfectants may alter the resistance to subsequent stressors present in food products and in the human host (Giotis *et al.*, 2008; Giotis *et al.*, 2010; Segal *et al.*, 1981; Taormina and Beuchat, 2002a), resulting in altered growth potential.

Food production companies and researchers have used challenge testing to estimate the storage time up to a 100-fold increase in concentration of *L. monocytogenes*, and to assess the storage time before *L. monocytogenes* represents a food safety risk (De Cesare *et al.* 2018; Mejlholm *et al.* 2010; Pal *et al* 2008; Skjerdal *et al* 2010; Skjerdal *et al* 2014). According to the guidelines, the inoculum should be prepared to obtain immediate growth and maximum growth rate in the food products. However, an environmental contamination route, including stress imposed by a disinfectant, will alter the physiological state of the bacterial inoculum, compared with an inoculum grown under traditional laboratory conditions (Eom *et al.*, 2009). This may result in a prolonged lag phase for stressed bacteria compared with unstressed bacteria (Guillier *et al.*, 2005). If *L. monocytogenes* contamination arises from an environmental contamination route, the cells may require an extended time to recover, showing reduced growth potential in food products compared with an inoculum in good physiological condition, even if cold-adapted. The presence of environmental stressors may thus cause a discrepancy between naturally contaminated samples and challenge test data, consequently affecting food safety, food economy and food waste.

L. monocytogenes is characterised as a hardy agent, able to grow under anaerobic conditions, at high salt concentrations and under refrigeration temperatures (Chan and Wiedmann, 2009; Liu, 2008; Lorentzen *et al.*, 2010; Schirmer *et al.*, 2014). The bacterial growth rate in food can be decreased with stressors such as low pH, organic acids, nitrite, low water activity, background flora, modified atmospheres and cold temperatures (Mejlholm *et al.*, 2010; Mejlholm and Dalgaard, 2015b). These stress factors function as hurdles and are used separately or in combination to reduce the growth rate of pathogens in food products.

Underestimations of pathogen growth in food products may lead to unacceptable high risks for consumers, but overestimation of growth may lead to unnecessary food waste. Considering the effect of relevant environmental stressors on the inoculum can lead to a more realistic *Listeria* shelf life without compromising food safety. In their review, Álvarez-Ordóñez *et al.* (2015) also pointed out that comparing the European guidelines with any alternative methodology is worthwhile.

The aim of this study was to evaluate how the inoculation procedure involving pre-exposure to a commercial chlorinated alkaline disinfectant influences the growth potential of *L. monocytogenes* in RTE food products. RTE chicken and RTE sliced deli meat were chosen as food model matrices because both products are widely used, have relatively long shelf lives and have been reported as food vehicles for *L. monocytogenes* transmission (Cartwright *et al.*, 2013).

Materials and Methods

■ *L. monocytogenes* strains and food products

Eight strains of *L. monocytogenes*, previously used in challenge tests to study growth in similar meat products, were used for inoculation of RTE food products (Skjerdal *et al.*, 2010). All strains are listed in Table 1. All these strains demonstrated rapid growth at 4°C in a previous study (Skjerdal *et al.*, 2010). Two laboratory strains, whereas Scott A was used as a reference strain, were included in the cocktail for both RTE chicken and RTE sliced deli meat. The respective cocktails further contained four isolates from similar food products and from food production facilities (Table 1). Because *L. monocytogenes* strains were selectively chosen in accordance with the specific product, statistical comparison of bacterial growth between these products was not performed.

TABLE 1 / Selected in-house *Listeria monocytogenes* strains for challenge testing.

ID number	Source	Used for inoculation of	Serotype*
VI 59788	Unknown product	RTE chicken	II c
VI 59789	RTE chicken	RTE chicken	II a
VI 59790	Sliced deli meat	RTE sliced deli meat	II a
VI 59791	Sliced deli meat	RTE sliced deli meat	II a
VI 59792	Meat balls	RTE chicken and sliced deli meat	II c
VI 59793	Wiener sausage	RTE chicken and sliced deli meat	II c
NVH-FMN	Laboratory	RTE chicken and sliced deli meat	IV b
Scott A	Laboratory	RTE chicken and sliced deli meat	IV b

*Serotype analysed by PCR (ANSES 2013, ANSES 2014)

RTE chicken and sliced deli meats were used as food matrices; they are heat-treated products with a commercial shelf life of 18 and 35 days, respectively. The package size was 200 g for the RTE chicken and 100 g for the RTE sliced deli meat. Food characteristics given on the product packages from the manufacturer are described in Table 2. In total, 369 packages of RTE chicken and 189 packages of RTE sliced deli meat from three different batches were included in the challenge test studies. All food packages were kindly provided by a private food business company. Challenge tests with BHI broth (BactoTM brain heart infusion, Becton, Dickinson and Company, Sparks, MD, USA) were performed in parallel with the challenge tests using food matrices to confirm the ability of the *L. monocytogenes* strains to grow. A potential effect of stress was expected to be more readily detectable in RTE chicken than in the RTE sliced deli meat, because previous challenge tests of the latter product have documented only limited growth of *L. monocytogenes*.

TABLE 2 / Food characteristics provided by the manufacturer on the product package.

	RTE chicken	RTE sliced deli meat
Shelf life	18 days	35 days
Ingredients in 100 g	109 g chicken[a] Water Salt (1.5%) Spices (including paprika) Glucose Garlic Rapeseed and sunflower oil	58% beef and pork Water Salt Spices Glucose Onion Smoke flavouring Starch
Preservation	E262 (sodium acetate) E325 (sodium lactate)	Anti-oxidant E315 E325 (sodium lactate) E261 (potassium acetate) E326 (potassium lactate)
Nutritional content in 100 g	980 KJ 25 g protein 0 g carbohydrate 15 g fat	998 KJ 12 g protein 6.5 g total carbohydrate, including 0.2 g sugars 18.6 g fat, including 7.3 g unsaturated fat, 8.5 g monounsaturated fat and 2.4 g polyunsaturated fat 1.7 g salt
Modified atmosphere	70% CO_2 and 30% N2	Yes, but not specified
Recommended storage temperature	0-4°C	0-4°C

[a] 109 g of raw chicken was needed for 100 g of the final chicken product

■ Preparation and characterisation of inoculum

The standard inoculation culture was prepared according to EURL *Lm* Technical Guidance Document for conducting shelf-life studies on *L. monocytogenes* in RTE foods, Version 3 – 6 June 2014 (Beaufort *et al.*, 2014). In brief, strains were inoculated from frozen stocks into BHI broth and cultured separately at 37°C for 24 h. For pre-adaptation to cold, in accordance with the food storage temperature, 100 µl of each pre-culture was transferred into 9 ml of BHI broth and incubated separately for 7 days at 4°C. Following this adaptation, equal volumes of all *L. monocytogenes* cultures were pooled into a mixed culture and enumerated in accordance with part 2 of the horizontal method for the detection and enumeration of *L. monocytogenes* (Anonymous *et al.*, 2004). The mixed culture was immediately diluted in BHI and subsequently in physiological saline water (sodium chloride, Merck, Darmstadt, Germany) aiming for a *L. monocytogenes* concentration in the food of 100 colony forming units (CFU)/g when inoculating with 100 µl (Beaufort *et al.*, 2014). The dilutions in physiological saline water were applied to ensure equal and minimal carry-over concentrations of BHI between standard inoculum and the chlorinated alkaline-stressed inoculum.

For the challenge tests with disinfectant-stressed inoculum, standard cultivation methods were used, except that the bacterial suspension was not diluted because the subsequent exposure to stress was expected to reduce the level of viable bacteria. The chlorinated alkaline disinfectant Titan Hypo (Lilleborg AS, Oslo, Norway) was diluted in physiological saline water to a concentration of 0.5 or 1% after addition of 1 ml of the BHI containing bacteria. After 5 min exposure to disinfectant, 1 ml of the bacterial suspension was transferred to 9 ml of physiological saline water for dilution as suggested by Eom *et al.* (2009). Both the concentration and the exposure time were in accordance with the producers' recommendations for disinfection of environmental surfaces in food processing plants. A preliminary experiment revealed that physiological saline water and the solutions containing 0.5 and 1% of Titan Hypo had pH values (AOAC 981.12, 1982) of 6.9, 10.6 and 11.1 respectively. After adding 1 ml of BHI containing the inoculum, the pH changed to 7.2, 7.8 and 8.3, respectively. The final pH values in the inoculum samples were 7.2 for the control, 7.5 for the 0.5% solution Titan Hypo and 8.2 for the 1% solution of Titan Hypo.

Inoculation and storage of food samples

The inoculation was performed on the production date or the day after the production date, except for the last batch of RTE sliced deli meat, which due to logistical reasons were inoculated 5 days after the production date.

The product packages from three different batches were inoculated with 100 µl of the mixed cultures through a septum (ø 15 mm white, hard, PBI Dansensor A/S, Ringsted, Denmark) using a needle (0.6*25 mm) and syringe. The needle was used to spread the bacteria on the surface. The inoculated area of the food package was marked to facilitate later quantification of 25 g food matrix (De Cesare *et al.*, 2018). After inoculation, the inoculated food packages and control broth were constantly stored at 4°C until eight days after the expiry date.

The concentration of *L. monocytogenes* in the challenge test food packages and corresponding BHI tubes was assessed three times during the storage time, except for three biological replicates of RTE chicken and respective BHI tubes, which were sampled nine times during the storage period. A preliminary experiment revealed more rapid growth in RTE chicken than in RTE sliced deli meat, and the RTE chicken was therefore prioritised for more frequent sampling. Quantification of *L. monocytogenes* was performed according to a modified version of ISO 11290-2 using buffered peptone water (BPW, Oxoid, Hampshire, England) as diluent and agar *Listeria* according to Ottaviani Agosti (ALOA) and ALOA® supplement (Biomérieux, Marcy L'Etoile, France) as the agar medium (Anonymous *et al.*, 2004). BPW was used for optimal recovery of stressed cells. In each challenge test, the level of *L. monocytogenes* was determined from at least three biological and technical replicate samples. To ensure a minimal effect of the inoculation in modified atmosphere (MAP) conditions, the MAP was measured prior to inoculation and at three days post-inoculation (DanSensors MAP analyser, Ringsted, Denmark).

Characterisation of RTE chicken and sliced deli meat

Control samples from all test batches were initially analysed for natural contamination of *L. monocytogenes* using the ISO 11290-1 standard method for *L. monocytogenes* detection. The total aerobic count of the challenge test batches was analysed at the beginning and at the end of the storage period. Briefly, after blending, samples were diluted in unbuffered peptone water (UPW) (Becton, Dickinson and Company), plated on plate count agar (PCA) (Becton, Dickinson and Company) and the plates were incubated at 20°C for three days before counting colonies. The water activity (NMKL No. 168) and the pH (AOAC 981.12; 1982) were also analysed both at the start and at the end of the storage period. Additional single food packages from three different batches (n = 3) of RTE chicken and sliced deli meat were analysed for both extrinsic (MAP) and intrinsic (pH, water activity, dry matter, organic acids, NaCl and lactic acid bacteria) properties (Table 3). The analyses of pH, water activity, dry matter (NMKL No 23, 1991), organic acids (internal method of the commercial laboratory) and NaCl concentration (internal method of the commercial laboratory using the chloride concentration and silver nitrate titration) were subcontracted to a commercial laboratory. The headspace MAP analysis in the food packages was performed using the PBI DanSensors CheckMate 9900 MAP analyser according to the manufacturer's instructions. The concentrations of organic acid in the water phase was calculated from the average dry matter weight and percentage of organic acid, using Food Spoilage and Safety Predictor (FSSP) software (Mejlholm, Gunvig *et al.* 2010, Mejlholm and Dalgaard 2013).

■ Statistical analysis

The food characteristic parameters were described with the mean and standard deviation (SD). Growth potentials were calculated from the log CFU/g difference of the median at the end and the median at the start (Beaufort *et al.*, 2014). The main aim of the study was to evaluate the effect of stress, not to categorise the food products in their respective growth category set by the regulations, and growth potentials below 0.5 log CFU/g were included in the regression analysis. The growth potentials were determined at the expiry dates and eight days after the expiry dates, because the sensory shelf life of the products were normally longer than the shelf life set by the food producer. The highest estimated growth potential among batches was used for final growth potential estimation of the specific product.

Statistical analyses were performed using Microsoft Excel 2010 and STATA, version 14. Multiple linear regression analysis was used to predict the growth potential, accounting for batch, level of stress exposure of the inoculum and inoculum concentration. The multiple regression model included predictors, which reached a p-value of < 0.2 in univariate regressions. The final model was determined by backward selection to obtain variables with p-values of < 0.05. Residuals were predicted and normality tested by using the Shapiro-Wilk test. Potential outliers were evaluated by their residual and leverage values.

Results

■ Growth potential of stressed and non-stressed *L. monocytogenes* in RTE chicken and sliced deli meat

L. monocytogenes strain mixtures were pre-exposed to either 0, 0.5 or 1% chlorinated alkaline disinfectant before inoculation of RTE chicken or sliced deli meat. The inoculum concentrations and the growth potentials of the *L. monocytogenes* strain mixtures in RTE chicken and sliced deli meat are given in Tables 4 and 5 and Figure 1. Growth of *L. monocytogenes* greater than 0.5 log CFU/g was observed for at least one of the challenge test repetitions within each category, except for the 0.5% stressed inoculum in RTE sliced deli meat.

■ Growth potential of *L. monocytogenes* in RTE chicken

Disinfectant exposure resulted in a concentration-dependent reduction in the growth potential of *L. monocytogenes* in chicken. A linear regression model, which included concentration of disinfectant and inoculum concentration as predictors for the growth potential estimations, revealed a significant effect of both inoculum concentration and the level of stress after 18 days of storage. The p-values were < 0.01 and 0.02, respectively, explaining 76% of the growth potentials (adj. R-squared). Potential batch variation had no significant effect on the growth potential for either of the products. A negligible batch effect is supported by the limited inter-batch variation observed for the food characteristics (Table 3). The inoculum concentration (p = 0.02) and the level of stress (p < 0.01) both had a significant effect on the final day of storage, explaining 70% of the growth potential estimates. There was an increased difference in growth potential in the RTE chicken between the stressed and non-stressed inoculum from the expiry date to eight days post-expiry.

TABLE 3 / Means and standard deviation (SD) of product characteristics for RTE chicken and RTE sliced deli meat, n=3.

Food characteristics	Batch	RTE chicken		RTE sliced deli meat	
		Mean	SD	Mean	SD
Total aerobic count, day 0 (Log CFU/g)	1, 2 and 3	1.75	0.23	1.91	1.08
pH, day 0		6.41	0.02	5.93	0.06
Water activity, day 0		0.98	0.00	0.97	0.01
Detection of *L. monocytogenes* in 25 g, day 0		ND[a]	ND	ND	ND
Total aerobic count, last day of storage (log CFU/g)	1, 2 and 3	6.86	0.37	7.07	0.66
pH, last day of storage		6.47	0.07	5.70	0.17
Water activity, last day of storage		0.98	0.00	0.97	0.00
Detection of *L. monocytogenes* in 25 g, last day of storage		ND	ND	ND	ND
Initial concentration of lactic acid bacteria (log CFU/g)	4, 5 and 6	1.70	0.19	1.90	0.44
NaCl (%)[b]		1.0	0.02	2.50	0.04
Dry matter (g/100 g)		34.9	0.67	37.2	0.59
pH		6.40	0.06	5.90	0.00
CO2 % in headspace gas at equilibrium		55.0	0.91	2.30	0.26
N2 % in headspace gas at equilibrium		45.0	0.92	97.7	0.28
O2 % in headspace gas at equilibrium		0.1	0.01	0.1	0.01
Nitrite (ppm)		<0.16	-	4.50	1.85
Acetic acid (ppm)[b]		307	17	981	40
Citric acid (ppm)[b,c]		56	6	-	-
Lactic acid (ppm)[b]		12096	82	17224	159

a Not detected (ND).
b In the aqueous phase of the product
c Values below the level of quantification (LOQ = 20) increased due to matrix effects and were <59, <99 and <63 for the three tested samples of sliced deli meat

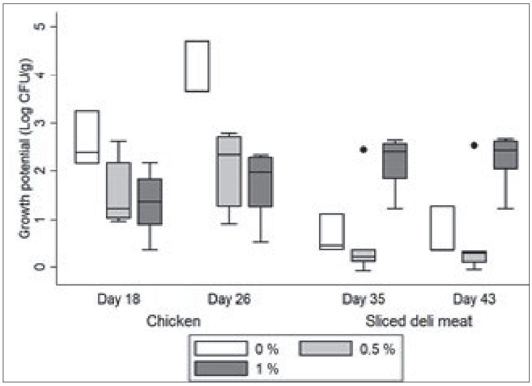

FIGURE 1 / Growth potentials of *L. monocytogenes* (log CFU/g) in RTE chicken and sliced deli meat at the expiry date (18 and 35 days, respectively) and eight days past the expiry date after exposure of the inoculum to 0, 0.5 and 1% chlorinated alkaline disinfection stress (n=3-5). Each box indicates the median (middle line in the box), the 25th (lower line of the box) and 75th (upper line of the box) percentiles, lower and upper adjacent value (single line) and outliers (dots)

Due to a potential compartment effect in solid foods, we compared the impact of disinfection on the growth parameters using BHI broth, representing more homogenous growth conditions than RTE chicken. The 1% stressed inoculum clearly demonstrated larger variance in *L. monocytogenes* concentration throughout the storage period, compared with the 0.5% stressed cells and the control (Figure 2).

■ Growth potentials of *L. monocytogenes* in RTE sliced deli meat

According to the linear regression model, disinfectant exposure resulted in a concentration-dependent increase in the growth potential in sliced deli meat (Table 4, 5 and Figure 1). In RTE sliced deli meat, stress and inoculum concentration had significant effects, with p-values of < 0.01 at both the expiry date and eight days past the expiry date and explained 89 and 86% of the observed growth potentials, respectively. One observation in the 0.5% stress exposed group for sliced deli meat (Figure 1) was defined as an outlier, because its residual value was 4.2 with a leverage of 0.8; it was therefore excluded from the regression model.

FIGURE 2 / Growth of a *L. monocytogenes* cocktail consisting of six strains (log CFU/g) in BHI broth and in RTE chicken from day 0 to day 26 (eight days post-expiry) after exposure of the inoculum to 0, 0.5 and 1% chlorinated alkaline disinfection stress (n=3-5). Each box indicates the median (middle line in the box) and the 25th (lower line of the box) and 75th (upper line of the box) percentiles. The high concentration of *L. monocytogenes* in BHI at day 26 may be due to sedimentation of cells.

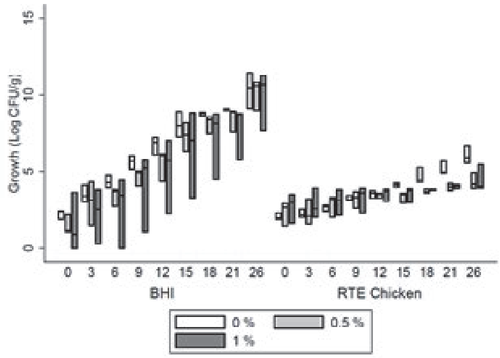

TABLE 4 / Challenge test data on RTE chicken.

			Expiry date		Eight days past expiry date	
Batch[a]	**Desinf.**[b]	**Day 0**[c]	**Day 18**[c]	**δ**[d]	**Day 26**[c]	**δ**[e]
1	0	2.3	4.5	2.2	6.0	3.7
2	0	1.9	4.3	2.4	5.6	3.7
3	0	2.0	5.3	3.3	6.7	4.7
1	0.5	1.5	3.7	2.2	4.2	2.7
2	0.5	2.7	3.7	1.0	3.9	1.3
3	0.5	2.9	3.9	1.0	4.9	2.0
3	0.5	2.8	3.9	1.1	5.4	2.6
3	0.5	1.0	3.6	2.6	4.6	0.9
3	0.5	3.3	4.7	1.3	6.1	2.8
1	1	1.7	3.8	2.2	4.0	2.3
2	1	3.5	3.9	0.4	4.1	0.5
3	1	3.0	3.9	0.9	5.4	1.3
3	1	2.0	3.8	1.8	4.2	2.2
3	1	2.0	3.8	1.7	4.3	2.3
3	1	3.6	4.5	1.0	5.4	1.8

[a] The original batch
[b] Level of chlorinated alkaline stress (%)
[c] Concentration on day 0, 18 and 26 (log CFU/g)
[d] Growth potential at expiry date (δ, log CFU/g)
[e] Growth potential eight days past expiry date (δ, log CFU/g)

TABLE 5 / Challenge test data on RTE sliced deli meat.

			Expiry date		Eight days past expiry date	
Batch[a]	**Desinf.[b]**	**Day 0[c]**	**Day 35[c]**	**δ[d]**	**Day43[c]**	**δ[e]**
1	0	2.2	2.5	0.4	2.5	0.4
2	0	2.4	3.5	1.1	3.7	1.3
3	0	1.9	2.4	0.4	2.3	0.4
1	0.5	3.3	3.6	0.4	3.6	0.3
2	0.5	3.8	4.1	0.2	4.2	0.3
2	0.5	4.0	4.1	0.1	4.1	0.1
2	0.5	1.5	3.9	2.5	4.0	2.6
3	0.5	3.8	3.7	-0.1	3.8	0.0
1	1	2.5	3.7	1.2	3.7	1.2
2	1	1.6	4.0	2.4	4.1	2.4
2	1	1.3	3.9	2.6	4.0	2.7
2	1	1.3	4.0	2.7	3.9	2.6
3	1	1.8	3.6	1.8	3.8	2.0

[a] The original batch
[b] Level of chlorinated alkaline stress (%)
[c] Concentration on day 0, 35 and 43 (log CFU/g)
[d] Growth potential at expiry date (δ, log CFU/g)
[e] Growth potential eight days past expiry date (δ, log CFU/g)

■ Characteristics of the food

Prior to inoculation, *L. monocytogenes* was not detected in any of the challenge test batches used. Regarding potential alteration of the MAP during inoculation, the inoculation procedure was evaluated as satisfactory, as shown in Table 6. The aerobic viable count increased in the challenge test batches of RTE chicken from an average ± standard error of the mean (SEM) of 1.8 ± 0.1 log CFU/g on the day of inoculation to 6.9 ± 0.2 log CFU/g at eight days after the expiry date (Table 3). In RTE sliced deli meat, the aerobic viable counts increased from 1.9 ± 0.3 log CFU/g on the day of inoculation to 7.1 ± 0.2 log CFU/g at eight days after the expiry date (Table 3). The water activity was consistent in both product types during storage and was considered to have a stable impact on *L. monocytogenes* growth during storage: 0.98 in the RTE chicken and 0.97 in the RTE sliced deli meat (Table 3). The pH was also stable in both products: 6.4 ± 0.0 and 5.9 ± 0.0 on the day of inoculation and 6.5 ± 0.0 and 5.7 ± 0 eight days after the expiry date in RTE chicken and sliced deli meat, respectively (Table 3). Additional characteristics of one sample, from three different batches of RTE sliced deli meat and RTE chicken, are also shown in Table 3. The level of dry matter was 34.9 ± 0.4% in the RTE chicken and 37.2 ± 0.3% (average ± SEM) in the RTE sliced deli meat (Table 3), and was used as input for the FSSP to calculate organic acid concentrations in the water phase of the products.

TABLE 6 / Control measurements of modified atmosphere packaging (MAP) 3 days after inoculation, means and standard deviation (SD), n =3, for CO_2, N_2 and O_2.

	CO_2 (%)		N_2 (%)		O_2 (%)	
	Mean	**SD**	**Mean**	**SD**	**Mean**	**SD**
RTE chicken, inoculated	56.1	0.5	43.9	0.5	0.0	0.0
RTE chicken, non-inoculated	53.8	0.6	46.2	0.6	0.1	0.1
RTE sliced deli meat, inoculated	2.6	0.4	97.3	0.4	0.1	0.0
RTE sliced deli meat, non-inoculated	2.4	0.1	97.5	0.1	0.1	0.0

Discussion

■ General considerations of the growth potential estimations

Maximising food safety and product shelf life and determining criteria for the withdrawal of foods require a correct estimation of the growth potential of *L. monocytogenes* in RTE foods at realistic production conditions. This study compared *L. monocytogenes* growth in RTE foods with a traditional inoculum preparation method and an alternative method including an environmental stressor, frequently used in food processing facilities. This new protocol for inoculum preparation was assumed to simulate a more realistic contamination route than the standard prepared inoculum for challenge testing. The "*Listeria* shelf life" of specific foods is often set as the time needed for a 2 log CFU/g increase in the *L. monocytogenes* level, based on the assumption that the concentration of *L. monocytogenes* is 1 CFU/g immediately after contamination. According to the guidelines for challenge tests (Beaufort *et al.*, 2014), the most important factors affecting *Listeria* shelf life and bacterial growth potential in food products are the properties of the inoculated strain(s), the inoculation level, the physiological state of the inoculated bacterial cell(s), the intrinsic properties of the food (*e.g.* pH, NaCl content, aw, associated microflora and antimicrobial constituents) and the extrinsic properties (*e.g.* time-temperature profile, gas atmosphere and moisture). The possible impact of these properties is assessed below.

All strains in the current study were either strains isolated from similar food products, or laboratory strains. Due to the food-matrix-specific composition of strains, to prepare a representative inoculum, only four of the strains were represented in both inoculums. Due to the different strains in the two products, the observed growth kinetic data for the two products cannot be compared and must be assessed separately.

As expected, the inoculation concentration significantly influenced the estimation of growth, and the inoculation concentration thereby had to be included in the linear regression analysis when analysing factors affecting growth potential. In contrast to naturally contaminated samples, where starting inoculum concentrations usually are below 1 log CFU/g (Beaufort *et al.*, 2007; Mejlholm *et al.*, 2015a; Pouillot *et al.*, 2007; Skjerdal *et al.*, 2014), the current study used starting concentrations between 1 and 4.0 log CFU/g. The European guidelines recommend a contamination level of 100 CFU/g in the food. However, one study claimed that the bacterial cell-to-cell variability has serious consequences for the challenge test design and that the inoculum concentration should be 3 log CFU/g to reach an acceptable level of variability and a consistent estimation of pathogen behaviour (Francois *et al.*, 2006). A low initial concentration of *L. monocytogenes* may also reduce growth potential due to lower ability to compete with the background flora and to the Jameson effect (Mellefont *et al.*, 2008). On the other hand, high inoculum concentrations may reduce the duration of the exponential growth phase, which may also lead to underestimation of growth potential (Francois *et al.*, 2006; Lardeux *et al.*, 2015). In the present study, the stressed inoculum concentration was challenging to standardise, despite preliminary studies and efforts to standardise the inoculum procedure. The protocol used in the current study may therefore introduce a bias to the growth potential estimates, as shown by the current results and by others (*e.g.* McManamon *et al.*, 2017). The stress exposure through the addition of a disinfectant agent in the current study likely introduced other caveats. However, removing any residual disinfectant agent by centrifugation prior to inoculation would not be representative of an environmental contamination route. Another alternative would be to use a reagent that chemically neutralises the stressor effect, but this is unrealistic for a natural contamination route and residuals from the neutralisers, which are not naturally present in the food industry plants, may potentially interact with the pathogen and the food matrix. Thus, it is difficult to make a stressed inoculum that contains a predictable concentration of bacteria and that is also representative of a realistic contamination route.

In addition to imposing increased stress on the inoculum, the disinfectants may have raised the pH of the food matrices, at least locally, which may have influenced the bacterial growth potential in the foods. If so, this pH effect can explain the contrasting effects of disinfectants in the chicken meat and in the sliced deli meat. Despite a 10-fold dilution of the disinfectant, disinfectant residues may interfere differently with the intrinsic qualities of the RTE chicken matrix compared with the sliced deli meat matrix. For example, the pH ranged by one unit between the stressed and non-stressed inoculum; thus the pH may change in the food matrix due to a carry-over effect of the alkaline disinfectant. The pH of chicken meat is closer to the optimum pH for growth of *L. monocytogenes* than the pH of sliced deli meat. A slightly increased pH due to the carry-over of disinfectants from the stressed inoculum could therefore lower the growth potential in chicken meat due to stress imposed on the bacteria, but give more favourable growth conditions in sliced deli meat due to a more favourable pH. However, higher pH in microenvironments in the inoculated samples due to carry-over of disinfectant was not possible to measure, because larger sample sizes are needed for pH measurements.

The decreasing growth potential in the RTE chicken may be due to a reduced physiological state of the bacterial cells after chlorinated alkaline stress (Eom *et al.*, 2009). Eom *et al.* (2009) reported that exposure to sodium hypochlorite affects both the lag-phase and the specific growth rate of *L. monocytogenes* strains. At 4°C, 75 ppm of sodium hypochlorite results in a higher specific growth rate than pre-exposure to 25 ppm, in broth and in a food matrix simulating crab meat (Eom *et al.*, 2009).

The food-specific intrinsic qualities also affect the behaviour of *L. monocytogenes* (Mejlholm *et al.*, 2015). An important difference between the RTE chicken and the sliced deli meat matrices is sodium nitrite, which is present in the sliced deli meat, but not in the chicken. Castellani and Niven (1955) showed that the bacteriostatic effect of nitrite was inversely proportional to pH. The chlorinated alkaline disinfectant may confer a local pH increase in the sliced deli meat during the inoculation procedure and thereby reduce the negative effect of nitrite and organic acids on the growth of *L. monocytogenes*.

The water activity and pH values were also consistent in both product types during storage. The variations in food characteristics in the current study are therefore not likely to provide any significant bias to the results.

■ Growth kinetics in RTE chicken versus BHI broth after stressing the inoculum

Due to the matrix effect in complex food products such as RTE chicken, it is also useful to analyse the effect of disinfection upon the growth in BHI broth, which is a more homogenous substrate. Therefore, RTE chicken and BHI broth were inoculated in parallel to compare the effect of disinfectant on growth of *L. monocytogenes*. The 1% stressed cells in broth clearly demonstrated larger variance in the concentration of *L. monocytogenes* than the 0.5% stressed cells and the controls throughout the storage period. The challenge of standardising the inoculum concentration when stressing the cells with disinfection was thereby further confirmed throughout the storage period (Figure 2).

■ Impact of sub-lethal stress on product categorisation according to EU microbiological criteria

According to the results from the current study, the level of stress imposed by the chlorinated alkaline disinfectant would not affect how the regulations categorise RTE chicken depending on growth potential. Except for one outlier in the 0.5% category of RTE sliced deli meat, all inoculated batches demonstrated *L. monocytogenes* growth levels of 0.5 log CFU/g or more, and are thereby categorised as “Ready to eat foods, able to support the growth of *L. monocytogenes* other than those intended for infants and special medical purposes” (Category 1.2) (European Commission, 2005). Nevertheless, the effect of disinfectant stress on the inoculum would affect how the food business operator would define a proper shelf life for this product.

The effect of chlorinated alkaline stress prior to contamination may have the potential to significantly alter the estimated concentration of *L. monocytogenes* in food products, thereby affecting food safety, food waste and the economy of the food industry. Further studies should be performed using single strains to determine the effect of stress imposed by disinfectants upon lag-phases and maximum growth rates of *L. monocytogenes* in food products.

Conclusion

The current study revealed significant changes in the growth potential of *L. monocytogenes* when the inoculum was pre-exposed to a commercial alkaline disinfection agent, consequently affecting the shelf life in terms of food safety. However, it is not clear whether the effect of the disinfectant was related to increased pH in the food matrix due to carry-over into the food matrix or to a change in the physiological condition of the inoculated bacteria. Furthermore, the significant impact of the inoculum concentration on growth potential and the challenge standardising the day 0 contamination levels indicate that the alternative method for inoculum preparation including stress is not recommended when performing traditional challenge tests with *L. monocytogenes* in RTE chicken and sliced deli meat.

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Paper II

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Survival of *Listeria monocytogenes* during *in vitro* gastrointestinal digestion after exposure to 5 and 0.5 % sodium chloride

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ABSTRACT

The food industry is under pressure to reduce the NaCl content in food, but the consequences on the ability of *L. monocytogenes* to survive in the human host and cause listeriosis is not known. In this study, a recently developed internationally harmonized static *in vitro* digestion (IVD) model was used to investigate the survival of *L. monocytogenes* in the gastric and intestinal phases after exposure to 5 or 0.5% NaCl. Six isolates from three Scandinavian foodborne listeriosis outbreaks, all related to NaCl containing foods, the EGDe reference strain and an EGDe mutant, deleted for the major stress regulator gene, *sigB,* were included. A ten-fold reduction of NaCl in the cultivation media significantly reduced the survival fraction of the EGDe strain in the IVD model while one of the clinical outbreak isolates showed a significantly increased survival fraction. Finally, the EGDe strain was able to attach and invade cultured HT-29 cells after passage through the IVD model. Altogether, these results suggest that a reduction of the NaCl content from 5 to 0.5% prior to exposure to the IVD model has the potential to cause a change in the relative survival fraction and that the effect is strain dependent.

1. Introduction

Listeria monocytogenes is a food-borne pathogen that causes the serious disease listeriosis in humans (Schlech et al., 1983). Listeriosis has the highest case fatality rate among all foodborne zoonotic diseases surveilled under the EU system (EFSA, 2017). In particular, immunosuppressed individuals, elderly, pregnant woman, fetuses and infants are at higher risk for invasive listeriosis. Despite improved control measurements since the 1990s, which have greatly reduced the prevalence of *L. monocytogenes* in many food products (Buchanan et al., 2017) there is an increase in invasive listeriosis reported within the EU (EFSA, 2018).

NaCl is one of the most widely used food preservatives but, today, the human intake of NaCl is considered to be too high (Kloss et al., 2015). Excessive dietary intake of NaCl, often related to commercially processed food, may lead to vascular hypertension and subsequent cardiovascular disease, the leading cause of death worldwide (Strazzullo et al., 2009). The food industry is therefore under great pressure to reduce the NaCl content in ready-to-eat (RTE) foods (Anderson et al., 2010). Several studies have explored the inhibitory effect of NaCl on the growth of *L. monocytogenes* in food and found it tolerant to high levels of salt stress (Bergholz et al., 2010; Lorentzen et al., 2010; Schirmer et al., 2014). Some of the genes responsible for such osmotolerance are under regulation of Sigma B, which is a key regulator for the *L. monocytogenes* stressosome (NicAogáin and O'Byrne, 2016). Sigma B regulates transcription of several virulence and stress-associated genes including those that facilitate survival during passage through the gastrointestinal system (NicAogáin and O'Byrne, 2016). Previous studies have also identified Sigma B as a critical regulon for *L. monocytogenes* to survive adverse and fluctuating stressors present in the gastro-intestinal tract. However, this has not been simulated by exposure to both the gastric and intestinal environment and by including key digestive enzymes (Garner et al., 2006; Sue et al., 2004).

Survival in the gastro-intestinal tract is a biological key-event for dose-response models (Buchanan et al., 2009). It has been described that the environment *L. monocytogenes* encounters prior to infection may influence its survival fitness in the human host and its pathogenic potential (Gahan and Hill, 2014). Previous studies report that pre-exposure to elevated osmolarity (0.3 M NaCl for 1 h) increases the tolerance of *L. monocytogenes* to lethal concentrations of bile (Begley et al., 2002; Sleator et al., 2009). RTE foods can impose a number of environmental stressors on *L. monocytogenes*, such as osmotic stress (NaCl

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or sugars), organic acid stress (fermentation), acidic pH and cold stress (refrigeration). However, there is still limited knowledge about how these factors influence the survival and fitness of the pathogen *in vivo*.

In vitro digestion models are widely used within food science as *in vivo* models are costly and may raise ethical issues (Minekus et al., 2014). However, the use of different non-standardized models for simulating the human digestive system has proved to be inconsistent when comparing results across research groups. Therefore, an international consensus for static *in vitro* digestion models was published in 2014 (Minekus et al., 2014) and harmonized by several laboratories in 2015 (Egger et al., 2016). The standardized *in vitro* digestion model was documented to be physiologically comparable to *in vivo* porcine digestion of skim milk powder with regard to protein degradation and peptide formation (Egger et al., 2017).

Responses to stressors in the food matrix may facilitate the survival of *L. monocytogenes* through the human digestive system and increase the number of cells able to invade intestinal epithelial cells (NicAogain and O'Byrne, 2016). The current study explores how adaptation to different levels of NaCl stress influences *L. monocytogenes* survival in the digestion system by using an internationally harmonized static *in vitro* digestion (IVD) model (Minekus et al., 2014). To study the importance of the stressosome regulator Sigma B for survival through the digestive barriers, an EGDe Δ*sigB* mutant strain was included in the study. To our knowledge, this is the first time that survival of a foodborne pathogen has been tested under gastrointestinal conditions using the standardized *in vitro* digestion model (Minekus et al., 2014).

2. Materials and methods

2.1. Selection of L. monocytogenes isolates and strains

Scandinavian outbreak isolates used in the current study are shown in Table 1. In general, *L. monocytogenes* food isolates from outbreaks are often challenging to get hold of due to the long clinical incubation time and the relatively short shelf life of the food products. The Norwegian isolate was from an outbreak in 2007, involving 17 patients and causing three deaths (Johnsen et al., 2010). The Danish isolate was from RTE spicy meat roll and collected during an outbreak in 2013/2014, which involved 41 cases, including 17 fatalities (Kvistholm Jensen et al., 2016). The Swedish isolates include two food isolates and two clinical isolates from a Swedish outbreak in 2013/2014, which involved 48 patients. All the Swedish outbreak isolates belonged to the same sequence type (ST-7) (Dahl et al., 2017). Whole genome sequencing revealed that the Patient 2 isolate differed by eight single nucleotide polymorphisms (SNPs) compared to the Patient 1 isolate and the food isolates (Dahl et al., 2017). The eight SNPs were found in genes encoding 6-phospho-beta-galactosidase, 30S ribosomal protein, endoglucanase, tRNA-binding protein, peptidase, cell surface protein and glycerol dehydratase (Cecilia Jernberg, Public Health Agency, Sweden, personal communication). The EGDe reference strain and an EGDe Δ*sigB* mutant are previously described (O'Donoghue et al., 2016) (Table 1).

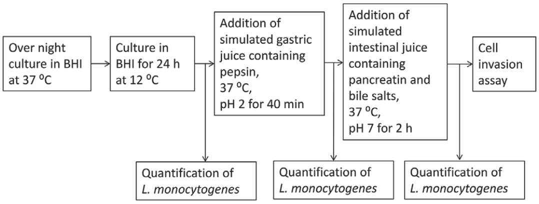

Fig. 1. Overview of the study design.

2.2. Exposure to NaCl

The experimental setup is outlined in Fig. 1. All isolates were grown in Brain Heart Infusion media (BHI, 237500, Bacto™ Becton, Dickinson and Company, Sparks, MID 21152 USA, 38800 Le Pont de Claix, France) to simulate the nutrient-rich environment of meat and other foods which are often associated with foodborne listeriosis (U.S Food and Drug Administration, 2003). The bacteria were first grown statically in a first pre-culture at 37 °C overnight and then transferred to a second pre-culture containing either 0.5% NaCl or 5% NaCl to simulate exposure to different salt concentrations in the water phase of food products. The second pre-culture was grown statically at 12 °C to simulate the growth conditions in solid food and temperature abuse (James et al., 2017). To reach a bacterial density of approximately 8 Log CFU/ml after 24 h of growth in pre-culture 2, different volumes of pre-culture 1 were transferred to pre-culture 2 to reach a total volume of 5 ml. Due to a lower growth rate at 5% NaCl than at 0.5% NaCl, 1 ml of pre-culture 1 was transferred to 4 ml of pre-culture 2 at 5% NaCl, and only 0.5 ml was transferred to 4.5 ml of pre-culture 2 at 0.5% NaCl. In pre-culture 2, *L. monocytogenes* was statically grown in 100 ml bottles with screw cap (not tightened) and wrapped in aluminum foil to ensure no exposure to light during the experiment.

2.3. Static in vitro digestion

A standardized *in vitro* digestion model was used to simulate the human gastrointestinal condition (Minekus et al., 2014). The digestive fate in the stomach and small intestine was investigated, while the oral phase was omitted since starch was not included in the substrate. After 24 h of growth in pre-culture 2, the bacteria were directly exposed to simulated gastric juice (Minekus et al., 2014). The time of gastric digestion for a liquid is reported to be between 5 and 45 min at 37 °C (Camilleri et al., 1989). The exposure time to pH 2 and porcine pepsin (2000U/ml, Sigma P7012) was therefore limited to 40 min and the incubation was performed at 37 °C with shaking (100 rpm). Subsequently, to simulate the intestinal phase, the pH was adjusted to 7 by adding 1 M NaOH, porcine pancreatin (trypsin 100U/ml, Sigma P7545) and porcine bile salts (10 mM, Sigma B8631) were added to the

Table 1
Isolates and strains used in the static *in vitro* digestion experiments.

Isolate	Reference	Isolated from	Provided by	Serogroup
1	EGDe wild type (O'Donoghue et al., 2016)	Rabbit	**	IIa (I/2a)
2	EGDe Δ*sigB* (O'Donoghue et al., 2016)	Laboratory	**	IIa (I/2a)
3	Outbreak, Norway (Johnsen et al., 2010)	Cheese brine	***	IIa (I/2a)
4	Outbreak, Denmark (Kvistholm Jensen et al., 2016)	Ready-to-eat spiced meat roll	****	IIb
5	Outbreak, Sweden* (Dahl et al., 2017)	Liver patê	*****	IIa
6	Outbreak, Sweden* (Dahl et al., 2017)	Boiled medwurst	*****	IIa
7	Outbreak, Sweden* (Dahl et al., 2017)	Patient 1	******	IIa
8	Outbreak, Sweden* (Dahl et al., 2017)	Patient 2	******	IIa

*Belong to the same outbreak. ** Department of Molecular Biology, Umeå University. *** Norwegian Veterinary Institute. ****National Food Institute, Technical University of Denmark. ***** National food agency, Sweden. ****** The public Health Agency of Sweden.

bacterial cultures. The cultures were then incubated for an additional 120 min at 37 °C with shaking (100 rpm). *L. monocytogenes* was quantified at the start and after each digestive step by plating tenfold dilution in BPW (Buffered Peptone Water ISO, CM 1049, Oxoid) on bovine blood agar plates (CM 02071, Oxoid). The pH was measured in all 48 samples during the intestinal phase (PHM92 LAB pH meter, Radiometer Copenhagen) but due to practical considerations, detailed pH measurements were performed for only 20 samples from the gastric phase. However, the pH was measured in all samples using pH indicator strips at the start of each digestive step, immediately after addition of the respective gastrointestinal enzymes and chemicals (Merck, 1.09584.001). For all strains and conditions, three independent experiments were performed.

2.4. Cell culture assay

HT-29 cells were grown overnight to 80% confluency in 24 well culture plates, using 0.6 ml of McCoy's 5A Modified Medium supplied with 10% fetal bovine serum. The cells were incubated at 37 °C in a 5% (vol/vol) CO_2 atmosphere. Six ml of the EGDe strain suspension, collected after passage through the intestinal phase of the IVD model, was washed once in PBS, centrifuged (10000 rpm, room temperature) and thereafter re-suspended in 1100 µl McCoy's Modified Medium. A volume of 100 µl of the bacterial suspension was diluted and spread on blood agar plates for bacterial enumeration.

For invasion assays, six ml of the EGDe strain suspension collected after passage through the intestinal phase of the IVD model was washed, as described above, and added to cell monolayers. After incubation at 37 °C for 1.5 h, the cell culture plates were washed three times in McCoys Modified Medium. A volume of 500 µl McCoy's Modified Medium supplemented with 1 mg/ml gentamicin (Sigma) was then added to each well of the cell culture plates to kill non-invading bacteria, and the plates were incubated for an additional 1.5 h under the same conditions. The monolayers were then washed with PBS and lysed with 250 µl of ice-cold 0.1% (vol/vol) Triton X-100 (Sigma) in PBS and spread on blood agar plates. The invasion capacity was determined by dividing the number of invading bacterial cells with the total number of bacterial cells added, multiplied by 100. Overnight cultures of the *L. innocua* CCUG 15531 and the EGDe strain (not exposed to the IVD model) were included as negative and positive controls, respectively.

2.5. Statistics

Linear regression analysis, oneway ANOVA and pairwise comparison of means (the pwmean command) were performed using Stata, version 14. When the oneway ANOVA subsequent Bartlett's test for equal variances was significant, the Kruskal-Wallis equality-of-populations rank test was used. Residuals from the linear regression analysis were considered normally distributed by graphical histogram display. P-values equal to or below 0.05 were considered significant.

3. Results

3.1. The effect of different NaCl concentrations on L. monocytogenes survival during gastrointestinal digestion using the IVD model

The average bacterial concentration for all isolates before exposure to the gastric juice, independently of the NaCl concentration, was 8.2 Log CFU/ml (CI: 8.1–8.2, n = 48) (Fig. 2). After the gastric phase, an average bacterial concentration of 3.3 Log CFU/ml (CI 3.1–3.5) was observed (not including the *ΔsigB* mutant). After the intestinal phase the average bacterial concentration was 3.4 Log CFU/ml (CI 3.2–3.5) (not including the *ΔsigB* mutant). The concentration of each strain during the IVD model is shown in Fig. 2.

Oneway ANOVA analysis of the EGDe strain and the outbreak isolates altogether, did not reveal any significant difference in survival in the IVD model depending on exposure to different NaCl concentrations. However, when analyzing the effect of the ten-fold reduction in NaCl for individual strains, the survival fraction after passage through the whole IVD model was significantly ($P < 0.01$), but contrastingly altered for the EGDe strain and one of the Swedish patient isolates (nr 1) (Fig. 3). The EGDe strain demonstrated a significantly reduced survival fraction while the Swedish patient 1 isolate demonstrated a significantly increased survival fraction when the NaCl concentration was reduced. The EGDe strain showed a significantly higher survival fraction ($P = 0.05$) in the intestinal phase when it was exposed to 5% NaCl compared to 0.5% NaCl. In contrast, the Swedish patient 1 isolate did not show any significantly altered survival in individual digestive phases depending on exposure to different NaCl concentrations, but only when considering both the gastric and intestinal survival fractions together (Fig. 3).

A pairwise comparison of means of the total survival fraction through the IVD model, after exposure to 5% NaCl, revealed no significant difference between the EGDe strain and/or between the outbreak isolates. However, the *ΔsigB* mutant strain demonstrated a significantly lower total survival fraction compared to its EGDe background strain ($P = 0.01$). The reduced survival fraction of the *ΔsigB* strain, after exposure to 5% NaCl, could only be observed in the intestinal phase ($P < 0.01$). A pairwise comparison of means between the strains of the total bacterial survival fraction through the IVD model, after exposure to 0.5% NaCl, only revealed a significant difference between the EGDe strain and the Danish meat roll isolate ($P = 0.05$). The *ΔsigB* strain demonstrated a survival fraction similar to its EGDe background strain. Subsequent analysis of the survival fractions in the gastric and intestinal phase separately, after exposure to 0.5% NaCl, revealed no significant difference between EGDe and the *ΔsigB* mutant strain, or the Danish meat roll isolate. All the outbreak isolates and the EGDe strain demonstrated similar survival fractions in the gastric phase. However, in the intestinal phase, the Norwegian outbreak isolate and both Swedish clinical isolates demonstrated significantly increased survival ($P \leq 0.05$) compared to the EGDe strain.

3.2. Invasiveness in HT-29 cells after passage through the IVD model

To study the ability of *L. monocytogenes* to invade epithelial cells after passage through the IVD model, a cell culture assay with HT-29 cells was applied immediately after the intestinal phase. The experiments were limited to the *L. monocytogenes* EGDe strain, exposed to 5 or 0.5% NaCl and the IVD model. The observed invasion percentage in HT-29 cells ranged from 0.0 to 0.4% and 1.3–7.6% when the EGDe strain was exposed to 5 and 0.5% NaCl, respectively (Table 2). Oneway ANOVA analysis revealed a significant result according to Bartlett's test for equal variances ($Prob > chi2 = 0.01$) when analyzing the effect of the NaCl concentration upon cell invasiveness by the EGDe strain. Therefore, the Kruskal Wallis test was used. This test indicated a significantly increased ability of the EGDe strain to invade HT-29 cells after a tenfold reduction in the NaCl concentration ($X^2 = 3.9$, $P = 0.05$). Control experiments of the assay with overnight cultures of *L. innocua* CCUG 15531 and *L. monocytogenes* EGDe strain not pre-exposed to the IVD model confirmed that *L. innocua* CCUG 15531 were not able to invade HT-29 cells while the *L. monocytogenes* EGDe strain was (data not shown).

3.3. Strain dependent survival through the IVD model, regardless of NaCl concentration

In order to assess the isolate variability and simulation of complex RTE foods, which contain a range of different NaCl concentrations, the survival fraction for both NaCl concentrations were pooled for each isolate. Linear regression analysis resulted in significant impact of the isolate upon total digestive survival ($Prob > F < 0.01$, Adj. R-squared = 0.35 and F(7,40)) Only the *ΔsigB* mutant demonstrated

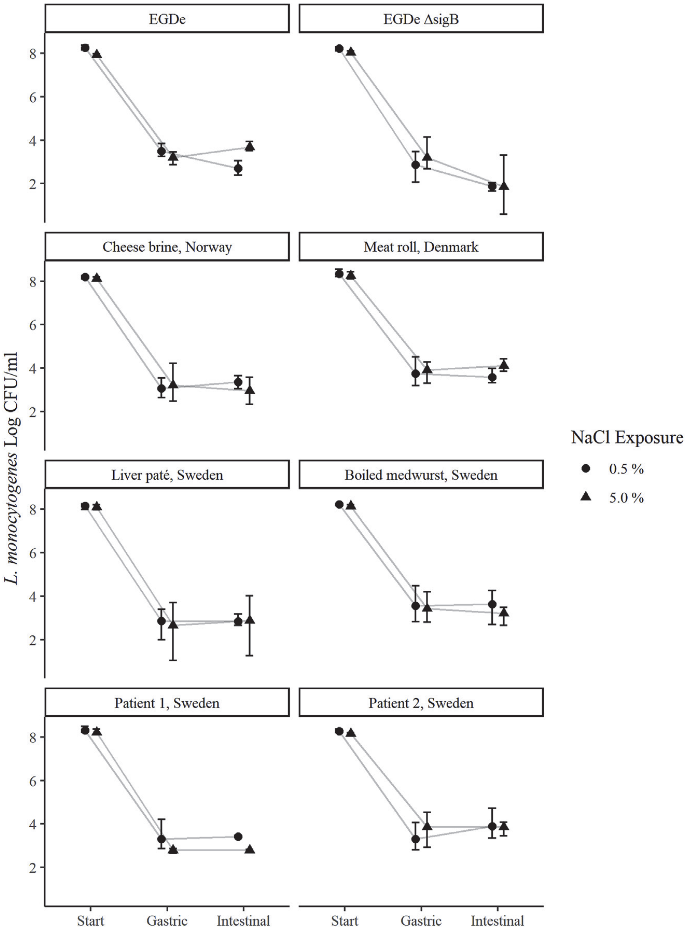

Fig. 2. Survival fraction of *L. monocytogenes* outbreak isolates and strains through the gastric and intestinal phases of the IVD model, divided by 0.5% NaCl (dot) and 5% NaCl (triangle) exposure (n = 3). The concentration (Log CFU/ml) is given at start, after the gastric phase (pH 2.1, 40 min) and after the intestinal phase (pH 7.0, 120 min). Data presented are mean values of three independent experiments and error bars representing the range.

significantly decreased survival ($P < 0.01$) in the IVD model compared to the EGDe wild type strain. The significant reduction in survival fraction occurred only after passing through the intestinal phase, and not in the gastric phase.

Among the outbreak isolates, the highest survival fraction mean was observed for the Swedish Patient 2 isolate (−4.3 Log CFU/ml, CI: −4.8 – (−3.8)), and the lowest survival fraction mean was observed for the Patient 1 isolate (−5.4 Log CFU/ml, CI: −5.5- (−4.4)), both originating from the Swedish outbreak.

4. Discussion

4.1. Exposure to different NaCl concentrations significantly affects the survival of L. monocytogenes in the IVD model

The aim of the current study was to explore how adaptation of *L. monocytogenes* to different levels of NaCl stress influences the survival fraction through the IVD model. Meat, meat products and dairy products are all NaCl-containing RTE food products often associated with *L. monocytogenes* contamination (U.S Food and Drug Administration, 2003). For public health reasons, many European countries have already started to reduce the NaCl content in RTE food. However, this may confer an adverse effect by resulting in faster growth of *L. monocytogenes* in the food products as the water activity increases. However, possible cross-protection against the digestive barriers after osmotic stress in the food products has been described (Sleator et al., 2009), which may lead to a higher survival fraction passing through the human digestive tract. Surprisingly, the present study detected no significant difference in survival fraction between isolates exposed to 5 and 0.5% NaCl when clustering the EGDe strain and the outbreak isolates altogether. The lower tolerance of the *ΔsigB* mutant was expected due to the likely reduced ability to cope with stress. However, when analyzing the isolates separately, exposure to different NaCl concentrations resulted in significant, but surprisingly contrasting survival fraction effects in the intestinal phase. The phenomena of cross-protection may explain why the EGDe strain demonstrated a significantly higher survival fraction in the intestinal phase when exposed to the higher NaCl concentration (Begley et al., 2002; Sleator et al., 2009). On the other hand, there are also studies reporting that exposure to osmotic stress may sensitize the bacteria to digestive stress (Barbosa et al., 2012; Garner

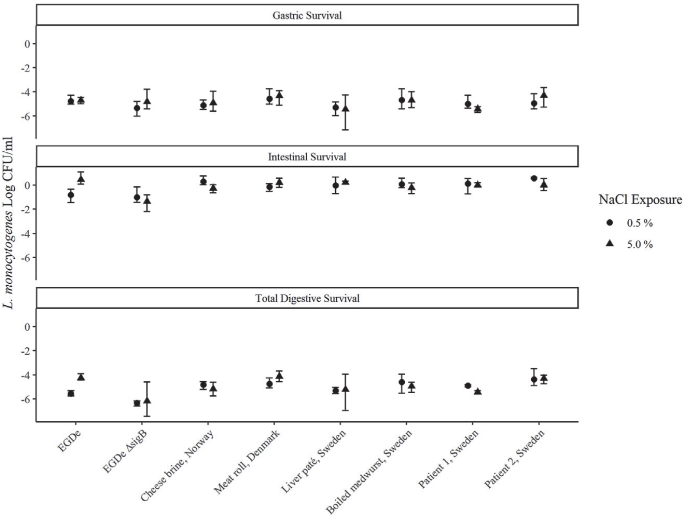

Fig. 3. Survival fraction of *L. monocytogenes* strains and isolates in the IVD model. The data represent the gastric step, the intestinal step and both steps together. Exposure to 0.5% NaCl (dot) and to 5% NaCl (triangle) is indicated by the mean values of three independent experiments and error bars representing the range.

Table 2
Invasivness of the EGDe strain in epithelial cells at 5 and 0.5% NaCl after *in vitro* digestion.

Experiment	NaCl (%)	Invasion (%)	Mean	Standard Error of the Mean
1	5.0	0.4	0.2	0.1
2	5.0	0.1		
3	5.0	0.0		
1	0.5	1.3	5.1	2
2	0.5	7.6		
3	0.5	6.5		

et al., 2006). This is in compliance with the significantly reduced survival fraction of the Swedish patient 1 isolate in the IVD model when the NaCl concentration was increased. Differences in survival fractions between the isolates were detected only in the intestinal phase, suggesting that stressors encountered in the intestine reveal more isolate dependent differences in stress tolerance than those encountered in the gastric phase. Our results suggest that exposure to NaCl may influence how strains and isolates of *L. monocytogenes* cope with stressors encountered in the digestive system and that there is a diversity among strains in how NaCl influence their stress resistance. After exposure to 0.5% NaCl, the Norwegian outbreak isolate, the Danish meat roll isolate and the two clinical Swedish outbreak isolates demonstrated significantly increased survival fractions in the IVD model compared to the EGDe strain. Such increased survival may have contributed to the severity of the respective listeriosis outbreaks. Surprisingly, such isolate-dependent differences in survival in the IVD model were not observed during exposure to 5% NaCl. In the current study, the initial concentration of *L. monocytogenes* was 8.2 Log CFU/g with a very low confidence interval, preventing potential bias in the results due to start concentration differences. By using a high inoculum concentration, it was still possible to quantify the bacteria after the intestinal step and to obtain enough cells to perform a cell culture assay, which is essential to document if the bacteria passing through the IVD model still have the potential to adhere, invade and cause disease. Barbosa et al. (2012) reported six *L. monocytogenes* isolates, isolated from cheese, to be more sensitive to acidic (pH 3.5) than osmotic stress (NaCl; 30–40%) prior to a static *in vitro* digestion model (Barbosa et al., 2012). After adding the bile salts to their IVD model, all strains decreased to a concentration below the level of detection, which is in contrast to the current study. However, Barbosa and colleagues exposed their strains to a higher NaCl concentration and used approximately a 6 Log in-put-concentration of *L. monocytogenes* and a longer digestion time than applied in the current study, which could explain the lower bacterial level after passage through the IVD model. Furthermore, it has been reported that *L. monocytogenes* isolates demonstrated different survival fractions after 90 min of exposure to the gastric environment (Barmpalia-Davis et al., 2008). Since the gastric phase lasted only 40 min in the present study, the short gastric exposure time may explain why no strain-dependent differences in survival were detected in the gastric phase.

The use of an in-put concentration of 8 Log CFU/g in the IVD model simulates a worst case scenario. However, given the low incidence of listeriosis in a population despite the ubiquitous nature of the causative bacterium, dose-response models presume illnesses results from exposure to high bacterial doses (Buchanan et al., 2017).

As expected, the *ΔsigB* mutant demonstrated a significantly lower survival fraction through the IVD model compared to its EGDe background strain, probably due to its inability to activate the stressosome. Surprisingly, deletion of *sigB* did not reduce the resistance to gastric pH, but rather sensitized the organism to the intestinal environment. Although Sigma B is regarded as the key stress regulator in *L. monocytogenes*, there are also other mechanisms responsible for coping with osmotic stress and low-pH stress, which do not belong to the Sigma B regulon, as reviewed by NicAogain and O'Byrne (2016). This may explain why deletion of *sigB* had a very limited effect on *L. monocytogenes* survival in the gastric phase (NicAogain and O'Byrne, 2016).

4.2. Invasion properties of the EGDe strain after passing through the IVD model

Key virulence genes in *L. monocytogenes* are important for attachment, invasion and the intracellular cycle. It has been reported that moderately increased salt stress could increase *L. monocytogenes* invasiveness in cell culture (Larsen and Jespersen, 2015; Lorentzen et al., 2011). However, the results in the current study demonstrated a significant lower invasion rate of HT-29 cells after the EGDe strain was exposed to 5% compared to when it was exposed 0.5% NaCl. Further experiments with more strains will be needed to reveal if the salt concentration also has a similar effect on cell invasiveness of other *L. monocytogenes* strains and isolates.

4.3. L. monocytogenes survival fractions through the IVD model, after exposure to either 5 or 0.5% NaCl

All *L. monocytogenes* strains and isolates used in the current study showed surprisingly high survival fractions in the IVD model (Fig. 2), even though the bacteria were exposed to the simulated digestive fluids and enzymes in pure broth with limited protective solid matrix effects. The protective effect of solid food matrix is assumed to increase the survival of *L. monocytogenes* during digestion (Barmpalia-Davis et al., 2009). However, *in vitro* digestion with Lactic Acid Bacteria (LAB) and *L. monocytogenes* in Latin-style fresh cheese revealed that the food matrix only had a protective effect on the LAB, but not on *L. monocytogenes* cells (Silva et al., 2015).

When comparing the total digestive survival of the Swedish outbreak isolates, the Liver patê isolate and the other clinical isolates, the patient isolate nr 1 demonstrated a significantly decreased total survival fraction through the IVD model compared to the patient 2 isolate and the Boiled medwurst isolate. They all originated from the same outbreak and belonged to the same sequence type (Dahl et al., 2017). The only reported genotypic differences between the Swedish outbreak isolates were the presences of eight SNPs in the patient 2 isolate (Dahl et al., 2017). However, the Boiled medwurst isolate did not demonstrate a significantly reduced total survival fraction compared to the patient nr 2 isolate. Although whole genome sequencing is a precious and powerful tool for outbreak investigation and public health, there are still considerations to be made before predicting the physiological and pathogenic potential of a strain or an isolate (Adhikari and Curtis, 2016; Gill A., 2017).

Altogether, the results suggest that a reduction of the NaCl content from 5 to 0.5% in the BHI growth media has the potential to alter the relative fraction of viable bacteria, which reach the intestine and that the effect is isolate and strain dependent. A tenfold reduction in NaCl concentration also conferred a potentially increased epithelial cell invasion. However, further studies are needed, including adjustments of the IVD model to make it more representative of individuals belonging to the high-risk group for achieving invasive listeriosis. Individual physiological differences in gastric pH, pepsin content, gastric lipase levels, bile concentrations, level of proteolytic enzymes and transit time, should therefore be considered and implemented (Shani-Levi et al., 2017).

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Appendix A. Supplementary data

Supplementary data related to this article can be found at https://doi.org/10.1016/j.fm.2018.08.010.

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July 14, 2020

Dear Editor,

We regret to inform you that we have discovered an error in the article "Survival of *Listeria monocytogenes* during *in vitro* gastrointestinal digestion after exposure to 5 and 0.5 % sodium chloride" published in Food Microbiology (DOI: https://doi.org/10.1016/j.fm.2018.08.010 , February 2019.

Our study describes how different *Listeria monocytogenes* strains survive through an *in vitro* digestion model after exposure to NaCl stress.

We have recently discovered that two numbers in Materials and methods, section 2.3, needs to be corrected:

2.3. Static *in vitro* digestion
A standardized *in vitro* digestion model was used to simulate the human gastrointestinal condition (Minekus et al., 2014). The digestive fate in the stomach and small intestine was investigated, while the oral phase was omitted since starch was not included in the substrate. After 24 h of growth in pre-culture 2, the bacteria were directly exposed to simulated gastric juice (Minekus et al., 2014). The time of gastric digestion for a liquid is reported to be between 5 and 45 min at 37 °C (Camilleri et al., 1989). The exposure time to pH 2 and porcine pepsin (**2000U**/ml, Sigma P7012) was therefore limited to 40 min and the incubation was performed at 37 °C with shaking (100 rpm). Subsequently, to simulate the intestinal phase, the pH was adjusted to 7 by adding 1 M NaOH, porcine pancreatin (trypsin **100U**/ml, Sigma P7545) and porcine bile salts (10 mM, Sigma B8631) were added to the bacterial cultures. The cultures were then incubated for an additional 120 min at 37 °C with shaking (100 rpm). *L. monocytogenes* was quantified at the start and after each digestive step by plating tenfold dilution in BPW (Buffered Peptone Water ISO, CM 1049, Oxoid) on bovine blood agar plates (CM 02071, Oxoid). The pH was measured in all 48 samples during the intestinal phase (PHM92 LAB pH meter, Radiometer Copenhagen) but due to practical considerations, detailed pH measurements were performed for only 20 samples from the gastric phase. However, the pH was measured in all samples using pH indicator strips at the start of each digestive step, immediately after addition of the respective gastrointestinal enzymes and chemicals (Merck, 1.09584.001). For all strains and conditions, three independent experiments were performed.

The correct values are 1000U/ml of pepsin and 30U/ml of pancreatin. We therefore suggest the following corrections to section 2.3 (in red):

2.3. Static in vitro digestion
A standardized in vitro digestion model was used to simulate the human gastrointestinal condition (Minekus et al., 2014). Adjustments regarding use of oral phase, length and pH of the gastric phase and enzyme activity were applied. The digestive phase in the stomach and small intestine was investigated, while the oral phase was omitted since starch was not included in the substrate. After 24 h of growth in pre-culture 2, the bacteria were directly exposed to simulated gastric juice

(Minekus et al., 2014). The time of gastric digestion for a liquid is reported to be between 5 and 45 min at 37 °C (Camilleri et al., 1989). The exposure time to pH 2 and porcine pepsin (1000U/ml, Sigma P7012) was therefore limited to 40 min and the incubation was performed at 37 °C with shaking (100 rpm). Subsequently, to simulate the intestinal phase, the pH was adjusted to 7 by adding 1 M NaOH, porcine pancreatin (trypsin 30U/ml, Sigma P7545) and porcine bile salts (10 mM, Sigma B8631) were added to the bacterial cultures. The cultures were then incubated for an additional 120 min at 37 °C with shaking (100 rpm). *L. monocytogenes* was quantified at the start and after each digestive step by plating tenfold dilution in BPW (Buffered Peptone Water ISO, CM 1049, Oxoid) on bovine blood agar plates (CM 02071, Oxoid). The pH was measured in all 48 samples during the intestinal phase (PHM92 LAB pH meter, Radiometer Copenhagen) but due to practical considerations, detailed pH measurements were performed for only 20 samples from the gastric phase. However, the pH was measured in all samples using pH indicator strips at the start of each digestive step, immediately after addition of the respective gastrointestinal enzymes and chemicals (Merck, 1.09584.001). For all strains and conditions, three independent experiments were performed.

We hope the editor will find these corrections within reason. All strains have been tested under the same conditions, and the conclusions of the study remains unchanged.

Sincerely,

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July 14, 2020

Paper III

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FOOD MICROBIOLOGY

Exposure to Broad-Spectrum Visible Light Causes Major Transcriptomic Changes in *Listeria monocytogenes* EGDe

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ABSTRACT *Listeria monocytogenes*, the causative agent of the serious foodborne disease listeriosis, can rapidly adapt to a wide range of environmental stresses, including visible light. This study shows that exposure of the *L. monocytogenes* EGDe strain to low-intensity, broad-spectrum visible light inhibited bacterial growth and caused altered multicellular behavior during growth on semisolid agar compared to when the bacteria were grown in complete darkness. These light-dependent changes were observed regardless of the presence of the blue light receptor (Lmo0799) and the stressosome regulator sigma B (SigB), which have been suggested to be important for the ability of *L. monocytogenes* to respond to blue light. A genome-wide transcriptional analysis revealed that exposure of *L. monocytogenes* EGDe to broad-spectrum visible light caused altered expression of 2,409 genes belonging to 18 metabolic pathways compared to bacteria grown in darkness. The light-dependent differentially expressed genes are involved in functions such as glycan metabolism, cell wall synthesis, chemotaxis, flagellar synthesis, and resistance to oxidative stress. Exposure to light conferred reduced bacterial motility in semisolid agar, which correlates well with the light-dependent reduction in transcript levels of flagellar and chemotaxis genes. Similar light-induced reduction in growth and motility was also observed in two different *L. monocytogenes* food isolates, suggesting that these responses are typical for *L. monocytogenes*. Together, the results show that even relatively small doses of broad-spectrum visible light cause genome-wide transcriptional changes, reduced growth, and motility in *L. monocytogenes*.

IMPORTANCE Despite major efforts to control *L. monocytogenes*, this pathogen remains a major problem for the food industry, where it poses a continuous risk of food contamination. The ability of *L. monocytogenes* to sense and adapt to different stressors in the environment enables it to persist in many different niches, including food production facilities and in food products. The present study shows that exposure of *L. monocytogenes* to low-intensity broad-spectrum visible light reduces its growth and motility and alters its multicellular behavior. Light exposure also caused genome-wide changes in transcript levels, affecting multiple metabolic pathways, which are likely to influence the bacterial physiology and lifestyle. In practical terms, the data presented in this study suggest that broad-spectrum visible light is an important environmental variable to consider as a strategy to improve food safety by reducing *L. monocytogenes* contamination in food production environments.

KEYWORDS EGDe, *Listeria monocytogenes*, broad-spectrum visible light, environmental stress, flagellar motility, growth inhibition, transcriptome

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Listeria monocytogenes is a foodborne opportunistic pathogen that causes the invasive disease listeriosis. Immunosuppressed individuals, the elderly, and pregnant women and their fetuses are at particularly high risk for acquiring invasive listeriosis (1). Listeriosis is characterized by bacteremia, meningoencephalitis, abortion, and neonatal sepsis (2). The overall fatality rate is between 20 and 30% of reported cases (1). *L. monocytogenes* exhibits tolerance to a wide range of environmental stressors, which facilitate its survival and replication in an extensive range of habitats, including soil, plant material, foods, food-processing environments, and the intestinal tracts of mammals (3–5). In order to develop innovative strategies to control this pathogen, it is crucial to understand how it responds and adapts to stressors encountered in different environments.

The damaging effect of UV light on bacteria is well documented and is often applied for reducing bacterial contamination (6). It has been shown that the blue part of the visible-light spectrum (400 to 500 nm) has a bactericidal effect (7–13). The bactericidal effect of visible light is suggested to be related to endogenous production of reactive oxygen species, which have a dose-dependent and multitarget oxidizing effect on cellular components (7–11). Several studies have been conducted to explore the bactericidal effect of blue light for decontamination purposes, especially in combination with other stressors such as low temperature, salt, acidic pH, or light sensitizers (8, 9, 14–19).

Many environmental nonphototrophic bacteria, including *L. monocytogenes*, can sense and modulate their gene expression profiles and phenotypes in response to visible light of different wavelengths (20). It has been suggested that visible light can provide an early warning that facilitates bacterial adaptation to upcoming osmotic stress caused by water evaporation under sunlight (20). There are also nonphototropic bacteria that regulate their surface attachment and biofilm formation according to the presence of visible light (20). Some pathogenic bacteria, such as *Brucella abortus* and *Acinetobacter baumannii*, use light to assess their environment and to regulate their transition between environmental and host-associated life styles (20, 22, 23).

In *L. monocytogenes*, exposure to blue and red light induces transcription of the gene encoding the stressosome regulator sigma B (SigB) and consequently of genes belonging to the SigB regulon (10, 21). *L. monocytogenes* senses blue light via the blue light photoreceptor (Lmo0799), whose activation triggers the transcription of *sigB* (21). Blue light is suggested to inhibit flagellar motility and increase invasiveness of Caco-2 enterocytes in a SigB- and blue light receptor-dependent manner (21). Furthermore, growth under oscillating light and dark conditions has been shown to cause an alternating translucent (not light exposed) and opaque (light exposed) ring pattern in *L. monocytogenes* colonies, indicating a blue-light-dependent and reversible multicellular behavior (11). The ring formation was dependent on both SigB and the blue light receptor, the positive regulatory factor A (PrfA) and the actin assembly-inducing protein (ActA) (11). *Bacillus subtilis*, which belongs to the same order as *L. monocytogenes* (i.e., the *Bacillales* order), contains a receptor which detects red light and has a broader spectral sensitivity than the blue light receptor (24). An orthologue to the *B. subtilis* red light receptor has not been identified in *L. monocytogenes*, and the mechanism behind the detection of red light is still unknown (21). The effect of red and blue light has been studied separately in *L. monocytogenes* and, based on mutational studies, it has been suggested that there is some cross talk or interference between red and blue light-triggered regulatory mechanisms (21). However, there is still very limited knowledge on the integrated response of *L. monocytogenes* to the full light spectrum and on how it regulates this bacterium's life style. In general, many questions regarding the physiological effects of visible light on nonphototrophic bacteria remain unanswered, and the use of "omics" technologies has been suggested as a tool to fill this knowledge gap (25).

The present study explored the effect of broad-spectrum visible light on *L. monocytogenes* by comparing the growth and transcriptomes of light-exposed cultures to those of cultures exposed to darkness. To capture the impact of temperature and

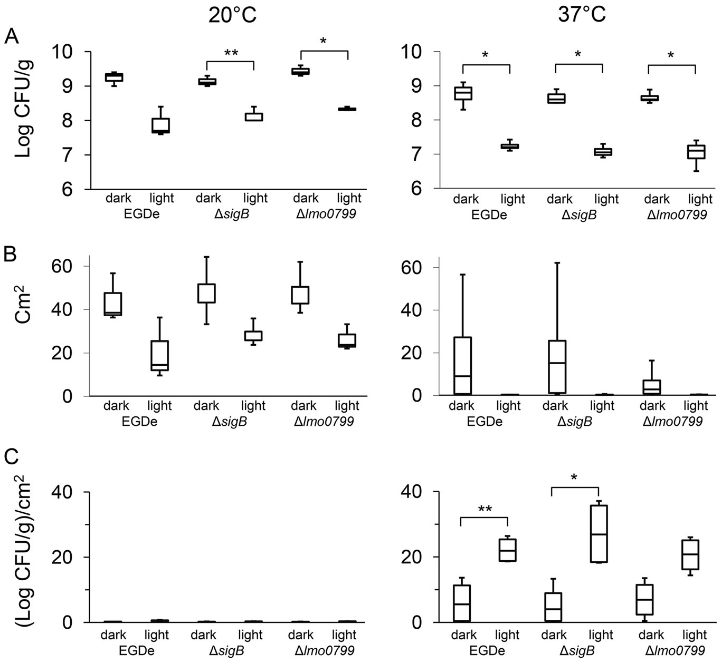

FIG 1 Growth of EGDe, EGDe Δ*sigB*, and EGDe Δ*lmo0799* strains, as indicated by log CFU/g (A), cm^2 (B), and bacterial density (C) after exposure to broad spectrum visible light at 20°C (N = 3) or 37°C (N = 4) for 12 and 7 days, respectively. In each box, the central mark indicates the median, and the bottom and top edges indicate the 25th and 75th percentiles, followed by the lower and upper adjacent values. Asterisks represent statistical differences from pairwise comparisons determined using two-tailed paired Student *t* tests (*, $P < 0.01$; **, $P < 0.05$).

exposure time on the transcriptomic response to light, the bacteria were exposed to visible light at 20°C for 20 and 180 min and at 37°C for 20 min. Functional analyses of selected significantly light-regulated pathways were performed to understand how altered gene regulation results in phenotypic differences between light- and dark-exposed samples. Together, the data presented here demonstrate that low-intensity, broad-spectrum visible light confers genome-wide changes in transcript levels and influences the growth and behavior of *L. monocytogenes*.

RESULTS AND DISCUSSION

Exposure to broad-spectrum visible light inhibits growth and causes altered multicellular behavior. To investigate the effect of low-intensity broad-spectrum visible light on the *L. monocytogenes* EGDe strain, it was grown for 7 days on semisolid agar plates under exposure of light or under complete darkness at 20 or 37°C. Exposure to light resulted in a reduced concentration of bacteria on the agar plates (log CFU/g agar) compared to cultures exposed to complete darkness at both temperature conditions tested, indicating that light exposure reduce bacterial growth (Fig. 1A). The colony areas were significantly reduced during light exposure at both 20 and 37°C (Fig. 1B), and a light-dependent increase in bacterial growth density was observed at 37°C (Fig. 1C). The differences in growth areas and growth densities observed between light- and dark-exposed cultures suggest that light exposure may alter the aggregative behavior of *L. monocytogenes*. The average dose of irradiance that each cell in a colony is exposed to will decrease when the cell density increases. The increased growth density may thus function as a protective strategy against light-induced stress. This assumption is supported by a previous study that shows that the inhibitory effect of

TABLE 1 Number of affected genes after light exposure at 20°C for 20 and 180 min and at 37°C for 20 min

		No. of affected genes[a]					
		<0.5 $\log_2$-fold change		0.5–2 $\log_2$-fold change		>2 $\log_2$-fold change	
Temp (°C)	Time (min)	+	–	+	–	+	–
20	20	184	172	470	645	141	123
20	180	196	279	424	412	7	18
37	20	172	274	334	471	127	36

[a] The numbers of genes are categorized according to the $\log_2$-fold change and extent of regulation. +, significantly upregulated genes; –, significantly downregulated genes.

blue light (470 nm) on *L. monocytogenes* was dependent on the cell density, since only cultures containing $<10^7$ CFU/ml were found to be growth inhibited by blue light exposure (10). Similarly, broad-spectrum, visible-light-induced growth inhibition was also observed when the EGDe strain and two different *L. monocytogenes* food isolates were cultured in liquid media at 20 and 37°C (see Table S1 in the supplemental material). The reduced growth of light-exposed cultures compared to cultures grown in darkness was more pronounced at earlier time points of growth, when the bacterial density in the cultures was lower, and decreased when the cultures reached higher densities.

Exposure to visible light alters *L. monocytogenes* gene expression profiles. To obtain a genome-wide view on how broad-spectrum visible light influences various biological activities in *L. monocytogenes*, a transcriptomic analysis was performed on the EGDe strain grown in liquid media under exposure to broad-spectrum visible light or complete darkness at 20°C for 20 min, 20°C for 180 min, or 37°C for 20 min. The transcriptomes of the light-exposed cultures were compared to cultures exposed to complete darkness under the same time-temperature conditions. The exposure times at 20°C were selected to investigate the immediate response (20 min) and longer-term (180 min) adaptation to light, and individual genes were defined as significantly differentially expressed based on a $\log_2$-fold difference between light- and dark-exposed samples and an adjusted *P* value of <0.05.

Exposure to broad-spectrum visible light at 20°C for 20 min changed the transcript levels of 1,735 genes, 54% of which were downregulated, and 46% of which were upregulated (Table 1 and Table S2). After 180 min of light exposure, the numbers of regulated genes were reduced to 1,336 (53% downregulated and 47% upregulated) and the numbers of >2 $\log_2$-fold up- and downregulated genes were also lower relative to cultures exposed to light for only 20 min (Table 1 and Table S2). Thus, the shift from darkness to light seemed to trigger a stronger and more complex transcriptional response compared to longer time exposures to light. However, a relatively large part of the regulated genes ($n = 1{,}006$) were shared between samples exposed to light for 20 and 180 min at 20°C, suggesting that they may represent a core set of genes regulated during light exposure at this temperature. Exposure to broad-spectrum visible light for 20 min at 37°C caused altered regulation of 1,414 genes, 55% of which were downregulated, and 45% of which were upregulated (Table 1 and Table S2). A total number of 913 differentially expressed genes were shared between light treatment at 20 and 37°C for 20 min. In all, 624 differentially expressed genes were shared across all time-temperature conditions (Fig. 2).

Light-dependent differently regulated metabolic pathways. KEGG pathway function analysis revealed that the differentially expressed genes (light versus darkness) participate in 18 metabolic pathways (Table 2). Altogether, six pathways (fructose mannose metabolism, pyrimidine metabolism, two-component system, bacterial chemotaxis, flagellar assembly, and the phosphotransferase system) were differentially regulated during light exposure across all time-temperature conditions tested. However, there were also differences between the conditions tested, which indicate that the

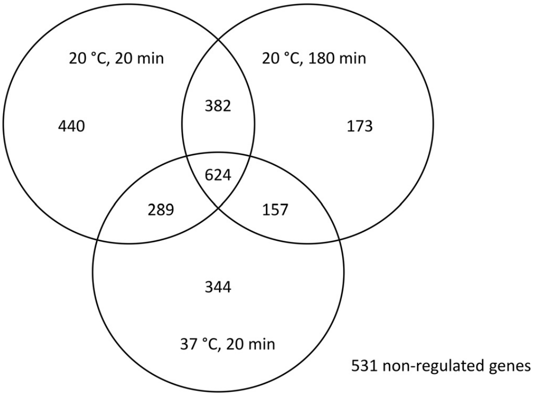

FIG 2 Venn diagram showing the number of differentially expressed genes across temperatures and time points and the overlap between the sets of differentially expressed genes.

response to light is both time and temperature dependent. During exposure to light for 20 min at 20°C, eight metabolic pathways were differently regulated. Seven of these pathways were also differently regulated after 180 min of light exposure at 20°C (Table 2 and Table S2). Furthermore, three pathways (pentose phosphate, microbial metabolism in diverse environments, and carbon metabolism) were differentially regulated only at the later time point. For several of the pathways that were differently regulated at both 20 and 180 min of light exposure at 20°C, a greater number of genes were affected at the earlier time point.

Light exposure at 37°C for 20 min resulted in altered regulation of genes belonging to 14 KEGG pathways, and 8 of these were also differentially regulated during light exposure at 20°C (Table 2 and Table S2). Six metabolic pathways, including the fatty acid biosynthesis, purine metabolism, peptidoglycan biosynthesis, aminoacyl-tRNA biosynthesis, amino sugar and nucleotide sugar metabolism, and the fatty acid metabolism, were differently regulated only during light exposure at 37°C. On the other hand, there were four pathways (pentose phosphate pathway, porphyrin metabolism, microbial metabolism in diverse environments, and carbon metabolism) that were

TABLE 2 KEGG pathways affected by light exposure and the number of genes being differentially expressed

KEGG pathway	No. of genes	No. of affected genes[a]		
		20°C, 20 min	20°C, 180 min	37°C, 20 min
lmo00030 pentose phosphate pathway	35	NA	16	NA
lmo00051 fructose and mannose metabolism	56	38	20	29
lmo00061 fatty acid biosynthesis	14	NA	NA	10
lmo00230 purine metabolism	54	NA	NA	38
lmo00240 pyrimidine metabolism	41	29	17	18
lmo00500 starch and sucrose metabolism	56	31	NA	21
lmo00520 amino sugar and nucleotide sugar metabolism	34	NA	NA	21
lmo00550 peptidoglycan biosynthesis	19	NA	NA	15
lmo00860 porphyrin and chlorophyll metabolism	35	32	23	NA
lmo00970 aminoacyl-tRNA biosynthesis	92	NA	NA	19
lmo01120 microbial metabolism in diverse environments	150	NA	70	NA
lmo01200 carbon metabolism	84	NA	32	NA
lmo01212 fatty acid metabolism	15	NA	NA	10
lmo02020 two-component system	47	31	30	30
lmo02030 bacterial chemotaxis	12	10	11	12
lmo02040 flagellar assembly	26	23	24	26
lmo02060 phosphotransferase system	85	60	22	38
lmo03010 ribosome	75	NA	14	48

[a] NA, not affected (i.e., the pathway was not significantly affected).

differentially regulated only during light exposure at 20°C (Table 2). A selection of the light-dependent differentially regulated pathways are further discussed below.

Porphyrins and flavins. A high number of the genes that were significantly downregulated during light exposure at 20°C are involved in porphyrin and flavin metabolism. A large proportion of these genes demonstrated a $>$2.0-log$_2$-fold downregulation after 20 min of light exposure. Both porphyrins and flavins function as endogenous photosensitizers in microbial cells (59). They contain large conjugated systems that absorb energy from visible light and transition it to an excited electronic state (26). The excited porphyrin molecules may react directly with biological structures (type I reactions) or with molecular oxygen, generating excited singlet oxygen (type II reactions), which may react with and cause damage to bacterial proteins or to the DNA (26). It could therefore be a beneficial strategy for the bacterial cell to lower the level of endogenous photosensitizers to reduce damage from oxidative stress. The porphyrin pathway ends up in reducing the cobalamin (vitamin B_{12}) coenzyme. Notably, the transcriptome analyses showed that multiple genes involved in vitamin B_{12} synthesis were significantly downregulated during light exposure at 20°C, particularly after 20 min. It has long been known that vitamin B_{12} functions as a cofactor for many enzymes that catalyze a range of important biochemical reactions (27). Recently, it was discovered that vitamin B_{12} also controls gene expression in response to light by binding covalently to transcription factors (27, 28). The use of B_{12} as a light sensor is suggested to be a feature with a deep evolutionary history as proteins with B_{12} binding domains are widespread among species belonging to the *Bacteria*, *Archaea*, and *Eukarya* kingdoms. Vitamin B_{12} has also been shown to influence gene expression in *L. monocytogenes* by binding to RNA-based riboswitches (29). Light-dependent downregulation of genes involved in vitamin B_{12} synthesis could therefore have an indirect effect on the expression of multiple genes in *L. monocytogenes*.

To investigate whether extracellular vitamin B_{12} increases the sensitivity of *L. monocytogenes* to broad-spectrum visible light, we cultured the EGDe strain in light and in darkness in the presence of vitamin B_{12}. Measurements of the optical density at 600 nm (OD_{600}) of the bacterial cultures did not show any significant differences in growth between bacteria grown in the presence of light with or without vitamin B_{12} (see Table S1 in the supplemental material). This may be due to absence of vitamin B_{12} uptake into the cell or indicate that other vitamin B_{12} derivatives are involved in light sensitivity. However, further studies are needed to understand the biological function of the light-dependent downregulation of vitamin B_{12} metabolism.

Protection against oxidative stress. Reactive oxygen species causes damage to carbohydrates, lipids, and proteins, and bacteria have evolved several different strategies to protect themselves against oxidative stress (30). The genes encoding superoxide dismutase (Lmo1439) and catalase (Lmo2785), which are both important for protection against oxidative stress, were upregulated during exposure to broad-spectrum visible light at all temperature conditions tested (Table 3). The pentose phosphate pathway, which produces NADPH, an important component in the defense mechanism against oxidative stress (31), was upregulated only after 180 min of light exposure at 20°C, which suggests that this protective mechanism comes into play after a longer time of light exposure.

Flagellar motility and chemotaxis. One of the most profound results from the transcriptomic analyses was the light-dependent downregulation of the flagellar assembly and chemotaxis genes (Fig. 3). Previous studies have shown that genes linked to flagellar motility in *L. monocytogenes* are expressed at temperatures between 20 and 25°C and transcriptionally downregulated at 37°C, although strain-dependent differences may occur (32–35). In the present study, exposure to broad-spectrum visible light resulted in downregulation of flagellar assembly genes at both 20 and 37°C. At 20°C, 23 of 26 (the total number of genes in the KEGG flagellar assembly pathway) flagellar assembly genes were downregulated after 20 min of light exposure. After 180 min of light exposure, 24 of the 26 flagellar assembly genes were downregulated. During light

TABLE 3 Regulation of virulence determinants and genes of special interest (log$_2$-fold change)

Gene	Log$_2$-fold change			Gene description
	20°C, 20 min	20°C, 180 min	37°C, 20 min	
prfA	2.1	0.7	–0.5	Transcriptional regulator
sigB	2.1	0.9		RNA polymerase sigma factor
inlA	2.3	1.9	1.3	Internalin A
inlB	2.6	1.3	1.3	Internalin B
hly		0.4	–0.4	Listeriolysin O precursor
actA	–1.0			Actin assembly-inducing protein precursor
lmo0799	0.4	0.4	0.3	Blue light receptor
lmo1439	1.7	0.9	1.0	Superoxide dismutase
lmo2785	0.9	0.6	0.5	Catalase
dgcB	1.0		–0.3	
dgcC	1.9	1.1	1.3	
mouR	1.0		0.5	Transcriptional regulator
mogR	0.3	–0.4	0.3	Transcriptional regulator

exposure at 37°C for 20 min, all 26 genes were downregulated. The downregulation of flagellar genes at 37°C ranged from -3.1- to -1.4-log$_2$-fold changes, while the downregulation at 20°C for 20 min was more variable, ranging from -4.4- to -0.5-log$_2$-fold changes (Table S2). To analyze the relative transcription level, compared to the normalization level across all samples, all light-temperature categories were gathered for comparison. In general, the flagellar assembly genes were most transcribed in the dark-exposed samples at 20°C, followed by light-exposed samples at 20°C (see Fig. S1 in the supplemental material). Consistent with what has been reported earlier, there was a much lower level of expression of flagellar genes at 37°C than at 20°C.

Two different food isolates (59792 and 59782) and the EGDe strain were tested for motility in soft agar, and all three strains showed the characteristic umbrella shaped motility when incubated in darkness at 20°C (Fig. S2). In contrast, the motility was

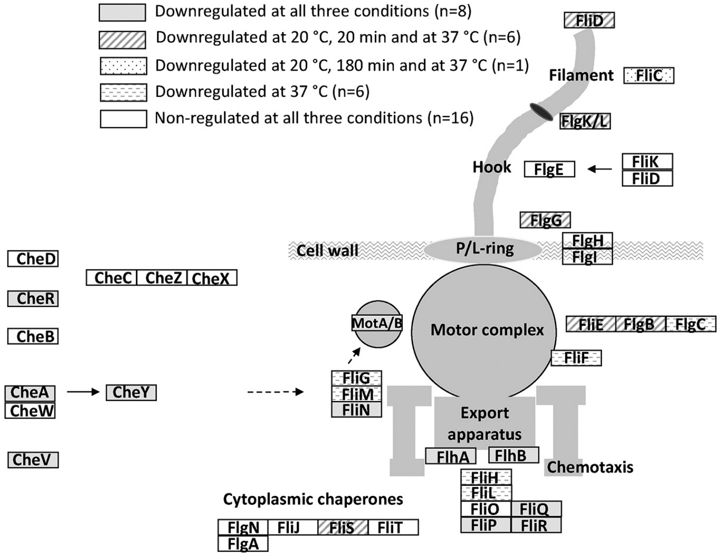

FIG 3 Downregulated genes (log$_2$-fold change of less than -1.0) in the chemotaxis and flagellar assembly pathways after exposure to broad-spectrum visible light. Different patterns of shading indicate the condition(s) under which the downregulations were observed, according to the key. White indicates nonregulated.

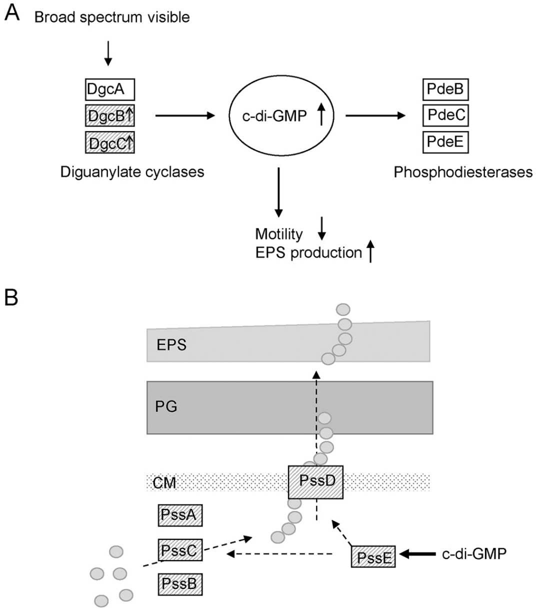

FIG 4 (A) Visible light causes upregulation of *dgcB* and *dgcC*, which likely will increase the intracellular concentration of c-di-GMP. (B) c-di-GMP positively regulates EPS production through PssE. Shaded boxes indicate genes encoding the proteins that are upregulated after exposure to light at 20°C. (The figure was adapted from reference 39 with permission from Oxford University.)

severely reduced when the soft agar cultures were exposed to light at 20°C (Fig. S2). At 37°C, no motility could be detected in either light- or dark-exposed cultures (Fig. S2). Together, these results indicate that visible light is an important factor that regulates flagellar motility in *L. monocytogenes* (21, 36, 37).

MogR is a transcriptional regulator that regulates swimming motility of *L. monocytogenes* in a temperature-dependent manner by repressing flagellar and chemotaxis genes (33, 38). In this study, only a slight upregulation of *mogR* was observed after 20 min of light exposure at both 20 and 37°C. After 180 min of light exposure at 20°C, it was −0.4 $\log_2$-fold downregulated (Table 3). This indicates that MogR is less important for light-dependent regulation of flagellar motility.

Light-induced expression of two diguanylate cyclases responsible for the synthesis of c-di-GMP. Numerous studies indicate that the second messenger 3′-5′ cyclic diguanylate monophosphate (c-di-GMP) negatively regulates flagellar motility and promotes bacterial adherence and biofilm formation (39). In *L. monocytogenes* it has previously been shown that c-di-GMP induces the expression of an exopolysaccharide that inhibits bacterial migration on semisolid agar, increases cellular aggregation, and confers enhanced tolerance to disinfectants and desiccation (40). Cyclic di-GMP is synthesized from two GTP molecules in a reaction catalyzed by diguanylate cyclase (Fig. 4A), and *L. monocytogenes* contains three genes encoding enzymes with diguanylate cyclase activity: *dgcA* (*lmo1911*), *dgcB* (*lmo1912*), and *dgcC* (*lmo2174*). In this study, exposure to broad-spectrum visible light triggered the upregulation of *dgcC* at all three time-temperature conditions tested (20°C and 20 min, a $\log_2$-fold change of 1.9; 20°C and 180 min, a $\log_2$-fold change of 1.1; and at 37°C and 20 min, a $\log_2$-fold change of 1.3), while *dgcB* was upregulated only during light exposure at 20°C for 20 min (a $\log_2$-fold change of 1.0). At 37°C, *dgcB* was weakly downregulated (a $\log_2$-fold change of −0.3). In contrast to the other two diguanylate cyclase genes in *L. monocytogenes*, *dgcA* was not differentially regulated during exposure to light at any of the time-temperature conditions tested.

Recent studies indicate that light exposure causes increased cell wall thickness in *L. monocytogenes*. Although not experimentally confirmed, this phenomenon was explained by increased production of extracellular polymeric substances (EPS) (10, 11). The *pss* operon comprising the *pssABCDE* genes (*pssA-E*; *lmo0527* to *lmo0531*) has been linked to c-di-GMP-induced EPS biosynthesis in *L. monocytogenes* (40, 41). In the present study, all *pssA-E* genes were upregulated during light exposure at 20°C for 20 min and 180 min (between 1.7 and 1.9 $\log_2$-fold and between 0.5 and 0.7 $\log_2$-fold, respectively) (Fig. 4B, Table S1). To explore the effect of visible light on EPS production, *L. monocytogenes* was cultured on agar plates containing Congo red either in the absence or presence of visible light. Dark- and light-exposed bacteria were also tested in a whole-cell Congo red depletion assay. No EPS production could be detected when the bacteria were grown at 20°C either in the presence of light or in darkness, even though transcriptional data indicated an increase in transcription of all *pssA-E* genes after light exposure at this temperature. At 37°C both methods detected EPS production, but there was no detectable difference in EPS production between light- and dark-exposed samples (data not shown). The latter result is in compliance with the transcriptional data which suggest that light exposure at 37°C do not affect transcription of the *pssA-E* genes.

***sigB* and the blue light receptor.** Upregulation of *sigB* was observed after exposure of the EGDe strain to broad-spectrum visible light for 20 and 180 min at 20°C ($\log_2$-fold changes of 2.1 and 0.9, respectively). However, this was not observed after light exposure at 37°C. The blue light receptor gene, Δ*lm0799*, was slightly upregulated in response to light exposure at all three time-temperature conditions tested (Table 3). The Δ*sigB* strain and the Δ*lm0799* strain, which lack SigB and the blue light receptor, respectively, did not demonstrate any observable differences in growth behavior on soft agar plates compared to the EGDe background strain (Fig. 1A). This is in contrast to what was reported by O'Donoghue et al., who observed that *L. monocytogenes* mutant strains lacking either SigB or the blue light receptor were less growth inhibited by blue light (460 to 470 nm, 1.5 to 2 mW cm^2) compared to the wild-type background strain (10). The different responses observed in the present study and in the study by O'Donoghue et al. (10) are likely due to differences in doses and wavelengths of the light the bacteria are exposed to. Similar to the results from the present study, NicAogáin et al. did not observe any significant difference in survival between the blue light receptor mutant (the strain used in the present study) and the wild-type EGDe background strain, when exposed to blue light (470 nm) in seawater (42). However, these researchers found that exposure to blue light reduced the survival of the Δ*sigB* mutant and suggested that the activity of SigB was regulated by other pathways than via the blue light receptor (42).

Virulence determinants and genes of special interest. In *L. monocytogenes*, the key virulence genes are expected to be most highly expressed at 37°C and almost silent at 30°C and are under the control of the temperature-sensing transcriptional regulator PrfA (43, 60, 61). Due to the complex regulatory network, it is difficult to predict the biological consequences of the broad-spectrum-visible-light-dependent upregulation of *prfA* transcription observed at 20°C. Only a slight upregulation of *prfA* expression was observed during light exposure at 37°C (Table 3). PrfA contributes to transcription of the membrane proteins Internalin A and Internalin B, which are involved in attachment and invasion of host cells, and they have also been suggested to mediate the adherence of *L. monocytogenes* to abiotic surfaces (44–46). In the present study, the genes encoding Internalin A and Internalin B (*inlA* and *inlB*, respectively) were upregulated under all light-temperature conditions tested (Table 3). This is consistent with results from a previous study, which showed that *inlA* and *inlB* were upregulated during exposure of *L. monocytogenes* to blue light (21). Since the *inl* genes were transcribed during light exposure at both 20 and 37°C, there could be other factors, in addition to PrfA, that are involved in the regulation of *inlA* and *inlB*. Further studies are required to elucidate whether light influences attachment of *L. monocytogenes* to abiotic and biotic surfaces.

It has been suggested that that the actin assembly-inducing protein (ActA) is essential for coordinated light- and dark-dependent colony differentiation in *L. monocytogenes* (11). In the present study, the gene encoding the ActA precursor was downregulated after light exposure at 20°C for 20 min, but not after 180 min of light exposure, indicating that the downregulation may be an immediate short-term response to light-induced stress.

Conclusion and further perspectives. To interpret the functional elements involved in the response of *L. monocytogenes* to broad-spectrum visible light, the EGDe strain was exposed to light of wavelengths between 390 and 780 nm, with a maximum irradiance within the blue-green wavelengths of the spectrum. The simulated daylight cannot directly be compared to natural daylight since natural light contains a wider range of wavelengths and the proportion of the different wavelengths constantly changes during the day and with the season (47). If only comparing total radiant exposure (J/cm^2) used in the present study, with the sunlight, it corresponds roughly to 8- and 60-s exposures for 20 and 180 min, respectively. However, the energy will not give full information about the effect, since the wavelength spectrum differs between sunlight and the current light source used (e.g., UV), and the comparison has been made with the assumption that sunlight results in 0.1 W/cm^2.

The data presented here show that exposure of *L. monocytogenes* to low intensities of broad-spectrum visible light reduces bacterial growth and induces major reprogramming of the bacterial transcriptome. Since light exposure at 20 and 37°C affects a different set of physiological pathways, the effect of light may be temperature dependent. The observed light-induced changes in transcription levels suggest that broad-spectrum visible light has a major influence on many biological processes in the bacterial cell and is an important environmental factor to consider both in research on this bacterium and for controlling it in food production environments. The use of low-intensity visible light as a mechanism to reduce growth of *L. monocytogenes* could have advantages compared to the use of high-intensity light (UV-light) for controlling this pathogen in food production facilities. For example, unlike UV-light, visible light passes through plastic, glass, and clear liquids. While rooms have to be evacuated when using high-intensity UV-light, one can still use rooms exposed to low-intensity visible light. Visible light can therefore potentially be used as a method for continuous low-level control of *L. monocytogenes*.

L. monocytogenes has the ability to colonize abiotic surfaces, which contributes to its persistence in food processing facilities and increases the risk for contamination of food products (48). Several studies have addressed the potential for applying the toxic effect of visible light for disinfection in the food industry, both for surface decontamination and in food, by coating food products with photosensitizing compounds (14, 16, 18). Knowledge of the response and adaptation of *L. monocytogenes* to different intensities and wavelengths of visible light is therefore highly relevant for the further development and innovation of these strategies. The present study has highlighted genes and metabolic pathways that are differentially expressed during exposure of *L. monocytogenes* to broad-spectrum visible light and provides a valuable basis for more-detailed functional analyses to understand how light affects the bacterial behavior.

MATERIALS AND METHODS

Bacterial strains and growth conditions on agar plates. All of the strains used in this study are listed in Table 4. The EGDe strain and its Δ*sigB* and Δ*lmo0799* derivative strains were kindly provided by Jörgen Johansson at Umeå University, Umeå, Sweden (10, 11). The EGDe strain was chosen since its whole-genome sequence is available and well annotated (49).

The bacteria were grown in brain heart infusion broth (BHI; catalog no. 237500, Bacto; Becton Dickinson, Sparks, MD) or on semisolid BHI agar (0.3%) and exposed to broad-spectrum visible light or kept in darkness at 20 or 37°C. Prior to growth on semisolid agar, bacteria from frozen stocks were grown on blood agar plates for 24 h at 37°C, transferred to BHI broth, and incubated overnight at 37°C. The OD_{600} of the overnight cultures was measured, and 2-μl portions were then transferred from the cultures to the center of 0.3% semisolid BHI agar plates. The plates were sealed with parafilm and incubated at

TABLE 4 *L. monocytogenes* strains used in the present study

Strain	Reference	Isolate source	Serogroup
EGDe	49	Rabbit	IIa (I/2a)
EGDe Δ*sigB*	10	Laboratory strain	
EGDe Δ*lmo0799*	10	Laboratory strain	
59789	58	RTE chicken	IIa
59792	58	Meatballs	IIc

20 or 37°C for 12 and 7 days, respectively, under continuous light exposure or in darkness. On the last day of incubation, the diameters of the growth zones were registered. To determine the bacterial concentration on the agar plates, the colonies and the agar from the culture plates were transferred to stomacher bags, weighed, diluted 1:2 (wt/wt) with BHI, and plated on blood agar in proper dilutions for enumeration. Linear regression analysis of the log CFU/g, including the presence of light, the effect of temperature, and the agar weight, resulted in an adjusted R^2 of 90.5 and a Prob $>$ F value of 0.000, meaning that the model can explain 90.5% of the variation in log CFU/g observed. However, only temperature and the presence of light were significant ($P > |t| = 0.000$) and the effect of weight was not significant ($P > |t| = 0.629$). When excluding weight as a predictor from the model, the adjusted R^2 value slightly improved, 90.7, and the Prob $>$ F value was 0.000. Therefore, the effect of the agar weight was assumed to be limited. All experiments were performed in triplicates or quadruplets.

To explore the effect of broad-spectrum visible light on growth in liquid medium, 4-ml portions of BHI cultures were grown in small cell-culture bottles (catalog no. 83.3911.002; Sarstedt AG & Co., Germany) at 20 or 37°C. The bottles were placed 17 to 20 cm from the light source. Growth was assessed by measuring the OD_{600}. To not expose "dark" cultures to light, a new parallel culture was used for each measurement both for dark- and light-exposed cultures. Dark-exposed culture bottles were wrapped in two layers of aluminum foil.

Preparation of RNA for sequencing. For the global transcriptomic analysis, *L. monocytogenes* EGDe strain was grown on blood agar plates for 24 h at 37°C. Seven single colonies, representing seven biological replicates, were transferred into seven separate tubes containing BHI broth, followed by incubation at 20 or 37°C until an OD_{600} of 0.8 was reached. Each of seven cultures was diluted 10,000 times in BHI broth before 4-ml portions of the cultures were transferred to six cell culture bottles (Sarstedt AG). All six bottles were wrapped up in aluminum foil and incubated at 20 or 37°C. After reaching an OD_{600} of 0.6 to 0.8, half of the bottles were exposed to light by removal of the aluminum foil. The control samples were incubated next to the light-exposed samples. Immediately after light/dark exposures, three bottles incubated under the same conditions were pooled, RNAprotect bacterial reagent (catalog no. 76506; Qiagen) was added according to the manufacturer's instructions, and the samples were stored at −80°C until RNA isolation. Three bottles were used per biological replicate to obtain enough cells without increasing the volume of the culture in one bottle. RNA isolation was performed by using an RNeasy minikit (Qiagen), including enzymatic lysis (lysozyme [50 μl of 100 mg/ml] and mutanolysin [Sigma-Aldrich, catalog no. M9901-5KU; 10 μl of 50 U]), proteinase K digestion (Qiagen, catalog no. 19131; 15 μl of 25 mg/ml) and mechanical disruption (bead beating at 6,200 rpm for 40 s using a Precellys lysing kit; Bertin Technologies, catalog no. 03961-1-005). DNase treatment was performed in columns (RNase-free DNase set; Qiagen, catalog no. 79254) according to the manufacturer's instructions. The quality and the quantity of the total RNA samples were estimated by using an Agilent Bioanalyzer (Agilent Technologies) and NanoDrop One (Thermo Scientific), respectively. RNA integrity number (RIN) values ranged from 8.8 to 9.9, the 260/280 ratio ranged from 1.8 to 2.1, and the 260/230 ratio ranged from 1.3 to 2.4; all samples were immediately depleted of rRNA by using Ribo-Zero magnetic kit bacteria (Illumina, catalog no. MRZB12424). The quality and quantity of the RNAs were measured after depletion using Bioanalyzer Pico Chips and a NanoDrop apparatus.

Light conditions. A Juwel Aquarium Discover Life light source (Day 24W T5; 9,000 K) was used to expose *L. monocytogenes* cultures to broad-spectrum visible light. The distance between the light source and the samples was held at 16 to 18 cm. Measurement of the blue light was done by using a Solar Light Co. PMA2100 detector (Blue Light Safety, serial number 2894; Solar Light Co., Philadelphia, PA), and the irradiation level was measured to $0.0002259\ \text{W/cm}^2 \times 60\ \text{s/min} \times x\ \text{min} = 0.014\ \text{J/cm}^2$ per min. The total radiant exposures (in J/cm²) were 0.8 and 6.1 for 20 and 180 min, respectively. The blue light radiant exposures (in J/cm²) were 0.3 and 2.4 for 20 and 180 min, respectively.

RNA sequencing. The transcriptomic analysis was performed on the EGDe strain grown under dark conditions in liquid media before exposure to light or darkness at 20°C for 20 min, at 20°C for 180 min, or at 37°C for 20 min. Two different exposure times were selected at 20°C to investigate the immediate (early) response to light exposure (20 min) and longer-term (180 min) adaptation to light. The longer exposure time was limited to 180 min to ensure RNA was harvested in the exponential growth phase. The light-exposed samples were compared only to corresponding samples kept in complete darkness (controls). Individual genes were defined as significantly differentially expressed based on a $\log_2$-fold difference between light- and dark-exposed samples and an adjusted P value of <0.05. Altogether, 42 libraries (7 biological replicates for each treatment) were prepared and sequenced on an Illumina HiSeq 3000 apparatus (150-bp paired-end reads) using a TruSeq stranded total RNA kit (Illumina) at the Norwegian Sequencing Centre, Oslo, Norway. The raw sequence reads were submitted to the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA506549. Bbduk v34.56 (50) was used for cleaning the raw data before alignment with Hisat2 v2.0.5 (51) using genome and annotation references from the ensemble bacteria (genome [Listeria_monocytogenes_egd_e.ASM19603v1.dna.toplevel.fa.gz from ENSEMBL BACTERIA] and annotation [Listeria_monocytogenes_egd_e.ASM19603v1.38.gtf.gz ENSEMBL BACTERIA]). Counting aligned reads was done with FeatureCounts v1.4.6-p1 (52), and finally DESeq2 v1.18.1 (53) was used for analysis of differentially regulated genes.

The experimental design included seven biological replicates from each condition. However, one control sample (dark) at 20°C for 20 min, two samples exposed to light at 20°C for 20 min, one sample exposed to light at 20°C for 180 min, and one sample exposed to light at 37°C for 20 min were removed due to low percentages of alignment (10.6 to 37.4% feature count alignment). In addition, due to outliers defined by the cluster dendrogram and principal component analysis (PCA) (Fig. S3), two more samples were removed (one control sample [dark] at 20°C for 20 min and one control sample [dark] at 37°C for 20 min). In all, five replicates were analyzed from both dark- and light-exposed cultures at 20°C for 20 min, six replicates were analyzed from both light conditions at 37°C for 20 min, and six and seven replicates were analyzed from light- and dark-exposed conditions, respectively, kept at 20°C for 180 min. Downstream analysis was performed according to the samples shown by the PCA analysis given in Fig. S1, which had a feature count alignment ranging from 71 to 83.4%. Output files from Deseq2 were first sorted on adjusted *P* values below 0.05. Conversion to the Entrez gene ID was performed using DAVID Bioinformatics Resources 6.8 (NIAID/NIH; https://david.ncifcrf.gov/tools.jsp [54]). After conversion, Pathview was used for functional pathway analysis and visualization (https://pathview.uncc.edu/ [55–57]).

Congo red assays. For visualization of EPS production, *L. monocytogenes* was grown on plates containing 20 g/liter TSB (Difco), 6.1 g/liter peptone (Difco), 3.5% agar (Oxoid), and 25 μg/ml Congo red. After incubation for 48 h, the colors of the colonies were compared by visual inspection. To detect differences in EPS production in liquid cultures, *L. monocytogenes* was cultured in a media containing 20 g/liter TSB and 6.1 g/liter peptone for 48 h in light or in darkness. After incubation, the cells were washed once in phosphate-buffered saline and adjusted to OD_{600} of 0.5, and Congo red was added to the cultures to a final concentration of 20 μg/ml, followed by further incubation for 20 min at room temperature. The cells were then pelleted at 10,000 × *g* for 5 min, and the absorbance of the supernatant was measured at 500 nm to detect the depletion of Congo red from the media.

Motility test. An umbrella motility test was performed in glass tubes containing 5 ml of soft agar (20 g/liter TSB [Difco], 6.1 g/liter peptone [Difco], 3.5% agar [Oxoid]). Overnight cultures of *L. monocytogenes* strains were inoculated into the soft agar, and the tubes were incubated under light exposure (17 to 20 cm next to the light source) or in darkness (wrapped in aluminum foil) for 24 h at 37°C or for 48 h at 20°C.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/AEM.01462-19.

SUPPLEMENTAL FILE 1, PDF file, 0.6 MB.

SUPPLEMENTAL FILE 2, XLSX file, 0.4 MB.

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K.S.P. and T.L. performed the experiments, with assistance from A.K. K.S.P. and A.Y.M.S. performed the bioinformatics analyses, the statistical analyses, and the initial interpretation. K.S.P. wrote the initial draft of the manuscript. All authors were involved in the study design, final interpretation, and manuscript preparation.

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Supplementary information

Exposure to broad-spectrum visible light causes major transcriptomic changes in the *L. monocytogenes* EGDe strain

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Table S1

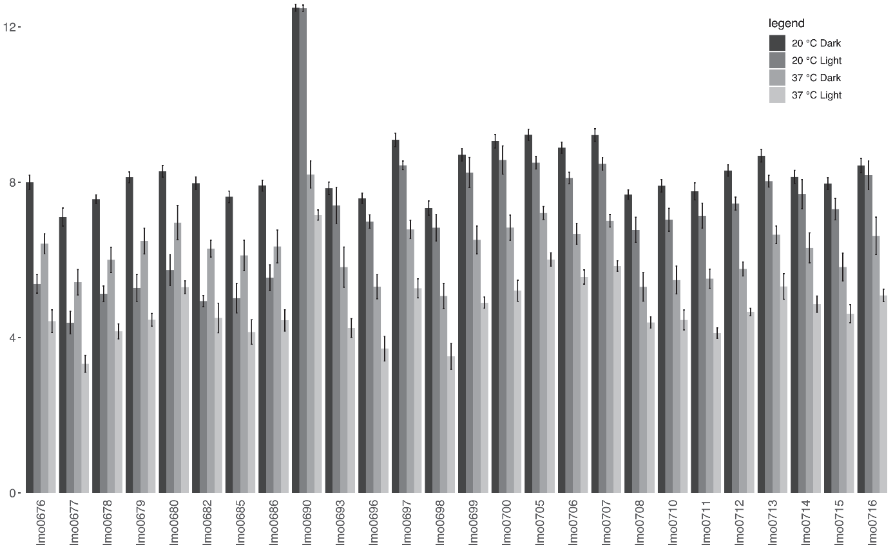
Reduction in growth shown by the ratio of OD_{600} between cultures exposed to broad-spectrum visible light and cultures grown in darkness.

Ratio OD_{600} light/dark						
	20°C[b]			37°C[b]		
	8 hrs	**12 hrs**	**24 hrs**	**3 hrs**	**5 hrs**	**24 hrs**
EGDe	0.5±0.2*	0.5±0.2*	1.0±0.2	0.6±0.1*	0.6±0.1*	0.9±0.0
59789	0.7±0.1	0.7±0.1*	1.0±0.0	0.7±0.1	0.7±0.1*	0.9±0.0*
59792	0.7±0.1*	0.7±0.1*	1.0±0.1	0.8±0.0*	0.9±0.0*	0.8±0.2
EGDe[a]	0.5±0.1	0.7±0.1*	1.1±0.1	0.6±0.0*	0.6±0.0*	0.9±0.3

[a] *L. monocytogenes* EGDe grown in presence of vitamin B_{12}.

[b] Asterisks represent statistical differences from pairwise comparisons using two-tailed paired Student t tests (*; P <0.05)

FIG S1



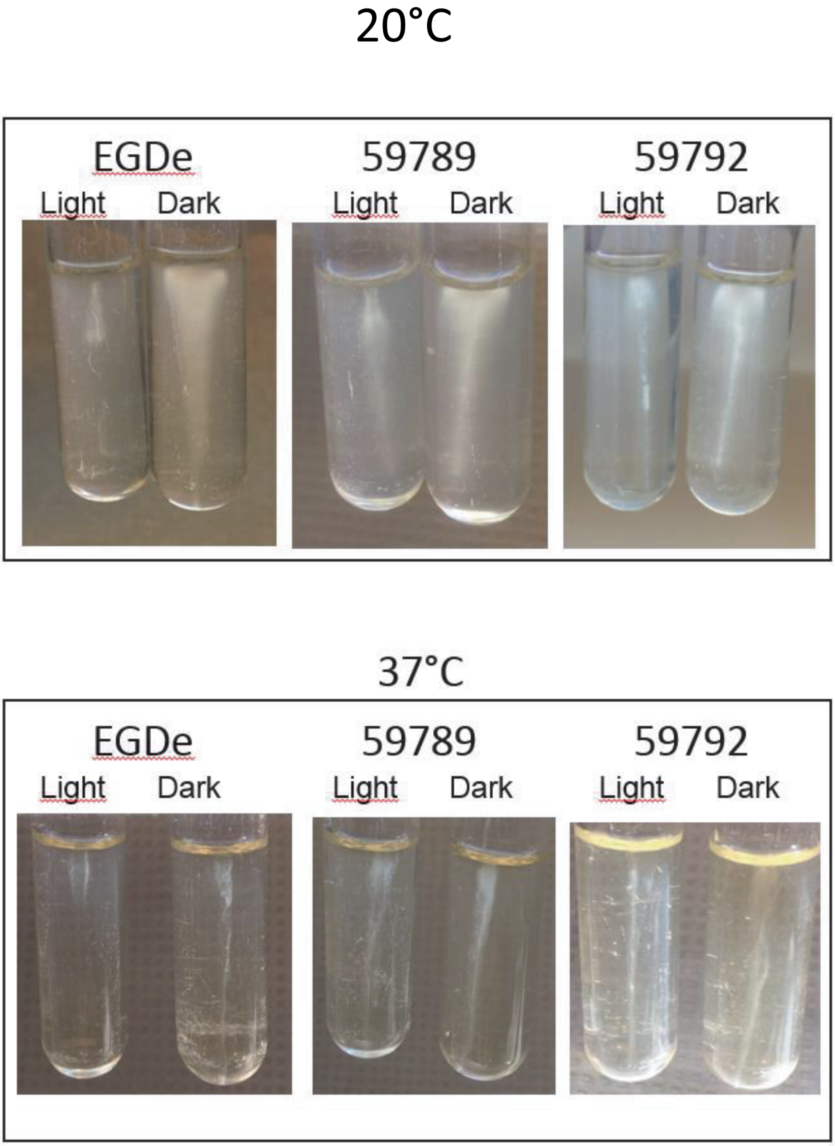
Transcription of flagellar synthesis genes. The bars represent the log mean of the normalized read count for the particular gene across all the replicates within each group and the corresponding standard deviation are shown as error bars.

TABLE S2

See appendix 1

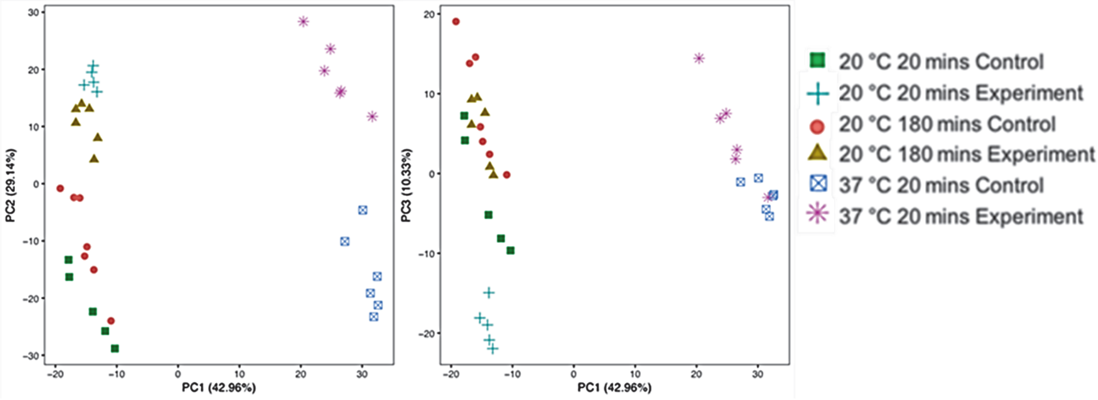
Transcriptome data of differentially expressed gene listed by treatment conditions

FIG S2



Differences in motility of *L. monocytogenes* strains incubated either under complete darkness or exposed to broad spectrum visible light at 20°C or 37°C. At 20°C the dark-incubated cultures show the typical umbrella-like lateral extension of growth caused by migration of the bacteria from the inoculation site. No motility was observed at 37°C.

FIG S3:



Principal Component Analysis (PCA) of biological replicates by each temperature and light exposure condition used for global transcriptomics.

20 degrees C, 20 min

ENSEMBL id	ENSEMBL gene	ENSEMBL biotype	ENTREZ id	ENTREZ gene description
CAC98216	dnaA	protein_coding	984365	chromosome replication initiator DnaA(dnaA)
CAC98217	dnaN	protein_coding	984379	DNA polymerase III subunit beta(dnaN)
CAC98218	lmo0003	protein_coding	984420	hypothetical protein(lmo0003)
CAC98221	gyrB	protein_coding	984708	DNA gyrase subunit B(gyrB)
CAC98223	lmo0008	protein_coding	984834	cardiolipin synthase(lmo0008)
CAC98224	lmo0009	protein_coding	984861	spermidine acetyltransferase(lmo0009)
CAC98227	lmo0012	protein_coding	984932	mevalonate kinase(lmo0012)
CAC98228	qoxA	protein_coding	984936	AA3-600 quinol oxidase subunit II(qoxA)
CAC98229	qoxB	protein_coding	984962	AA3-600 quinol oxidase subunit I(qoxB)
CAC98230	qoxC	protein_coding	984980	AA3-600 quinol oxidase subunit III(qoxC)
CAC98231	qoxD	protein_coding	984983	quinol oxidase aa3-600 subunit IV(qoxD)
CAC98232	lmo0017	protein_coding	984984	CapA protein (polyglutamate capsule biosynthesis)(lmo0017)
CAC98234	lmo0019	protein_coding	985005	lmo0019(lmo0019)
CAC98236	lmo0021	protein_coding	985040	PTS fructose transporter subunit IIA(lmo0021)
CAC98237	lmo0022	protein_coding	985051	PTS fructose transporter subunit IIB(lmo0022)
CAC98238	lmo0023	protein_coding	985053	PTS fructose transporter subunit IIC(lmo0023)
CAC98239	lmo0024	protein_coding	985058	PTS mannose transporter subunit IID(lmo0024)
CAC98240	lmo0025	protein_coding	985061	phosphoheptose isomerase(lmo0025)
CAC98242	lmo0027	protein_coding	985074	PTS beta-glucoside transporter subunit IIABC(lmo0027)
CAC98243	lmo0028	protein_coding	985088	microcin C7 self-immunity protein MccF(lmo0028)
CAC98245	lmo0030	protein_coding	985106	hypothetical protein(lmo0030)
CAC98246	lmo0031	protein_coding	985116	LacI family transcription regulator(lmo0031)
CAC98247	lmo0032	protein_coding	985121	xylose repressor(lmo0032)
CAC98248	lmo0033	protein_coding	985131	endoglucanase(lmo0033)
CAC98249	lmo0034	protein_coding	985136	PTS cellbiose transporter subunit IIC(lmo0034)
CAC98250	lmo0035	protein_coding	985145	glucosamine--fructose-6-phosphate aminotransferase(lmo0035)
CAC98251	lmo0036	protein_coding	985152	putrescine carbamoyltransferase(lmo0036)
CAC98252	lmo0037	protein_coding	985153	amino acid transporter(lmo0037)
CAC98253	lmo0038	protein_coding	985162	agmatine deiminase 1(lmo0038)
CAC98254	lmo0039	protein_coding	985163	carbamate kinase(lmo0039)
CAC98256	lmo0041	protein_coding	985277	hypothetical protein(lmo0041)
CAC98257	lmo0042	protein_coding	985331	DedA protein(lmo0042)
CAC98258	lmo0043	protein_coding	985417	arginine deiminase(lmo0043)
CAC98263	lmo0048	protein_coding	985598	sensor histidine kinase AgrB(lmo0048)
CAC98264	lmo0049	protein_coding	985690	lmo0049(lmo0049)
CAC98265	lmo0050	protein_coding	985694	histidine kinase(lmo0050)
CAC98266	lmo0051	protein_coding	985847	response regulator(lmo0051)
CAC98270	purA	protein_coding	986069	adenylosuccinate synthetase(purA)
CAC98272	lmo0057	protein_coding	986071	hypothetical protein(lmo0057)
CAC98273	lmo0058	protein_coding	986073	lmo0058(lmo0058)
CAC98274	lmo0059	protein_coding	986184	hypothetical protein(lmo0059)
CAC98275	lmo0060	protein_coding	986285	hypothetical protein(lmo0060)
CAC98276	lmo0061	protein_coding	986287	hypothetical protein(lmo0061)
CAC98277	lmo0062	protein_coding	986293	lmo0062(lmo0062)
CAC98281	lmo0066	protein_coding	986392	toxin(lmo0066)

CAC98283	lmo0068	protein_coding	986408	lmo0068(lmo0068)
CAC98285	lmo0070	protein_coding	986434	lmo0070(lmo0070)
CAC98286	lmo0071	protein_coding	986441	lmo0071(lmo0071)
CAC98287	lmo0072	protein_coding	986445	hypothetical protein(lmo0072)
CAC98291	lmo0076	protein_coding	986519	O6-methylguanine-DNA methyltransferase(lmo0076)
CAC98292	lmo0077	protein_coding	986552	hypothetical protein(lmo0077)
CAC98293	lmo0078	protein_coding	986565	phosphoglycerate dehydrogenase(lmo0078)
CAC98294	lmo0079	protein_coding	986575	lmo0079(lmo0079)
CAC98295	lmo0080	protein_coding	986576	lmo0080(lmo0080)
CAC98296	lmo0081	protein_coding	986577	lmo0081(lmo0081)
CAC98297	lmo0082	protein_coding	986579	lmo0082(lmo0082)
CAC98300	lmo0085	protein_coding	986582	lmo0085(lmo0085)
CAC98305	lmo0090	protein_coding	986589	ATP synthase F0F1 subunit alpha(lmo0090)
CAC98306	lmo0091	protein_coding	986593	ATP synthase subunit gamma(lmo0091)
CAC98307	lmo0092	protein_coding	986598	ATP synthase F0F1 subunit beta(lmo0092)
CAC98310	lmo0095	protein_coding	986608	lmo0095(lmo0095)
CAC98311	lmo0096	protein_coding	986611	PTS mannose transporter subunit IIAB(lmo0096)
CAC98312	lmo0097	protein_coding	986614	PTS mannose transporter subunit IIC(lmo0097)
CAC98313	lmo0098	protein_coding	986620	PTS mannose transporter subunit IID(lmo0098)
CAC98314	lmo0099	protein_coding	986621	lmo0099(lmo0099)
CAC98315	lmo0100	protein_coding	986623	lmo0100(lmo0100)
CAC98317	lmo0102	protein_coding	986630	lmo0102(lmo0102)
CAC98318	lmo0103	protein_coding	986631	NADH oxidase(lmo0103)
CAC98319	lmo0104	protein_coding	986632	lmo0104(lmo0104)
CAC98320	lmo0105	protein_coding	986634	chitinase B(lmo0105)
CAC98321	lmo0106	protein_coding	986639	transcriptional regulator(lmo0106)
CAC98322	lmo0107	protein_coding	986644	ABC transporter ATP-binding protein(lmo0107)
CAC98323	lmo0108	protein_coding	986645	ABC transporter ATP-binding protein(lmo0108)
CAC98328	lmo0113	protein_coding	986656	hypothetical protein(lmo0113)
CAC98345	lmo0130	protein_coding	986721	5'-nucleotidase(lmo0130)
CAC98347	lmo0132	protein_coding	986732	inosine 5-monophosphate dehydrogenase(lmo0132)
CAC98348	lmo0133	protein_coding	986735	hypothetical protein(lmo0133)
CAC98349	lmo0134	protein_coding	986737	hypothetical protein(lmo0134)
CAC98351	lmo0136	protein_coding	986752	peptide ABC transporter permease(lmo0136)
CAC98352	lmo0137	protein_coding	986757	peptide ABC transporter permease(lmo0137)
CAC98353	lmo0138	protein_coding	986772	lmo0138(lmo0138)
CAC98355	lmo0140	protein_coding	986783	lmo0140(lmo0140)
CAC98356	lmo0141	protein_coding	986784	lmo0141(lmo0141)
CAC98357	lmo0142	protein_coding	986788	lmo0142(lmo0142)
CAC98358	lmo0143	protein_coding	986794	lmo0143(lmo0143)
CAC98361	lmo0146	protein_coding	986800	hypothetical protein(lmo0146)
CAC98362	lmo0147	protein_coding	986802	lmo0147(lmo0147)
CAC98364	lmo0149	protein_coding	986806	lmo0149(lmo0149)
CAC98365	lmo0150	protein_coding	986809	lmo0150(lmo0150)
CAC98367	lmo0152	protein_coding	986821	peptide ABC transporter substrate-binding protein(lmo0152)
CAC98368	lmo0153	protein_coding	986823	zinc ABC transporter substrate-binding protein(lmo0153)
CAC98369	lmo0154	protein_coding	986826	zinc ABC transporter ATP-binding protein(lmo0154)
CAC98373	lmo0158	protein_coding	986836	hypothetical protein(lmo0158)

CAC98375	lmo0160	protein_coding	986846	peptidoglycan binding protein(lmo0160)
CAC98376	lmo0161	protein_coding	986851	lmo0161(lmo0161)
CAC98377	lmo0162	protein_coding	986854	DNA polymerase III subunit delta'(lmo0162)
CAC98378	lmo0163	protein_coding	986862	lmo0163(lmo0163)
CAC98380	lmo0165	protein_coding	986872	hypothetical protein(lmo0165)
CAC98383	lmo0168	protein_coding	986889	AbrB family transcriptional regulator(lmo0168)
CAC98384	lmo0169	protein_coding	986890	glucose transporter(lmo0169)
CAC98385	lmo0170	protein_coding	986891	lmo0170(lmo0170)
CAC98389	lmo0174	protein_coding	985368	transposase(lmo0827)
CAC98390	lmo0175	protein_coding	986928	peptidoglycan-binding protein(lmo0175)
CAC98391	lmo0176	protein_coding	986935	glucose transporter(lmo0176)
CAC98392	metS	protein_coding	986940	methionyl-tRNA synthetase(metS)
CAC98393	lmo0178	protein_coding	986964	xylose repressor(lmo0178)
CAC98394	lmo0179	protein_coding	986967	sugar ABC transporter permease(lmo0179)
CAC98395	lmo0180	protein_coding	986972	sugar ABC transporter permease(lmo0180)
CAC98396	lmo0181	protein_coding	986977	sugar ABC transporter substrate-binding protein(lmo0181)
CAC98397	lmo0182	protein_coding	986983	alpha-glucosidase(lmo0182)
CAC98399	lmo0184	protein_coding	987008	oligo-1,6-glucosidase(lmo0184)
CAC98400	lmo0185	protein_coding	987009	hypothetical protein(lmo0185)
CAC98402	lmo0187	protein_coding	987012	hypothetical protein(lmo0187)
CAC98403	ksgA	protein_coding	987014	dimethyladenosine transferase(ksgA)
CAC98404	lmo0189	protein_coding	987015	Veg protein(lmo0189)
CAC98405	lmo0190	protein_coding	987016	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase(ipk)
CAC98406	lmo0191	protein_coding	987017	phospho-beta-glucosidase(lmo0191)
CAC98412	lmo0333	protein_coding	987568	internalin(lmo0333)
CAC98413	lmo0334	protein_coding	987569	lmo0334(lmo0334)
CAC98414	lmo0335	protein_coding	987570	lmo0335(lmo0335)
CAC98415	lmo0336	protein_coding	987572	lmo0336(lmo0336)
CAC98416	lmo0337	protein_coding	987574	lmo0337(lmo0337)
CAC98417	lmo0338	protein_coding	987576	lmo0338(lmo0338)
CAC98418	lmo0339	protein_coding	987577	hypothetical protein(lmo0339)
CAC98419	lmo0340	protein_coding	987578	lmo0340(lmo0340)
CAC98422	lmo0343	protein_coding	987583	translaldolase(lmo0343)
CAC98424	lmo0345	protein_coding	987586	sugar-phosphate isomerase(lmo0345)
CAC98425	lmo0346	protein_coding	987587	triosephosphate isomerase(lmo0346)
CAC98427	lmo0348	protein_coding	987591	dihydroxyacetone kinase(lmo0348)
CAC98428	lmo0349	protein_coding	987592	lmo0349(lmo0349)
CAC98429	lmo0350	protein_coding	987593	lmo0350(lmo0350)
CAC98430	lmo0351	protein_coding	987594	phosphotransferase mannnose-specific family component IIA(lmo0351)
CAC98431	lmo0352	protein_coding	987595	DeoR family transcriptional regulator(lmo0352)
CAC98432	lmo0353	protein_coding	987596	hypothetical protein(lmo0353)
CAC98433	lmo0354	protein_coding	987600	fatty-acid--CoA ligase(lmo0354)
CAC98434	lmo0355	protein_coding	987602	fumarate reductase subunit A(lmo0355)
CAC98435	lmo0356	protein_coding	987603	oxidoreductase(lmo0356)
CAC98440	lmo0361	protein_coding	987609	membrane protein(lmo0361)
CAC98441	lmo0362	protein_coding	987610	hypothetical protein(lmo0362)
CAC98442	lmo0363	protein_coding	987612	peptidase E(lmo0363)
CAC98444	lmo0365	protein_coding	987614	hypothetical protein(lmo0365)

CAC98445	lmo0366	protein_coding	987616	hypothetical protein(lmo0366)
CAC98447	lmo0368	protein_coding	987618	hypothetical protein(lmo0368)
CAC98448	lmo0369	protein_coding	987619	hypothetical protein(lmo0369)
CAC98449	lmo0370	protein_coding	987620	hypothetical protein(lmo0370)
CAC98450	lmo0371	protein_coding	987623	GntR family transcriptional regulator(lmo0371)
CAC98451	lmo0372	protein_coding	987624	beta-glucosidase(lmo0372)
CAC98452	lmo0373	protein_coding	987627	PTS beta-glucoside transporter subunit IIC(lmo0373)
CAC98455	lmo0376	protein_coding	987632	transcriptional regulator(lmo0376)
CAC98456	lmo0377	protein_coding	987633	lmo0377(lmo0377)
CAC98457	lmo0378	protein_coding	987634	lmo0378(lmo0378)
CAC98458	lmo0379	protein_coding	987635	lmo0379(lmo0379)
CAC98459	lmo0380	protein_coding	987636	lmo0380(lmo0380)
CAC98462	lmo0383	protein_coding	987639	methylmalonate-semialdehyde dehydrogenase(lmo0383)
CAC98463	lmo0384	protein_coding	987640	IolB protein(lmo0384)
CAC98466	lmo0387	protein_coding	987643	hypothetical protein(lmo0387)
CAC98468	ltrA	protein_coding	987647	low temperature requirement protein A(ltrA)
CAC98469	lmo0390	protein_coding	987648	uracil-DNA glycosylase(lmo0390)
CAC98470	lmo0391	protein_coding	987649	lmo0391(lmo0391)
CAC98471	lmo0392	protein_coding	987651	hypothetical protein(lmo0392)
CAC98472	lmo0393	protein_coding	987652	lmo0393(lmo0393)
CAC98473	lmo0394	protein_coding	987653	P60 protein(lmo0394)
CAC98474	lmo0395	protein_coding	987654	blasticidin S-acetyltransferase(lmo0395)
CAC98475	lmo0396	protein_coding	987655	pyrroline-5-carboxylate reductase(proC)
CAC98476	lmo0397	protein_coding	987657	hypothetical protein(lmo0397)
CAC98477	lmo0398	protein_coding	987659	PTS sugar transporter subunit IIA(lmo0398)
CAC98478	lmo0399	protein_coding	987673	PTS fructose transporter subunit IIB(lmo0399)
CAC98479	lmo0400	protein_coding	987677	PTS fructose transporter subunit IIC(lmo0400)
CAC98482	lmo0403	protein_coding	987752	lmo0403(lmo0403)
CAC98483	lmo0404	protein_coding	987761	lmo0404(lmo0404)
CAC98484	lmo0405	protein_coding	987767	phosphate transporter(lmo0405)
CAC98485	lmo0406	protein_coding	987775	hypothetical protein(lmo0406)
CAC98486	lmo0407	protein_coding	987777	lmo0407(lmo0407)
CAC98487	lmo0408	protein_coding	987782	lmo0408(lmo0408)
CAC98488	lmo0409	protein_coding	987787	internalin(lmo0409)
CAC98490	lmo0411	protein_coding	987794	phosphoenolpyruvate synthase(lmo0411)
CAC98491	lmo0412	protein_coding	987812	lmo0412(lmo0412)
CAC98493	lmo0414	protein_coding	987822	hypothetical protein(lmo0414)
CAC98494	lmo0415	protein_coding	987823	endo-1,4-beta-xylanase(lmo0415)
CAC98495	lmo0416	protein_coding	987824	transcriptional regulator(lmo0416)
CAC98496	lmo0417	protein_coding	987835	lmo0417(lmo0417)
CAC98500	lmo0421	protein_coding	987848	rod shape-determining protein RodA(lmo0421)
CAC98501	lmo0422	protein_coding	987850	lineage-specific thermal regulator protein(lstR)
CAC98502	lmo0423	protein_coding	987863	RNA polymerase factor sigma C(lmo0423)
CAC98503	lmo0424	protein_coding	987866	glucose uptake protein(lmo0424)
CAC98504	lmo0425	protein_coding	987867	transcriptional antiterminator BglG(lmo0425)
CAC98505	lmo0426	protein_coding	987869	PTS fructose transporter subunit IIA(lmo0426)
CAC98506	lmo0427	protein_coding	984685	PTS fructose transporter subunit IIB(lmo0427)
CAC98507	lmo0428	protein_coding	984384	PTS fructose transporter subunit IIC(lmo0428)

CAC98508	lmo0429	protein_coding	985137	sugar hydrolase(lmo0429)
CAC98509	lmo0430	protein_coding	986731	LysR family transcriptional regulator(lmo0430)
CAC98510	lmo0431	protein_coding	986199	acetyltransferase(lmo0431)
CAC98511	lmo0432	protein_coding	985147	oxidoreductase(lmo0432)
CAC98512	inlA	protein_coding	985151	internalin A(inlA)
CAC98513	inlB	protein_coding	986892	internalin B(inlB)
CAC98514	lmo0435	protein_coding	985154	peptidoglycan binding protein(lmo0435)
CAC98516	lmo0437	protein_coding	985156	hypothetical protein(lmo0437)
CAC98517	lmo0438	protein_coding	985161	lmo0438(lmo0438)
CAC98518	lmo0439	protein_coding	985164	hypothetical protein(lmo0439)
CAC98520	lmo0441	protein_coding	985168	D-alanyl-D-alanine carboxypeptidase(lmo0441)
CAC98521	lmo0442	protein_coding	985171	lmo0442(lmo0442)
CAC98522	lmo0443	protein_coding	985172	LytR family transcriptional regulator(lmo0443)
CAC98524	lmo0445	protein_coding	985175	transcripitonal regulator(lmo0445)
CAC98526	lmo0447	protein_coding	986724	glutamate decarboxylase(lmo0447)
CAC98528	lmo0449	protein_coding	985180	lmo0449(lmo0449)
CAC98529	lmo0450	protein_coding	985181	hypothetical protein(lmo0450)
CAC98530	lmo0451	protein_coding	985185	lmo0451(lmo0451)
CAC98531	lmo0452	protein_coding	985178	hypothetical protein(lmo0452)
CAC98532	lmo0453	protein_coding	985179	hypothetical protein(lmo0453)
CAC98533	lmo0454	protein_coding	985184	hypothetical protein(lmo0454)
CAC98534	lmo0455	protein_coding	985188	hypothetical protein(lmo0455)
CAC98535	lmo0456	protein_coding	985191	permease(lmo0456)
CAC98536	lmo0457	protein_coding	985189	hypothetical protein(lmo0457)
CAC98538	lmo0459	protein_coding	985370	transcriptional regulator(lmo0459)
CAC98539	lmo0460	protein_coding	985198	membrane associated lipoprotein(lmo0460)
CAC98540	lmo0461	protein_coding	985193	lmo0461(lmo0461)
CAC98541	lmo0462	protein_coding	985196	lmo0462(lmo0462)
CAC98542	lmo0463	protein_coding	985195	lmo0463(lmo0463)
CAC98543	lmo0464	protein_coding	985200	transposase(lmo0464)
CAC98547	lmo0468	protein_coding	984468	lmo0468(lmo0468)
CAC98548	lmo0469	protein_coding	985204	lmo0469(lmo0469)
CAC98549	lmo0470	protein_coding	985233	hypothetical protein(lmo0470)
CAC98550	lmo0471	protein_coding	985203	lmo0471(lmo0471)
CAC98551	lmo0472	protein_coding	985207	lmo0472(lmo0472)
CAC98553	lmo0474	protein_coding	985208	lmo0474(lmo0474)
CAC98555	lmo0476	protein_coding	985213	oxetanocin A resistance protein OxrB(lmo0476)
CAC98556	lmo0477	protein_coding	985893	secreted protein(lmo0477)
CAC98557	lmo0478	protein_coding	985211	secreted protein(lmo0478)
CAC98558	lmo0479	protein_coding	985210	secreted protein(lmo0479)
CAC98560	lmo0481	protein_coding	985215	hypothetical protein(lmo0481)
CAC98561	lmo0482	protein_coding	986229	ribosomal RNA large subunit methyltransferase N(lmo0482)
CAC98564	lmo0485	protein_coding	985219	lmo0485(lmo0485)
CAC98567	lmo0488	protein_coding	985225	LysR family transcriptional regulator(lmo0488)
CAC98568	lmo0489	protein_coding	984913	NADH:flavin oxidoreductase(lmo0489)
CAC98569	lmo0490	protein_coding	985396	shikimate 5-dehydrogenase(aroE)
CAC98573	lmo0494	protein_coding	985230	hypothetical protein(lmo0494)
CAC98574	lmo0495	protein_coding	985247	hypothetical protein(lmo0495)

CAC98575	lmo0496	protein_coding	984435	hypothetical protein(lmo0496)
CAC98577	lmo0498	protein_coding	985236	5-phosphate isomerase(lmo0498)
CAC98578	lmo0499	protein_coding	985241	ribulose-5-phosphate 3 epimerase(lmo0499)
CAC98579	lmo0500	protein_coding	985240	transaldolase(lmo0500)
CAC98580	lmo0501	protein_coding	985244	transcriptional antiterminator BglG(lmo0501)
CAC98581	lmo0502	protein_coding	985250	sugar-phosphate isomerase(lmo0502)
CAC98583	lmo0504	protein_coding	985256	lmo0504(lmo0504)
CAC98584	lmo0505	protein_coding	985251	ribulose-5-phosphate 3-epimerase(lmo0505)
CAC98585	lmo0506	protein_coding	986275	sorbitol dehydrogenase(lmo0506)
CAC98587	lmo0508	protein_coding	985255	PTS galactitol transporter subunit IIC(lmo0508)
CAC98588	prs	protein_coding	985257	phosphoribosyl pyrophosphate synthetase(prs)
CAC98589	lmo0510	protein_coding	985258	lmo0510(lmo0510)
CAC98590	lmo0511	protein_coding	985259	hypothetical protein(lmo0511)
CAC98591	lmo0512	protein_coding	985264	lmo0512(lmo0512)
CAC98592	lmo0513	protein_coding	985263	hypothetical protein(lmo0513)
CAC98593	lmo0514	protein_coding	985260	internalin(lmo0514)
CAC98594	lmo0515	protein_coding	986558	hypothetical protein(lmo0515)
CAC98595	lmo0516	protein_coding	985267	encapsulation protein CapA(lmo0516)
CAC98596	lmo0517	protein_coding	985270	phosphoglycerate mutase(lmo0517)
CAC98598	lmo0519	protein_coding	985272	multidrug resistance protein(lmo0519)
CAC98601	lmo0522	protein_coding	985274	transcriptional regulator(lmo0522)
CAC98602	lmo0523	protein_coding	985275	hypothetical protein(lmo0523)
CAC98603	lmo0524	protein_coding	985278	sulfate transporter(lmo0524)
CAC98604	lmo0525	protein_coding	985282	lmo0525(lmo0525)
CAC98606	lmo0527	protein_coding	985287	transmembrane protein(lmo0527)
CAC98607	lmo0528	protein_coding	985299	hypothetical secreted protein(lmo0528)
CAC98608	lmo0529	protein_coding	985294	glucosaminyltransferase(lmo0529)
CAC98609	lmo0530	protein_coding	984571	lmo0530(lmo0530)
CAC98610	lmo0531	protein_coding	985297	lmo0531(lmo0531)
CAC98611	lmo0532	protein_coding	985308	lmo0532(lmo0532)
CAC98612	lmo0533	protein_coding	985302	hypothetical protein(lmo0533)
CAC98615	lmo0536	protein_coding	985314	6-phospho-beta-glucosidase(lmo0536)
CAC98616	lmo0537	protein_coding	985309	allantoate amidohydrolase(lmo0537)
CAC98617	lmo0538	protein_coding	985381	N-acyl-L-amino acid amidohydrolase(lmo0538)
CAC98618	lmo0539	protein_coding	985316	tagatose 1,6-diphosphate aldolase(lmo0539)
CAC98619	lmo0540	protein_coding	985229	penicillin-binding protein(lmo0540)
CAC98623	lmo0544	protein_coding	986622	PTS sorbitol transporter subunit IIC(lmo0544)
CAC98625	lmo0546	protein_coding	985462	NAD(P)-dependent oxidoreductase(lmo0546)
CAC98630	lmo0551	protein_coding	984417	lmo0551(lmo0551)
CAC98631	lmo0552	protein_coding	986885	hypothetical protein(lmo0552)
CAC98633	lmo0554	protein_coding	984446	NADH-dependent butanol dehydrogenase(lmo0554)
CAC98634	lmo0555	protein_coding	984577	di-tripeptide transporter(lmo0555)
CAC98635	lmo0556	protein_coding	984853	phosphoglycerate mutase(lmo0556)
CAC98636	lmo0557	protein_coding	984617	phosphoglycerate mutase(lmo0557)
CAC98637	lmo0558	protein_coding	984498	hypothetical protein(lmo0558)
CAC98639	lmo0560	protein_coding	986813	glutamate dehydrogenase(lmo0560)
CAC98648	hisZ	protein_coding	984506	ATP phosphoribosyltransferase(hisZ)
CAC98649	hisJ	protein_coding	984572	histidinol-phosphatase(hisJ)

CAC98650	lmo0571	protein_coding	985060	methyltransferase(lmo0571)
CAC98651	lmo0572	protein_coding	986053	lmo0572(lmo0572)
CAC98652	lmo0573	protein_coding	985853	hypothetical protein(lmo0573)
CAC98653	lmo0574	protein_coding	984589	beta-glucosidase(lmo0574)
CAC98655	lmo0576	protein_coding	985083	hypothetical cell wall associated protein(lmo0576)
CAC98656	lmo0577	protein_coding	984939	lmo0577(lmo0577)
CAC98657	lmo0578	protein_coding	984630	hypothetical protein(lmo0578)
CAC98658	lmo0579	protein_coding	986865	hypothetical protein(lmo0579)
CAC98659	lmo0580	protein_coding	986638	hypothetical protein(lmo0580)
CAC98663	lmo0584	protein_coding	984661	hypothetical protein(lmo0584)
CAC98664	lmo0585	protein_coding	984672	secreted protein(lmo0585)
CAC98666	lmo0587	protein_coding	986515	secreted protein(lmo0587)
CAC98667	lmo0588	protein_coding	984699	DNA photolyase(lmo0588)
CAC98668	lmo0589	protein_coding	985047	lmo0589(lmo0589)
CAC98669	lmo0590	protein_coding	985311	hypothetical protein(lmo0590)
CAC98670	lmo0591	protein_coding	984755	hypothetical protein(lmo0591)
CAC98671	lmo0592	protein_coding	986217	lmo0592(lmo0592)
CAC98675	lmo0596	protein_coding	985266	hypothetical protein(lmo0596)
CAC98677	lmo0599	protein_coding	985146	hypothetical protein(lmo0599)
CAC98678	lmo0600	protein_coding	985344	lmo0600(lmo0600)
CAC98679	lmo0601	protein_coding	984830	cell surface protein(lmo0601)
CAC98680	lmo0602	protein_coding	984599	transcripitonal regulator(lmo0602)
CAC98682	lmo0604	protein_coding	985855	hypothetical protein(lmo0604)
CAC98683	lmo0605	protein_coding	985094	hypothetical protein(lmo0605)
CAC98684	lmo0606	protein_coding	985290	MarR family transcriptional regulator(lmo0606)
CAC98685	lmo0607	protein_coding	985501	ABC transporter ATP-binding protein(lmo0607)
CAC98686	lmo0608	protein_coding	984780	ABC transporter ATP-binding protein(lmo0608)
CAC98687	lmo0609	protein_coding	986403	phage shock protein E(lmo0609)
CAC98688	lmo0610	protein_coding	985509	internalin(lmo0610)
CAC98689	lmo0611	protein_coding	985209	azoreductase(acpD)
CAC98690	lmo0612	protein_coding	984912	MarR family transcriptional evidence(lmo0612)
CAC98691	lmo0613	protein_coding	987413	oxidoreductase(lmo0613)
CAC98693	lmo0615	protein_coding	984917	lmo0615(lmo0615)
CAC98694	lmo0616	protein_coding	985453	glycerophosphoryl diester phosphodiesterase(lmo0616)
CAC98695	lmo0617	protein_coding	985148	lmo0617(lmo0617)
CAC98696	lmo0618	protein_coding	984940	protein kinase(lmo0618)
CAC98697	lmo0619	protein_coding	984942	lmo0619(lmo0619)
CAC98698	lmo0620	protein_coding	985155	lmo0620(lmo0620)
CAC98699	lmo0621	protein_coding	985249	hypothetical protein(lmo0621)
CAC98702	lmo0624	protein_coding	985292	hypothetical protein(lmo0624)
CAC98703	lmo0625	protein_coding	985881	lmo0625(lmo0625)
CAC98704	lmo0626	protein_coding	985506	hypothetical protein(lmo0626)
CAC98705	lmo0627	protein_coding	984956	pepdidoglycan bound protein(lmo0627)
CAC98706	lmo0628	protein_coding	984963	lmo0628(lmo0628)
CAC98707	lmo0629	protein_coding	984966	lmo0629(lmo0629)
CAC98708	lmo0630	protein_coding	984967	transcriptional antiterminator BglG(lmo0630)
CAC98710	lmo0632	protein_coding	984378	PTS fructose transporter subunit IIC(lmo0632)
CAC98711	lmo0633	protein_coding	984968	PTS fructose transporter subunit IIB(lmo0633)

CAC98712	lmo0634	protein_coding	987068	tagatose 6-phosphate kinase(lmo0634)
CAC98713	lmo0635	protein_coding	984974	lmo0635(lmo0635)
CAC98716	lmo0638	protein_coding	984973	lmo0638(lmo0638)
CAC98717	lmo0639	protein_coding	984972	transcripitonal regulator(lmo0639)
CAC98719	lmo0641	protein_coding	985323	heavy metal-transporting ATPase(lmo0641)
CAC98720	lmo0642	protein_coding	984976	lmo0642(lmo0642)
CAC98721	lmo0643	protein_coding	984977	transaldolase(lmo0643)
CAC98722	lmo0644	protein_coding	984979	hypothetical protein(lmo0644)
CAC98723	lmo0645	protein_coding	984978	amino acid transporter(lmo0645)
CAC98724	lmo0646	protein_coding	984982	hypothetical protein(lmo0646)
CAC98725	lmo0647	protein_coding	985414	lmo0647(lmo0647)
CAC98726	lmo0648	protein_coding	987051	hypothetical protein(lmo0648)
CAC98727	lmo0649	protein_coding	986557	transcriptional regulator(lmo0649)
CAC98728	lmo0650	protein_coding	984986	hypothetical protein(lmo0650)
CAC98729	lmo0651	protein_coding	984985	transcriptional regulator(lmo0651)
CAC98730	lmo0652	protein_coding	984987	hypothetical protein(lmo0652)
CAC98731	lmo0653	protein_coding	985279	lmo0653(lmo0653)
CAC98732	lmo0654	protein_coding	984989	lmo0654(lmo0654)
CAC98733	lmo0655	protein_coding	984992	phosphoprotein phosphatase(lmo0655)
CAC98735	lmo0657	protein_coding	985003	lmo0657(lmo0657)
CAC98736	lmo0658	protein_coding	985006	hypothetical protein(lmo0658)
CAC98737	lmo0659	protein_coding	984988	transcriptional regulator(lmo0659)
CAC98739	lmo0661	protein_coding	984999	hypothetical protein(lmo0661)
CAC98740	thiD	protein_coding	985000	phosphomethylpyrimidine kinase(thiD)
CAC98741	lmo0663	protein_coding	985001	hypothetical protein(lmo0663)
CAC98742	lmo0664	protein_coding	987123	acetyl transferase(lmo0664)
CAC98745	lmo0667	protein_coding	985013	ABC transporter ATP-binding protein(lmo0667)
CAC98746	lmo0668	protein_coding	987144	ABC transporter permease(lmo0668)
CAC98747	lmo0669	protein_coding	987147	oxidoreductase(lmo0669)
CAC98748	lmo0670	protein_coding	985009	lmo0670(lmo0670)
CAC98749	lmo0671	protein_coding	985011	lmo0671(lmo0671)
CAC98752	lmo0674	protein_coding	985015	lmo0674(lmo0674)
CAC98753	lmo0675	protein_coding	987142	lmo0675(lmo0675)
CAC98754	lmo0676	protein_coding	985021	flagellar biosynthesis protein FliP(fliP)
CAC98755	lmo0677	protein_coding	985022	flagellar biosynthesis protein FliQ(fliQ)
CAC98756	lmo0678	protein_coding	985024	flagellar biosynthesis protein FliR(fliR)
CAC98757	lmo0679	protein_coding	986322	flagellar biosynthesis protein FlhB(flhB)
CAC98758	lmo0680	protein_coding	986323	flagellar biosynthesis protein FlhA(flhA)
CAC98759	lmo0681	protein_coding	985019	flagellar biosynthesis regulator FlhF(lmo0681)
CAC98760	lmo0682	protein_coding	985030	flagellar basal body rod protein FlgG(flgG)
CAC98761	lmo0683	protein_coding	985031	chemotaxis protein CheR(lmo0683)
CAC98762	lmo0684	protein_coding	985027	lmo0684(lmo0684)
CAC98763	lmo0685	protein_coding	985036	flagellar motor protein MotA(lmo0685)
CAC98764	motB	protein_coding	986861	flagellar motor rotation MotB(motB)
CAC98765	lmo0687	protein_coding	985029	lmo0687(lmo0687)
CAC98766	lmo0688	protein_coding	986281	hypothetical protein(lmo0688)
CAC98767	lmo0689	protein_coding	987162	chemotaxis protein CheV(lmo0689)
CAC98769	cheY	protein_coding	985049	chemotaxis response regulator CheY(cheY)

CAC98770	cheA	protein_coding	985032	two-component sensor histidine kinase CheA(cheA)
CAC98772	lmo0694	protein_coding	985033	lmo0694(lmo0694)
CAC98773	lmo0695	protein_coding	985037	lmo0695(lmo0695)
CAC98774	lmo0696	protein_coding	985038	flagellar basal body rod modification protein(flgD)
CAC98775	lmo0697	protein_coding	985043	flagellar hook protein FlgE(flgE)
CAC98776	lmo0698	protein_coding	985039	flagellar motor switch protein(lmo0698)
CAC98777	lmo0699	protein_coding	987173	flagellar motor switch protein FliM(fliM)
CAC98778	lmo0700	protein_coding	985046	flagellar motor switch protein FliY(lmo0700)
CAC98779	lmo0701	protein_coding	985048	lmo0701(lmo0701)
CAC98780	lmo0702	protein_coding	985034	lmo0702(lmo0702)
CAC98781	lmo0703	protein_coding	985050	lmo0703(lmo0703)
CAC98782	lmo0704	protein_coding	985042	lmo0704(lmo0704)
CAC98783	lmo0705	protein_coding	985054	flagellar hook-associated protein FlgK(flgK)
CAC98784	lmo0706	protein_coding	985052	flagellar hook-associated protein FlgL(flgL)
CAC98785	lmo0707	protein_coding	985041	flagellar capping protein FliD(fliD)
CAC98786	lmo0708	protein_coding	985045	flagellar protein(lmo0708)
CAC98787	lmo0709	protein_coding	985079	lmo0709(lmo0709)
CAC98788	lmo0710	protein_coding	985059	flagellar basal-body rod protein FlgB(flgB)
CAC98789	lmo0711	protein_coding	984818	flagellar basal body rod protein FlgC(flgC)
CAC98790	lmo0712	protein_coding	985062	flagellar hook-basal body protein FliE(fliE)
CAC98791	lmo0713	protein_coding	985064	flagellar MS-ring protein FliF(fliF)
CAC98792	lmo0714	protein_coding	985067	flagellar motor switch protein FliG(fliG)
CAC98793	lmo0715	protein_coding	985068	lmo0715(fliH)
CAC98795	lmo0717	protein_coding	987208	transglycosylase(lmo0717)
CAC98796	lmo0718	protein_coding	985076	lmo0718(lmo0718)
CAC98799	lmo0721	protein_coding	987135	fibronectin-binding protein(lmo0721)
CAC98800	lmo0722	protein_coding	986726	pyruvate oxidase(lmo0722)
CAC98804	lmo0726	protein_coding	986355	hypothetical protein(lmo0726)
CAC98805	lmo0727	protein_coding	986353	glucosamine--fructose-6-phosphate aminotransferase(lmo0727)
CAC98806	lmo0728	protein_coding	986299	riboflavin kinase / FAD synthase(lmo0728)
CAC98808	lmo0730	protein_coding	986268	lmo0730(lmo0730)
CAC98810	lmo0732	protein_coding	985958	peptidoglycan binding protein(lmo0732)
CAC98811	lmo0733	protein_coding	985919	transcriptional regulator(lmo0733)
CAC98813	lmo0735	protein_coding	985578	ribulose-5-phosphate 3-epimerase(lmo0735)
CAC98814	lmo0736	protein_coding	985545	ribose-5-phosphate isomerase B(lmo0736)
CAC98815	lmo0737	protein_coding	985544	lmo0737(lmo0737)
CAC98819	lmo0741	protein_coding	985539	GntR family transcriptional regulator(lmo0741)
CAC98820	lmo0742	protein_coding	985536	ABC transporter ATP-binding protein(lmo0742)
CAC98821	lmo0743	protein_coding	985534	lmo0743(lmo0743)
CAC98824	lmo0746	protein_coding	985530	hypothetical protein(lmo0746)
CAC98833	lmo0755	protein_coding	985516	hypothetical protein(lmo0755)
CAC98836	lmo0758	protein_coding	985508	lmo0758(lmo0758)
CAC98837	lmo0759	protein_coding	985503	lmo0759(lmo0759)
CAC98838	lmo0760	protein_coding	985499	lmo0760(lmo0760)
CAC98839	lmo0761	protein_coding	985498	hypothetical protein(lmo0761)
CAC98840	lmo0762	protein_coding	985496	ATP/GTP-binding protein(lmo0762)
CAC98841	lmo0763	protein_coding	985495	hypothetical protein(lmo0763)
CAC98842	lmo0764	protein_coding	985491	lipoate-protein ligase(lmo0764)

CAC98843	lmo0765	protein_coding	985489	lmo0765(lmo0765)
CAC98844	lmo0766	protein_coding	985488	sugar ABC transporter permease(lmo0766)
CAC98845	lmo0767	protein_coding	985486	ABC transporter permease(lmo0767)
CAC98846	lmo0768	protein_coding	985485	sugar ABC transporter substrate-binding protein(lmo0768)
CAC98847	lmo0769	protein_coding	985482	alpha-1,6-mannanase(lmo0769)
CAC98851	lmo0773	protein_coding	985473	alcohol dehydrogenase(lmo0773)
CAC98852	lmo0774	protein_coding	985472	hypothetical protein(lmo0774)
CAC98853	lmo0775	protein_coding	985469	lmo0775(lmo0775)
CAC98854	lmo0776	protein_coding	985467	transcriptional regulator(lmo0776)
CAC98856	lmo0778	protein_coding	985465	lmo0778(lmo0778)
CAC98857	lmo0779	protein_coding	985463	lmo0779(lmo0779)
CAC98858	lmo0780	protein_coding	985461	lmo0780(lmo0780)
CAC98859	lmo0781	protein_coding	985460	PTS mannose transporter subunit IID(lmo0781)
CAC98860	lmo0782	protein_coding	985459	PTS mannose transporter subunit IIC(lmo0782)
CAC98861	lmo0783	protein_coding	985458	PTS mannose transporter subunit IIB(lmo0783)
CAC98862	lmo0784	protein_coding	985456	PTS mannose transporter subunit IIB(lmo0784)
CAC98863	lmo0785	protein_coding	985452	transcriptional regulator(lmo0785)
CAC98864	lmo0786	protein_coding	985450	ACP phosphodiesterase(lmo0786)
CAC98865	lmo0787	protein_coding	985449	amino acid transporter(lmo0787)
CAC98867	lmo0789	protein_coding	985444	hypothetical protein(lmo0789)
CAC98868	lmo0790	protein_coding	985443	transcriptional regulator(lmo0790)
CAC98871	lmo0793	protein_coding	985432	hypothetical protein(lmo0793)
CAC98872	lmo0794	protein_coding	985430	hypothetical protein(lmo0794)
CAC98873	lmo0795	protein_coding	985429	hypothetical protein(lmo0795)
CAC98874	lmo0796	protein_coding	985428	hypothetical protein(lmo0796)
CAC98875	lmo0797	protein_coding	985426	lmo0797(lmo0797)
CAC98876	lmo0798	protein_coding	985421	lysine-specific permease(lmo0798)
CAC98877	lmo0799	protein_coding	985420	lmo0799(lmo0799)
CAC98878	lmo0800	protein_coding	985418	hypothetical protein(lmo0800)
CAC98880	lmo0802	protein_coding	985413	hypothetical protein(lmo0802)
CAC98881	lmo0803	protein_coding	985412	Na+/H+ antiporter(lmo0803)
CAC98883	lmo0805	protein_coding	985405	lmo0805(lmo0805)
CAC98884	lmo0806	protein_coding	985404	transcriptional regulator(lmo0806)
CAC98885	lmo0807	protein_coding	985403	spermidine/putrescine ABC transporter ATP-binding protein(lmo0807)
CAC98886	lmo0808	protein_coding	985401	spermidine/putrescine ABC transporter permease(lmo0808)
CAC98887	lmo0809	protein_coding	985399	spermidine/putrescine ABC transporter permease(lmo0809)
CAC98888	lmo0810	protein_coding	985395	spermidine/putrescine ABC transporter substrate-binding protein(lmo0810)
CAC98889	lmo0811	protein_coding	985394	carbonic anhydrase(lmo0811)
CAC98890	lmo0812	protein_coding	985393	lmo0812(lmo0812)
CAC98891	lmo0813	protein_coding	985392	fructokinase(lmo0813)
CAC98892	lmo0814	protein_coding	985391	oxidoreductase(lmo0814)
CAC98894	lmo0816	protein_coding	985388	regulatory protein PaiA(lmo0816)
CAC98896	lmo0818	protein_coding	985383	cation-transporting ATPase(lmo0818)
CAC98897	lmo0819	protein_coding	985382	lmo0819(lmo0819)
CAC98898	lmo0820	protein_coding	985380	acetyltransferase(lmo0820)
CAC98899	lmo0821	protein_coding	985377	lmo0821(lmo0821)
CAC98900	lmo0822	protein_coding	985376	transcriptional regulator(lmo0822)
CAC98901	lmo0823	protein_coding	985374	oxidoreductase(lmo0823)

CAC98902	lmo0824	protein_coding	985373	lmo0824(lmo0824)
CAC98903	lmo0825	protein_coding	985372	3-hydroxy-3-methylglutaryl-CoA reductase(lmo0825)
CAC98904	lmo0826	protein_coding	985369	transporter(lmo0826)
CAC98907	nifJ	protein_coding	985364	pyruvate-flavodoxin oxidoreductase(nifJ)
CAC98908	fbp	protein_coding	985361	fructose-1,6-bisphosphatase(fbp)
CAC98909	lmo0831	protein_coding	985359	lmo0831(lmo0831)
CAC98911	lmo0833	protein_coding	985354	transcriptional regulator(lmo0833)
CAC98912	lmo0834	protein_coding	985353	lmo0834(lmo0834)
CAC98913	lmo0835	protein_coding	985352	peptidoglycan binding protein(lmo0835)
CAC98919	lmo0841	protein_coding	985338	calcium-transporting ATPase(lmo0841)
CAC98920	lmo0842	protein_coding	985337	peptidoglycan binding protein(lmo0842)
CAC98923	lmo0845	protein_coding	985330	hypothetical protein(lmo0845)
CAC98924	lmo0846	protein_coding	985329	excinuclease ABC subunit C(lmo0846)
CAC98925	lmo0847	protein_coding	985328	glutamine ABC transporter(lmo0847)
CAC98927	lmo0849	protein_coding	985321	amidase(lmo0849)
CAC98928	lmo0850	protein_coding	985319	hypothetical protein(lmo0850)
CAC98929	lmo0851	protein_coding	985315	lmo0851(lmo0851)
CAC98930	lmo0852	protein_coding	985313	TetR family transcriptional regulator(lmo0852)
CAC98931	lmo0853	protein_coding	985304	SugE protein(lmo0853)
CAC98932	lmo0854	protein_coding	985242	SugE protein(lmo0854)
CAC98933	ddlA	protein_coding	985238	D-alanyl-alanine synthetase A(ddl)
CAC98935	lmo0857	protein_coding	985170	carboxylesterase(lmo0857)
CAC98937	lmo0859	protein_coding	985026	sugar ABC transporter substrate-binding protein(lmo0859)
CAC98938	lmo0860	protein_coding	984935	sugar ABC transporter permease(lmo0860)
CAC98939	lmo0861	protein_coding	984876	sugar ABC transporter permease(lmo0861)
CAC98940	lmo0862	protein_coding	984847	oligo-1,6-glucosidase(lmo0862)
CAC98941	lmo0863	protein_coding	984720	lmo0863(lmo0863)
CAC98943	lmo0865	protein_coding	984615	phosphomannomutase(lmo0865)
CAC98944	lmo0866	protein_coding	984613	ATP-dependent RNA helicase(lmo0866)
CAC98945	lmo0867	protein_coding	984585	lmo0867(lmo0867)
CAC98947	lmo0869	protein_coding	984542	lmo0869(lmo0869)
CAC98948	lmo0870	protein_coding	984493	lmo0870(lmo0870)
CAC98949	lmo0871	protein_coding	984472	hypothetical protein(lmo0871)
CAC98951	lmo0873	protein_coding	984373	transcriptional regulator(lmo0873)
CAC98952	lmo0874	protein_coding	986569	PTS sugar transporter subunit IIA(lmo0874)
CAC98953	lmo0875	protein_coding	986563	PTS beta-glucoside transporter subunit IIB(lmo0875)
CAC98954	lmo0876	protein_coding	986296	PTS sugar transporter subunit IIC(lmo0876)
CAC98956	lmo0878	protein_coding	986549	oxidoreductase(lmo0878)
CAC98958	lmo0880	protein_coding	986636	wall associated protein precursor(lmo0880)
CAC98960	lmo0882	protein_coding	986548	hypothetical protein(lmo0882)
CAC98961	lmo0883	protein_coding	986544	hypothetical protein(lmo0883)
CAC98962	lmo0884	protein_coding	986422	protoporphyrinogen oxidase(lmo0884)
CAC98964	dal	protein_coding	986294	alanine racemase(dal)
CAC98966	lmo0888	protein_coding	986538	hypothetical protein(lmo0888)
CAC98967	RsbR	protein_coding	986201	positive regulator of sigma-B activity(RsbR)
CAC98969	rsbT	protein_coding	986533	positive regulation of sigma-B activity(rsbT)
CAC98970	rsbU	protein_coding	986534	serine phosphatase(rsbU)
CAC98971	rsbV	protein_coding	986526	anti-anti-sigma factor (antagonist of RsbW)(rsbV)

CAC98972	rsbW	protein_coding	986524	serine-protein kinase RsbW(rsbW)
CAC98973	sigB	protein_coding	986527	RNA polymerase sigma factor SigB(sigB)
CAC98974	rsbX	protein_coding	986520	indirect negative regulation of sigma B dependant gene expression (serine phosphatase)(rsbX)
CAC98975	lmo0897	protein_coding	984941	transporter(lmo0897)
CAC98978	lmo0900	protein_coding	987809	lmo0900(lmo0900)
CAC98980	lmo0902	protein_coding	986980	GntR family transcriptional regulator(lmo0902)
CAC98982	lmo0904	protein_coding	986917	lmo0904(lmo0904)
CAC98983	lmo0905	protein_coding	986916	lmo0905(lmo0905)
CAC98984	lmo0906	protein_coding	986897	glutathione reductase(lmo0906)
CAC98985	lmo0907	protein_coding	986931	phosphoglycerate mutase(lmo0907)
CAC98987	lmo0909	protein_coding	986502	GntR family transcriptional regulator(lmo0909)
CAC98988	lmo0910	protein_coding	984497	lmo0910(lmo0910)
CAC98989	lmo0911	protein_coding	986500	lmo0911(lmo0911)
CAC98990	lmo0912	protein_coding	986984	formate transporter(lmo0912)
CAC98991	lmo0913	protein_coding	986938	succinate semialdehyde dehydrogenase(lmo0913)
CAC98992	lmo0914	protein_coding	987760	PTS sugar transporter subunit IIB(lmo0914)
CAC98993	lmo0915	protein_coding	987872	PTS sugar transporter subunit IIC(lmo0915)
CAC98994	lmo0916	protein_coding	987774	PTS sugar transporter subunit IIA(lmo0916)
CAC98997	lmo0919	protein_coding	986830	antibiotic ABC transporter ATP-binding protein(lmo0919)
CAC99000	lmo0922	protein_coding	986345	pantothenate kinase(lmo0922)
CAC99005	lmo0927	protein_coding	986782	hypothetical protein(lmo0927)
CAC99006	lmo0928	protein_coding	985312	3-methyladenine DNA glycosylase(lmo0928)
CAC99007	lmo0929	protein_coding	986837	sortase(lmo0929)
CAC99010	lmo0932	protein_coding	987846	hypothetical protein(lmo0932)
CAC99011	lmo0933	protein_coding	984547	sugar transferase(lmo0933)
CAC99015	lmo0937	protein_coding	987860	lmo0937(lmo0937)
CAC99016	lmo0938	protein_coding	987839	protein-tyrosine-phosphatase(lmo0938)
CAC99017	lmo0939	protein_coding	985869	lmo0939(lmo0939)
CAC99018	lmo0940	protein_coding	987854	lmo0940(lmo0940)
CAC99020	lmo0942	protein_coding	986476	heat shock protein 90(lmo0942)
CAC99021	fri	protein_coding	986847	non-heme iron-binding ferritin(fri)
CAC99022	lmo0944	protein_coding	986825	hypothetical protein(lmo0944)
CAC99025	lmo0947	protein_coding	986474	hypothetical transport protein(lmo0947)
CAC99026	lmo0948	protein_coding	986781	transcriptional regulator(lmo0948)
CAC99027	lmo0949	protein_coding	987856	hypothetical protein(lmo0949)
CAC99028	lmo0950	protein_coding	987861	lmo0950(lmo0950)
CAC99029	lmo0951	protein_coding	987836	lmo0951(lmo0951)
CAC99030	lmo0952	protein_coding	986763	lmo0952(lmo0952)
CAC99031	lmo0953	protein_coding	986396	lmo0953(lmo0953)
CAC99034	lmo0956	protein_coding	986776	N-acetylglucosamine-6P-phosphate deacetylase(lmo0956)
CAC99035	lmo0957	protein_coding	986480	glucosamine-6-phosphate isomerase(lmo0957)
CAC99036	lmo0958	protein_coding	986478	GntR family transcirptional regulator(lmo0958)
CAC99038	lmo0960	protein_coding	986469	protease(lmo0960)
CAC99039	lmo0961	protein_coding	986465	protease(lmo0961)
CAC99040	lemA	protein_coding	986467	LemA protein(lemA)
CAC99042	lmo0964	protein_coding	986468	hypothetical protein(lmo0964)
CAC99043	lmo0965	protein_coding	985451	hypothetical protein(lmo0965)

CAC99044	lmo0966	protein_coding	986839	lmo0966(lmo0966)
CAC99045	lmo0967	protein_coding	986471	hypothetical protein(lmo0967)
CAC99048	lmo0970	protein_coding	987821	enoyl-ACP reductase(lmo0970)
CAC99049	dltD	protein_coding	986447	DltD protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid(dltD)
CAC99050	dltC	protein_coding	986460	D-alanine--poly(phosphoribitol) ligase subunit 2(dltC)
CAC99051	dltB	protein_coding	986448	DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid(dltB)
CAC99052	dltA	protein_coding	986449	D-alanine--poly(phosphoribitol) ligase subunit 1(dltA)
CAC99054	lmo0976	protein_coding	986442	hypothetical protein(lmo0976)
CAC99055	lmo0977	protein_coding	986913	hypothetical protein(lmo0977)
CAC99056	lmo0978	protein_coding	986440	branched-chain amino acid aminotransferase(lmo0978)
CAC99059	lmo0981	protein_coding	986765	transporter(lmo0981)
CAC99060	lmo0982	protein_coding	986804	peptidase(lmo0982)
CAC99061	lmo0983	protein_coding	986438	glutathione peroxidase(lmo0983)
CAC99062	lmo0984	protein_coding	986785	hypothetical protein(lmo0984)
CAC99063	lmo0985	protein_coding	986431	lmo0985(lmo0985)
CAC99064	lmo0986	protein_coding	986427	antibiotic ABC transporter ATP-binding protein(lmo0986)
CAC99065	lmo0987	protein_coding	986424	CylB protein(lmo0987)
CAC99068	lmo0990	protein_coding	986420	hypothetical protein(lmo0990)
CAC99069	lmo0991	protein_coding	986787	hypothetical protein(lmo0991)
CAC99072	lmo0994	protein_coding	986414	lmo0994(lmo0994)
CAC99073	lmo0995	protein_coding	986413	hypothetical protein(lmo0995)
CAC99075	clpE	protein_coding	986780	ATP-dependent protease(clpE)
CAC99076	lmo0998	protein_coding	986409	hypothetical protein(lmo0998)
CAC99078	lmo1000	protein_coding	986831	phytoene dehydrogenase(lmo1000)
CAC99084	lmo1006	protein_coding	986673	aminotransferase(lmo1006)
CAC99085	lmo1007	protein_coding	986404	lmo1007(lmo1007)
CAC99087	lmo1009	protein_coding	986412	hypothetical protein(lmo1009)
CAC99088	lmo1010	protein_coding	986367	LysR family transcriptional regulator(lmo1010)
CAC99089	lmo1011	protein_coding	986298	tetrahydrodipicolinate succinylase(lmo1011)
CAC99090	lmo1012	protein_coding	986510	N-acyl-L-amino acid amidohydrolase(lmo1012)
CAC99092	gbuA	protein_coding	986360	glycine/betaine ABC transporter ATP-binding protein(gbuA)
CAC99093	gbuB	protein_coding	985002	glycine/betaine ABC transporter permease(gbuB)
CAC99094	gbuC	protein_coding	986358	glycine/betaine ABC transporter substrate-binding protein(gbuC)
CAC99095	lmo1017	protein_coding	986356	PTS glucose transporter subunit IIA(lmo1017)
CAC99096	lmo1018	protein_coding	986357	copper homeostasis protein CutC(lmo1018)
CAC99101	lmo1023	protein_coding	985239	potassium transporter(lmo1023)
CAC99105	lmo1027	protein_coding	986344	hypothetical protein(lmo1027)
CAC99106	lmo1028	protein_coding	986595	hypothetical protein(lmo1028)
CAC99108	lmo1030	protein_coding	986852	LacI family transcriptional regulator(lmo1030)
CAC99109	lmo1031	protein_coding	986327	hypothetical protein(lmo1031)
CAC99112	lmo1034	protein_coding	986330	glycerol kinase(lmo1034)
CAC99113	lmo1035	protein_coding	985245	PTS beta-glucoside transporter subunit IIABC(lmo1035)
CAC99114	lmo1036	protein_coding	984797	lmo1036(lmo1036)
CAC99116	lmo1038	protein_coding	986325	hypothetical protein(lmo1038)
CAC99126	lmo1048	protein_coding	986817	molybdenum cofactor biosynthesis protein B(lmo1048)
CAC99130	pdhA	protein_coding	986808	pyruvate dehydrogenase subunit E1 alpha(pdhA)
CAC99131	PdhB	protein_coding	984409	pyruvate dehydrogenase subunit E1 beta(PdhB)

CAC99132	pdhC	protein_coding	986301	dihydrolipoamide acetyltransferase(pdhC)
CAC99133	PdhD	protein_coding	986542	dihydrolipoamide dehydrogenase(PdhD)
CAC99134	lmo1056	protein_coding	986297	lmo1056(lmo1056)
CAC99135	lmo1057	protein_coding	986824	L-lactate dehydrogenase(lmo1057)
CAC99136	lmo1058	protein_coding	986292	hypothetical protein(lmo1058)
CAC99137	lmo1059	protein_coding	984717	lmo1059(lmo1059)
CAC99138	lmo1060	protein_coding	984788	transcriptional regulator(lmo1060)
CAC99139	lmo1061	protein_coding	986289	two-component sensor histidine kinase(lmo1061)
CAC99143	lmo1065	protein_coding	984607	hypothetical protein(lmo1065)
CAC99148	lmo1070	protein_coding	986295	hypothetical protein(lmo1070)
CAC99154	lmo1076	protein_coding	986264	autolysin(lmo1076)
CAC99157	lmo1079	protein_coding	986262	hypothetical protein(lmo1079)
CAC99160	lmo1082	protein_coding	986259	dTDP-sugar epimerase(lmo1082)
CAC99161	lmo1083	protein_coding	986257	dTDP-D-glucose 4,6-dehydratase(lmo1083)
CAC99166	tagB	protein_coding	986255	teichoic acid biosynthesis protein B(tagB)
CAC99168	lmo1090	protein_coding	986248	glycosyltransferase(lmo1090)
CAC99170	lmo1092	protein_coding	986245	nicotinate phosphoribosyltransferase(lmo1092)
CAC99171	lmo1093	protein_coding	986246	NAD synthetase(nadE)
CAC99173	lmo1095	protein_coding	986241	PTS cellbiose transporter subunit IIB(lmo1095)
CAC99174	guaA	protein_coding	986238	GMP synthase(guaA)
CAC99175	lmo1097	protein_coding	986237	integrase(lmo1097)
CAC99180	lmo1102	protein_coding	987644	cadmium efflux system accessory protein(lmo1102)
CAC99190	lmo1112	protein_coding	986216	hypothetical protein(lmo1112)
CAC99191	lmo1113	protein_coding	986214	hypothetical protein(lmo1113)
CAC99192	lmo1114	protein_coding	986213	hypothetical protein(lmo1114)
CAC99193	lmo1115	protein_coding	986211	fibrinogen-binding protein(lmo1115)
CAC99194	lmo1116	protein_coding	986570	regulatory protein(lmo1116)
CAC99195	lmo1117	protein_coding	986210	lmo1117(lmo1117)
CAC99198	lmo1120	protein_coding	986206	lmo1120(lmo1120)
CAC99199	lmo1121	protein_coding	986205	lmo1121(lmo1121)
CAC99200	lmo1122	protein_coding	986203	lmo1122(lmo1122)
CAC99202	lmo1124	protein_coding	986198	lmo1124(lmo1124)
CAC99203	lmo1125	protein_coding	986200	lmo1125(lmo1125)
CAC99205	lmo1127	protein_coding	986196	lmo1127(lmo1127)
CAC99212	lmo1134	protein_coding	986190	regulatory protein(lmo1134)
CAC99213	lmo1135	protein_coding	986189	lmo1135(lmo1135)
CAC99214	lmo1136	protein_coding	986166	internalin(lmo1136)
CAC99218	lmo1140	protein_coding	986180	lmo1140(lmo1140)
CAC99219	lmo1141	protein_coding	986179	uroporphyrin-III C-methyltransferase(lmo1141)
CAC99220	lmo1142	protein_coding	986177	PduS protein(lmo1142)
CAC99221	lmo1143	protein_coding	986169	PduT protein(lmo1143)
CAC99222	lmo1144	protein_coding	986310	PduU protein(lmo1144)
CAC99223	lmo1145	protein_coding	986160	PduV protein(lmo1145)
CAC99224	lmo1146	protein_coding	986162	lmo1146(lmo1146)
CAC99225	lmo1147	protein_coding	986161	cobalamin biosynthesis protein CopB(lmo1147)
CAC99226	lmo1148	protein_coding	986158	cobalamin (5'-phosphatase) synthetase(lmo1148)
CAC99227	lmo1149	protein_coding	986156	alpha-ribazole-5'-phosphatase(lmo1149)
CAC99229	lmo1151	protein_coding	986164	PduA protein(lmo1151)

CAC99230	lmo1152	protein_coding	986154	PduB protein(lmo1152)
CAC99231	lmo1153	protein_coding	986155	propanediol dehydratase subunit alpha(lmo1153)
CAC99246	AckA2	protein_coding	986132	acetate kinase(AckA2)
CAC99248	lmo1170	protein_coding	986128	PduX protein(lmo1170)
CAC99249	pduQ	protein_coding	986125	NADPH-dependent butanol dehydrogenase(pduQ)
CAC99250	lmo1172	protein_coding	986126	two-component response regulator(lmo1172)
CAC99251	lmo1173	protein_coding	986122	two-component sensor histidine kinase(lmo1173)
CAC99252	eutA	protein_coding	986123	ethanolamine utilization protein EutA(eutA)
CAC99253	eutB	protein_coding	986127	ethanolamine ammonia-lyase large subunit(eutB)
CAC99254	eutC	protein_coding	986120	ethanolamine ammonia-lyase small subunit(eutC)
CAC99255	lmo1177	protein_coding	986121	carboxysome structural protein EutL(lmo1177)
CAC99256	lmo1178	protein_coding	986118	carboxysome structural protein(lmo1178)
CAC99257	lmo1179	protein_coding	986119	alcohol dehydrogenase(lmo1179)
CAC99258	lmo1180	protein_coding	986115	carboxysome structural protein(lmo1180)
CAC99259	lmo1181	protein_coding	986116	cobalamin adenosyl transferase(lmo1181)
CAC99260	lmo1182	protein_coding	986114	PduL protein(lmo1182)
CAC99261	lmo1183	protein_coding	986117	lmo1183(lmo1183)
CAC99262	lmo1184	protein_coding	986113	carbon dioxide concentrating mechanism protein(lmo1184)
CAC99263	lmo1185	protein_coding	986110	PduT protein(lmo1185)
CAC99264	lmo1186	protein_coding	986111	ethanolamine utilization protein EutH(lmo1186)
CAC99265	lmo1187	protein_coding	986106	ethanolamine utilization protein EutQ(lmo1187)
CAC99266	lmo1188	protein_coding	986112	lmo1188(lmo1188)
CAC99267	lmo1189	protein_coding	986109	transcriptional regulator(lmo1189)
CAC99268	lmo1190	protein_coding	986103	lmo1190(lmo1190)
CAC99269	cbiA	protein_coding	986099	cobyrinic acid a,c-diamide synthase(cbiA)
CAC99270	lmo1192	protein_coding	986098	cobalamin biosynthesis protein(cobD)
CAC99271	lmo1193	protein_coding	986096	cobalt-precorrin-8X methylmutase(cbiC)
CAC99272	cbiD	protein_coding	986097	cobalt-precorrin-6A synthase(cbiD)
CAC99273	cbiE	protein_coding	986100	cobalt-precorrin-6Y C(5)-methyltransferase(cbiE)
CAC99274	lmo1196	protein_coding	986101	cobalt-precorrin-6Y C(15)-methyltransferase(lmo1196)
CAC99275	cbiF	protein_coding	986091	precorrin-3 methylase(cbiF)
CAC99276	cbiG	protein_coding	986089	cobalamin biosynthesis protein CbiG(cbiG)
CAC99277	cbiH	protein_coding	986093	precorrin-3B C17-methyltransferase(cbiH)
CAC99278	lmo1200	protein_coding	986085	cobalamin biosynthesis protein CbiJ(lmo1200)
CAC99279	lmo1201	protein_coding	986081	uroporphyrinogen-III methyltransferase/uroporphyrinogen-III synthase (lmo1201)
CAC99280	cbiK	protein_coding	986086	cobalt chelatase(cbiK)
CAC99281	cbiL	protein_coding	986075	cobalt-precorrin-2 C(20)-methyltransferase(cbiL)
CAC99282	lmo1204	protein_coding	984567	cobalamin biosynthesis protein CbiM(lmo1204)
CAC99283	lmo1205	protein_coding	986083	cobalamin biosynthesis protein CbiN(lmo1205)
CAC99284	cbiQ	protein_coding	986065	cobalamin biosynthesis protein CbiQ(cbiQ)
CAC99285	lmo1207	protein_coding	986074	cobalt transporter ATP-binding protein CbiO(lmo1207)
CAC99286	cbiP	protein_coding	986064	cobyric acid synthase CbiP(cbiP)
CAC99287	lmo1209	protein_coding	986058	hypothetical protein(lmo1209)
CAC99288	lmo1210	protein_coding	986061	hypothetical protein(lmo1210)
CAC99289	lmo1211	protein_coding	986063	hypothetical protein(lmo1211)
CAC99291	lmo1213	protein_coding	986048	hypothetical protein(lmo1213)
CAC99292	lmo1214	protein_coding	986223	lmo1214(lmo1214)

CAC99293	lmo1215	protein_coding	986221	N-acetylmuramoyl-L-alanine amidase(lmo1215)
CAC99298	lmo1220	protein_coding	986047	hypothetical protein(lmo1220)
CAC99301	lmo1223	protein_coding	986045	ABC transporter ATP-binding proteins(lmo1223)
CAC99302	lmo1224	protein_coding	986043	hypothetical protein(lmo1224)
CAC99303	lmo1225	protein_coding	986044	MarR family transcriptional regulator(lmo1225)
CAC99304	lmo1226	protein_coding	986040	transporter(lmo1226)
CAC99308	lmo1230	protein_coding	986037	hypothetical protein(lmo1230)
CAC99309	lmo1231	protein_coding	986038	DNA polymerase beta(lmo1231)
CAC99310	lmo1232	protein_coding	986039	recombination and DNA strand exchange inhibitor protein(lmo1232)
CAC99311	trxA	protein_coding	986032	thioredoxin(trxA)
CAC99312	uvrC	protein_coding	986033	excinuclease ABC subunit C(uvrC)
CAC99313	lmo1235	protein_coding	986030	aspartate kinase(lmo1235)
CAC99314	lmo1236	protein_coding	986036	hypothetical protein(lmo1236)
CAC99315	racE	protein_coding	986027	glutamate racemase(racE)
CAC99316	lmo1238	protein_coding	986029	ribonuclease PH(rph)
CAC99317	lmo1239	protein_coding	986028	nucleoside-triphosphatase(lmo1239)
CAC99318	lmo1240	protein_coding	986025	hypothetical protein(lmo1240)
CAC99319	lmo1241	protein_coding	986024	lmo1241(lmo1241)
CAC99320	lmo1242	protein_coding	986021	hypothetical protein(lmo1242)
CAC99321	lmo1243	protein_coding	986018	lmo1243(lmo1243)
CAC99322	lmo1244	protein_coding	986020	phosphoglycerate mutase(lmo1244)
CAC99323	lmo1245	protein_coding	986013	lmo1245(lmo1245)
CAC99324	lmo1246	protein_coding	986011	ATP-dependent RNA helicase(lmo1246)
CAC99326	lmo1248	protein_coding	986009	hypothetical protein(lmo1248)
CAC99327	lmo1249	protein_coding	986015	lmo1249(lmo1249)
CAC99328	lmo1250	protein_coding	986007	antibiotic resistance protein(lmo1250)
CAC99329	lmo1251	protein_coding	986006	Fnr/Crp family transcriptional regulator(lmo1251)
CAC99331	lmo1253	protein_coding	984383	GntR family transcriptional regulator(lmo1253)
CAC99332	lmo1254	protein_coding	986004	alpha,alpha-phosphotrehalase(lmo1254)
CAC99333	lmo1255	protein_coding	986002	PTS trehalose transporter subunit IIBC(lmo1255)
CAC99335	lmo1257	protein_coding	985997	lmo1257(lmo1257)
CAC99336	lmo1258	protein_coding	985992	lmo1258(lmo1258)
CAC99337	proA	protein_coding	985995	gamma-glutamyl phosphate reductase(proA)
CAC99338	proB	protein_coding	985996	gamma-glutamyl kinase(proB)
CAC99339	lmo1261	protein_coding	985993	lmo1261(lmo1261)
CAC99340	lmo1262	protein_coding	985990	transcriptional regulator(lmo1262)
CAC99344	lmo1266	protein_coding	985084	lmo1266(lmo1266)
CAC99346	clpX	protein_coding	985086	ATP-dependent protease ATP-binding subunit ClpX(clpX)
CAC99347	lmo1269	protein_coding	985087	type I signal peptidase(lmo1269)
CAC99348	lmo1270	protein_coding	985113	type I signal peptidase(lmo1270)
CAC99351	rnhB	protein_coding	985073	ribonuclease HII(rnhB)
CAC99352	lmo1274	protein_coding	987273	polypeptide deformylase(lmo1274)
CAC99353	topA	protein_coding	985095	DNA topoisomerase I(topA)
CAC99354	gid	protein_coding	985107	tRNA (uracil-5-)-methyltransferase Gid(gid)
CAC99361	lmo1283	protein_coding	985110	LacX protein(lmo1283)
CAC99363	lmo1285	protein_coding	985138	hypothetical protein(lmo1285)
CAC99368	lmo1290	protein_coding	985114	internalin(lmo1290)
CAC99370	lmo1292	protein_coding	985112	glycerophosphodiester phosphodiesterase(lmo1292)

CAC99371	glpD	protein_coding	985350	glycerol-3-phosphate dehydrogenase(glpD)
CAC99372	miaA	protein_coding	985128	tRNA delta(2)-isopentenylpyrophosphate transferase(miaA)
CAC99373	lmo1295	protein_coding	985120	host factor-1 protein(lmo1295)
CAC99376	glnR	protein_coding	985126	glutamine synthetase repressor(glnR)
CAC99378	lmo1300	protein_coding	985130	arsenic transporter(lmo1300)
CAC99380	lmo1302	protein_coding	985139	LexA family transcriptional regulator(lmo1302)
CAC99381	lmo1303	protein_coding	987680	cell division suppressor(lmo1303)
CAC99384	lmo1306	protein_coding	987683	hypothetical protein(lmo1306)
CAC99394	cdsA	protein_coding	987695	phosphatidate cytidylyltransferase(cdsA)
CAC99395	lmo1317	protein_coding	987697	1-deoxy-D-xylulose 5-phosphate reductoisomerase(lmo1317)
CAC99396	lmo1318	protein_coding	987698	zinc metalloprotease Lmo1318(lmo1318)
CAC99401	lmo1323	protein_coding	987703	hypothetical protein(lmo1323)
CAC99403	infB	protein_coding	987704	translation initiation factor IF-2(infB)
CAC99404	lmo1326	protein_coding	987708	hypothetical protein(lmo1326)
CAC99405	rbfA	protein_coding	987713	ribosome-binding factor A(rbfA)
CAC99407	ribC	protein_coding	987710	riboflavin kinase(ribC)
CAC99409	pnpA	protein_coding	987712	polynucleotide phosphorylase(pnpA)
CAC99412	lmo1334	protein_coding	987718	hypothetical protein(lmo1334)
CAC99414	lmo1336	protein_coding	987720	5-formyltetrahydrofolate cyclo-ligase(lmo1336)
CAC99415	lmo1337	protein_coding	987722	hypothetical protein(lmo1337)
CAC99416	lmo1338	protein_coding	987721	hypothetical protein(lmo1338)
CAC99418	lmo1340	protein_coding	987724	hypothetical protein(lmo1340)
CAC99423	lmo1345	protein_coding	987732	competence protein ComGC(lmo1345)
CAC99424	comGB	protein_coding	987733	competence protein ComGB(comGB)
CAC99425	comGA	protein_coding	987735	competence protein ComGA(comGA)
CAC99429	lmo1351	protein_coding	987739	lmo1351(lmo1351)
CAC99430	lmo1352	protein_coding	987741	lmo1352(lmo1352)
CAC99431	lmo1353	protein_coding	987743	hypothetical protein(lmo1353)
CAC99432	lmo1354	protein_coding	987742	aminopeptidase P(lmo1354)
CAC99433	efp	protein_coding	987744	elongation factor P(efp)
CAC99435	lmo1357	protein_coding	987387	acetyl-CoA carboxylase biotin carboxylase subunit(lmo1357)
CAC99437	lmo1359	protein_coding	987880	transcription antitermination protein NusB(nusB)
CAC99438	folD	protein_coding	987879	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase(folD)
CAC99439	lmo1361	protein_coding	987878	exodeoxyribonuclease VII large subunit(xseA)
CAC99440	lmo1362	protein_coding	987876	exodeoxyribonuclease VII small subunit(lmo1362)
CAC99441	lmo1363	protein_coding	987873	geranyltranstransferase(lmo1363)
CAC99444	lmo1366	protein_coding	986969	hypothetical protein(lmo1366)
CAC99446	recN	protein_coding	987672	DNA repair protein(recN)
CAC99448	lmo1370	protein_coding	987676	butyrate kinase(lmo1370)
CAC99449	lmo1371	protein_coding	987674	dihydrolipoamide dehydrogenase(lmo1371)
CAC99450	lmo1372	protein_coding	987855	branched-chain alpha-keto acid dehydrogenase subunit E1(lmo1372)
CAC99451	lmo1373	protein_coding	987859	branched-chain alpha-keto acid dehydrogenase subunit E1(lmo1373)
CAC99452	lmo1374	protein_coding	987858	branched-chain alpha-keto acid dehydrogenase subunit E2(lmo1374)
CAC99453	lmo1375	protein_coding	987853	aminotripeptidase(lmo1375)
CAC99454	lmo1376	protein_coding	987851	6-phosphogluconate dehydrogenase(lmo1376)
CAC99455	lisR	protein_coding	987849	two-component response regulator(lisR)
CAC99456	lisK	protein_coding	987844	two-component sensor histidine kinase(lisK)

CAC99457	lmo1379	protein_coding	987847	sporulation protein SpoJ(lmo1379)
CAC99458	lmo1380	protein_coding	987834	lmo1380(lmo1380)
CAC99459	lmo1381	protein_coding	987841	lmo1381(lmo1381)
CAC99460	lmo1382	protein_coding	987840	lmo1382(lmo1382)
CAC99461	lmo1383	protein_coding	987838	isopentenyl pyrophosphate isomerase(lmo1383)
CAC99462	lmo1384	protein_coding	987831	hypothetical protein(lmo1384)
CAC99463	lmo1385	protein_coding	987832	hypothetical protein(lmo1385)
CAC99465	lmo1387	protein_coding	987829	pyrroline-5-carboxylate reductase(lmo1387)
CAC99466	tcsA	protein_coding	984815	CD4+ T cell-stimulating antigen, lipoprotein(tcsA)
CAC99467	lmo1389	protein_coding	984826	sugar ABC transporter ATP-binding protein(lmo1389)
CAC99468	lmo1390	protein_coding	984893	ABC transporter permease(lmo1390)
CAC99469	lmo1391	protein_coding	986482	sugar ABC transporter permease(lmo1391)
CAC99470	lmo1392	protein_coding	986324	peptidase(lmo1392)
CAC99471	lmo1393	protein_coding	986760	peptidase(lmo1393)
CAC99472	lmo1394	protein_coding	984737	3-ketoacyl-ACP reductase(lmo1394)
CAC99473	lmo1395	protein_coding	986796	hypothetical protein(lmo1395)
CAC99474	lmo1396	protein_coding	985296	phosphatidylglycerophosphate synthase(lmo1396)
CAC99475	cinA	protein_coding	987615	competence damage-inducible protein CinA(cinA)
CAC99476	recA	protein_coding	984485	recombinase A(recA)
CAC99481	mutS	protein_coding	985419	DNA mismatch repair protein MutS(mutS)
CAC99483	lmo1405	protein_coding	986841	anti-terminator regulatory protein(lmo1405)
CAC99484	pflB	protein_coding	986171	pyruvate formate-lyase(pflB)
CAC99485	pflC	protein_coding	986485	pyruvate-formate lyase activating enzyme(pflC)
CAC99487	lmo1409	protein_coding	986419	multidrug transporter(lmo1409)
CAC99490	lmo1412	protein_coding	986461	modulates DNA topology(lmo1412)
CAC99492	lmo1414	protein_coding	986819	acetyl-CoA:acetyltransferase(lmo1414)
CAC99493	lmo1415	protein_coding	986439	hydroxy-3-methylglutaryl-CoA synthase(lmo1415)
CAC99496	lmo1418	protein_coding	986995	hypothetical protein(lmo1418)
CAC99497	lmo1419	protein_coding	986497	hypothetical protein(lmo1419)
CAC99498	lmo1420	protein_coding	984666	UDP-N-acetylenolpyruvoylglucosamine reductase(murB)
CAC99499	lmo1421	protein_coding	984736	glycine/betaine ABC transporter ATP-binding protein(lmo1421)
CAC99500	lmo1422	protein_coding	986774	glycine/betaine ABC transporter permease(lmo1422)
CAC99501	lmo1423	protein_coding	986759	lmo1423(lmo1423)
CAC99502	lmo1424	protein_coding	986818	manganese transporter(lmo1424)
CAC99503	opuCD	protein_coding	984750	glycine/betaine ABC transporter permease(opuCD)
CAC99504	opuCC	protein_coding	986463	glycine/betaine ABC transporter substrate-binding protein(opuCC)
CAC99505	opuCB	protein_coding	985838	glycine/betaine ABC transporter permease(opuCB)
CAC99506	opuCA	protein_coding	987882	glycine/betaine ABC transporter ATP-binding protein(opuCA)
CAC99510	lmo1432	protein_coding	986495	lmo1432(lmo1432)
CAC99511	lmo1433	protein_coding	985502	glutathione reductase(lmo1433)
CAC99512	lmo1434	protein_coding	984605	hypothetical protein(lmo1434)
CAC99513	lmo1435	protein_coding	986494	dihydrodipicolinate synthase(dapA)
CAC99517	sod	protein_coding	986791	superoxide dismutase(sod)
CAC99518	lmo1440	protein_coding	986499	hypothetical protein(lmo1440)
CAC99519	lmo1441	protein_coding	986437	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase(ispG)
CAC99520	lmo1442	protein_coding	986764	transporter(lmo1442)
CAC99523	zurR	protein_coding	986176	ZurR family transcriptional regulator(zurR)
CAC99525	zurA	protein_coding	986711	metal (zinc) transport protein(ABC transporter, ATP-binding protein)(zurA)

CAC99529	lmo1451	protein_coding	987625	4-hydroxy-3-methylbut-2-enyl diphosphate reductase(ispH)
CAC99530	lmo1452	protein_coding	986883	hypothetical protein(lmo1452)
CAC99531	lmo1453	protein_coding	984399	hypothetical protein(lmo1453)
CAC99532	rpoD	protein_coding	984456	RNA polymerase sigma factor RpoD(rpoD)
CAC99539	lmo1461	protein_coding	987662	lmo1461(lmo1461)
CAC99544	lmo1466	protein_coding	987828	hypothetical protein(lmo1466)
CAC99547	rpsU	protein_coding	987865	30S ribosomal protein S21(rpsU)
CAC99548	lmo1470	protein_coding	986707	16S ribosomal RNA methyltransferase RsmE(lmo1470)
CAC99550	dnaJ	protein_coding	987063	molecular chaperone DnaJ(dnaJ)
CAC99551	dnaK	protein_coding	986290	molecular chaperone DnaK(dnaK)
CAC99552	grpE	protein_coding	986715	heat shock protein GrpE(grpE)
CAC99553	hrcA	protein_coding	986933	heat-inducible transcription repressor(hrcA)
CAC99556	lmo1478	protein_coding	986291	MerR family transcriptional regulator(lmo1478)
CAC99557	lepA	protein_coding	986365	GTP-binding protein LepA(lepA)
CAC99559	lmo1481	protein_coding	986943	DNA polymerase III subunit delta(holA)
CAC99561	comEB	protein_coding	986960	competence protein ComEB(comEB)
CAC99565	lmo1487	protein_coding	986903	hypothetical protein(lmo1487)
CAC99566	lmo1488	protein_coding	986963	nicotinic acid mononucleotide adenylyltransferase(nadD)
CAC99570	lmo1492	protein_coding	986939	hypothetical protein(lmo1492)
CAC99572	lmo1494	protein_coding	986944	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase(lmo1494)
CAC99573	lmo1495	protein_coding	986966	hypothetical protein(lmo1495)
CAC99574	lmo1496	protein_coding	986962	transcription elongation factor GreA(greA)
CAC99575	udk	protein_coding	986986	uridine kinase(udk)
CAC99576	lmo1498	protein_coding	986934	O-methyltransferase(lmo1498)
CAC99577	lmo1499	protein_coding	987003	hypothetical protein(lmo1499)
CAC99578	lmo1500	protein_coding	986971	hypothetical protein(lmo1500)
CAC99582	alaS	protein_coding	987749	alanyl-tRNA synthetase(alaS)
CAC99583	lmo1505	protein_coding	987751	ABC transporter ATP-binding protein(lmo1505)
CAC99587	lmo1509	protein_coding	987759	exodeoxyribonuclease V(lmo1509)
CAC99590	lmo1512	protein_coding	987757	tRNA-specific 2-thiouridylase(mnmA)
CAC99591	lmo1513	protein_coding	987764	iron-sulfur cofactor synthesis protein(lmo1513)
CAC99593	lmo1515	protein_coding	987766	hypothetical protein(lmo1515)
CAC99594	lmo1516	protein_coding	987771	ammonium transporter NrgA(lmo1516)
CAC99596	lmo1518	protein_coding	987772	lmo1518(lmo1518)
CAC99598	hisS	protein_coding	987781	histidyl-tRNA synthetase(hisS)
CAC99599	lmo1521	protein_coding	987780	N-acetylmuramoyl-L-alanine amidase(lmo1521)
CAC99604	lmo1526	protein_coding	987791	hypothetical protein(lmo1526)
CAC99605	lmo1527	protein_coding	987793	preprotein translocase SecDF(lmo1527)
CAC99609	lmo1531	protein_coding	987806	S-adenosylmethionine:tRNA ribosyltransferase-isomerase(queA)
CAC99610	ruvB	protein_coding	987802	Holliday junction DNA helicase RuvB(ruvB)
CAC99611	ruvA	protein_coding	987805	Holliday junction DNA helicase RuvA(ruvA)
CAC99612	lmo1534	protein_coding	987808	L-lactate dehydrogenase(lmo1534)
CAC99616	lmo1538	protein_coding	987807	glycerol kinase(glpK)
CAC99617	lmo1539	protein_coding	987817	glycerol transporter(lmo1539)
CAC99626	mreB	protein_coding	986954	rod shape-determining protein MreB(mreB)
CAC99630	valS	protein_coding	986904	valyl-tRNA synthetase(valS)
CAC99631	hemL	protein_coding	986918	glutamate-1-semialdehyde aminotransferase(hemL)
CAC99632	hemB	protein_coding	986926	delta-aminolevulinic acid dehydratase(hemB)

CAC99634	hemC	protein_coding	986927	porphobilinogen deaminase(hemC)
CAC99635	hemA	protein_coding	986920	glutamyl-tRNA reductase(hemA)
CAC99636	lmo1558	protein_coding	986915	GTP-binding protein EngB(engB)
CAC99637	thrS	protein_coding	986974	threonyl-tRNA synthetase(thrS)
CAC99641	lmo1563	protein_coding	986899	dephospho-CoA kinase(coaE)
CAC99642	mutM	protein_coding	986950	formamidopyrimidine-DNA glycosylase(mutM)
CAC99643	polA	protein_coding	986949	DNA polymerase I(polA)
CAC99644	citC	protein_coding	986955	isocitrate dehydrogenase(citC)
CAC99645	citZ	protein_coding	986909	citrate synthase(citZ)
CAC99646	lmo1568	protein_coding	986923	hypothetical protein(lmo1568)
CAC99653	lmo1575	protein_coding	986973	hypothetical protein(lmo1575)
CAC99656	lmo1578	protein_coding	986985	X-Pro dipeptidase(lmo1578)
CAC99657	lmo1579	protein_coding	986945	alanine dehydrogenase(lmo1579)
CAC99658	lmo1580	protein_coding	986961	hypothetical protein(lmo1580)
CAC99661	lmo1583	protein_coding	987763	thiol peroxidase(tpx)
CAC99662	lmo1584	protein_coding	986942	hypothetical protein(lmo1584)
CAC99663	lmo1585	protein_coding	987795	peptidase(lmo1585)
CAC99664	lmo1586	protein_coding	987765	inorganic polyphosphate/ATP-NAD kinase(ppnK)
CAC99670	lmo1592	protein_coding	986418	thiamine biosynthesis protein ThiI(lmo1592)
CAC99671	lmo1593	protein_coding	985205	iron-sulfur cofactor synthesis protein NifS(lmo1593)
CAC99673	lmo1595	protein_coding	986055	hypothetical protein(lmo1595)
CAC99675	lmo1597	protein_coding	984705	lmo1597(lmo1597)
CAC99676	tyrS	protein_coding	985752	tyrosyl-tRNA synthetase(tyrS)
CAC99678	aroA	protein_coding	985307	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase (aroA)
CAC99679	lmo1601	protein_coding	985749	general stress protein(lmo1601)
CAC99680	lmo1602	protein_coding	985745	hypothetical protein(lmo1602)
CAC99681	lmo1603	protein_coding	985743	aminopeptidase(lmo1603)
CAC99682	lmo1604	protein_coding	985746	2-cys peroxiredoxin(lmo1604)
CAC99683	murC	protein_coding	985741	UDP-N-acetylmuramate--L-alanine ligase(murC)
CAC99684	lmo1606	protein_coding	985737	DNA translocase(lmo1606)
CAC99685	pheT	protein_coding	985742	phenylalanyl-tRNA synthetase subunit beta(pheT)
CAC99686	lmo1608	protein_coding	986017	hypothetical protein(lmo1608)
CAC99687	lmo1609	protein_coding	985740	thioredoxin(lmo1609)
CAC99690	lmo1612	protein_coding	985731	hypothetical protein(lmo1612)
CAC99693	lmo1615	protein_coding	985730	tRNA (guanine-N(7)-)-methyltransferase(trmB)
CAC99695	lmo1617	protein_coding	985727	multidrug transporter(lmo1617)
CAC99696	lmo1618	protein_coding	985724	MarR family transcriptional regulator(lmo1618)
CAC99697	daaA	protein_coding	985722	D-amino acid aminotransferase(daaA)
CAC99698	lmo1620	protein_coding	985721	dipeptidase PepV(lmo1620)
CAC99700	lmo1622	protein_coding	985726	hypothetical protein(lmo1622)
CAC99701	lmo1623	protein_coding	985719	hypothetical protein(lmo1623)
CAC99702	lmo1624	protein_coding	985718	transporter(lmo1624)
CAC99703	lmo1625	protein_coding	985717	transporter(lmo1625)
CAC99704	lmo1626	protein_coding	985552	lmo1626(lmo1626)
CAC99705	trpA	protein_coding	985711	tryptophan synthase subunit alpha(trpA)
CAC99706	trpB	protein_coding	985710	tryptophan synthase subunit beta(trpB)
CAC99707	trpF	protein_coding	985716	N-(5'-phosphoribosyl)anthranilate isomerase(trpF)

CAC99708	trpC	protein_coding	985709	indole-3-glycerol phosphate synthase(trpC)
CAC99709	trpD	protein_coding	985706	anthranilate phosphoribosyltransferase(trpD)
CAC99710	trpG	protein_coding	985715	anthranilate synthase subunit beta(trpG)
CAC99711	trpE	protein_coding	985705	anthranilate synthase subunit alpha(trpE)
CAC99712	lmo1634	protein_coding	985703	bifunctional acetaldehyde-CoA/alcohol dehydrogenase(lmo1634)
CAC99713	lmo1635	protein_coding	985702	hypothetical protein(lmo1635)
CAC99714	lmo1636	protein_coding	985701	ABC transporter ATP-binding protein(lmo1636)
CAC99715	lmo1637	protein_coding	985693	hypothetical protein(lmo1637)
CAC99719	citB	protein_coding	985689	aconitate hydratase(citB)
CAC99722	lmo1644	protein_coding	985681	helicase SNF2(lmo1644)
CAC99726	lmo1648	protein_coding	985680	lmo1648(lmo1648)
CAC99727	lmo1649	protein_coding	985678	lmo1649(lmo1649)
CAC99728	lmo1650	protein_coding	985591	hypothetical protein(lmo1650)
CAC99732	lmo1654	protein_coding	985673	cell surface protein(lmo1654)
CAC99733	lmo1655	protein_coding	985665	hypothetical protein(lmo1655)
CAC99734	lmo1656	protein_coding	985594	lmo1656(lmo1656)
CAC99736	rpsB	protein_coding	985326	30S ribosomal protein S2(rpsB)
CAC99738	leuS	protein_coding	985669	leucyl-tRNA synthetase(leuS)
CAC99739	lmo1661	protein_coding	985668	hypothetical protein(lmo1661)
CAC99740	lmo1662	protein_coding	985666	hypothetical protein(lmo1662)
CAC99742	metK	protein_coding	985664	methionine adenosyltransferase(metK)
CAC99744	lmo1666	protein_coding	985661	peptidoglycan-linked protein(lmo1666)
CAC99745	lmo1667	protein_coding	985660	L-lactate dehydrogenase(lmo1667)
CAC99746	lmo1668	protein_coding	985659	hypothetical protein(lmo1668)
CAC99747	lmo1669	protein_coding	985657	hypothetical protein(lmo1669)
CAC99750	menE	protein_coding	985655	O-succinylbenzoic acid--CoA ligase(menE)
CAC99751	menB	protein_coding	985651	naphthoate synthase(menB)
CAC99752	lmo1674	protein_coding	985652	prolyl aminopetidase(lmo1674)
CAC99753	menD	protein_coding	985654	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase (menD)
CAC99754	menF	protein_coding	985649	menaquinone-specific isochorismate synthase(menF)
CAC99757	lmo1679	protein_coding	985644	cystathionine beta-lyase(lmo1679)
CAC99758	lmo1680	protein_coding	985641	cystathionine gamma-synthase(lmo1680)
CAC99759	lmo1681	protein_coding	985640	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (lmo1681)
CAC99762	lmo1684	protein_coding	985633	glycerate dehydrogenase(lmo1684)
CAC99763	gsaB	protein_coding	985629	glutamate-1-semialdehyde aminotransferase(gsaB)
CAC99764	lmo1686	protein_coding	985630	hypothetical protein(lmo1686)
CAC99766	lmo1688	protein_coding	985625	enoyl-ACP reductase(lmo1688)
CAC99767	lmo1689	protein_coding	985627	A/G-specific adenine glycosylase(lmo1689)
CAC99771	lmo1693	protein_coding	985620	Regulatory protein recX.(recX)
CAC99772	lmo1694	protein_coding	985624	CDP-abequose synthase(lmo1694)
CAC99773	lmo1695	protein_coding	985618	hypothetical protein(lmo1695)
CAC99774	lmo1696	protein_coding	985619	hypothetical protein(lmo1696)
CAC99776	lmo1698	protein_coding	985612	ribosomal-protein-alanine N-acetyltransferase(lmo1698)
CAC99777	lmo1699	protein_coding	985617	chemotaxis protein(lmo1699)
CAC99778	lmo1700	protein_coding	985611	lmo1700(lmo1700)
CAC99782	lmo1704	protein_coding	985606	hypothetical protein(lmo1704)
CAC99784	lmo1706	protein_coding	985609	transporter(lmo1706)

CAC99786	lmo1708	protein_coding	985601	aminoglycoside N3'-acetyltransferase(lmo1708)
CAC99787	lmo1709	protein_coding	985602	methionine aminopeptidase(lmo1709)
CAC99788	lmo1710	protein_coding	985600	flavodoxin(lmo1710)
CAC99789	lmo1711	protein_coding	985599	aminopeptidase(lmo1711)
CAC99790	lmo1712	protein_coding	985590	multidrug resistance protein(lmo1712)
CAC99791	lmo1713	protein_coding	985588	rod shape-determining protein MreB(lmo1713)
CAC99793	lmo1715	protein_coding	985568	hypothetical protein(lmo1715)
CAC99795	lmo1717	protein_coding	985593	hypothetical protein(lmo1717)
CAC99800	lmo1722	protein_coding	985584	ATP-dependent RNA helicase(lmo1722)
CAC99804	lmo1726	protein_coding	985614	hypothetical protein(lmo1726)
CAC99805	lmo1727	protein_coding	986088	LacI family transcriptional regulator(lmo1727)
CAC99811	lmo1733	protein_coding	984552	glutamate synthase subunit beta(gltD)
CAC99812	lmo1734	protein_coding	986573	glutamate synthase large subunit(lmo1734)
CAC99813	gltC	protein_coding	985367	transcription activator of glutamate synthase operon GltC(gltC)
CAC99814	lmo1736	protein_coding	986571	hypothetical protein(lmo1736)
CAC99815	lmo1737	protein_coding	985567	glycerol dehydrogenase(lmo1737)
CAC99819	lmo1741	protein_coding	985955	histidine kinase(lmo1741)
CAC99821	lmo1743	protein_coding	986834	lmo1743(lmo1743)
CAC99822	lmo1744	protein_coding	985378	hypothetical protein(lmo1744)
CAC99823	lmo1745	protein_coding	985561	two-component response regulator(lmo1745)
CAC99824	lmo1746	protein_coding	985569	ABC transporter permease(lmo1746)
CAC99825	lmo1747	protein_coding	985559	ABC transporter ATP-binding protein(lmo1747)
CAC99826	lmo1748	protein_coding	986669	lmo1748(lmo1748)
CAC99828	lmo1750	protein_coding	985557	hypothetical protein(lmo1750)
CAC99829	lmo1751	protein_coding	985554	Uncharacterized RNA methyltransferase lmo1751(lmo1751)
CAC99831	lmo1753	protein_coding	985555	lipid kinase(lmo1753)
CAC99833	gatA	protein_coding	985546	aspartyl/glutamyl-tRNA amidotransferase subunit A(gatA)
CAC99834	gatC	protein_coding	985549	aspartyl/glutamyl-tRNA amidotransferase subunit C(gatC)
CAC99835	lmo1757	protein_coding	987885	hypothetical protein(lmo1757)
CAC99837	pcrA	protein_coding	985986	ATP-dependent DNA helicase(pcrA)
CAC99838	lmo1760	protein_coding	985989	geranylgeranylglyceryl phosphate synthase-like protein(lmo1760)
CAC99839	lmo1761	protein_coding	985984	sodium-dependent transporter(lmo1761)
CAC99853	purE	protein_coding	985964	phosphoribosylaminoimidazole carboxylase catalytic subunit(purE)
CAC99855	lmo1777	protein_coding	985957	hypothetical protein(lmo1777)
CAC99857	lmo1779	protein_coding	985954	lmo1779(lmo1779)
CAC99859	lmo1781	protein_coding	985951	lmo1781(lmo1781)
CAC99860	lmo1782	protein_coding	985950	3'-exo-deoxyribonuclease(lmo1782)
CAC99862	rpmI	protein_coding	985946	50S ribosomal protein L35(rpmI)
CAC99866	lmo1788	protein_coding	985948	transcriptional regulator(lmo1788)
CAC99867	lmo1789	protein_coding	985940	hypothetical protein(lmo1789)
CAC99868	lmo1790	protein_coding	985953	hypothetical protein(lmo1790)
CAC99869	lmo1791	protein_coding	985939	lmo1791(lmo1791)
CAC99870	trmD	protein_coding	985936	tRNA (guanine-N(1)-)-methyltransferase(trmD)
CAC99873	lmo1795	protein_coding	985941	hypothetical protein(lmo1795)
CAC99878	lmo1800	protein_coding	985934	protein-tyrosine phosphatase(lmo1800)
CAC99883	rncS	protein_coding	985924	ribonuclease III(rnc)
CAC99889	lmo1811	protein_coding	985917	ATP-dependent DNA helicase RecG(lmo1811)
CAC99890	lmo1812	protein_coding	985916	L-serine dehydratase(lmo1812)

CAC99891	lmo1813	protein_coding	985914	phosphoglycerate dehydrogenase(lmo1813)
CAC99893	lmo1815	protein_coding	985911	hypothetical protein(lmo1815)
CAC99901	fmt	protein_coding	985899	methionyl-tRNA formyltransferase(fmt)
CAC99904	lmo1826	protein_coding	985894	lmo1826(rpoZ)
CAC99905	lmo1827	protein_coding	985464	guanylate kinase(gmk)
CAC99906	lmo1828	protein_coding	985886	hypothetical protein(lmo1828)
CAC99907	lmo1829	protein_coding	985887	fibronectin-binding proteins(lmo1829)
CAC99908	lmo1830	protein_coding	984389	short-chain dehydrogenase(lmo1830)
CAC99909	pyrE	protein_coding	985882	orotate phosphoribosyltransferase(pyrE)
CAC99910	pyrF	protein_coding	985880	orotidine 5'-phosphate decarboxylase(pyrF)
CAC99911	pyrD	protein_coding	985875	dihydroorotate dehydrogenase(pyrD)
CAC99912	pyrDII	protein_coding	985877	dihydroorotate dehydrogenase electron transfer subunit(pyrDII)
CAC99913	pyrAB	protein_coding	985876	carbamoyl-phosphate synthetase(carB)
CAC99914	pyrAa	protein_coding	985872	carbamoyl phosphate synthase small subunit(pyrAa)
CAC99915	pyrC	protein_coding	985870	dihydroorotase(pyrC)
CAC99916	pyrB	protein_coding	985866	aspartate carbamoyltransferase(pyrB)
CAC99917	pyrP	protein_coding	985867	uracil permease(pyrP)
CAC99918	pyrR	protein_coding	985861	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase(pyrR)
CAC99920	lmo1842	protein_coding	985864	hypothetical protein(lmo1842)
CAC99921	lmo1843	protein_coding	985856	hypothetical protein(lmo1843)
CAC99922	lsp	protein_coding	985858	lipoprotein signal peptidase(lspA)
CAC99924	lmo1846	protein_coding	985857	multidrug transporter(lmo1846)
CAC99928	lmo1850	protein_coding	985846	MarR family transcriptional regulator(lmo1850)
CAC99929	lmo1851	protein_coding	985844	carboxy-terminal processing proteinase(lmo1851)
CAC99930	lmo1852	protein_coding	985843	mercury-binding protein(lmo1852)
CAC99931	lmo1853	protein_coding	985841	heavy metal-transporting ATPase(lmo1853)
CAC99933	lmo1855	protein_coding	985842	D-alanyl-D-alanine carboxypeptidase(lmo1855)
CAC99934	deoD	protein_coding	985839	purine nucleoside phosphorylase(deoD)
CAC99935	lmo1857	protein_coding	985942	hypothetical protein(lmo1857)
CAC99937	lmo1859	protein_coding	985834	methionine sulfoxide reductase B(lmo1859)
CAC99938	lmo1860	protein_coding	985835	methionine sulfoxide reductase A(lmo1860)
CAC99940	lmo1862	protein_coding	985832	hypothetical protein(lmo1862)
CAC99941	lmo1863	protein_coding	985833	hypothetical protein(lmo1863)
CAC99944	lmo1866	protein_coding	985829	hypothetical protein(lmo1866)
CAC99945	lmo1867	protein_coding	985826	pyruvate phosphate dikinase(lmo1867)
CAC99946	lmo1868	protein_coding	986136	hypothetical protein(lmo1868)
CAC99947	lmo1869	protein_coding	985825	hypothetical protein(lmo1869)
CAC99948	lmo1870	protein_coding	985824	alkaline phosphatase(lmo1870)
CAC99949	lmo1871	protein_coding	985905	phosphoglucomutase(lmo1871)
CAC99951	lmo1873	protein_coding	985819	dihydrofolate reductase(lmo1873)
CAC99952	lmo1874	protein_coding	985817	thymidylate synthase(thyA)
CAC99953	lmo1875	protein_coding	985821	ABC transporter ATP-binding protein(lmo1875)
CAC99955	lmo1877	protein_coding	985815	formyl-tetrahydrofolate synthetase(lmo1877)
CAC99956	lmo1878	protein_coding	985816	manganese transport transcriptional regulator(lmo1878)
CAC99957	cspD	protein_coding	985814	cold-shock protein(cspD)
CAC99958	lmo1880	protein_coding	985813	RNase HI(lmo1880)
CAC99959	lmo1881	protein_coding	985812	5'-3' exonuclease(lmo1881)

CAC99960	lmo1882	protein_coding	985810	30S ribosomal protein S14(rpsN)
CAC99961	lmo1883	protein_coding	986008	chitinase(lmo1883)
CAC99962	lmo1884	protein_coding	985809	xanthine permease(lmo1884)
CAC99963	lmo1885	protein_coding	985807	xanthine phosphoribosyltransferase(lmo1885)
CAC99967	lmo1889	protein_coding	985803	hypothetical protein(lmo1889)
CAC99968	lmo1890	protein_coding	986335	hypothetical protein(lmo1890)
CAC99975	aspB	protein_coding	985794	aspartate aminotransferase(aspB)
CAC99977	dinG	protein_coding	985791	bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon(dinG)
CAC99978	panD	protein_coding	985787	aspartate alpha-decarboxylase(panD)
CAC99982	birA	protein_coding	985785	transcriptional regulator(birA)
CAC99983	cca	protein_coding	985781	tRNA CCA-pyrophosphorylase(cca)
CAC99984	lmo1906	protein_coding	985777	methylglyoxal synthase(mgsA)
CAC99985	dapB	protein_coding	985778	dihydrodipicolinate reductase(dapB)
CAC99988	lmo1910	protein_coding	985775	oxidoreductase(lmo1910)
CAC99990	lmo1912	protein_coding	985772	histidine kinase(lmo1912)
CAC99991	lmo1913	protein_coding	985769	hypothetical protein(lmo1913)
CAC99993	lmo1915	protein_coding	985767	malate dehydrogenase(lmo1915)
CAC99994	lmo1916	protein_coding	985771	peptidase(lmo1916)
CAC99995	pflA	protein_coding	985766	pyruvate formate-lyase(pflA)
CAC99997	lmo1919	protein_coding	985763	hypothetical protein(lmo1919)
CAC99999	lmo1921	protein_coding	985800	hypothetical protein(lmo1921)
CAD00000	lmo1922	protein_coding	985760	hypothetical protein(lmo1922)
CAD00001	aroE	protein_coding	985759	3-phosphoshikimate 1-carboxyvinyltransferase(aroE)
CAD00007	ndk	protein_coding	984899	nucleoside diphosphate kinase(ndk)
CAD00008	lmo1930	protein_coding	987985	heptaprenyl diphosphate synthase subunit II(lmo1930)
CAD00009	menH	protein_coding	987989	ubiquinone/menaquinone biosynthesis methyltransferase(ubiE)
CAD00010	lmo1932	protein_coding	987988	heptaprenyl diphosphate synthase subunit I(lmo1932)
CAD00011	lmo1933	protein_coding	987987	GTP cyclohydrolase I(folE)
CAD00015	lmo1937	protein_coding	986528	GTP-binding protein EngA(engA)
CAD00016	lmo1938	protein_coding	987984	30S ribosomal protein S1(rpsA)
CAD00017	cmk	protein_coding	984888	cytidylate kinase(cmk)
CAD00018	lmo1940	protein_coding	987982	asparaginase(lmo1940)
CAD00020	recS	protein_coding	987981	ATP-dependent DNA helicase(recS)
CAD00021	lmo1943	protein_coding	984735	hypothetical protein(lmo1943)
CAD00022	lmo1944	protein_coding	984673	ferredoxin(lmo1944)
CAD00023	lmo1945	protein_coding	984894	hypothetical protein(lmo1945)
CAD00024	lmo1946	protein_coding	987980	acyl-CoA hydrolase(lmo1946)
CAD00026	resD	protein_coding	984889	two-component response regulator ResD(resD)
CAD00027	lmo1949	protein_coding	984426	hypothetical protein(lmo1949)
CAD00028	lmo1950	protein_coding	985025	hypothetical protein(lmo1950)
CAD00029	lmo1951	protein_coding	987973	segregation and condensation protein A(scpA)
CAD00030	lysA	protein_coding	987983	diaminopimelate decarboxylase(lysA)
CAD00031	pnp	protein_coding	987976	purine nucleoside phosphorylase(pnp)
CAD00032	drm	protein_coding	987977	phosphopentomutase(drm)
CAD00033	lmo1955	protein_coding	987975	integrase/recombinase(lmo1955)
CAD00034	fur	protein_coding	987991	Fur family transcriptional regulator(fur)
CAD00046	lmo1968	protein_coding	984877	creatinine amidohydrolase(lmo1968)

CAD00049	lmo1971	protein_coding	984874	PTS ascorbate transporter subunit IIC(ulaA)
CAD00051	lmo1973	protein_coding	987968	PTS sugar transporter subunit IIA(lmo1973)
CAD00052	lmo1974	protein_coding	984870	GntR family transcriptional regulator(lmo1974)
CAD00056	lmo1978	protein_coding	984868	glucose-6-phosphate 1-dehydrogenase(lmo1978)
CAD00059	lmo1981	protein_coding	987963	hypothetical protein(lmo1981)
CAD00060	lmo1982	protein_coding	984865	hypothetical protein(lmo1982)
CAD00061	ilvD	protein_coding	984864	dihydroxy-acid dehydratase(ilvD)
CAD00062	ilvB	protein_coding	984805	acetolactate synthase(ilvB)
CAD00063	ilvN	protein_coding	987961	acetolactate synthase small subunit(ilvH)
CAD00064	ilvC	protein_coding	986504	ketol-acid reductoisomerase(ilvC)
CAD00065	leuA	protein_coding	984863	2-isopropylmalate synthase(leuA)
CAD00066	leuB	protein_coding	984909	3-isopropylmalate dehydrogenase(leuB)
CAD00068	leuD	protein_coding	984859	isopropylmalate isomerase small subunit(leuD)
CAD00070	lmo1992	protein_coding	986230	alpha-acetolactate decarboxylase(lmo1992)
CAD00071	pdp	protein_coding	984377	pyrimidine-nucleoside phosphorylase(pdp)
CAD00072	lmo1994	protein_coding	984855	LacI family transcriptional regulator(lmo1994)
CAD00073	dra	protein_coding	984581	deoxyribose-phosphate aldolase(dra)
CAD00074	lmo1996	protein_coding	984762	DeoR family transcriptional regulator(lmo1996)
CAD00075	lmo1997	protein_coding	984854	PTS mannose transporter subunit IIA(lmo1997)
CAD00076	lmo1998	protein_coding	987959	opine catabolism protein(lmo1998)
CAD00077	lmo1999	protein_coding	984760	hypothetical protein(lmo1999)
CAD00078	lmo2000	protein_coding	984850	PTS mannose transporter subunit IID(lmo2000)
CAD00079	lmo2001	protein_coding	987965	PTS mannose transporter subunit IIC(lmo2001)
CAD00080	lmo2002	protein_coding	984415	PTS mannose transporter subunit IIB(lmo2002)
CAD00081	lmo2003	protein_coding	984849	GntR family transcriptional regulator(lmo2003)
CAD00082	lmo2004	protein_coding	987958	GntR family transcriptional regulator(lmo2004)
CAD00084	alsS	protein_coding	987957	acetolactate synthase(alsS)
CAD00091	lmo2013	protein_coding	986399	hypothetical protein(lmo2013)
CAD00092	lmo2014	protein_coding	984835	sugar hydrolase(lmo2014)
CAD00093	lmo2015	protein_coding	984770	alpha-mannosidase(lmo2015)
CAD00094	cspB	protein_coding	985343	cold-shock protein(cspB)
CAD00095	lmo2017	protein_coding	987951	hypothetical protein(lmo2017)
CAD00096	lmo2018	protein_coding	985823	diaminopimelate epimerase(dapF)
CAD00099	lmo2021	protein_coding	984837	hypothetical protein(lmo2021)
CAD00100	lmo2022	protein_coding	987950	carbon-sulfur lyase(lmo2022)
CAD00106	lmo2028	protein_coding	987967	hypothetical protein(lmo2028)
CAD00107	lmo2029	protein_coding	987945	hypothetical protein(lmo2029)
CAD00108	lmo2030	protein_coding	984817	hypothetical protein(lmo2030)
CAD00109	lmo2031	protein_coding	987935	hypothetical protein(lmo2031)
CAD00112	divIB	protein_coding	988005	cell division protein FtsQ(divIB)
CAD00117	pbpB	protein_coding	984823	penicillin-binding protein 2B(pbpB)
CAD00122	lmo2044	protein_coding	984734	peptide ABC transporter substrate-binding protein(lmo2044)
CAD00127	lmo2049	protein_coding	987928	hypothetical protein(lmo2049)
CAD00128	lmo2050	protein_coding	987929	excinuclease ABC subunit A(lmo2050)
CAD00129	lmo2051	protein_coding	987932	hypothetical protein(lmo2051)
CAD00130	lmo2052	protein_coding	987934	phosphopantetheine adenylyltransferase(coaD)
CAD00133	lmo2055	protein_coding	984919	hypothetical protein(lmo2055)
CAD00134	lmo2056	protein_coding	984807	hypothetical protein(lmo2056)

CAD00135	ctaB	protein_coding	984806	protoheme IX farnesyltransferase(ctaB)
CAD00136	ctaA	protein_coding	984460	heme O oxygenase(ctaA)
CAD00137	lmo2059	protein_coding	988010	potassium channel protein(lmo2059)
CAD00138	lmo2060	protein_coding	984801	hypothetical protein(lmo2060)
CAD00139	lmo2061	protein_coding	987917	hypothetical protein(lmo2061)
CAD00140	lmo2062	protein_coding	987920	copper transporter(lmo2062)
CAD00141	lmo2063	protein_coding	984792	lmo2063(lmo2063)
CAD00142	lmo2064	protein_coding	984800	large-conductance mechanosensitive channel protein(mscL)
CAD00143	lmo2065	protein_coding	987927	lmo2065(lmo2065)
CAD00145	lmo2067	protein_coding	984795	bile acid hydrolase(lmo2067)
CAD00146	groEL	protein_coding	987925	molecular chaperone GroEL(groEL)
CAD00147	groES	protein_coding	985586	co-chaperonin GroES(groES)
CAD00150	lmo2072	protein_coding	984371	redox-sensing transcriptional repressor Rex(lmo2072)
CAD00156	lmo2078	protein_coding	987047	hypothetical protein(lmo2078)
CAD00157	lmo2079	protein_coding	984776	lmo2079(lmo2079)
CAD00158	lmo2080	protein_coding	984774	lmo2080(lmo2080)
CAD00161	lmo2083	protein_coding	984857	lmo2083(lmo2083)
CAD00162	lmo2084	protein_coding	984631	lmo2084(lmo2084)
CAD00163	lmo2085	protein_coding	984772	peptidoglycan binding protein(lmo2085)
CAD00164	lmo2086	protein_coding	987915	hypothetical protein(lmo2086)
CAD00167	lmo2089	protein_coding	984766	lipase(lmo2089)
CAD00168	argG	protein_coding	984368	argininosuccinate synthase(argG)
CAD00169	argH	protein_coding	987914	argininosuccinate lyase(argH)
CAD00170	betL	protein_coding	987924	glycine betaine transporter BetL(betL)
CAD00176	lmo2098	protein_coding	984757	PTS galacticol transporter subunit IIA(lmo2098)
CAD00177	lmo2099	protein_coding	987911	transcriptional antiterminator(lmo2099)
CAD00178	lmo2100	protein_coding	987909	GntR family transcriptional regulator(lmo2100)
CAD00179	lmo2101	protein_coding	984461	pyridoxal biosynthesis lyase PdxS(lmo2101)
CAD00180	lmo2102	protein_coding	984751	lmo2102(lmo2102)
CAD00182	lmo2104	protein_coding	984430	lmo2104(lmo2104)
CAD00183	lmo2105	protein_coding	987907	ferrous iron transport protein B(lmo2105)
CAD00185	lmo2107	protein_coding	984748	DeoR family transcriptional regulator(lmo2107)
CAD00187	lmo2109	protein_coding	984746	hydrolase(lmo2109)
CAD00189	lmo2111	protein_coding	984745	nitroreductase(lmo2111)
CAD00190	lmo2112	protein_coding	985597	lmo2112(lmo2112)
CAD00191	lmo2113	protein_coding	984744	heme peroxidase(lmo2113)
CAD00192	lmo2114	protein_coding	987889	ABC transporter ATP-binding protein(lmo2114)
CAD00193	lmo2115	protein_coding	987993	ABC transporter permease(lmo2115)
CAD00196	lmo2118	protein_coding	984740	phosphoglucosamine mutase(glmM)
CAD00197	lmo2119	protein_coding	985280	hypothetical protein(lmo2119)
CAD00201	lmo2123	protein_coding	984732	sugar ABC transporter permease(lmo2123)
CAD00202	lmo2124	protein_coding	987890	sugar ABC transporter permease(lmo2124)
CAD00203	lmo2125	protein_coding	987894	sugar ABC transporter substrate-binding protein(lmo2125)
CAD00204	lmo2126	protein_coding	984730	maltogenic amylase(lmo2126)
CAD00205	lmo2127	protein_coding	984729	lmo2127(lmo2127)
CAD00206	lmo2128	protein_coding	987887	LacI family transcriptional regulator(lmo2128)
CAD00207	lmo2129	protein_coding	984728	lmo2129(lmo2129)
CAD00208	lmo2130	protein_coding	984779	hypothetical protein(lmo2130)

CAD00209	lmo2131	protein_coding	984721	lmo2131(lmo2131)
CAD00210	lmo2132	protein_coding	985218	lmo2132(lmo2132)
CAD00212	lmo2134	protein_coding	986514	fructose-1,6-biphosphate aldolase type II(lmo2134)
CAD00213	lmo2135	protein_coding	984713	PTS fructose transporter subunit IIC(lmo2135)
CAD00216	lmo2138	protein_coding	984707	transcriptional regulator(lmo2138)
CAD00220	lmo2142	protein_coding	985289	lmo2142(lmo2142)
CAD00221	lmo2143	protein_coding	984703	hypothetical protein(lmo2143)
CAD00222	lmo2144	protein_coding	984704	GntR family transcriptional regulator(lmo2144)
CAD00224	lmo2146	protein_coding	984701	LysR family transcriptional regulator(lmo2146)
CAD00225	lmo2147	protein_coding	984698	hypothetical protein(lmo2147)
CAD00227	lmo2149	protein_coding	984696	hypothetical protein(lmo2149)
CAD00228	lmo2150	protein_coding	984695	lmo2150(lmo2150)
CAD00230	lmo2152	protein_coding	984598	thioredoxin(lmo2152)
CAD00231	lmo2153	protein_coding	985637	flavodoxin(lmo2153)
CAD00234	lmo2156	protein_coding	988000	lmo2156(lmo2156)
CAD00235	sepA	protein_coding	987998	sepA(sepA)
CAD00236	lmo2158	protein_coding	984441	hypothetical protein(lmo2158)
CAD00238	lmo2160	protein_coding	984686	hypothetical protein(lmo2160)
CAD00242	lmo2164	protein_coding	986022	AraC family transcriptional regulator(lmo2164)
CAD00243	lmo2165	protein_coding	985896	Crp/Fnr family transcriptional regulator(lmo2165)
CAD00244	lmo2166	protein_coding	984431	lmo2166(lmo2166)
CAD00246	lmo2168	protein_coding	984676	glyoxalase(lmo2168)
CAD00250	lmo2172	protein_coding	984671	propionate CoA-transferase(lmo2172)
CAD00252	lmo2174	protein_coding	986302	hypothetical protein(lmo2174)
CAD00254	lmo2176	protein_coding	984665	TetR family transcriptional regulator(lmo2176)
CAD00255	lmo2177	protein_coding	984664	hypothetical protein(lmo2177)
CAD00256	lmo2178	protein_coding	984662	peptidoglycan binding protein(lmo2178)
CAD00257	lmo2179	protein_coding	984658	peptidoglycan binding protein(lmo2179)
CAD00261	lmo2183	protein_coding	984509	ferrichrome ABC transporter permease(lmo2183)
CAD00263	lmo2185	protein_coding	984803	lmo2185(lmo2185)
CAD00264	lmo2186	protein_coding	984742	lmo2186(lmo2186)
CAD00265	lmo2187	protein_coding	984649	lmo2187(lmo2187)
CAD00266	lmo2188	protein_coding	984648	oligoendopeptidase(lmo2188)
CAD00267	lmo2189	protein_coding	988007	competence protein CoiA(lmo2189)
CAD00268	mecA	protein_coding	984925	adaptor protein(mecA)
CAD00269	lmo2191	protein_coding	988006	ArsC family transcriptional regulator(spxA)
CAD00274	lmo2196	protein_coding	984918	peptide ABC transporter substrate-binding protein(lmo2196)
CAD00275	lmo2197	protein_coding	984643	lmo2197(lmo2197)
CAD00277	lmo2199	protein_coding	984811	hypothetical protein(lmo2199)
CAD00278	lmo2200	protein_coding	984642	MarR family transcriptional regulator(lmo2200)
CAD00283	lmo2205	protein_coding	986282	phosphoglyceromutase(lmo2205)
CAD00285	lmo2207	protein_coding	984638	hypothetical protein(lmo2207)
CAD00289	hemH	protein_coding	984632	ferrochelatase(hemH)
CAD00290	hemE	protein_coding	984388	uroporphyrinogen decarboxylase(hemE)
CAD00291	lmo2213	protein_coding	984794	hypothetical protein(lmo2213)
CAD00292	lmo2214	protein_coding	985371	ABC transporter permease(lmo2214)
CAD00296	lmo2218	protein_coding	985873	lmo2218(lmo2218)
CAD00297	lmo2219	protein_coding	984626	foldase(lmo2219)

CAD00299	lmo2221	protein_coding	984625	hypothetical protein(lmo2221)
CAD00300	lmo2222	protein_coding	984624	hypothetical protein(lmo2222)
CAD00304	lmo2226	protein_coding	985438	hypothetical protein(lmo2226)
CAD00305	lmo2227	protein_coding	984938	ABC transporter ATP-binding protein(lmo2227)
CAD00306	lmo2228	protein_coding	985739	hypothetical protein(lmo2228)
CAD00307	lmo2229	protein_coding	984619	penicillin-binding protein(lmo2229)
CAD00308	lmo2230	protein_coding	986212	arsenate reductase(lmo2230)
CAD00309	lmo2231	protein_coding	984616	hypothetical protein(lmo2231)
CAD00310	lmo2232	protein_coding	984442	hypothetical protein(lmo2232)
CAD00311	lmo2233	protein_coding	986617	LysR family transcriptional regulator(lmo2233)
CAD00312	lmo2234	protein_coding	984614	hypothetical protein(lmo2234)
CAD00313	lmo2235	protein_coding	984612	NADH oxidase(lmo2235)
CAD00314	lmo2236	protein_coding	984609	shikimate 5-dehydrogenase(lmo2236)
CAD00315	lmo2237	protein_coding	987939	MFS transporter permease(lmo2237)
CAD00316	lmo2238	protein_coding	984611	MFS transporter(lmo2238)
CAD00318	lmo2240	protein_coding	984621	ABC transporter ATP-binding protein(lmo2240)
CAD00319	lmo2241	protein_coding	984595	GntR family transcriptional regulator(lmo2241)
CAD00321	lmo2243	protein_coding	984592	AraC family transcriptional regulator(lmo2243)
CAD00322	lmo2244	protein_coding	984802	ribosomal large subunit pseudouridine synthase(lmo2244)
CAD00326	lmo2248	protein_coding	984588	hypothetical protein(lmo2248)
CAD00327	lmo2249	protein_coding	984840	low-affinity inorganic phosphate transporter(lmo2249)
CAD00328	arpJ	protein_coding	984583	amino acid ABC transporter permease(arpJ)
CAD00329	lmo2251	protein_coding	984693	amino acid ABC transporter ATP-binding protein(lmo2251)
CAD00330	lmo2252	protein_coding	984582	aspartate aminotransferase(lmo2252)
CAD00331	lmo2253	protein_coding	984901	phosphoglucomutase(lmo2253)
CAD00332	lmo2254	protein_coding	984903	hypothetical protein(lmo2254)
CAD00333	lmo2255	protein_coding	985217	lmo2255(lmo2255)
CAD00334	lmo2256	protein_coding	986867	hypothetical protein(lmo2256)
CAD00337	lmo2259	protein_coding	984570	PTS beta-glucoside transporter subunit IIA(lmo2259)
CAD00338	lmo2260	protein_coding	984702	hypothetical protein(lmo2260)
CAD00340	lmo2262	protein_coding	984566	hypothetical protein(lmo2262)
CAD00341	lmo2263	protein_coding	984709	hypothetical protein(lmo2263)
CAD00343	lmo2265	protein_coding	984574	hypothetical protein(lmo2265)
CAD00344	lmo2266	protein_coding	984562	hypothetical protein(lmo2266)
CAD00345	lmo2267	protein_coding	985303	ATP-dependent deoxyribonuclease subunit A(lmo2267)
CAD00346	addB	protein_coding	984656	ATP-dependent deoxyribonuclease subunit B(addB)
CAD00347	lmo2269	protein_coding	988009	lmo2269(lmo2269)
CAD00348	comK'	protein_coding	986337	competence protein ComK(comK')
CAD00353	lmo2275	protein_coding	984548	protein gp28(lmo2275)
CAD00354	lmo2276	protein_coding	984564	hypothetical protein(lmo2276)
CAD00381	lmo2303	protein_coding	984511	hypothetical protein(lmo2303)
CAD00407	lmo2329	protein_coding	988012	hypothetical protein(lmo2329)
CAD00408	lmo2330	protein_coding	985317	hypothetical protein(lmo2330)
CAD00409	lmo2331	protein_coding	985570	hypothetical protein(lmo2331)
CAD00416	pepC	protein_coding	984466	aminopeptidase(pepC)
CAD00417	lmo2339	protein_coding	984799	hypothetical protein(lmo2339)
CAD00421	lmo2343	protein_coding	984458	nitrilotriacetate monooxygenase(lmo2343)
CAD00422	lmo2344	protein_coding	984568	hypothetical protein(lmo2344)

CAD00423	lmo2345	protein_coding	987930	hypothetical protein(lmo2345)
CAD00424	lmo2346	protein_coding	984455	amino acid ABC transporter ATP-binding protein(lmo2346)
CAD00425	lmo2347	protein_coding	984476	amino acid ABC transporter permease(lmo2347)
CAD00426	lmo2348	protein_coding	984447	amino acid ABC transporter permease(lmo2348)
CAD00427	lmo2349	protein_coding	985790	amino acid ABC transporter substrate-binding protein(lmo2349)
CAD00428	lmo2350	protein_coding	984858	hypothetical protein(lmo2350)
CAD00429	lmo2351	protein_coding	984660	FMN reductase(lmo2351)
CAD00430	lmo2352	protein_coding	986168	LysR family transcriptional regulator(lmo2352)
CAD00431	lmo2353	protein_coding	984445	Na+/H+ antiporter(lmo2353)
CAD00432	lmo2354	protein_coding	984444	hypothetical protein(lmo2354)
CAD00433	lmo2355	protein_coding	985985	multidrug resistance protein(lmo2355)
CAD00434	lmo2356	protein_coding	984439	lmo2356(lmo2356)
CAD00435	lmo2357	protein_coding	984422	hypothetical protein(lmo2357)
CAD00436	lmo2358	protein_coding	984434	N-acetylglucosamine-6-phosphate isomerase(lmo2358)
CAD00437	lmo2359	protein_coding	984722	hypothetical protein(lmo2359)
CAD00438	lmo2360	protein_coding	984433	transmembrane protein(lmo2360)
CAD00440	lmo2362	protein_coding	984369	amino acid antiporter(lmo2362)
CAD00441	lmo2363	protein_coding	985123	glutamate decarboxylase(lmo2363)
CAD00442	lmo2364	protein_coding	984429	hypothetical protein(lmo2364)
CAD00443	lmo2365	protein_coding	984424	RofA family transcriptional regulator(lmo2365)
CAD00445	pgi	protein_coding	984404	glucose-6-phosphate isomerase(pgi)
CAD00446	lmo2368	protein_coding	985492	lmo2368(lmo2368)
CAD00448	lmo2370	protein_coding	984540	aminotransferase(lmo2370)
CAD00449	lmo2371	protein_coding	984414	ABC transporter permease(lmo2371)
CAD00450	lmo2372	protein_coding	984413	ABC transporter ATP-binding protein(lmo2372)
CAD00452	lmo2374	protein_coding	984416	aspartate kinase(lmo2374)
CAD00455	lmo2377	protein_coding	987926	multidrug transporter(lmo2377)
CAD00456	lmo2378	protein_coding	984923	monovalent cation/H+ antiporter subunit A(lmo2378)
CAD00457	lmo2379	protein_coding	984386	monovalent cation/H+ antiporter subunit B(lmo2379)
CAD00458	lmo2380	protein_coding	987938	monovalent cation/H+ antiporter subunit C(lmo2380)
CAD00459	lmo2381	protein_coding	985605	monovalent cation/H+ antiporter subunit D(lmo2381)
CAD00460	lmo2382	protein_coding	984482	monovalent cation/H+ antiporter subunit E(lmo2382)
CAD00461	lmo2383	protein_coding	987601	monovalent cation/H+ antiporter subunit F(lmo2383)
CAD00462	lmo2384	protein_coding	987553	monovalent cation/H+ antiporter subunit G(lmo2384)
CAD00463	lmo2385	protein_coding	987552	hypothetical protein(lmo2385)
CAD00464	lmo2386	protein_coding	987551	hypothetical protein(lmo2386)
CAD00465	lmo2387	protein_coding	987550	hypothetical protein(lmo2387)
CAD00467	lmo2389	protein_coding	987546	NADH dehydrogenase(lmo2389)
CAD00468	lmo2390	protein_coding	987545	hypothetical thioredoxine reductase(lmo2390)
CAD00469	lmo2391	protein_coding	987544	hypothetical protein(lmo2391)
CAD00470	lmo2392	protein_coding	987541	hypothetical protein(lmo2392)
CAD00471	lmo2393	protein_coding	987540	hypothetical protein(lmo2393)
CAD00473	lmo2395	protein_coding	987504	lmo2395(lmo2395)
CAD00474	lmo2396	protein_coding	987503	internalin(lmo2396)
CAD00475	lmo2397	protein_coding	987502	NifU protein(lmo2397)
CAD00476	ltrC	protein_coding	987501	hypothetical protein(ltrC)
CAD00477	lmo2399	protein_coding	987500	hypothetical protein(lmo2399)
CAD00478	lmo2400	protein_coding	987499	acetyltransferase(lmo2400)

CAD00479	lmo2401	protein_coding	987498	hypothetical protein(lmo2401)
CAD00482	lmo2404	protein_coding	987494	hypothetical protein(lmo2404)
CAD00483	lmo2405	protein_coding	987492	lmo2405(lmo2405)
CAD00484	lmo2406	protein_coding	987489	hypothetical protein(lmo2406)
CAD00487	lmo2409	protein_coding	987484	lmo2409(lmo2409)
CAD00488	lmo2410	protein_coding	987480	lmo2410(lmo2410)
CAD00489	lmo2411	protein_coding	987479	hypothetical protein(lmo2411)
CAD00494	lmo2416	protein_coding	987472	lmo2416(lmo2416)
CAD00495	lmo2417	protein_coding	987469	ABC transporter substrate-binding protein(lmo2417)
CAD00499	lmo2421	protein_coding	987464	two-component sensor histidine kinase(lmo2421)
CAD00501	lmo2423	protein_coding	987460	hypothetical protein(lmo2423)
CAD00502	lmo2424	protein_coding	987459	thioredoxin(lmo2424)
CAD00506	lmo2428	protein_coding	987433	cell division protein FtsW(lmo2428)
CAD00507	lmo2429	protein_coding	987431	ferrichrome ABC transporter ATP-binding protein(lmo2429)
CAD00508	lmo2430	protein_coding	987428	ferrichrome ABC transporter permease(lmo2430)
CAD00509	lmo2431	protein_coding	987425	ferrichrome ABC transporter substrate-binding protein(lmo2431)
CAD00511	lmo2433	protein_coding	987422	acetylesterase(lmo2433)
CAD00512	lmo2434	protein_coding	987419	glutamate decarboxylase(lmo2434)
CAD00514	lmo2436	protein_coding	987417	transcription antiterminator(lmo2436)
CAD00517	lmo2439	protein_coding	987411	lmo2439(lmo2439)
CAD00518	lmo2440	protein_coding	987409	lmo2440(lmo2440)
CAD00523	lmo2445	protein_coding	987394	internalin(lmo2445)
CAD00524	lmo2446	protein_coding	987393	glycosidase(lmo2446)
CAD00525	lmo2447	protein_coding	987392	transcriptional regulator(lmo2447)
CAD00526	lmo2448	protein_coding	987391	SsrA-binding protein.(smpB)
CAD00527	lmo2449	protein_coding	987390	exoribonuclease RNase-R(lmo2449)
CAD00528	lmo2450	protein_coding	987389	carboxylesterase(lmo2450)
CAD00530	lmo2452	protein_coding	987385	carboxylesterase(lmo2452)
CAD00531	lmo2453	protein_coding	987384	epoxide hydrolase(lmo2453)
CAD00532	lmo2454	protein_coding	987383	lmo2454(lmo2454)
CAD00537	gap	protein_coding	987377	glyceraldehyde-3-phosphate dehydrogenase(gap)
CAD00540	lmo2462	protein_coding	987372	dipeptidase(lmo2462)
CAD00541	lmo2463	protein_coding	987371	multidrug transporter(lmo2463)
CAD00542	lmo2464	protein_coding	987370	transcriptional regulator(lmo2464)
CAD00543	lmo2465	protein_coding	987367	lmo2465(lmo2465)
CAD00544	lmo2466	protein_coding	987366	lmo2466(lmo2466)
CAD00545	lmo2467	protein_coding	987365	chitin-binding protein(lmo2467)
CAD00546	clpP	protein_coding	987364	ATP-dependent Clp protease proteolytic subunit(clpP)
CAD00547	lmo2469	protein_coding	987361	amino acid transporter(lmo2469)
CAD00548	lmo2470	protein_coding	987359	internalin(lmo2470)
CAD00549	lmo2471	protein_coding	987354	NADPH dehydrogenase(lmo2471)
CAD00550	lmo2472	protein_coding	987353	hypothetical protein(lmo2472)
CAD00551	lmo2473	protein_coding	987352	hypothetical protein(lmo2473)
CAD00552	lmo2474	protein_coding	987349	hypothetical protein(lmo2474)
CAD00556	trxB	protein_coding	987338	thioredoxin reductase(trxB)
CAD00557	lmo2479	protein_coding	987336	lmo2479(lmo2479)
CAD00561	lmo2483	protein_coding	987330	HPr kinase/phosphorylase(lmo2483)
CAD00562	lmo2484	protein_coding	987328	hypothetical protein(lmo2484)

CAD00563	lmo2485	protein_coding	987327	hypothetical protein(lmo2485)
CAD00566	uvrA	protein_coding	987320	excinuclease ABC subunit A(uvrA)
CAD00567	uvrB	protein_coding	987319	excinuclease ABC subunit B(uvrB)
CAD00568	lmo2490	protein_coding	987317	CsbA protein(lmo2490)
CAD00569	lmo2491	protein_coding	987316	lmo2491(lmo2491)
CAD00570	lmo2492	protein_coding	987892	lmo2492(lmo2492)
CAD00571	lmo2493	protein_coding	987893	ArsR family transcriptional regulator(lmo2493)
CAD00572	lmo2494	protein_coding	987895	PhoU family transcriptional regulator(lmo2494)
CAD00573	lmo2495	protein_coding	987314	phosphate ABC transporter ATP-binding protein(lmo2495)
CAD00577	lmo2499	protein_coding	987906	phosphate ABC transporter substrate-binding protein(lmo2499)
CAD00581	lmo2503	protein_coding	987903	cardiolipin synthase(lmo2503)
CAD00586	lmo2508	protein_coding	984634	hypothetical protein(lmo2508)
CAD00587	prfB	protein_coding	986491	peptide chain release factor 2(prfB)
CAD00589	lmo2511	protein_coding	986743	hypothetical protein(lmo2511)
CAD00590	comFC	protein_coding	987303	competence protein ComFC(comFC)
CAD00591	comFA	protein_coding	987745	competence protein comFA(comFA)
CAD00592	lmo2514	protein_coding	985904	hypothetical protein(lmo2514)
CAD00593	lmo2515	protein_coding	987300	two-component response regulator DegU(lmo2515)
CAD00594	lmo2516	protein_coding	987299	hypothetical protein(lmo2516)
CAD00595	lmo2517	protein_coding	987297	lmo2517(lmo2517)
CAD00596	lmo2518	protein_coding	984500	LytR family transcriptional regulator(lmo2518)
CAD00602	lmo2524	protein_coding	987293	(3R)-hydroxymyristoyl-ACP dehydratase(fabZ)
CAD00603	mbl	protein_coding	986838	rod shape-determining protein MreB(mbl)
CAD00604	murA	protein_coding	984514	UDP-N-acetylglucosamine 1-carboxyvinyltransferase(murA)
CAD00613	atpB	protein_coding	987279	ATP synthase F0F1 subunit A(atpB)
CAD00614	atpI	protein_coding	986740	ATP synthase subunit I(atpI)
CAD00616	upp	protein_coding	986484	uracil phosphoribosyltransferase(upp)
CAD00617	glyA	protein_coding	986768	serine hydroxymethyltransferase(glyA)
CAD00618	lmo2540	protein_coding	987277	phosphatase(lmo2540)
CAD00619	lmo2541	protein_coding	986761	tRNA threonylcarbamoyladenosine biosynthesis protein(lmo2541)
CAD00620	lmo2542	protein_coding	986635	protoporphyrinogen oxidase(lmo2542)
CAD00621	prf1	protein_coding	986736	peptide chain release factor 1(prfA)
CAD00622	lmo2544	protein_coding	986601	thymidine kinase(lmo2544)
CAD00623	thrB	protein_coding	984754	homoserine kinase(thrB)
CAD00624	thrC	protein_coding	986503	threonine synthase(thrC)
CAD00625	hom	protein_coding	987269	homoserine dehydrogenase(hom)
CAD00626	rpmE	protein_coding	987268	50S ribosomal protein L31(rpmE2)
CAD00629	rho	protein_coding	987264	transcription termination factor Rho(rho)
CAD00631	lmo2553	protein_coding	987259	hypothetical protein(lmo2553)
CAD00632	lmo2554	protein_coding	987257	galactosyltransferase(lmo2554)
CAD00634	fbaA	protein_coding	986313	fructose-1,6-bisphosphate aldolase(fbaA)
CAD00635	lmo2557	protein_coding	987255	lipid kinase(lmo2557)
CAD00636	ami	protein_coding	987254	autolysin, amidase(ami)
CAD00637	pyrG	protein_coding	987251	CTP synthase(pyrG)
CAD00641	lmo2563	protein_coding	987248	hypothetical protein(lmo2563)
CAD00643	lmo2565	protein_coding	984565	hypothetical protein(lmo2565)
CAD00644	lmo2566	protein_coding	984810	lmo2566(lmo2566)
CAD00647	lmo2569	protein_coding	987245	peptide ABC transporter substrate-binding protein(lmo2569)

CAD00648	lmo2570	protein_coding	984821	lmo2570(lmo2570)
CAD00649	lmo2571	protein_coding	987244	nicotinamidase(lmo2571)
CAD00650	lmo2572	protein_coding	985849	dihydrofolate reductase subunit A(lmo2572)
CAD00651	lmo2573	protein_coding	987242	zinc-binding dehydrogenase(lmo2573)
CAD00653	lmo2575	protein_coding	986612	cation transporter(lmo2575)
CAD00654	lmo2576	protein_coding	986661	colossin A(lmo2576)
CAD00655	lmo2577	protein_coding	987240	hypothetical protein(lmo2577)
CAD00662	lmo2584	protein_coding	987234	formate dehydrogenase accessory protein(lmo2584)
CAD00663	lmo2585	protein_coding	987233	hypothetical protein(lmo2585)
CAD00666	lmo2588	protein_coding	987224	multidrug transporter(lmo2588)
CAD00669	lmo2591	protein_coding	984569	N-acetylmuramoyl-L-alanine amidase(lmo2591)
CAD00670	lmo2592	protein_coding	987219	aldo/keto reductase(lmo2592)
CAD00673	lmo2595	protein_coding	986306	hypothetical protein(lmo2595)
CAD00680	lmo2602	protein_coding	987211	hypothetical protein(lmo2602)
CAD00681	lmo2603	protein_coding	987210	lmo2603(lmo2603)
CAD00682	lmo2604	protein_coding	987206	lmo2604(lmo2604)
CAD00683	rplQ	protein_coding	987205	50S ribosomal protein L17(rplQ)
CAD00713	lmo2635	protein_coding	987177	1,4-dihydroxy-2-naphthoate octaprenyltransferase(lmo2635)
CAD00714	lmo2636	protein_coding	987176	hypothetical protein(lmo2636)
CAD00715	lmo2637	protein_coding	987175	hypothetical protein(lmo2637)
CAD00716	lmo2638	protein_coding	986300	NADH dehydrogenase(lmo2638)
CAD00717	lmo2639	protein_coding	984401	lmo2639(lmo2639)
CAD00720	lmo2642	protein_coding	984410	lmo2642(lmo2642)
CAD00724	lmo0197	protein_coding	987024	regulatory protein SpoVG(lmo0197)
CAD00727	prfA	protein_coding	987031	listeriolysin positive regulatory protein(prfA)
CAD00728	plcA	protein_coding	987032	phosphatidylinositol-specific phospholipase c(plcA)
CAD00730	mpl	protein_coding	987034	Zinc metalloproteinase precursor(mpl)
CAD00731	actA	protein_coding	987035	actin-assembly inducing protein precursor(actA)
CAD00734	lmo0207	protein_coding	987038	Uncharacterized lipoprotein Lmo0207 precursor.(lmo0207)
CAD00737	ldh	protein_coding	987043	L-lactate dehydrogenase(ldh)
CAD00738	ctc	protein_coding	987044	50S ribosomal protein L25(ctc)
CAD00739	lmo0212	protein_coding	987045	lmo0212(lmo0212)
CAD00740	pth	protein_coding	987046	peptidyl-tRNA hydrolase(pth)
CAD00741	mfd	protein_coding	987048	transcription-repair coupling factor(mfd)
CAD00742	lmo0215	protein_coding	987049	hypothetical protein(lmo0215)
CAD00743	lmo0216	protein_coding	987050	hypothetical protein(lmo0216)
CAD00747	ftsH	protein_coding	987058	cell division protein FtsH(ftsH)
CAD00748	lmo0221	protein_coding	987060	Type III pantothenate kinase(lmo0221)
CAD00749	lmo0222	protein_coding	987062	heat shock protein 33(hslO)
CAD00750	cysK	protein_coding	987069	cysteine synthase(cysK)
CAD00751	sul	protein_coding	987081	dihydropteroate synthases(sul)
CAD00752	folA	protein_coding	987089	dihydroneopterin aldolase(folA)
CAD00753	folK	protein_coding	987097	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase(folK)
CAD00755	lysS	protein_coding	987100	lysyl-tRNA synthetase(lysS)
CAD00757	lmo0230	protein_coding	987194	hypothetical protein(lmo0230)
CAD00758	lmo0231	protein_coding	987202	ATP:guanido phosphotransferase(lmo0231)
CAD00759	clpC	protein_coding	987203	endopeptidase Clp ATP-binding chain C(clpC)
CAD00760	lmo0233	protein_coding	987204	DNA repair protein RadA(lmo0233)

CAD00764	gltX	protein_coding	987229	glutamyl-tRNA synthetase(gltX)
CAD00771	lmo0244	protein_coding	987282	50S ribosomal protein L33 type II(rpmG)
CAD00779	lmo0252	protein_coding	987321	penicilinase repressor(lmo0252)
CAD00780	lmo0253	protein_coding	987325	penicillinase antirepressor(lmo0253)
CAD00781	lmo0254	protein_coding	987329	lmo0254(lmo0254)
CAD00782	lmo0255	protein_coding	987335	hypothetical protein(lmo0255)
CAD00783	lmo0256	protein_coding	987337	hypothetical protein(lmo0256)
CAD00785	rpoB	protein_coding	987342	DNA-directed RNA polymerase subunit beta(rpoB)
CAD00786	rpoC	protein_coding	987344	DNA-directed RNA polymerase subunit beta'(rpoC)
CAD00787	lmo0260	protein_coding	987345	hypothetical protein(lmo0260)
CAD00790	inlH	protein_coding	987355	internalin H(inlH)
CAD00792	lmo0265	protein_coding	987360	succinyl-diaminopimelate desuccinylase(lmo0265)
CAD00793	lmo0266	protein_coding	987368	transcriptional regulator(lmo0266)
CAD00794	lmo0267	protein_coding	987388	hypothetical protein(lmo0267)
CAD00795	lmo0268	protein_coding	987396	phosphoglycerate mutase(lmo0268)
CAD00796	lmo0269	protein_coding	987397	transporter(lmo0269)
CAD00798	lmo0271	protein_coding	987399	phospho-beta-glucosidase(lmo0271)
CAD00799	lmo0272	protein_coding	987400	hypothetical protein(lmo0272)
CAD00801	lmo0274	protein_coding	987410	lmo0274(lmo0274)
CAD00802	lmo0275	protein_coding	987414	hypothetical protein(lmo0275)
CAD00803	lmo0276	protein_coding	987415	hypothetical protein(lmo0276)
CAD00805	lmo0278	protein_coding	987432	sugar ABC transporter ATP-binding protein(lmo0278)
CAD00806	lmo0279	protein_coding	987434	anaerobic ribonucleoside triphosphate reductase(lmo0279)
CAD00807	lmo0280	protein_coding	987436	anaerobic ribonucleotide reductase activator protein(lmo0280)
CAD00808	lmo0281	protein_coding	987437	lmo0281(lmo0281)
CAD00810	lmo0283	protein_coding	987440	ABC transporter permease(lmo0283)
CAD00811	lmo0284	protein_coding	987441	ABC transporter ATP-binding protein(lmo0284)
CAD00812	lmo0285	protein_coding	987445	lipoprotein(lmo0285)
CAD00813	lmo0286	protein_coding	987447	aminotransferase(lmo0286)
CAD00814	lmo0287	protein_coding	987448	two-component response regulator(lmo0287)
CAD00815	lmo0288	protein_coding	987449	two-component sensor histidine kinase(lmo0288)
CAD00816	lmo0289	protein_coding	987451	hypothetical protein(lmo0289)
CAD00818	lmo0291	protein_coding	987454	hypothetical protein(lmo0291)
CAD00819	lmo0292	protein_coding	987455	heat-shock protein htrA serine protease(lmo0292)
CAD00820	lmo0293	protein_coding	987456	rRNA large subunit methyltransferase(lmo0293)
CAD00822	lmo0295	protein_coding	987458	FMN-containing NADPH-linked nitro/flavin reductase(lmo0295)
CAD00824	lmo0297	protein_coding	987506	transcriptional antiterminator BglG(lmo0297)
CAD00825	lmo0298	protein_coding	987507	PTS beta-glucoside transporter subunit IIC(lmo0298)
CAD00826	lmo0299	protein_coding	987508	PTS beta-glucoside transporter subunit IIB(lmo0299)
CAD00827	lmo0300	protein_coding	987510	phospho-beta-galactosidase(lmo0300)
CAD00828	lmo0301	protein_coding	987511	PTS beta-glucoside transporter subunit IIA(lmo0301)
CAD00830	lmo0303	protein_coding	987514	putaive secreted, lysin rich protein(lmo0303)
CAD00831	lmo0304	protein_coding	987515	lmo0304(lmo0304)
CAD00834	lmo0307	protein_coding	987521	lmo0307(lmo0307)
CAD00836	lmo0309	protein_coding	987523	hypothetical protein(lmo0309)
CAD00841	lmo0314	protein_coding	987529	hypothetical protein(lmo0314)
CAD00842	lmo0315	protein_coding	987530	thiamin biosynthesis protein(lmo0315)
CAD00844	lmo0317	protein_coding	987534	phosphomethylpyrimidine kinase(lmo0317)

CAD00848	lmo0321	protein_coding	987539	hypothetical protein(lmo0321)
CAD00849	lmo0322	protein_coding	987554	hypothetical protein(lmo0322)
CAD00851	lmo0324	protein_coding	987558	lmo0324(lmo0324)
CAD00852	lmo0325	protein_coding	987559	transcriptional regulator(lmo0325)
CAD00854	lmo0327	protein_coding	987561	cell surface protein(lmo0327)
CAD00855	lmo0328	protein_coding	987562	lmo0328(lmo0328)
CAD00859	lmo2646	protein_coding	985483	lmo2646(lmo2646)
CAD00860	lmo2647	protein_coding	987172	creatinine amidohydrolase(lmo2647)
CAD00861	lmo2648	protein_coding	987171	phosphotriesterase(lmo2648)
CAD00862	lmo2649	protein_coding	987170	PTS system ascorbate transporter subunit IIC(ulaA)
CAD00863	lmo2650	protein_coding	987169	MFS transporter(lmo2650)
CAD00864	lmo2651	protein_coding	984393	PTS mannitol transporter subunit IIA(lmo2651)
CAD00865	lmo2652	protein_coding	985080	transcriptional antiterminator(lmo2652)
CAD00866	tufA	protein_coding	987166	elongation factor Tu(tuf)
CAD00870	lmo2657	protein_coding	985613	deoxyguanosinetriphosphate triphosphohydrolase(lmo2657)
CAD00871	lmo2658	protein_coding	984905	acyltransferase(lmo2658)
CAD00872	lmo2659	protein_coding	985991	ribulose-phosphate 3-epimerase(lmo2659)
CAD00873	lmo2660	protein_coding	986863	transketolase(lmo2660)
CAD00874	lmo2661	protein_coding	984667	ribulose-5-phosphate 3-epimerase(lmo2661)
CAD00876	lmo2663	protein_coding	984376	polyol dehydrogenase(lmo2663)
CAD00877	lmo2664	protein_coding	987161	sorbitol dehydrogenase(lmo2664)
CAD00878	lmo2665	protein_coding	987160	PTS galacticol transporter subunit IIC(lmo2665)
CAD00879	lmo2666	protein_coding	987159	PTS galacticol transporter subunit IIB(lmo2666)
CAD00880	lmo2667	protein_coding	987158	PTS galacticol transporter subunit IIA(lmo2667)
CAD00881	lmo2668	protein_coding	987157	transcriptional antiterminator BglG(lmo2668)
CAD00882	lmo2669	protein_coding	987156	lmo2669(lmo2669)
CAD00883	lmo2670	protein_coding	984436	hypothetical protein(lmo2670)
CAD00884	lmo2671	protein_coding	987155	lmo2671(lmo2671)
CAD00885	lmo2672	protein_coding	987154	AraC family transcriptional regulator(lmo2672)
CAD00886	lmo2673	protein_coding	987153	hypothetical protein(lmo2673)
CAD00887	lmo2674	protein_coding	987152	ribose-5-phosphate isomerase B(lmo2674)
CAD00893	kdpC	protein_coding	987150	potassium-transporting ATPase subunit C(kdpC)
CAD00895	kdpA	protein_coding	987148	potassium-transporting ATPase subunit A(kdpA)
CAD00896	lmo2683	protein_coding	987143	PTS cellbiose transporter subunit IIB(lmo2683)
CAD00899	lmo2686	protein_coding	986869	lmo2686(lmo2686)
CAD00900	lmo2687	protein_coding	987138	cell division protein FtsW(lmo2687)
CAD00901	lmo2688	protein_coding	985360	cell division protein FtsW(lmo2688)
CAD00902	lmo2689	protein_coding	987136	magnesium-translocating P-type ATPase(lmo2689)
CAD00903	lmo2690	protein_coding	987134	TetR family transcriptional regulator(lmo2690)
CAD00904	lmo2691	protein_coding	987132	autolysin(lmo2691)
CAD00905	lmo2692	protein_coding	984921	lmo2692(lmo2692)
CAD00908	lmo2695	protein_coding	987129	dihydroxyacetone kinase subunit DhaK(lmo2695)
CAD00909	lmo2696	protein_coding	987127	dihydroxyacetone kinase(lmo2696)
CAD00910	lmo2697	protein_coding	987124	PTS mannose transporter subunit IIA(lmo2697)
CAD00911	lmo2698	protein_coding	987122	RpiR family transcriptional regulator(lmo2698)
CAD00912	lmo2699	protein_coding	987121	hypothetical protein(lmo2699)
CAD00913	lmo2700	protein_coding	987120	aldo/keto reductase(lmo2700)
CAD00923	lmo2710	protein_coding	987111	lmo2710(lmo2710)

CAD00924	lmo2711	protein_coding	987108	hypothetical protein(lmo2711)
CAD00927	lmo2714	protein_coding	987103	pepdidoglycan bound protein(lmo2714)
CAD00928	cydD	protein_coding	984392	ABC transporter ATP-binding protein(cydD)
CAD00930	cydB	protein_coding	987101	cytochrome D ubiquinol oxidase subunit II(cydB)
CAD00931	cydA	protein_coding	987099	cytochrome D ubiquinol oxidase subunit I(cydA)
CAD00932	lmo2719	protein_coding	987096	hypothetical protein(lmo2719)
CAD00934	lmo2721	protein_coding	984959	6-phosphogluconolactonase(lmo2721)
CAD00935	lmo2722	protein_coding	985237	MerR family transcripitonal regulator(lmo2722)
CAD00937	lmo2724	protein_coding	984922	hypothetical protein(lmo2724)
CAD00940	lmo2727	protein_coding	987088	hypothetical protein(lmo2727)
CAD00943	lmo2730	protein_coding	987083	phosphatase(lmo2730)
CAD00944	lmo2731	protein_coding	987082	RpiR family transcriptional regulator(lmo2731)
CAD00946	lmo2733	protein_coding	987079	PTS fructose transporter subunit IIABC(lmo2733)
CAD00947	lmo2734	protein_coding	987078	sugar hydrolase(lmo2734)
CAD00948	lmo2735	protein_coding	987075	sucrose phosphorylase(lmo2735)
CAD00949	lmo2736	protein_coding	987073	hypothetical protein(lmo2736)
CAD00950	lmo2737	protein_coding	987071	LacI family transcriptional regulator(lmo2737)
CAD00951	lmo2738	protein_coding	987070	hemolysin(lmo2738)
CAD00952	lmo2739	protein_coding	987067	NAD-dependent deacetylase(lmo2739)
CAD00953	lmo2740	protein_coding	985142	lmo2740(lmo2740)
CAD00954	lmo2741	protein_coding	987061	multidrug transporter(lmo2741)
CAD00955	lmo2742	protein_coding	987057	lmo2742(lmo2742)
CAD00956	lmo2743	protein_coding	987056	translaldolase(lmo2743)
CAD00959	lmo2746	protein_coding	987030	lmo2746(lmo2746)
CAD00961	lmo2748	protein_coding	984689	hypothetical protein(lmo2748)
CAD00962	lmo2749	protein_coding	984910	glutamine amidotransferase(lmo2749)
CAD00963	lmo2750	protein_coding	986907	para-aminobenzoate synthase subunit I(lmo2750)
CAD00964	lmo2751	protein_coding	984683	ABC transporter ATP-binding protein(lmo2751)
CAD00965	lmo2752	protein_coding	984457	ABC transporter ATP-binding protein(lmo2752)
CAD00966	lmo2753	protein_coding	984463	lmo2753(lmo2753)
CAD00967	lmo2754	protein_coding	986888	D-alanyl-D-alanine carboxypeptidase(lmo2754)
CAD00969	topB	protein_coding	985520	DNA topoisomerase III(topB)
CAD00970	lmo2757	protein_coding	986884	ATP-dependent DNA helicase(lmo2757)
CAD00972	lmo2759	protein_coding	986677	hypothetical protein(lmo2759)
CAD00975	lmo2762	protein_coding	986856	PTS cellbiose transporter subunit IIB(lmo2762)
CAD00976	lmo2763	protein_coding	986739	PTS cellbiose transporter subunit IIC(lmo2763)
CAD00979	lmo2766	protein_coding	986816	RpiR family transcriptional regulator(lmo2766)
CAD00980	lmo2767	protein_coding	986810	lmo2767(lmo2767)
CAD00981	lmo2768	protein_coding	986273	hypothetical membrane protein(lmo2768)
CAD00982	lmo2769	protein_coding	986801	ABC transporter ATP-binding protein(lmo2769)
CAD00983	lmo2770	protein_coding	986798	bifunctional glutamate--cysteine ligase/glutathione synthetase(lmo2770)
CAD00984	lmo2771	protein_coding	986786	beta-glucosidase(lmo2771)
CAD00985	lmo2772	protein_coding	986779	PTS beta-glucoside transporter subunit IIABC(lmo2772)
CAD00986	lmo2773	protein_coding	986771	transcriptional antiterminator(lmo2773)
CAD00987	lmo2774	protein_coding	986770	ABC transporter ATP-binding protein(lmo2774)
CAD00989	lmo2776	protein_coding	986012	lmo2776(lmo2776)
CAD00992	lmo2779	protein_coding	986766	GTP-binding protein EngD(lmo2779)
CAD00995	lmo2782	protein_coding	984812	PTS cellbiose transporter subunit IIB(lmo2782)

CAD00996	lmo2783	protein_coding	984856	PTS cellbiose transporter subunit IIC(lmo2783)
CAD00998	kat	protein_coding	984948	catalase(kat)
CAD00999	bvrC	protein_coding	986755	bvrC(bvrC)
CAD01000	bvrB	protein_coding	986754	beta-glucoside-specific phosphotransferase enzyme II ABC component(bvrB)
CAD01001	bvrA	protein_coding	986751	transcription antiterminator(bvrA)
CAD01005	lmo2792	protein_coding	986982	lmo2792(lmo2792)
CAD01008	lmo2795	protein_coding	986746	RpiR family transcription regulator(lmo2795)
CAD01010	lmo2797	protein_coding	986733	PTS mannitol transporter subunit IIA(lmo2797)
CAD01011	lmo2798	protein_coding	986730	phosphatase(lmo2798)
CAD01012	lmo2799	protein_coding	986729	PTS mannitol transporter subunit IIBC(lmo2799)
CAD01013	lmo2800	protein_coding	984411	dehydrogenase(lmo2800)
CAD01014	lmo2801	protein_coding	986720	N-acetylmannosamine-6-phosphate 2-epimerase(lmo2801)
CAD01017	lmo2804	protein_coding	986717	lmo2804(lmo2804)
CAD01018	lmo2805	protein_coding	986900	hypothetical secreted protein(lmo2805)
CAD01021	lmo2808	protein_coding	986698	hypothetical secreted protein(lmo2808)
CAD01022	lmo2809	protein_coding	986696	hypothetical secreted protein(lmo2809)
CAD01026	lmo2813	protein_coding	986694	lmo2813(lmo2813)
CAD01027	lmo2814	protein_coding	986681	TetR family transcriptional regulator(lmo2814)
CAD01028	lmo2815	protein_coding	984831	3-ketoacyl-ACP reductase(fabG)
CAD01029	lmo2816	protein_coding	985339	MFS transporter(lmo2816)
CAD01030	lmo2817	protein_coding	984784	peptidase(lmo2817)
CAD01031	lmo2818	protein_coding	984714	MFS transporter(lmo2818)
CAD01032	lmo2819	protein_coding	986663	carboxypeptidase(lmo2819)
CAD01033	lmo2820	protein_coding	986657	amino-terminal domain-containing protein(lmo2820)
CAD01034	lmo2821	protein_coding	984504	internalin(lmo2821)
CAD01041	lmo2828	protein_coding	986627	lmo2828(lmo2828)
CAD01043	lmo2830	protein_coding	984904	thioredoxin(lmo2830)
CAD01047	lmo2834	protein_coding	986600	oxidoreductase(lmo2834)
CAD01048	lmo2835	protein_coding	986592	xylose isomerase(lmo2835)
CAD01050	lmo2837	protein_coding	986555	sugar ABC transporter permease(lmo2837)
CAD01051	lmo2838	protein_coding	986547	sugar ABC transporter permease(lmo2838)
CAD01052	lmo2839	protein_coding	987883	sugar ABC transporter substrate-binding protein(lmo2839)
CAD01053	lmo2840	protein_coding	986521	sucrose phosphorylase(lmo2840)
CAD01054	lmo2841	protein_coding	986398	sucrose phosphorylase(lmo2841)
CAD01056	lmo2843	protein_coding	986395	lmo2843(lmo2843)
CAD01057	lmo2844	protein_coding	986394	hypothetical protein(lmo2844)
CAD01061	lmo2848	protein_coding	986386	L-rhamnose isomerase(lmo2848)
CAD01062	lmo2849	protein_coding	986385	rhamnulokinase(lmo2849)
CAD01063	lmo2850	protein_coding	986384	sugar transporter(lmo2850)
CAD01064	lmo2851	protein_coding	986382	AraC family transcriptional regulator(lmo2851)
CAD01065	lmo2852	protein_coding	986380	lmo2852(lmo2852)
CAD01067	lmo2854	protein_coding	986378	sporulation protein SpoJ(lmo2854)
EBG00000016607	'comK	pseudogene		
EBG00000016610	lmo0837	pseudogene		
EBG00000016613	lmo0173	pseudogene		
EBG00000016619	lmo0410	pseudogene		
EBG00000016628	lmo0473	pseudogene		
EBG00000016642	transfert RNA-Thr	tRNA		

EBG00000016650	rRNA-23s	rRNA
EBG00000016656	rRNA-16s	rRNA
EBG00000016664	rRNA-5s	rRNA
EBG00000016668	transfert RNA-Gly	tRNA
EBG00000016671	rRNA-23s	rRNA
EBG00000016676	rRNA-16s	rRNA
EBG00000016677	transfert RNA-Glu	tRNA
EBG00000016682	rRNA-16s	rRNA
EBG00000016684	transfert RNA-Arg	tRNA
EBG00000016686	transfert RNA-Asn	tRNA
EBG00000016695	rRNA-16s	rRNA
EBG00000016702	rRNA-23s	rRNA
EBG00000016708	transfert RNA-Ser	tRNA
EBG00000016709	rRNA-23s	rRNA
EBG00000016711	rRNA-16s	rRNA
EBG00000016713	transfert RNA-Glu	tRNA
EBG00000016714	transfert RNA-Lys	tRNA
EBG00000016715	rRNA-16s	rRNA

20 degrees C, 180 min

ENSEMBL gene id	ENSEMBL gene	ENSEMBL biotype	ENTREZ id	ENTREZ gene description
CAC98216	dnaA	protein_coding	984365	chromosome replication initiator DnaA(dnaA)
CAC98217	dnaN	protein_coding	984379	DNA polymerase III subunit beta(dnaN)
CAC98219	lmo0004	protein_coding	984453	hypothetical protein(lmo0004)
CAC98221	gyrB	protein_coding	984708	DNA gyrase subunit B(gyrB)
CAC98228	qoxA	protein_coding	984936	AA3-600 quinol oxidase subunit II(qoxA)
CAC98229	qoxB	protein_coding	984962	AA3-600 quinol oxidase subunit I(qoxB)
CAC98230	qoxC	protein_coding	984980	AA3-600 quinol oxidase subunit III(qoxC)
CAC98232	lmo0017	protein_coding	984984	CapA protein (polyglutamate capsule biosynthesis)(lmo0017)
CAC98234	lmo0019	protein_coding	985005	lmo0019(lmo0019)
CAC98240	lmo0025	protein_coding	985061	phosphoheptose isomerase(lmo0025)
CAC98241	lmo0026	protein_coding	985069	copper homeostasis protein CutC(lmo0026)
CAC98243	lmo0028	protein_coding	985088	microcin C7 self-immunity protein MccF(lmo0028)
CAC98245	lmo0030	protein_coding	985106	hypothetical protein(lmo0030)
CAC98246	lmo0031	protein_coding	985116	LacI family transcription regulator(lmo0031)
CAC98247	lmo0032	protein_coding	985121	xylose repressor(lmo0032)
CAC98248	lmo0033	protein_coding	985131	endoglucanase(lmo0033)
CAC98249	lmo0034	protein_coding	985136	PTS cellbiose transporter subunit IIC(lmo0034)
CAC98250	lmo0035	protein_coding	985145	glucosamine--fructose-6-phosphate aminotransferase(lmo0035)
CAC98251	lmo0036	protein_coding	985152	putrescine carbamoyltransferase(lmo0036)
CAC98252	lmo0037	protein_coding	985153	amino acid transporter(lmo0037)
CAC98253	lmo0038	protein_coding	985162	agmatine deiminase 1(lmo0038)
CAC98254	lmo0039	protein_coding	985163	carbamate kinase(lmo0039)
CAC98257	lmo0042	protein_coding	985331	DedA protein(lmo0042)
CAC98258	lmo0043	protein_coding	985417	arginine deiminase(lmo0043)
CAC98261	rpsR	protein_coding	985537	30S ribosomal protein S18(rpsR)
CAC98262	lmo0047	protein_coding	985583	lmo0047(lmo0047)
CAC98263	lmo0048	protein_coding	985598	sensor histidine kinase AgrB(lmo0048)
CAC98264	lmo0049	protein_coding	985690	lmo0049(lmo0049)
CAC98265	lmo0050	protein_coding	985694	histidine kinase(lmo0050)
CAC98266	lmo0051	protein_coding	985847	response regulator(lmo0051)
CAC98270	purA	protein_coding	986069	adenylosuccinate synthetase(purA)
CAC98271	lmo0056	protein_coding	986070	heat shock protein(lmo0056)
CAC98272	lmo0057	protein_coding	986071	hypothetical protein(lmo0057)
CAC98273	lmo0058	protein_coding	986073	lmo0058(lmo0058)
CAC98276	lmo0061	protein_coding	986287	hypothetical protein(lmo0061)
CAC98279	lmo0064	protein_coding	986373	lmo0064(lmo0064)
CAC98280	lmo0065	protein_coding	986383	lmo0065(lmo0065)
CAC98291	lmo0076	protein_coding	986519	O6-methylguanine-DNA methyltransferase(lmo0076)
CAC98292	lmo0077	protein_coding	986552	hypothetical protein(lmo0077)
CAC98295	lmo0080	protein_coding	986576	lmo0080(lmo0080)
CAC98298	lmo0083	protein_coding	986580	MerR family transcriptional regulator(lmo0083)
CAC98299	lmo0084	protein_coding	986581	oxidoreductase(lmo0084)
CAC98301	lmo0086	protein_coding	986583	lmo0086(lmo0086)
CAC98302	lmo0087	protein_coding	986585	lmo0087(lmo0087)
CAC98304	lmo0089	protein_coding	986587	ATP synthase subunit delta(lmo0089)
CAC98305	lmo0090	protein_coding	986589	ATP synthase F0F1 subunit alpha(lmo0090)

CAC98306	lmo0091	protein_coding	986593	ATP synthase subunit gamma(lmo0091)
CAC98307	lmo0092	protein_coding	986598	ATP synthase F0F1 subunit beta(lmo0092)
CAC98311	lmo0096	protein_coding	986611	PTS mannose transporter subunit IIAB(lmo0096)
CAC98312	lmo0097	protein_coding	986614	PTS mannose transporter subunit IIC(lmo0097)
CAC98313	lmo0098	protein_coding	986620	PTS mannose transporter subunit IID(lmo0098)
CAC98314	lmo0099	protein_coding	986621	lmo0099(lmo0099)
CAC98321	lmo0106	protein_coding	986639	transcriptional regulator(lmo0106)
CAC98345	lmo0130	protein_coding	986721	5'-nucleotidase(lmo0130)
CAC98348	lmo0133	protein_coding	986735	hypothetical protein(lmo0133)
CAC98349	lmo0134	protein_coding	986737	hypothetical protein(lmo0134)
CAC98350	lmo0135	protein_coding	986748	peptide ABC transporter substrate-binding protein(lmo0135)
CAC98353	lmo0138	protein_coding	986772	lmo0138(lmo0138)
CAC98357	lmo0142	protein_coding	986788	lmo0142(lmo0142)
CAC98358	lmo0143	protein_coding	986794	lmo0143(lmo0143)
CAC98359	lmo0144	protein_coding	986795	lmo0144(lmo0144)
CAC98361	lmo0146	protein_coding	986800	hypothetical protein(lmo0146)
CAC98365	lmo0150	protein_coding	986809	lmo0150(lmo0150)
CAC98366	lmo0151	protein_coding	986811	lmo0151(lmo0151)
CAC98367	lmo0152	protein_coding	986821	peptide ABC transporter substrate-binding protein(lmo0152)
CAC98368	lmo0153	protein_coding	986823	zinc ABC transporter substrate-binding protein(lmo0153)
CAC98369	lmo0154	protein_coding	986826	zinc ABC transporter ATP-binding protein(lmo0154)
CAC98373	lmo0158	protein_coding	986836	hypothetical protein(lmo0158)
CAC98374	lmo0159	protein_coding	986840	peptidoglycan binding protein(lmo0159)
CAC98376	lmo0161	protein_coding	986851	lmo0161(lmo0161)
CAC98377	lmo0162	protein_coding	986854	DNA polymerase III subunit delta'(lmo0162)
CAC98378	lmo0163	protein_coding	986862	lmo0163(lmo0163)
CAC98379	lmo0164	protein_coding	986868	DNA replication intiation control protein YabA(lmo0164)
CAC98380	lmo0165	protein_coding	986872	hypothetical protein(lmo0165)
CAC98384	lmo0169	protein_coding	986890	glucose transporter(lmo0169)
CAC98385	lmo0170	protein_coding	986891	lmo0170(lmo0170)
CAC98391	lmo0176	protein_coding	986935	glucose transporter(lmo0176)
CAC98392	metS	protein_coding	986940	methionyl-tRNA synthetase(metS)
CAC98398	lmo0183	protein_coding	987006	alpha-glucosidase(lmo0183)
CAC98400	lmo0185	protein_coding	987009	hypothetical protein(lmo0185)
CAC98402	lmo0187	protein_coding	987012	hypothetical protein(lmo0187)
CAC98403	ksgA	protein_coding	987014	dimethyladenosine transferase(ksgA)
CAC98404	lmo0189	protein_coding	987015	Veg protein(lmo0189)
CAC98406	lmo0191	protein_coding	987017	phospho-beta-glucosidase(lmo0191)
CAC98407	lmo0192	protein_coding	987018	PurR family transcriptional regulator(lmo0192)
CAC98411	lmo0332	protein_coding	987567	lmo0332(lmo0332)
CAC98412	lmo0333	protein_coding	987568	internalin(lmo0333)
CAC98413	lmo0334	protein_coding	987569	lmo0334(lmo0334)
CAC98415	lmo0336	protein_coding	987572	lmo0336(lmo0336)
CAC98416	lmo0337	protein_coding	987574	lmo0337(lmo0337)
CAC98417	lmo0338	protein_coding	987576	lmo0338(lmo0338)
CAC98418	lmo0339	protein_coding	987577	hypothetical protein(lmo0339)
CAC98419	lmo0340	protein_coding	987578	lmo0340(lmo0340)
CAC98421	lmo0342	protein_coding	987582	transketolase(lmo0342)

CAC98422	lmo0343	protein_coding	987583	translaldolase(lmo0343)
CAC98424	lmo0345	protein_coding	987586	sugar-phosphate isomerase(lmo0345)
CAC98427	lmo0348	protein_coding	987591	dihydroxyacetone kinase(lmo0348)
CAC98428	lmo0349	protein_coding	987592	lmo0349(lmo0349)
CAC98433	lmo0354	protein_coding	987600	fatty-acid--CoA ligase(lmo0354)
CAC98434	lmo0355	protein_coding	987602	fumarate reductase subunit A(lmo0355)
CAC98435	lmo0356	protein_coding	987603	oxidoreductase(lmo0356)
CAC98447	lmo0368	protein_coding	987618	hypothetical protein(lmo0368)
CAC98448	lmo0369	protein_coding	987619	hypothetical protein(lmo0369)
CAC98449	lmo0370	protein_coding	987620	hypothetical protein(lmo0370)
CAC98450	lmo0371	protein_coding	987623	GntR family transcriptional regulator(lmo0371)
CAC98451	lmo0372	protein_coding	987624	beta-glucosidase(lmo0372)
CAC98452	lmo0373	protein_coding	987627	PTS beta-glucoside transporter subunit IIC(lmo0373)
CAC98455	lmo0376	protein_coding	987632	transcriptional regulator(lmo0376)
CAC98456	lmo0377	protein_coding	987633	lmo0377(lmo0377)
CAC98457	lmo0378	protein_coding	987634	lmo0378(lmo0378)
CAC98458	lmo0379	protein_coding	987635	lmo0379(lmo0379)
CAC98459	lmo0380	protein_coding	987636	lmo0380(lmo0380)
CAC98462	lmo0383	protein_coding	987639	methylmalonate-semialdehyde dehydrogenase(lmo0383)
CAC98464	lmo0385	protein_coding	987641	IolC protein(lmo0385)
CAC98465	lmo0386	protein_coding	987642	IolD protein(lmo0386)
CAC98466	lmo0387	protein_coding	987643	hypothetical protein(lmo0387)
CAC98468	ltrA	protein_coding	987647	low temperature requirement protein A(ltrA)
CAC98469	lmo0390	protein_coding	987648	uracil-DNA glycosylase(lmo0390)
CAC98471	lmo0392	protein_coding	987651	hypothetical protein(lmo0392)
CAC98472	lmo0393	protein_coding	987652	lmo0393(lmo0393)
CAC98476	lmo0397	protein_coding	987657	hypothetical protein(lmo0397)
CAC98482	lmo0403	protein_coding	987752	lmo0403(lmo0403)
CAC98483	lmo0404	protein_coding	987761	lmo0404(lmo0404)
CAC98484	lmo0405	protein_coding	987767	phosphate transporter(lmo0405)
CAC98485	lmo0406	protein_coding	987775	hypothetical protein(lmo0406)
CAC98486	lmo0407	protein_coding	987777	lmo0407(lmo0407)
CAC98487	lmo0408	protein_coding	987782	lmo0408(lmo0408)
CAC98488	lmo0409	protein_coding	987787	internalin(lmo0409)
CAC98490	lmo0411	protein_coding	987794	phosphoenolpyruvate synthase(lmo0411)
CAC98491	lmo0412	protein_coding	987812	lmo0412(lmo0412)
CAC98493	lmo0414	protein_coding	987822	hypothetical protein(lmo0414)
CAC98494	lmo0415	protein_coding	987823	endo-1,4-beta-xylanase(lmo0415)
CAC98500	lmo0421	protein_coding	987848	rod shape-determining protein RodA(lmo0421)
CAC98502	lmo0423	protein_coding	987863	RNA polymerase factor sigma C(lmo0423)
CAC98512	inlA	protein_coding	985151	internalin A(inlA)
CAC98513	inlB	protein_coding	986892	internalin B(inlB)
CAC98514	lmo0435	protein_coding	985154	peptidoglycan binding protein(lmo0435)
CAC98518	lmo0439	protein_coding	985164	hypothetical protein(lmo0439)
CAC98520	lmo0441	protein_coding	985168	D-alanyl-D-alanine carboxypeptidase(lmo0441)
CAC98523	lmo0444	protein_coding	985173	hypothetical protein(lmo0444)
CAC98524	lmo0445	protein_coding	985175	transcripitonal regulator(lmo0445)
CAC98525	lmo0446	protein_coding	985176	penicillin acylase(lmo0446)

CAC98526	lmo0447	protein_coding	986724	glutamate decarboxylase(lmo0447)
CAC98527	lmo0448	protein_coding	985174	amino acid antiporter(lmo0448)
CAC98530	lmo0451	protein_coding	985185	lmo0451(lmo0451)
CAC98531	lmo0452	protein_coding	985178	hypothetical protein(lmo0452)
CAC98532	lmo0453	protein_coding	985179	hypothetical protein(lmo0453)
CAC98533	lmo0454	protein_coding	985184	hypothetical protein(lmo0454)
CAC98534	lmo0455	protein_coding	985188	hypothetical protein(lmo0455)
CAC98538	lmo0459	protein_coding	985370	transcriptional regulator(lmo0459)
CAC98539	lmo0460	protein_coding	985198	membrane associated lipoprotein(lmo0460)
CAC98540	lmo0461	protein_coding	985193	lmo0461(lmo0461)
CAC98541	lmo0462	protein_coding	985196	lmo0462(lmo0462)
CAC98543	lmo0464	protein_coding	985200	transposase(lmo0464)
CAC98545	lmo0466	protein_coding	985199	lmo0466(lmo0466)
CAC98546	lmo0467	protein_coding	985201	lmo0467(lmo0467)
CAC98556	lmo0477	protein_coding	985893	secreted protein(lmo0477)
CAC98557	lmo0478	protein_coding	985211	secreted protein(lmo0478)
CAC98558	lmo0479	protein_coding	985210	secreted protein(lmo0479)
CAC98559	lmo0480	protein_coding	985214	transcriptional regulator(lmo0480)
CAC98560	lmo0481	protein_coding	985215	hypothetical protein(lmo0481)
CAC98561	lmo0482	protein_coding	986229	ribosomal RNA large subunit methyltransferase N(lmo0482)
CAC98564	lmo0485	protein_coding	985219	lmo0485(lmo0485)
CAC98568	lmo0489	protein_coding	984913	NADH:flavin oxidoreductase(lmo0489)
CAC98569	lmo0490	protein_coding	985396	shikimate 5-dehydrogenase(aroE)
CAC98573	lmo0494	protein_coding	985230	hypothetical protein(lmo0494)
CAC98576	lmo0497	protein_coding	984596	sugar transferase(lmo0497)
CAC98577	lmo0498	protein_coding	985236	5-phosphate isomerase(lmo0498)
CAC98578	lmo0499	protein_coding	985241	ribulose-5-phosphate 3 epimerase(lmo0499)
CAC98583	lmo0504	protein_coding	985256	lmo0504(lmo0504)
CAC98585	lmo0506	protein_coding	986275	sorbitol dehydrogenase(lmo0506)
CAC98588	prs	protein_coding	985257	phosphoribosyl pyrophosphate synthetase(prs)
CAC98589	lmo0510	protein_coding	985258	lmo0510(lmo0510)
CAC98594	lmo0515	protein_coding	986558	hypothetical protein(lmo0515)
CAC98595	lmo0516	protein_coding	985267	encapsulation protein CapA(lmo0516)
CAC98599	lmo0520	protein_coding	985284	transcriptional regulator(lmo0520)
CAC98602	lmo0523	protein_coding	985275	hypothetical protein(lmo0523)
CAC98603	lmo0524	protein_coding	985278	sulfate transporter(lmo0524)
CAC98604	lmo0525	protein_coding	985282	lmo0525(lmo0525)
CAC98606	lmo0527	protein_coding	985287	transmembrane protein(lmo0527)
CAC98607	lmo0528	protein_coding	985299	hypothetical secreted protein(lmo0528)
CAC98608	lmo0529	protein_coding	985294	glucosaminyltransferase(lmo0529)
CAC98609	lmo0530	protein_coding	984571	lmo0530(lmo0530)
CAC98610	lmo0531	protein_coding	985297	lmo0531(lmo0531)
CAC98612	lmo0533	protein_coding	985302	hypothetical protein(lmo0533)
CAC98614	lmo0535	protein_coding	985755	LacI family transcriptional regulator(lmo0535)
CAC98616	lmo0537	protein_coding	985309	allantoate amidohydrolase(lmo0537)
CAC98617	lmo0538	protein_coding	985381	N-acyl-L-amino acid amidohydrolase(lmo0538)
CAC98618	lmo0539	protein_coding	985316	tagatose 1,6-diphosphate aldolase(lmo0539)
CAC98619	lmo0540	protein_coding	985229	penicillin-binding protein(lmo0540)

CAC98622	lmo0543	protein_coding	984396	PTS sorbitol transporter subunit IIBC(lmo0543)
CAC98628	lmo0549	protein_coding	984412	internalin(lmo0549)
CAC98630	lmo0551	protein_coding	984417	lmo0551(lmo0551)
CAC98631	lmo0552	protein_coding	986885	hypothetical protein(lmo0552)
CAC98633	lmo0554	protein_coding	984446	NADH-dependent butanol dehydrogenase(lmo0554)
CAC98634	lmo0555	protein_coding	984577	di-tripeptide transporter(lmo0555)
CAC98636	lmo0557	protein_coding	984617	phosphoglycerate mutase(lmo0557)
CAC98638	lmo0559	protein_coding	985234	hypothetical protein(lmo0559)
CAC98639	lmo0560	protein_coding	986813	glutamate dehydrogenase(lmo0560)
CAC98640	lmo0561	protein_coding	984508	phosphoribosyl-ATP pyrophosphatase(hisE)
CAC98643	hisA	protein_coding	984608	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase(hisA)
CAC98646	hisD	protein_coding	985596	histidinol dehydrogenase(hisD)
CAC98647	hisG	protein_coding	985390	ATP phosphoribosyltransferase(hisG)
CAC98649	hisJ	protein_coding	984572	histidinol-phosphatase(hisJ)
CAC98651	lmo0572	protein_coding	986053	lmo0572(lmo0572)
CAC98652	lmo0573	protein_coding	985853	hypothetical protein(lmo0573)
CAC98653	lmo0574	protein_coding	984589	beta-glucosidase(lmo0574)
CAC98656	lmo0577	protein_coding	984939	lmo0577(lmo0577)
CAC98657	lmo0578	protein_coding	984630	hypothetical protein(lmo0578)
CAC98658	lmo0579	protein_coding	986865	hypothetical protein(lmo0579)
CAC98659	lmo0580	protein_coding	986638	hypothetical protein(lmo0580)
CAC98661	iap	protein_coding	985140	invasion associated secreted endopeptidase(iap)
CAC98663	lmo0584	protein_coding	984661	hypothetical protein(lmo0584)
CAC98664	lmo0585	protein_coding	984672	secreted protein(lmo0585)
CAC98666	lmo0587	protein_coding	986515	secreted protein(lmo0587)
CAC98667	lmo0588	protein_coding	984699	DNA photolyase(lmo0588)
CAC98668	lmo0589	protein_coding	985047	lmo0589(lmo0589)
CAC98669	lmo0590	protein_coding	985311	hypothetical protein(lmo0590)
CAC98670	lmo0591	protein_coding	984755	hypothetical protein(lmo0591)
CAC98671	lmo0592	protein_coding	986217	lmo0592(lmo0592)
CAC98673	lmo0594	protein_coding	985447	homoserine O-acetyltransferase(metX)
CAC98675	lmo0596	protein_coding	985266	hypothetical protein(lmo0596)
CAC98680	lmo0602	protein_coding	984599	transcripitonal regulator(lmo0602)
CAC98682	lmo0604	protein_coding	985855	hypothetical protein(lmo0604)
CAC98683	lmo0605	protein_coding	985094	hypothetical protein(lmo0605)
CAC98685	lmo0607	protein_coding	985501	ABC transporter ATP-binding protein(lmo0607)
CAC98686	lmo0608	protein_coding	984780	ABC transporter ATP-binding protein(lmo0608)
CAC98688	lmo0610	protein_coding	985509	internalin(lmo0610)
CAC98689	lmo0611	protein_coding	985209	azoreductase(acpD)
CAC98690	lmo0612	protein_coding	984912	MarR family transcriptional evidence(lmo0612)
CAC98691	lmo0613	protein_coding	987413	oxidoreductase(lmo0613)
CAC98692	lmo0614	protein_coding	985507	hypothetical protein(lmo0614)
CAC98693	lmo0615	protein_coding	984917	lmo0615(lmo0615)
CAC98694	lmo0616	protein_coding	985453	glycerophosphoryl diester phosphodiesterase(lmo0616)
CAC98695	lmo0617	protein_coding	985148	lmo0617(lmo0617)
CAC98698	lmo0620	protein_coding	985155	lmo0620(lmo0620)
CAC98702	lmo0624	protein_coding	985292	hypothetical protein(lmo0624)

CAC98703	lmo0625	protein_coding	985881	lmo0625(lmo0625)
CAC98704	lmo0626	protein_coding	985506	hypothetical protein(lmo0626)
CAC98705	lmo0627	protein_coding	984956	pepdidoglycan bound protein(lmo0627)
CAC98706	lmo0628	protein_coding	984963	lmo0628(lmo0628)
CAC98707	lmo0629	protein_coding	984966	lmo0629(lmo0629)
CAC98712	lmo0634	protein_coding	987068	tagatose 6-phosphate kinase(lmo0634)
CAC98713	lmo0635	protein_coding	984974	lmo0635(lmo0635)
CAC98716	lmo0638	protein_coding	984973	lmo0638(lmo0638)
CAC98718	lmo0640	protein_coding	987093	oxidoreductase(lmo0640)
CAC98719	lmo0641	protein_coding	985323	heavy metal-transporting ATPase(lmo0641)
CAC98720	lmo0642	protein_coding	984976	lmo0642(lmo0642)
CAC98722	lmo0644	protein_coding	984979	hypothetical protein(lmo0644)
CAC98723	lmo0645	protein_coding	984978	amino acid transporter(lmo0645)
CAC98724	lmo0646	protein_coding	984982	hypothetical protein(lmo0646)
CAC98726	lmo0648	protein_coding	987051	hypothetical protein(lmo0648)
CAC98727	lmo0649	protein_coding	986557	transcriptional regulator(lmo0649)
CAC98728	lmo0650	protein_coding	984986	hypothetical protein(lmo0650)
CAC98731	lmo0653	protein_coding	985279	lmo0653(lmo0653)
CAC98732	lmo0654	protein_coding	984989	lmo0654(lmo0654)
CAC98733	lmo0655	protein_coding	984992	phosphoprotein phosphatase(lmo0655)
CAC98736	lmo0658	protein_coding	985006	hypothetical protein(lmo0658)
CAC98737	lmo0659	protein_coding	984988	transcriptional regulator(lmo0659)
CAC98738	lmo0660	protein_coding	985017	transposase(lmo0660)
CAC98739	lmo0661	protein_coding	984999	hypothetical protein(lmo0661)
CAC98741	lmo0663	protein_coding	985001	hypothetical protein(lmo0663)
CAC98745	lmo0667	protein_coding	985013	ABC transporter ATP-binding protein(lmo0667)
CAC98746	lmo0668	protein_coding	987144	ABC transporter permease(lmo0668)
CAC98747	lmo0669	protein_coding	987147	oxidoreductase(lmo0669)
CAC98748	lmo0670	protein_coding	985009	lmo0670(lmo0670)
CAC98749	lmo0671	protein_coding	985011	lmo0671(lmo0671)
CAC98752	lmo0674	protein_coding	985015	lmo0674(lmo0674)
CAC98753	lmo0675	protein_coding	987142	lmo0675(lmo0675)
CAC98754	lmo0676	protein_coding	985021	flagellar biosynthesis protein FliP(fliP)
CAC98755	lmo0677	protein_coding	985022	flagellar biosynthesis protein FliQ(fliQ)
CAC98756	lmo0678	protein_coding	985024	flagellar biosynthesis protein FliR(fliR)
CAC98757	lmo0679	protein_coding	986322	flagellar biosynthesis protein FlhB(flhB)
CAC98758	lmo0680	protein_coding	986323	flagellar biosynthesis protein FlhA(flhA)
CAC98759	lmo0681	protein_coding	985019	flagellar biosynthesis regulator FlhF(lmo0681)
CAC98760	lmo0682	protein_coding	985030	flagellar basal body rod protein FlgG(flgG)
CAC98761	lmo0683	protein_coding	985031	chemotaxis protein CheR(lmo0683)
CAC98762	lmo0684	protein_coding	985027	lmo0684(lmo0684)
CAC98763	lmo0685	protein_coding	985036	flagellar motor protein MotA(lmo0685)
CAC98764	motB	protein_coding	986861	flagellar motor rotation MotB(motB)
CAC98765	lmo0687	protein_coding	985029	lmo0687(lmo0687)
CAC98766	lmo0688	protein_coding	986281	hypothetical protein(lmo0688)
CAC98767	lmo0689	protein_coding	987162	chemotaxis protein CheV(lmo0689)
CAC98768	flaA	protein_coding	987167	flagellin(flaA)
CAC98769	cheY	protein_coding	985049	chemotaxis response regulator CheY(cheY)

CAC98770	cheA	protein_coding	985032	two-component sensor histidine kinase CheA(cheA)
CAC98771	lmo0693	protein_coding	985035	flagellar motor switch protein FliY(lmo0693)
CAC98772	lmo0694	protein_coding	985033	lmo0694(lmo0694)
CAC98773	lmo0695	protein_coding	985037	lmo0695(lmo0695)
CAC98774	lmo0696	protein_coding	985038	flagellar basal body rod modification protein(flgD)
CAC98775	lmo0697	protein_coding	985043	flagellar hook protein FlgE(flgE)
CAC98776	lmo0698	protein_coding	985039	flagellar motor switch protein(lmo0698)
CAC98777	lmo0699	protein_coding	987173	flagellar motor switch protein FliM(fliM)
CAC98778	lmo0700	protein_coding	985046	flagellar motor switch protein FliY(lmo0700)
CAC98779	lmo0701	protein_coding	985048	lmo0701(lmo0701)
CAC98780	lmo0702	protein_coding	985034	lmo0702(lmo0702)
CAC98781	lmo0703	protein_coding	985050	lmo0703(lmo0703)
CAC98782	lmo0704	protein_coding	985042	lmo0704(lmo0704)
CAC98783	lmo0705	protein_coding	985054	flagellar hook-associated protein FlgK(flgK)
CAC98784	lmo0706	protein_coding	985052	flagellar hook-associated protein FlgL(flgL)
CAC98785	lmo0707	protein_coding	985041	flagellar capping protein FliD(fliD)
CAC98786	lmo0708	protein_coding	985045	flagellar protein(lmo0708)
CAC98787	lmo0709	protein_coding	985079	lmo0709(lmo0709)
CAC98788	lmo0710	protein_coding	985059	flagellar basal-body rod protein FlgB(flgB)
CAC98789	lmo0711	protein_coding	984818	flagellar basal body rod protein FlgC(flgC)
CAC98790	lmo0712	protein_coding	985062	flagellar hook-basal body protein FliE(fliE)
CAC98791	lmo0713	protein_coding	985064	flagellar MS-ring protein FliF(fliF)
CAC98793	lmo0715	protein_coding	985068	lmo0715(fliH)
CAC98796	lmo0718	protein_coding	985076	lmo0718(lmo0718)
CAC98797	lmo0719	protein_coding	985078	hypothetical protein(lmo0719)
CAC98799	lmo0721	protein_coding	987135	fibronectin-binding protein(lmo0721)
CAC98800	lmo0722	protein_coding	986726	pyruvate oxidase(lmo0722)
CAC98801	lmo0723	protein_coding	986712	metyl-accepting chemotaxis protein(lmo0723)
CAC98802	lmo0724	protein_coding	986702	hypothetical protein(lmo0724)
CAC98803	lmo0725	protein_coding	986516	peptidoglycan-binding protein(lmo0725)
CAC98804	lmo0726	protein_coding	986355	hypothetical protein(lmo0726)
CAC98806	lmo0728	protein_coding	986299	riboflavin kinase / FAD synthase(lmo0728)
CAC98809	lmo0731	protein_coding	986215	lmo0731(lmo0731)
CAC98810	lmo0732	protein_coding	985958	peptidoglycan binding protein(lmo0732)
CAC98819	lmo0741	protein_coding	985539	GntR family transcriptional regulator(lmo0741)
CAC98820	lmo0742	protein_coding	985536	ABC transporter ATP-binding protein(lmo0742)
CAC98821	lmo0743	protein_coding	985534	lmo0743(lmo0743)
CAC98822	lmo0744	protein_coding	985533	ABC transporter ATP-binding protein(lmo0744)
CAC98827	lmo0749	protein_coding	985526	lmo0749(lmo0749)
CAC98828	lmo0750	protein_coding	985524	lmo0750(lmo0750)
CAC98829	lmo0751	protein_coding	985522	lmo0751(lmo0751)
CAC98836	lmo0758	protein_coding	985508	lmo0758(lmo0758)
CAC98837	lmo0759	protein_coding	985503	lmo0759(lmo0759)
CAC98838	lmo0760	protein_coding	985499	lmo0760(lmo0760)
CAC98839	lmo0761	protein_coding	985498	hypothetical protein(lmo0761)
CAC98840	lmo0762	protein_coding	985496	ATP/GTP-binding protein(lmo0762)
CAC98846	lmo0768	protein_coding	985485	sugar ABC transporter substrate-binding protein(lmo0768)
CAC98851	lmo0773	protein_coding	985473	alcohol dehydrogenase(lmo0773)

CAC98854	lmo0776	protein_coding	985467	transcriptional regulator(lmo0776)
CAC98856	lmo0778	protein_coding	985465	lmo0778(lmo0778)
CAC98859	lmo0781	protein_coding	985460	PTS mannose transporter subunit IID(lmo0781)
CAC98860	lmo0782	protein_coding	985459	PTS mannose transporter subunit IIC(lmo0782)
CAC98861	lmo0783	protein_coding	985458	PTS mannose transporter subunit IIB(lmo0783)
CAC98862	lmo0784	protein_coding	985456	PTS mannose transporter subunit IIB(lmo0784)
CAC98864	lmo0786	protein_coding	985450	ACP phosphodiesterase(lmo0786)
CAC98865	lmo0787	protein_coding	985449	amino acid transporter(lmo0787)
CAC98867	lmo0789	protein_coding	985444	hypothetical protein(lmo0789)
CAC98871	lmo0793	protein_coding	985432	hypothetical protein(lmo0793)
CAC98872	lmo0794	protein_coding	985430	hypothetical protein(lmo0794)
CAC98874	lmo0796	protein_coding	985428	hypothetical protein(lmo0796)
CAC98875	lmo0797	protein_coding	985426	lmo0797(lmo0797)
CAC98876	lmo0798	protein_coding	985421	lysine-specific permease(lmo0798)
CAC98877	lmo0799	protein_coding	985420	lmo0799(lmo0799)
CAC98884	lmo0806	protein_coding	985404	transcriptional regulator(lmo0806)
CAC98885	lmo0807	protein_coding	985403	spermidine/putrescine ABC transporter ATP-binding protein(lmo0807)
CAC98886	lmo0808	protein_coding	985401	spermidine/putrescine ABC transporter permease(lmo0808)
CAC98889	lmo0811	protein_coding	985394	carbonic anhydrase(lmo0811)
CAC98891	lmo0813	protein_coding	985392	fructokinase(lmo0813)
CAC98892	lmo0814	protein_coding	985391	oxidoreductase(lmo0814)
CAC98893	lmo0815	protein_coding	985389	transcriptional regulator(lmo0815)
CAC98894	lmo0816	protein_coding	985388	regulatory protein PaiA(lmo0816)
CAC98896	lmo0818	protein_coding	985383	cation-transporting ATPase(lmo0818)
CAC98897	lmo0819	protein_coding	985382	lmo0819(lmo0819)
CAC98898	lmo0820	protein_coding	985380	acetyltransferase(lmo0820)
CAC98899	lmo0821	protein_coding	985377	lmo0821(lmo0821)
CAC98901	lmo0823	protein_coding	985374	oxidoreductase(lmo0823)
CAC98902	lmo0824	protein_coding	985373	lmo0824(lmo0824)
CAC98908	fbp	protein_coding	985361	fructose-1,6-bisphosphatase(fbp)
CAC98911	lmo0833	protein_coding	985354	transcriptional regulator(lmo0833)
CAC98912	lmo0834	protein_coding	985353	lmo0834(lmo0834)
CAC98913	lmo0835	protein_coding	985352	peptidoglycan binding protein(lmo0835)
CAC98916	uhpT	protein_coding	985347	sugar:phosphate antiporter(uhpT)
CAC98917	lmo0839	protein_coding	985342	tetracycline resistance protein(lmo0839)
CAC98919	lmo0841	protein_coding	985338	calcium-transporting ATPase(lmo0841)
CAC98920	lmo0842	protein_coding	985337	peptidoglycan binding protein(lmo0842)
CAC98924	lmo0846	protein_coding	985329	excinuclease ABC subunit C(lmo0846)
CAC98925	lmo0847	protein_coding	985328	glutamine ABC transporter(lmo0847)
CAC98926	lmo0848	protein_coding	985325	amino acid ABC transporter ATP-binding protein(lmo0848)
CAC98933	ddlA	protein_coding	985238	D-alanyl-alanine synthetase A(ddl)
CAC98935	lmo0857	protein_coding	985170	carboxylesterase(lmo0857)
CAC98938	lmo0860	protein_coding	984935	sugar ABC transporter permease(lmo0860)
CAC98939	lmo0861	protein_coding	984876	sugar ABC transporter permease(lmo0861)
CAC98945	lmo0867	protein_coding	984585	lmo0867(lmo0867)
CAC98947	lmo0869	protein_coding	984542	lmo0869(lmo0869)
CAC98948	lmo0870	protein_coding	984493	lmo0870(lmo0870)
CAC98949	lmo0871	protein_coding	984472	hypothetical protein(lmo0871)

CAC98950	lmo0872	protein_coding	984428	antibiotic resistance protein(lmo0872)
CAC98954	lmo0876	protein_coding	986296	PTS sugar transporter subunit IIC(lmo0876)
CAC98955	lmo0877	protein_coding	986454	glucosamine-6-phosphate isomerase(lmo0877)
CAC98956	lmo0878	protein_coding	986549	oxidoreductase(lmo0878)
CAC98957	lmo0879	protein_coding	986553	lmo0879(lmo0879)
CAC98958	lmo0880	protein_coding	986636	wall associated protein precursor(lmo0880)
CAC98960	lmo0882	protein_coding	986548	hypothetical protein(lmo0882)
CAC98961	lmo0883	protein_coding	986544	hypothetical protein(lmo0883)
CAC98966	lmo0888	protein_coding	986538	hypothetical protein(lmo0888)
CAC98967	RsbR	protein_coding	986201	positive regulator of sigma-B activity(RsbR)
CAC98970	rsbU	protein_coding	986534	serine phosphatase(rsbU)
CAC98971	rsbV	protein_coding	986526	anti-anti-sigma factor (antagonist of RsbW)(rsbV)
CAC98972	rsbW	protein_coding	986524	serine-protein kinase RsbW(rsbW)
CAC98973	sigB	protein_coding	986527	RNA polymerase sigma factor SigB(sigB)
CAC98974	rsbX	protein_coding	986520	indirect negative regulation of sigma B dependant gene expression (serine phosphatase)(rsbX)
CAC98975	lmo0897	protein_coding	984941	transporter(lmo0897)
CAC98978	lmo0900	protein_coding	987809	lmo0900(lmo0900)
CAC98979	lmo0901	protein_coding	986930	PTS cellbiose transporter subunit IIC(lmo0901)
CAC98980	lmo0902	protein_coding	986980	GntR family transcriptional regulator(lmo0902)
CAC98981	lmo0903	protein_coding	986912	hypothetical protein(lmo0903)
CAC98982	lmo0904	protein_coding	986917	lmo0904(lmo0904)
CAC98983	lmo0905	protein_coding	986916	lmo0905(lmo0905)
CAC98984	lmo0906	protein_coding	986897	glutathione reductase(lmo0906)
CAC98985	lmo0907	protein_coding	986931	phosphoglycerate mutase(lmo0907)
CAC98987	lmo0909	protein_coding	986502	GntR family transcriptional regulator(lmo0909)
CAC98989	lmo0911	protein_coding	986500	lmo0911(lmo0911)
CAC98990	lmo0912	protein_coding	986984	formate transporter(lmo0912)
CAC98991	lmo0913	protein_coding	986938	succinate semialdehyde dehydrogenase(lmo0913)
CAC99000	lmo0922	protein_coding	986345	pantothenate kinase(lmo0922)
CAC99004	lmo0926	protein_coding	984510	TetR family transcriptional regulator(lmo0926)
CAC99005	lmo0927	protein_coding	986782	hypothetical protein(lmo0927)
CAC99008	lmo0930	protein_coding	986560	hypothetical protein(lmo0930)
CAC99011	lmo0933	protein_coding	984547	sugar transferase(lmo0933)
CAC99012	lmo0934	protein_coding	986642	hypothetical protein(lmo0934)
CAC99015	lmo0937	protein_coding	987860	lmo0937(lmo0937)
CAC99016	lmo0938	protein_coding	987839	protein-tyrosine-phosphatase(lmo0938)
CAC99017	lmo0939	protein_coding	985869	lmo0939(lmo0939)
CAC99027	lmo0949	protein_coding	987856	hypothetical protein(lmo0949)
CAC99028	lmo0950	protein_coding	987861	lmo0950(lmo0950)
CAC99029	lmo0951	protein_coding	987836	lmo0951(lmo0951)
CAC99030	lmo0952	protein_coding	986763	lmo0952(lmo0952)
CAC99031	lmo0953	protein_coding	986396	lmo0953(lmo0953)
CAC99034	lmo0956	protein_coding	986776	N-acetylglucosamine-6P-phosphate deacetylase(lmo0956)
CAC99035	lmo0957	protein_coding	986480	glucosamine-6-phosphate isomerase(lmo0957)
CAC99036	lmo0958	protein_coding	986478	GntR family transcirptional regulator(lmo0958)
CAC99038	lmo0960	protein_coding	986469	protease(lmo0960)
CAC99040	lemA	protein_coding	986467	LemA protein(lemA)

CAC99043	lmo0965	protein_coding	985451	hypothetical protein(lmo0965)
CAC99044	lmo0966	protein_coding	986839	lmo0966(lmo0966)
CAC99048	lmo0970	protein_coding	987821	enoyl-ACP reductase(lmo0970)
CAC99049	dltD	protein_coding	986447	DltD protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid (dltD)
CAC99050	dltC	protein_coding	986460	D-alanine--poly(phosphoribitol) ligase subunit 2(dltC)
CAC99051	dltB	protein_coding	986448	DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid (dltB)
CAC99052	dltA	protein_coding	986449	D-alanine--poly(phosphoribitol) ligase subunit 1(dltA)
CAC99056	lmo0978	protein_coding	986440	branched-chain amino acid aminotransferase(lmo0978)
CAC99059	lmo0981	protein_coding	986765	transporter(lmo0981)
CAC99062	lmo0984	protein_coding	986785	hypothetical protein(lmo0984)
CAC99064	lmo0986	protein_coding	986427	antibiotic ABC transporter ATP-binding protein(lmo0986)
CAC99067	lmo0989	protein_coding	986432	MarR family transcriptional regulator(lmo0989)
CAC99068	lmo0990	protein_coding	986420	hypothetical protein(lmo0990)
CAC99072	lmo0994	protein_coding	986414	lmo0994(lmo0994)
CAC99073	lmo0995	protein_coding	986413	hypothetical protein(lmo0995)
CAC99074	lmo0996	protein_coding	986513	methylated-DNA-protein-cysteine methyltransferase(lmo0996)
CAC99078	lmo1000	protein_coding	986831	phytoene dehydrogenase(lmo1000)
CAC99079	lmo1001	protein_coding	986350	hypothetical protein(lmo1001)
CAC99084	lmo1006	protein_coding	986673	aminotransferase(lmo1006)
CAC99086	lmo1008	protein_coding	986444	hypothetical protein(lmo1008)
CAC99089	lmo1011	protein_coding	986298	tetrahydrodipicolinate succinylase(lmo1011)
CAC99097	lmo1019	protein_coding	986368	hypothetical protein(lmo1019)
CAC99105	lmo1027	protein_coding	986344	hypothetical protein(lmo1027)
CAC99110	lmo1032	protein_coding	986336	transketolase(lmo1032)
CAC99111	lmo1033	protein_coding	986331	transketolase(lmo1033)
CAC99113	lmo1035	protein_coding	985245	PTS beta-glucoside transporter subunit IIABC(lmo1035)
CAC99114	lmo1036	protein_coding	984797	lmo1036(lmo1036)
CAC99122	lmo1044	protein_coding	986188	molybdopterin converting factor subunit 2(lmo1044)
CAC99123	lmo1045	protein_coding	985638	molybdopterin converting factor subunit 1(lmo1045)
CAC99124	lmo1046	protein_coding	986305	molybdenum cofactor biosynthesis protein MoaC(moaC)
CAC99125	lmo1047	protein_coding	984816	molybdenum cofactor biosynthesis protein A(moaA)
CAC99128	lmo1050	protein_coding	986511	hypothetical protein(lmo1050)
CAC99130	pdhA	protein_coding	986808	pyruvate dehydrogenase subunit E1 alpha(pdhA)
CAC99131	PdhB	protein_coding	984409	pyruvate dehydrogenase subunit E1 beta(PdhB)
CAC99132	pdhC	protein_coding	986301	dihydrolipoamide acetyltransferase(pdhC)
CAC99133	PdhD	protein_coding	986542	dihydrolipoamide dehydrogenase(PdhD)
CAC99134	lmo1056	protein_coding	986297	lmo1056(lmo1056)
CAC99135	lmo1057	protein_coding	986824	L-lactate dehydrogenase(lmo1057)
CAC99136	lmo1058	protein_coding	986292	hypothetical protein(lmo1058)
CAC99139	lmo1061	protein_coding	986289	two-component sensor histidine kinase(lmo1061)
CAC99140	lmo1062	protein_coding	986633	ABC transporters permease(lmo1062)
CAC99141	lmo1063	protein_coding	986288	ABC transporter ATP binding protein(lmo1063)
CAC99142	lmo1064	protein_coding	986286	transporter(lmo1064)
CAC99143	lmo1065	protein_coding	984607	hypothetical protein(lmo1065)
CAC99144	lmo1066	protein_coding	986059	myo-inositol-1(or 4)-monophosphatase(lmo1066)
CAC99145	lmo1067	protein_coding	986279	GTP-binding elongation factor(lmo1067)
CAC99151	lmo1073	protein_coding	986508	metal ABC transporter substrate-binding protein(lmo1073)

CAC99152	lmo1074	protein_coding	986267	teichoic acid translocation permease TagG(lmo1074)
CAC99153	lmo1075	protein_coding	986506	teichoic acid ABC transporter ATP-binding protein(lmo1075)
CAC99154	lmo1076	protein_coding	986264	autolysin(lmo1076)
CAC99161	lmo1083	protein_coding	986257	dTDP-D-glucose 4,6-dehydratase(lmo1083)
CAC99162	lmo1084	protein_coding	986256	DTDP-L-rhamnose synthetase(lmo1084)
CAC99163	lmo1085	protein_coding	986253	teichoic acid biosynthesis protein B(lmo1085)
CAC99168	lmo1090	protein_coding	986248	glycosyltransferase(lmo1090)
CAC99169	lmo1091	protein_coding	986251	glysosyltransferase(lmo1091)
CAC99172	lmo1094	protein_coding	986243	lmo1094(lmo1094)
CAC99174	guaA	protein_coding	986238	GMP synthase(guaA)
CAC99175	lmo1097	protein_coding	986237	integrase(lmo1097)
CAC99177	lmo1099	protein_coding	986219	hypothetical protein(lmo1099)
CAC99182	lmo1104	protein_coding	986227	P60 protein(lmo1104)
CAC99183	lmo1105	protein_coding	986240	hypothetical protein(lmo1105)
CAC99184	lmo1106	protein_coding	986235	hypothetical protein(lmo1106)
CAC99186	lmo1108	protein_coding	986222	hypothetical protein(lmo1108)
CAC99190	lmo1112	protein_coding	986216	hypothetical protein(lmo1112)
CAC99191	lmo1113	protein_coding	986214	hypothetical protein(lmo1113)
CAC99192	lmo1114	protein_coding	986213	hypothetical protein(lmo1114)
CAC99194	lmo1116	protein_coding	986570	regulatory protein(lmo1116)
CAC99195	lmo1117	protein_coding	986210	lmo1117(lmo1117)
CAC99196	lmo1118	protein_coding	986207	lmo1118(lmo1118)
CAC99202	lmo1124	protein_coding	986198	lmo1124(lmo1124)
CAC99206	lmo1128	protein_coding	985150	lmo1128(lmo1128)
CAC99209	lmo1131	protein_coding	986529	ABC transporter ATP-binding protein(lmo1131)
CAC99210	lmo1132	protein_coding	986192	ABC transporter ATP-binding protein(lmo1132)
CAC99214	lmo1136	protein_coding	986166	internalin(lmo1136)
CAC99218	lmo1140	protein_coding	986180	lmo1140(lmo1140)
CAC99220	lmo1142	protein_coding	986177	PduS protein(lmo1142)
CAC99221	lmo1143	protein_coding	986169	PduT protein(lmo1143)
CAC99222	lmo1144	protein_coding	986310	PduU protein(lmo1144)
CAC99223	lmo1145	protein_coding	986160	PduV protein(lmo1145)
CAC99224	lmo1146	protein_coding	986162	lmo1146(lmo1146)
CAC99229	lmo1151	protein_coding	986164	PduA protein(lmo1151)
CAC99232	lmo1154	protein_coding	986151	diol dehydratase subunit gamma(lmo1154)
CAC99234	lmo1156	protein_coding	986150	diol dehydratase-reactivating factor large subunit(lmo1156)
CAC99236	lmo1158	protein_coding	986149	PduK protein(lmo1158)
CAC99239	lmo1161	protein_coding	986144	ethanolamine utilization protein EutJ(lmo1161)
CAC99242	lmo1164	protein_coding	986139	ATP:cob(I)alamin adenosyltransferase PduO(lmo1164)
CAC99245	glpF	protein_coding	986131	glycerol uptake facilitator protein(glpF)
CAC99246	AckA2	protein_coding	986132	acetate kinase(AckA2)
CAC99248	lmo1170	protein_coding	986128	PduX protein(lmo1170)
CAC99249	pduQ	protein_coding	986125	NADPH-dependent butanol dehydrogenase(pduQ)
CAC99250	lmo1172	protein_coding	986126	two-component response regulator(lmo1172)
CAC99251	lmo1173	protein_coding	986122	two-component sensor histidine kinase(lmo1173)
CAC99252	eutA	protein_coding	986123	ethanolamine utilization protein EutA(eutA)
CAC99253	eutB	protein_coding	986127	ethanolamine ammonia-lyase large subunit(eutB)
CAC99254	eutC	protein_coding	986120	ethanolamine ammonia-lyase small subunit(eutC)

CAC99255	lmo1177	protein_coding	986121	carboxysome structural protein EutL(lmo1177)
CAC99256	lmo1178	protein_coding	986118	carboxysome structural protein(lmo1178)
CAC99257	lmo1179	protein_coding	986119	alcohol dehydrogenase(lmo1179)
CAC99258	lmo1180	protein_coding	986115	carboxysome structural protein(lmo1180)
CAC99259	lmo1181	protein_coding	986116	cobalamin adenosyl transferase(lmo1181)
CAC99260	lmo1182	protein_coding	986114	PduL protein(lmo1182)
CAC99261	lmo1183	protein_coding	986117	lmo1183(lmo1183)
CAC99262	lmo1184	protein_coding	986113	carbon dioxide concentrating mechanism protein(lmo1184)
CAC99263	lmo1185	protein_coding	986110	PduT protein(lmo1185)
CAC99264	lmo1186	protein_coding	986111	ethanolamine utilization protein EutH(lmo1186)
CAC99265	lmo1187	protein_coding	986106	ethanolamine utilization protein EutQ(lmo1187)
CAC99266	lmo1188	protein_coding	986112	lmo1188(lmo1188)
CAC99267	lmo1189	protein_coding	986109	transcriptional regulator(lmo1189)
CAC99268	lmo1190	protein_coding	986103	lmo1190(lmo1190)
CAC99269	cbiA	protein_coding	986099	cobyrinic acid a,c-diamide synthase(cbiA)
CAC99270	lmo1192	protein_coding	986098	cobalamin biosynthesis protein(cobD)
CAC99271	lmo1193	protein_coding	986096	cobalt-precorrin-8X methylmutase(cbiC)
CAC99272	cbiD	protein_coding	986097	cobalt-precorrin-6A synthase(cbiD)
CAC99273	cbiE	protein_coding	986100	cobalt-precorrin-6Y C(5)-methyltransferase(cbiE)
CAC99274	lmo1196	protein_coding	986101	cobalt-precorrin-6Y C(15)-methyltransferase(lmo1196)
CAC99275	cbiF	protein_coding	986091	precorrin-3 methylase(cbiF)
CAC99276	cbiG	protein_coding	986089	cobalamin biosynthesis protein CbiG(cbiG)
CAC99277	cbiH	protein_coding	986093	precorrin-3B C17-methyltransferase(cbiH)
CAC99278	lmo1200	protein_coding	986085	cobalamin biosynthesis protein CbiJ(lmo1200)
CAC99279	lmo1201	protein_coding	986081	uroporphyrinogen-III methyltransferase/uroporphyrinogen-III synthase(lmo1201)
CAC99280	cbiK	protein_coding	986086	cobalt chelatase(cbiK)
CAC99281	cbiL	protein_coding	986075	cobalt-precorrin-2 C(20)-methyltransferase(cbiL)
CAC99282	lmo1204	protein_coding	984567	cobalamin biosynthesis protein CbiM(lmo1204)
CAC99283	lmo1205	protein_coding	986083	cobalamin biosynthesis protein CbiN(lmo1205)
CAC99284	cbiQ	protein_coding	986065	cobalamin biosynthesis protein CbiQ(cbiQ)
CAC99285	lmo1207	protein_coding	986074	cobalt transporter ATP-binding protein CbiO(lmo1207)
CAC99301	lmo1223	protein_coding	986045	ABC transporter ATP-binding proteins(lmo1223)
CAC99302	lmo1224	protein_coding	986043	hypothetical protein(lmo1224)
CAC99304	lmo1226	protein_coding	986040	transporter(lmo1226)
CAC99306	rnhC	protein_coding	987663	ribonuclease HIII(rnhC)
CAC99313	lmo1235	protein_coding	986030	aspartate kinase(lmo1235)
CAC99314	lmo1236	protein_coding	986036	hypothetical protein(lmo1236)
CAC99315	racE	protein_coding	986027	glutamate racemase(racE)
CAC99316	lmo1238	protein_coding	986029	ribonuclease PH(rph)
CAC99317	lmo1239	protein_coding	986028	nucleoside-triphosphatase(lmo1239)
CAC99318	lmo1240	protein_coding	986025	hypothetical protein(lmo1240)
CAC99319	lmo1241	protein_coding	986024	lmo1241(lmo1241)
CAC99326	lmo1248	protein_coding	986009	hypothetical protein(lmo1248)
CAC99327	lmo1249	protein_coding	986015	lmo1249(lmo1249)
CAC99328	lmo1250	protein_coding	986007	antibiotic resistance protein(lmo1250)
CAC99329	lmo1251	protein_coding	986006	Fnr/Crp family transcriptional regulator(lmo1251)
CAC99331	lmo1253	protein_coding	984383	GntR family transcriptional regulator(lmo1253)
CAC99335	lmo1257	protein_coding	985997	lmo1257(lmo1257)

CAC99336	lmo1258	protein_coding	985992	lmo1258(lmo1258)
CAC99337	proA	protein_coding	985995	gamma-glutamyl phosphate reductase(proA)
CAC99338	proB	protein_coding	985996	gamma-glutamyl kinase(proB)
CAC99339	lmo1261	protein_coding	985993	lmo1261(lmo1261)
CAC99340	lmo1262	protein_coding	985990	transcriptional regulator(lmo1262)
CAC99343	lmo1265	protein_coding	985747	hypothetical protein(lmo1265)
CAC99345	tig	protein_coding	985096	trigger factor(tig)
CAC99347	lmo1269	protein_coding	985087	type I signal peptidase(lmo1269)
CAC99349	lmo1271	protein_coding	985089	type I signal peptidase(lmo1271)
CAC99352	lmo1274	protein_coding	987273	polypeptide deformylase(lmo1274)
CAC99357	clpY	protein_coding	985103	ATP-dependent protease ATP-binding subunit HslU(hslU)
CAC99358	codY	protein_coding	985108	transcriptional repressor CodY(codY)
CAC99359	lmo1281	protein_coding	985105	hypothetical protein(lmo1281)
CAC99363	lmo1285	protein_coding	985138	hypothetical protein(lmo1285)
CAC99365	parC	protein_coding	985091	DNA topoisomerase IV subunit A(parC)
CAC99370	lmo1292	protein_coding	985112	glycerophosphodiester phosphodiesterase(lmo1292)
CAC99371	glpD	protein_coding	985350	glycerol-3-phosphate dehydrogenase(glpD)
CAC99372	miaA	protein_coding	985128	tRNA delta(2)-isopentenylpyrophosphate transferase(miaA)
CAC99373	lmo1295	protein_coding	985120	host factor-1 protein(lmo1295)
CAC99375	lmo1297	protein_coding	985127	aluminum resistance protein(lmo1297)
CAC99376	glnR	protein_coding	985126	glutamine synthetase repressor(glnR)
CAC99378	lmo1300	protein_coding	985130	arsenic transporter(lmo1300)
CAC99384	lmo1306	protein_coding	987683	hypothetical protein(lmo1306)
CAC99387	lmo1309	protein_coding	987686	hypothetical protein(lmo1309)
CAC99388	lmo1310	protein_coding	987688	hypothetical protein(lmo1310)
CAC99389	lmo1311	protein_coding	987689	lmo1311(lmo1311)
CAC99390	lmo1312	protein_coding	987691	lmo1312(lmo1312)
CAC99399	lmo1321	protein_coding	987701	hypothetical protein(lmo1321)
CAC99407	ribC	protein_coding	987710	riboflavin kinase(ribC)
CAC99409	pnpA	protein_coding	987712	polynucleotide phosphorylase(pnpA)
CAC99411	lmo1333	protein_coding	987717	hypothetical protein(lmo1333)
CAC99412	lmo1334	protein_coding	987718	hypothetical protein(lmo1334)
CAC99413	rpmG	protein_coding	987719	50S ribosomal protein L33(rpmG)
CAC99414	lmo1336	protein_coding	987720	5-formyltetrahydrofolate cyclo-ligase(lmo1336)
CAC99415	lmo1337	protein_coding	987722	hypothetical protein(lmo1337)
CAC99419	lmo1341	protein_coding	987725	competence protein ComG(lmo1341)
CAC99423	lmo1345	protein_coding	987732	competence protein ComGC(lmo1345)
CAC99429	lmo1351	protein_coding	987739	lmo1351(lmo1351)
CAC99431	lmo1353	protein_coding	987743	hypothetical protein(lmo1353)
CAC99433	efp	protein_coding	987744	elongation factor P(efp)
CAC99442	cspL	protein_coding	987871	cold-shock protein(cspL)
CAC99446	recN	protein_coding	987672	DNA repair protein(recN)
CAC99452	lmo1374	protein_coding	987858	branched-chain alpha-keto acid dehydrogenase subunit E2(lmo1374)
CAC99453	lmo1375	protein_coding	987853	aminotripeptidase(lmo1375)
CAC99454	lmo1376	protein_coding	987851	6-phosphogluconate dehydrogenase(lmo1376)
CAC99458	lmo1380	protein_coding	987834	lmo1380(lmo1380)
CAC99459	lmo1381	protein_coding	987841	lmo1381(lmo1381)
CAC99461	lmo1383	protein_coding	987838	isopentenyl pyrophosphate isomerase(lmo1383)

CAC99464	lmo1386	protein_coding	987830	DNA translocase(lmo1386)
CAC99465	lmo1387	protein_coding	987829	pyrroline-5-carboxylate reductase(lmo1387)
CAC99466	tcsA	protein_coding	984815	CD4+ T cell-stimulating antigen, lipoprotein(tcsA)
CAC99468	lmo1390	protein_coding	984893	ABC transporter permease(lmo1390)
CAC99469	lmo1391	protein_coding	986482	sugar ABC transporter permease(lmo1391)
CAC99470	lmo1392	protein_coding	986324	peptidase(lmo1392)
CAC99471	lmo1393	protein_coding	986760	peptidase(lmo1393)
CAC99483	lmo1405	protein_coding	986841	anti-terminator regulatory protein(lmo1405)
CAC99484	pflB	protein_coding	986171	pyruvate formate-lyase(pflB)
CAC99485	pflC	protein_coding	986485	pyruvate-formate lyase activating enzyme(pflC)
CAC99487	lmo1409	protein_coding	986419	multidrug transporter(lmo1409)
CAC99492	lmo1414	protein_coding	986819	acetyl-CoA:acetyltransferase(lmo1414)
CAC99494	lmo1416	protein_coding	986348	lmo1416(lmo1416)
CAC99495	lmo1417	protein_coding	986745	hypothetical protein(lmo1417)
CAC99498	lmo1420	protein_coding	984666	UDP-N-acetylenolpyruvoylglucosamine reductase(murB)
CAC99499	lmo1421	protein_coding	984736	glycine/betaine ABC transporter ATP-binding protein(lmo1421)
CAC99500	lmo1422	protein_coding	986774	glycine/betaine ABC transporter permease(lmo1422)
CAC99503	opuCD	protein_coding	984750	glycine/betaine ABC transporter permease(opuCD)
CAC99504	opuCC	protein_coding	986463	glycine/betaine ABC transporter substrate-binding protein(opuCC)
CAC99505	opuCB	protein_coding	985838	glycine/betaine ABC transporter permease(opuCB)
CAC99506	opuCA	protein_coding	987882	glycine/betaine ABC transporter ATP-binding protein(opuCA)
CAC99510	lmo1432	protein_coding	986495	lmo1432(lmo1432)
CAC99511	lmo1433	protein_coding	985502	glutathione reductase(lmo1433)
CAC99513	lmo1435	protein_coding	986494	dihydrodipicolinate synthase(dapA)
CAC99517	sod	protein_coding	986791	superoxide dismutase(sod)
CAC99518	lmo1440	protein_coding	986499	hypothetical protein(lmo1440)
CAC99519	lmo1441	protein_coding	986437	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase(ispG)
CAC99520	lmo1442	protein_coding	986764	transporter(lmo1442)
CAC99523	zurR	protein_coding	986176	ZurR family transcriptional regulator(zurR)
CAC99525	zurA	protein_coding	986711	metal (zinc) transport protein(ABC transporter, ATP-binding protein)(zurA)
CAC99526	lmo1448	protein_coding	986727	manganese-dependent inorganic pyrophosphatase(lmo1448)
CAC99528	lmo1450	protein_coding	987133	DEAD/DEAH box helicase(lmo1450)
CAC99529	lmo1451	protein_coding	987625	4-hydroxy-3-methylbut-2-enyl diphosphate reductase(ispH)
CAC99531	lmo1453	protein_coding	984399	hypothetical protein(lmo1453)
CAC99532	rpoD	protein_coding	984456	RNA polymerase sigma factor RpoD(rpoD)
CAC99533	dnaG	protein_coding	986564	DNA primase(dnaG)
CAC99534	lmo1456	protein_coding	986822	hypothetical protein(lmo1456)
CAC99538	lmo1460	protein_coding	987669	DNA repair protein RecO(recO)
CAC99539	lmo1461	protein_coding	987662	lmo1461(lmo1461)
CAC99547	rpsU	protein_coding	987865	30S ribosomal protein S21(rpsU)
CAC99557	lepA	protein_coding	986365	GTP-binding protein LepA(lepA)
CAC99558	rpsT	protein_coding	986932	30S ribosomal protein S20(rpsT)
CAC99559	lmo1481	protein_coding	986943	DNA polymerase III subunit delta(holA)
CAC99561	comEB	protein_coding	986960	competence protein ComEB(comEB)
CAC99563	lmo1485	protein_coding	987000	hypothetical protein(lmo1485)
CAC99564	lmo1486	protein_coding	986988	lmo1486(lmo1486)
CAC99565	lmo1487	protein_coding	986903	hypothetical protein(lmo1487)
CAC99566	lmo1488	protein_coding	986963	nicotinic acid mononucleotide adenylyltransferase(nadD)

CAC99569	lmo1491	protein_coding	986978	GTP-binding protein(lmo1491)
CAC99570	lmo1492	protein_coding	986939	hypothetical protein(lmo1492)
CAC99571	lmo1493	protein_coding	986970	oligopeptidase(lmo1493)
CAC99573	lmo1495	protein_coding	986966	hypothetical protein(lmo1495)
CAC99575	udk	protein_coding	986986	uridine kinase(udk)
CAC99576	lmo1498	protein_coding	986934	O-methyltransferase(lmo1498)
CAC99577	lmo1499	protein_coding	987003	hypothetical protein(lmo1499)
CAC99583	lmo1505	protein_coding	987751	ABC transporter ATP-binding protein(lmo1505)
CAC99584	lmo1506	protein_coding	987750	transporter(lmo1506)
CAC99593	lmo1515	protein_coding	987766	hypothetical protein(lmo1515)
CAC99594	lmo1516	protein_coding	987771	ammonium transporter NrgA(lmo1516)
CAC99595	lmo1517	protein_coding	987779	nitrogen regulatory PII protein(lmo1517)
CAC99597	aspS	protein_coding	987778	aspartyl-tRNA synthetase(aspS)
CAC99598	hisS	protein_coding	987781	histidyl-tRNA synthetase(hisS)
CAC99600	lmo1522	protein_coding	987785	D-tyrosyl-tRNA(Tyr) deacylase(lmo1522)
CAC99601	relA	protein_coding	987788	(p)ppGpp synthetase(relA)
CAC99604	lmo1526	protein_coding	987791	hypothetical protein(lmo1526)
CAC99607	lmo1529	protein_coding	987799	hypothetical protein(lmo1529)
CAC99608	lmo1530	protein_coding	987798	queuine tRNA-ribosyltransferase(tgt)
CAC99614	lmo1536	protein_coding	987813	prephenate dehydratase(lmo1536)
CAC99615	lmo1537	protein_coding	987811	GTPase ObgE(obgE)
CAC99616	lmo1538	protein_coding	987807	glycerol kinase(glpK)
CAC99617	lmo1539	protein_coding	987817	glycerol transporter(lmo1539)
CAC99627	lmo1549	protein_coding	986979	DNA repair protein RadC(radC)
CAC99631	hemL	protein_coding	986918	glutamate-1-semialdehyde aminotransferase(hemL)
CAC99633	lmo1555	protein_coding	986929	uroporphyrinogen-III synthase(hemD)
CAC99634	hemC	protein_coding	986927	porphobilinogen deaminase(hemC)
CAC99635	hemA	protein_coding	986920	glutamyl-tRNA reductase(hemA)
CAC99636	lmo1558	protein_coding	986915	GTP-binding protein EngB(engB)
CAC99641	lmo1563	protein_coding	986899	dephospho-CoA kinase(coaE)
CAC99642	mutM	protein_coding	986950	formamidopyrimidine-DNA glycosylase(mutM)
CAC99643	polA	protein_coding	986949	DNA polymerase I(polA)
CAC99655	lmo1577	protein_coding	986999	metal-dependent hydrolase(lmo1577)
CAC99656	lmo1578	protein_coding	986985	X-Pro dipeptidase(lmo1578)
CAC99657	lmo1579	protein_coding	986945	alanine dehydrogenase(lmo1579)
CAC99658	lmo1580	protein_coding	986961	hypothetical protein(lmo1580)
CAC99660	lmo1582	protein_coding	986947	hypothetical protein(lmo1582)
CAC99662	lmo1584	protein_coding	986942	hypothetical protein(lmo1584)
CAC99663	lmo1585	protein_coding	987795	peptidase(lmo1585)
CAC99669	argC	protein_coding	984694	N-acetyl-gamma-glutamyl-phosphate reductase(argC)
CAC99670	lmo1592	protein_coding	986418	thiamine biosynthesis protein ThiI(lmo1592)
CAC99671	lmo1593	protein_coding	985205	iron-sulfur cofactor synthesis protein NifS(lmo1593)
CAC99672	lmo1594	protein_coding	986850	septation ring formation regulator EzrA(lmo1594)
CAC99673	lmo1595	protein_coding	986055	hypothetical protein(lmo1595)
CAC99675	lmo1597	protein_coding	984705	lmo1597(lmo1597)
CAC99678	aroA	protein_coding	985307	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase(aroA)
CAC99679	lmo1601	protein_coding	985749	general stress protein(lmo1601)
CAC99680	lmo1602	protein_coding	985745	hypothetical protein(lmo1602)

CAC99681	lmo1603	protein_coding	985743	aminopeptidase(lmo1603)
CAC99682	lmo1604	protein_coding	985746	2-cys peroxiredoxin(lmo1604)
CAC99684	lmo1606	protein_coding	985737	DNA translocase(lmo1606)
CAC99685	pheT	protein_coding	985742	phenylalanyl-tRNA synthetase subunit beta(pheT)
CAC99693	lmo1615	protein_coding	985730	tRNA (guanine-N(7)-)-methyltransferase(trmB)
CAC99694	lmo1616	protein_coding	985729	hypothetical protein(lmo1616)
CAC99695	lmo1617	protein_coding	985727	multidrug transporter(lmo1617)
CAC99696	lmo1618	protein_coding	985724	MarR family transcriptional regulator(lmo1618)
CAC99697	daaA	protein_coding	985722	D-amino acid aminotransferase(daaA)
CAC99698	lmo1620	protein_coding	985721	dipeptidase PepV(lmo1620)
CAC99700	lmo1622	protein_coding	985726	hypothetical protein(lmo1622)
CAC99702	lmo1624	protein_coding	985718	transporter(lmo1624)
CAC99704	lmo1626	protein_coding	985552	lmo1626(lmo1626)
CAC99705	trpA	protein_coding	985711	tryptophan synthase subunit alpha(trpA)
CAC99706	trpB	protein_coding	985710	tryptophan synthase subunit beta(trpB)
CAC99707	trpF	protein_coding	985716	N-(5'-phosphoribosyl)anthranilate isomerase(trpF)
CAC99708	trpC	protein_coding	985709	indole-3-glycerol phosphate synthase(trpC)
CAC99709	trpD	protein_coding	985706	anthranilate phosphoribosyltransferase(trpD)
CAC99710	trpG	protein_coding	985715	anthranilate synthase subunit beta(trpG)
CAC99711	trpE	protein_coding	985705	anthranilate synthase subunit alpha(trpE)
CAC99712	lmo1634	protein_coding	985703	bifunctional acetaldehyde-CoA/alcohol dehydrogenase(lmo1634)
CAC99713	lmo1635	protein_coding	985702	hypothetical protein(lmo1635)
CAC99714	lmo1636	protein_coding	985701	ABC transporter ATP-binding protein(lmo1636)
CAC99715	lmo1637	protein_coding	985693	hypothetical protein(lmo1637)
CAC99726	lmo1648	protein_coding	985680	lmo1648(lmo1648)
CAC99727	lmo1649	protein_coding	985678	lmo1649(lmo1649)
CAC99728	lmo1650	protein_coding	985591	hypothetical protein(lmo1650)
CAC99735	tsf	protein_coding	985671	elongation factor Ts(tsf)
CAC99738	leuS	protein_coding	985669	leucyl-tRNA synthetase(leuS)
CAC99739	lmo1661	protein_coding	985668	hypothetical protein(lmo1661)
CAC99740	lmo1662	protein_coding	985666	hypothetical protein(lmo1662)
CAC99742	metK	protein_coding	985664	methionine adenosyltransferase(metK)
CAC99744	lmo1666	protein_coding	985661	peptidoglycan-linked protein(lmo1666)
CAC99749	lmo1671	protein_coding	985656	ABC transporter(lmo1671)
CAC99750	menE	protein_coding	985655	O-succinylbenzoic acid--CoA ligase(menE)
CAC99751	menB	protein_coding	985651	naphthoate synthase(menB)
CAC99756	lmo1678	protein_coding	985643	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase(lmo1678)
CAC99758	lmo1680	protein_coding	985641	cystathionine gamma-synthase(lmo1680)
CAC99759	lmo1681	protein_coding	985640	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (lmo1681)
CAC99762	lmo1684	protein_coding	985633	glycerate dehydrogenase(lmo1684)
CAC99767	lmo1689	protein_coding	985627	A/G-specific adenine glycosylase(lmo1689)
CAC99770	lmo1692	protein_coding	985622	lmo1692(lmo1692)
CAC99772	lmo1694	protein_coding	985624	CDP-abequose synthase(lmo1694)
CAC99773	lmo1695	protein_coding	985618	hypothetical protein(lmo1695)
CAC99774	lmo1696	protein_coding	985619	hypothetical protein(lmo1696)
CAC99776	lmo1698	protein_coding	985612	ribosomal-protein-alanine N-acetyltransferase(lmo1698)
CAC99777	lmo1699	protein_coding	985617	chemotaxis protein(lmo1699)

CAC99778	lmo1700	protein_coding	985611	lmo1700(lmo1700)
CAC99782	lmo1704	protein_coding	985606	hypothetical protein(lmo1704)
CAC99784	lmo1706	protein_coding	985609	transporter(lmo1706)
CAC99786	lmo1708	protein_coding	985601	aminoglycoside N3'-acetyltransferase(lmo1708)
CAC99788	lmo1710	protein_coding	985600	flavodoxin(lmo1710)
CAC99791	lmo1713	protein_coding	985588	rod shape-determining protein MreB(lmo1713)
CAC99795	lmo1717	protein_coding	985593	hypothetical protein(lmo1717)
CAC99799	lmo1721	protein_coding	985585	transcriptional regulator(lmo1721)
CAC99800	lmo1722	protein_coding	985584	ATP-dependent RNA helicase(lmo1722)
CAC99805	lmo1727	protein_coding	986088	LacI family transcriptional regulator(lmo1727)
CAC99806	lmo1728	protein_coding	985695	cellobiose phosphorylase(lmo1728)
CAC99807	lmo1729	protein_coding	985699	beta-glucosidase(lmo1729)
CAC99808	lmo1730	protein_coding	985575	sugar ABC transporter substrate-binding protein(lmo1730)
CAC99809	lmo1731	protein_coding	985577	sugar ABC transporter permease(lmo1731)
CAC99810	lmo1732	protein_coding	985574	sugar ABC transporter permease(lmo1732)
CAC99811	lmo1733	protein_coding	984552	glutamate synthase subunit beta(gltD)
CAC99812	lmo1734	protein_coding	986573	glutamate synthase large subunit(lmo1734)
CAC99813	gltC	protein_coding	985367	transcription activator of glutamate synthase operon GltC(gltC)
CAC99814	lmo1736	protein_coding	986571	hypothetical protein(lmo1736)
CAC99815	lmo1737	protein_coding	985567	glycerol dehydrogenase(lmo1737)
CAC99821	lmo1743	protein_coding	986834	lmo1743(lmo1743)
CAC99822	lmo1744	protein_coding	985378	hypothetical protein(lmo1744)
CAC99823	lmo1745	protein_coding	985561	two-component response regulator(lmo1745)
CAC99824	lmo1746	protein_coding	985569	ABC transporter permease(lmo1746)
CAC99825	lmo1747	protein_coding	985559	ABC transporter ATP-binding protein(lmo1747)
CAC99826	lmo1748	protein_coding	986669	lmo1748(lmo1748)
CAC99827	lmo1749	protein_coding	986346	shikimate kinase(lmo1749)
CAC99828	lmo1750	protein_coding	985557	hypothetical protein(lmo1750)
CAC99838	lmo1760	protein_coding	985989	geranylgeranylglyceryl phosphate synthase-like protein(lmo1760)
CAC99839	lmo1761	protein_coding	985984	sodium-dependent transporter(lmo1761)
CAC99840	lmo1762	protein_coding	985983	lmo1762(lmo1762)
CAC99841	lmo1763	protein_coding	985981	hypothetical protein(lmo1763)
CAC99842	purD	protein_coding	985980	phosphoribosylamine--glycine ligase(purD)
CAC99843	purH	protein_coding	985977	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase(purH)
CAC99844	purN	protein_coding	985978	phosphoribosylglycinamide formyltransferase(purN)
CAC99845	purM	protein_coding	985975	phosphoribosylaminoimidazole synthetase(purM)
CAC99846	purF	protein_coding	985974	amidophosphoribosyltransferase(purF)
CAC99847	purQ	protein_coding	985972	phosphoribosylformylglycinamidine synthase II(purQ)
CAC99848	purL	protein_coding	985306	phosphoribosylformylglycinamidine synthase I(purL)
CAC99851	purB	protein_coding	985967	adenylosuccinate lyase(purB)
CAC99852	purK	protein_coding	985968	phosphoribosylaminoimidazole carboxylase ATPase subunit(purK)
CAC99853	purE	protein_coding	985964	phosphoribosylaminoimidazole carboxylase catalytic subunit(purE)
CAC99856	lmo1778	protein_coding	985960	ABC transporter ATP-binding protein(lmo1778)
CAC99858	lmo1780	protein_coding	985952	aminotripeptidase(lmo1780)
CAC99860	lmo1782	protein_coding	985950	3'-exo-deoxyribonuclease(lmo1782)
CAC99861	rplT	protein_coding	985949	50S ribosomal protein L20(rplT)
CAC99862	rpmI	protein_coding	985946	50S ribosomal protein L35(rpmI)

CAC99863	infC	protein_coding	985947	translation initiation factor IF-3(infC)
CAC99864	inlC	protein_coding	985945	internalin C(inlC)
CAC99865	rplS	protein_coding	985943	50S ribosomal protein L19(rplS)
CAC99866	lmo1788	protein_coding	985948	transcriptional regulator(lmo1788)
CAC99867	lmo1789	protein_coding	985940	hypothetical protein(lmo1789)
CAC99868	lmo1790	protein_coding	985953	hypothetical protein(lmo1790)
CAC99869	lmo1791	protein_coding	985939	lmo1791(lmo1791)
CAC99870	trmD	protein_coding	985936	tRNA (guanine-N(1)-)-methyltransferase(trmD)
CAC99873	lmo1795	protein_coding	985941	hypothetical protein(lmo1795)
CAC99875	rpsP	protein_coding	985931	30S ribosomal protein S16(rpsP)
CAC99876	lmo1798	protein_coding	985932	hypothetical protein(lmo1798)
CAC99877	lmo1799	protein_coding	985930	peptidoglycan binding protein(lmo1799)
CAC99878	lmo1800	protein_coding	985934	protein-tyrosine phosphatase(lmo1800)
CAC99879	ffh	protein_coding	985929	signal recognition particle protein Ffh(ffh)
CAC99880	lmo1802	protein_coding	985927	DNA-binding protein(lmo1802)
CAC99883	rncS	protein_coding	985924	ribonuclease III(rnc)
CAC99884	acpA	protein_coding	986035	acyl carrier protein(acpP)
CAC99891	lmo1813	protein_coding	985914	phosphoglycerate dehydrogenase(lmo1813)
CAC99893	lmo1815	protein_coding	985911	hypothetical protein(lmo1815)
CAC99894	rpmB	protein_coding	985895	50S ribosomal protein L28(rpmB)
CAC99904	lmo1826	protein_coding	985894	lmo1826(rpoZ)
CAC99905	lmo1827	protein_coding	985464	guanylate kinase(gmk)
CAC99906	lmo1828	protein_coding	985886	hypothetical protein(lmo1828)
CAC99907	lmo1829	protein_coding	985887	fibronectin-binding proteins(lmo1829)
CAC99908	lmo1830	protein_coding	984389	short-chain dehydrogenase(lmo1830)
CAC99918	pyrR	protein_coding	985861	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase(pyrR)
CAC99920	lmo1842	protein_coding	985864	hypothetical protein(lmo1842)
CAC99921	lmo1843	protein_coding	985856	hypothetical protein(lmo1843)
CAC99922	lsp	protein_coding	985858	lipoprotein signal peptidase(lspA)
CAC99924	lmo1846	protein_coding	985857	multidrug transporter(lmo1846)
CAC99925	lmo1847	protein_coding	985848	metal ABC transporter(lmo1847)
CAC99926	lmo1848	protein_coding	985850	metal ABC transporter permease(lmo1848)
CAC99927	lmo1849	protein_coding	985851	metal ABC transporter ATP-binding protein(lmo1849)
CAC99928	lmo1850	protein_coding	985846	MarR family transcriptional regulator(lmo1850)
CAC99929	lmo1851	protein_coding	985844	carboxy-terminal processing proteinase(lmo1851)
CAC99933	lmo1855	protein_coding	985842	D-alanyl-D-alanine carboxypeptidase(lmo1855)
CAC99936	lmo1858	protein_coding	985865	dehydrogenase(lmo1858)
CAC99937	lmo1859	protein_coding	985834	methionine sulfoxide reductase B(lmo1859)
CAC99938	lmo1860	protein_coding	985835	methionine sulfoxide reductase A(lmo1860)
CAC99940	lmo1862	protein_coding	985832	hypothetical protein(lmo1862)
CAC99941	lmo1863	protein_coding	985833	hypothetical protein(lmo1863)
CAC99946	lmo1868	protein_coding	986136	hypothetical protein(lmo1868)
CAC99947	lmo1869	protein_coding	985825	hypothetical protein(lmo1869)
CAC99949	lmo1871	protein_coding	985905	phosphoglucomutase(lmo1871)
CAC99952	lmo1874	protein_coding	985817	thymidylate synthase(thyA)
CAC99957	cspD	protein_coding	985814	cold-shock protein(cspD)
CAC99961	lmo1883	protein_coding	986008	chitinase(lmo1883)

CAC99962	lmo1884	protein_coding	985809	xanthine permease(lmo1884)
CAC99963	lmo1885	protein_coding	985807	xanthine phosphoribosyltransferase(lmo1885)
CAC99969	recU	protein_coding	985797	Holliday junction-specific endonuclease(recU)
CAC99986	lmo1908	protein_coding	985779	hypothetical protein(lmo1908)
CAC99988	lmo1910	protein_coding	985775	oxidoreductase(lmo1910)
CAC99995	pflA	protein_coding	985766	pyruvate formate-lyase(pflA)
CAC99997	lmo1919	protein_coding	985763	hypothetical protein(lmo1919)
CAD00007	ndk	protein_coding	984899	nucleoside diphosphate kinase(ndk)
CAD00008	lmo1930	protein_coding	987985	heptaprenyl diphosphate synthase subunit II(lmo1930)
CAD00011	lmo1933	protein_coding	987987	GTP cyclohydrolase I(folE)
CAD00015	lmo1937	protein_coding	986528	GTP-binding protein EngA(engA)
CAD00016	lmo1938	protein_coding	987984	30S ribosomal protein S1(rpsA)
CAD00017	cmk	protein_coding	984888	cytidylate kinase(cmk)
CAD00019	lmo1941	protein_coding	987990	hypothetical protein(lmo1941)
CAD00020	recS	protein_coding	987981	ATP-dependent DNA helicase(recS)
CAD00021	lmo1943	protein_coding	984735	hypothetical protein(lmo1943)
CAD00027	lmo1949	protein_coding	984426	hypothetical protein(lmo1949)
CAD00028	lmo1950	protein_coding	985025	hypothetical protein(lmo1950)
CAD00029	lmo1951	protein_coding	987973	segregation and condensation protein A(scpA)
CAD00030	lysA	protein_coding	987983	diaminopimelate decarboxylase(lysA)
CAD00031	pnp	protein_coding	987976	purine nucleoside phosphorylase(pnp)
CAD00033	lmo1955	protein_coding	987975	integrase/recombinase(lmo1955)
CAD00034	fur	protein_coding	987991	Fur family transcriptional regulator(fur)
CAD00036	fhuB	protein_coding	984897	ferrichrome ABC transporter permease(fhuB)
CAD00039	lmo1961	protein_coding	984397	oxidoreductase(lmo1961)
CAD00040	lmo1962	protein_coding	987974	TetR family transcriptional regulator(lmo1962)
CAD00046	lmo1968	protein_coding	984877	creatinine amidohydrolase(lmo1968)
CAD00047	lmo1969	protein_coding	984879	2-keto-3-deoxygluconate-6-phosphate aldolase(lmo1969)
CAD00048	lmo1970	protein_coding	984875	phosphotriesterase(lmo1970)
CAD00049	lmo1971	protein_coding	984874	PTS ascorbate transporter subunit IIC(ulaA)
CAD00050	lmo1972	protein_coding	984873	PTS pentitol transporter subunit IIB(lmo1972)
CAD00052	lmo1974	protein_coding	984870	GntR family transcriptional regulator(lmo1974)
CAD00056	lmo1978	protein_coding	984868	glucose-6-phosphate 1-dehydrogenase(lmo1978)
CAD00059	lmo1981	protein_coding	987963	hypothetical protein(lmo1981)
CAD00060	lmo1982	protein_coding	984865	hypothetical protein(lmo1982)
CAD00061	ilvD	protein_coding	984864	dihydroxy-acid dehydratase(ilvD)
CAD00064	ilvC	protein_coding	986504	ketol-acid reductoisomerase(ilvC)
CAD00065	leuA	protein_coding	984863	2-isopropylmalate synthase(leuA)
CAD00072	lmo1994	protein_coding	984855	LacI family transcriptional regulator(lmo1994)
CAD00074	lmo1996	protein_coding	984762	DeoR family transcriptional regulator(lmo1996)
CAD00083	lmo2005	protein_coding	987954	oxidoreductase(lmo2005)
CAD00086	lmo2008	protein_coding	985318	ABC transporter permease(lmo2008)
CAD00087	lmo2009	protein_coding	984845	sugar ABC transporter permease(lmo2009)
CAD00089	lmo2011	protein_coding	987955	two-component sensor histidine kinase(lmo2011)
CAD00090	lmo2012	protein_coding	987952	hypothetical protein(lmo2012)
CAD00091	lmo2013	protein_coding	986399	hypothetical protein(lmo2013)
CAD00092	lmo2014	protein_coding	984835	sugar hydrolase(lmo2014)
CAD00098	divIVA	protein_coding	984838	chemotaxis protein CheY(divIVA)

CAD00099	lmo2021	protein_coding	984837	hypothetical protein(lmo2021)
CAD00101	nadB	protein_coding	986699	L-aspartate oxidase(nadB)
CAD00102	nadC	protein_coding	984833	nicotinate-nucleotide pyrophosphorylase(nadC)
CAD00103	nadA	protein_coding	987946	quinolinate synthetase(nadA)
CAD00112	divIB	protein_coding	988005	cell division protein FtsQ(divIB)
CAD00118	ftsL	protein_coding	987937	cell division protein FtsL(ftsL)
CAD00119	lmo2041	protein_coding	984957	S-adenosyl-methyltransferase MraW(mraW)
CAD00126	lmo2048	protein_coding	987933	hypothetical protein(lmo2048)
CAD00134	lmo2056	protein_coding	984807	hypothetical protein(lmo2056)
CAD00135	ctaB	protein_coding	984806	protoheme IX farnesyltransferase(ctaB)
CAD00137	lmo2059	protein_coding	988010	potassium channel protein(lmo2059)
CAD00138	lmo2060	protein_coding	984801	hypothetical protein(lmo2060)
CAD00139	lmo2061	protein_coding	987917	hypothetical protein(lmo2061)
CAD00140	lmo2062	protein_coding	987920	copper transporter(lmo2062)
CAD00143	lmo2065	protein_coding	987927	lmo2065(lmo2065)
CAD00144	lmo2066	protein_coding	984796	lmo2066(lmo2066)
CAD00145	lmo2067	protein_coding	984795	bile acid hydrolase(lmo2067)
CAD00151	lmo2073	protein_coding	984372	ABC transporter ATP-binding protein(lmo2073)
CAD00152	lmo2074	protein_coding	987923	hypothetical protein(lmo2074)
CAD00157	lmo2079	protein_coding	984776	lmo2079(lmo2079)
CAD00158	lmo2080	protein_coding	984774	lmo2080(lmo2080)
CAD00159	lmo2081	protein_coding	987918	camphor resistance protein CrcB(lmo2081)
CAD00163	lmo2085	protein_coding	984772	peptidoglycan binding protein(lmo2085)
CAD00164	lmo2086	protein_coding	987915	hypothetical protein(lmo2086)
CAD00167	lmo2089	protein_coding	984766	lipase(lmo2089)
CAD00168	argG	protein_coding	984368	argininosuccinate synthase(argG)
CAD00169	argH	protein_coding	987914	argininosuccinate lyase(argH)
CAD00170	betL	protein_coding	987924	glycine betaine transporter BetL(betL)
CAD00174	lmo2096	protein_coding	987825	PTS galacticol transporter subunit IIC(lmo2096)
CAD00189	lmo2111	protein_coding	984745	nitroreductase(lmo2111)
CAD00190	lmo2112	protein_coding	985597	lmo2112(lmo2112)
CAD00191	lmo2113	protein_coding	984744	heme peroxidase(lmo2113)
CAD00192	lmo2114	protein_coding	987889	ABC transporter ATP-binding protein(lmo2114)
CAD00193	lmo2115	protein_coding	987993	ABC transporter permease(lmo2115)
CAD00197	lmo2119	protein_coding	985280	hypothetical protein(lmo2119)
CAD00198	lmo2120	protein_coding	984739	hypothetical protein(lmo2120)
CAD00205	lmo2127	protein_coding	984729	lmo2127(lmo2127)
CAD00206	lmo2128	protein_coding	987887	LacI family transcriptional regulator(lmo2128)
CAD00208	lmo2130	protein_coding	984779	hypothetical protein(lmo2130)
CAD00209	lmo2131	protein_coding	984721	lmo2131(lmo2131)
CAD00210	lmo2132	protein_coding	985218	lmo2132(lmo2132)
CAD00211	lmo2133	protein_coding	984718	fructose-1,6-biphosphate aldolase type II(lmo2133)
CAD00213	lmo2135	protein_coding	984713	PTS fructose transporter subunit IIC(lmo2135)
CAD00215	lmo2137	protein_coding	986283	PTS fructose transporter subunit IIA(lmo2137)
CAD00220	lmo2142	protein_coding	985289	lmo2142(lmo2142)
CAD00224	lmo2146	protein_coding	984701	LysR family transcriptional regulator(lmo2146)
CAD00227	lmo2149	protein_coding	984696	hypothetical protein(lmo2149)
CAD00234	lmo2156	protein_coding	988000	lmo2156(lmo2156)

CAD00235	sepA	protein_coding	987998	sepA(sepA)
CAD00236	lmo2158	protein_coding	984441	hypothetical protein(lmo2158)
CAD00237	lmo2159	protein_coding	986640	oxidoreductase(lmo2159)
CAD00238	lmo2160	protein_coding	984686	hypothetical protein(lmo2160)
CAD00239	lmo2161	protein_coding	984682	lmo2161(lmo2161)
CAD00240	lmo2162	protein_coding	984679	hypothetical protein(lmo2162)
CAD00242	lmo2164	protein_coding	986022	AraC family transcriptional regulator(lmo2164)
CAD00246	lmo2168	protein_coding	984676	glyoxalase(lmo2168)
CAD00249	lmo2171	protein_coding	984675	MFS transporter(lmo2171)
CAD00250	lmo2172	protein_coding	984671	propionate CoA-transferase(lmo2172)
CAD00252	lmo2174	protein_coding	986302	hypothetical protein(lmo2174)
CAD00257	lmo2179	protein_coding	984658	peptidoglycan binding protein(lmo2179)
CAD00261	lmo2183	protein_coding	984509	ferrichrome ABC transporter permease(lmo2183)
CAD00265	lmo2187	protein_coding	984649	lmo2187(lmo2187)
CAD00266	lmo2188	protein_coding	984648	oligoendopeptidase(lmo2188)
CAD00267	lmo2189	protein_coding	988007	competence protein CoiA(lmo2189)
CAD00269	lmo2191	protein_coding	988006	ArsC family transcriptional regulator(spxA)
CAD00273	lmo2195	protein_coding	984916	peptide ABC transporter permease(lmo2195)
CAD00274	lmo2196	protein_coding	984918	peptide ABC transporter substrate-binding protein(lmo2196)
CAD00275	lmo2197	protein_coding	984643	lmo2197(lmo2197)
CAD00276	trpS	protein_coding	984829	tryptophanyl-tRNA synthetase(trpS)
CAD00279	lmo2201	protein_coding	985883	3-oxoacyl-ACP synthase(lmo2201)
CAD00281	lmo2203	protein_coding	984639	N-acetylmuramoyl-L-alanine amidase(lmo2203)
CAD00283	lmo2205	protein_coding	986282	phosphoglyceromutase(lmo2205)
CAD00288	lmo2210	protein_coding	984633	lmo2210(lmo2210)
CAD00289	hemH	protein_coding	984632	ferrochelatase(hemH)
CAD00290	hemE	protein_coding	984388	uroporphyrinogen decarboxylase(hemE)
CAD00291	lmo2213	protein_coding	984794	hypothetical protein(lmo2213)
CAD00292	lmo2214	protein_coding	985371	ABC transporter permease(lmo2214)
CAD00295	lmo2217	protein_coding	984627	hypothetical protein(lmo2217)
CAD00296	lmo2218	protein_coding	985873	lmo2218(lmo2218)
CAD00297	lmo2219	protein_coding	984626	foldase(lmo2219)
CAD00299	lmo2221	protein_coding	984625	hypothetical protein(lmo2221)
CAD00300	lmo2222	protein_coding	984624	hypothetical protein(lmo2222)
CAD00303	citG	protein_coding	987997	fumarate hydratase(fumC)
CAD00308	lmo2230	protein_coding	986212	arsenate reductase(lmo2230)
CAD00309	lmo2231	protein_coding	984616	hypothetical protein(lmo2231)
CAD00311	lmo2233	protein_coding	986617	LysR family transcriptional regulator(lmo2233)
CAD00316	lmo2238	protein_coding	984611	MFS transporter(lmo2238)
CAD00321	lmo2243	protein_coding	984592	AraC family transcriptional regulator(lmo2243)
CAD00322	lmo2244	protein_coding	984802	ribosomal large subunit pseudouridine synthase(lmo2244)
CAD00324	lmo2246	protein_coding	984843	hypothetical protein(lmo2246)
CAD00325	lmo2247	protein_coding	984590	oxidoreductase(lmo2247)
CAD00326	lmo2248	protein_coding	984588	hypothetical protein(lmo2248)
CAD00327	lmo2249	protein_coding	984840	low-affinity inorganic phosphate transporter(lmo2249)
CAD00328	arpJ	protein_coding	984583	amino acid ABC transporter permease(arpJ)
CAD00329	lmo2251	protein_coding	984693	amino acid ABC transporter ATP-binding protein(lmo2251)
CAD00330	lmo2252	protein_coding	984582	aspartate aminotransferase(lmo2252)

CAD00332	lmo2254	protein_coding	984903	hypothetical protein(lmo2254)
CAD00334	lmo2256	protein_coding	986867	hypothetical protein(lmo2256)
CAD00340	lmo2262	protein_coding	984566	hypothetical protein(lmo2262)
CAD00344	lmo2266	protein_coding	984562	hypothetical protein(lmo2266)
CAD00347	lmo2269	protein_coding	988009	lmo2269(lmo2269)
CAD00348	comK'	protein_coding	986337	competence protein ComK(comK')
CAD00350	lmo2272	protein_coding	984555	lmo2272(lmo2272)
CAD00351	lmo2273	protein_coding	985897	hypothetical protein(lmo2273)
CAD00354	lmo2276	protein_coding	984564	hypothetical protein(lmo2276)
CAD00382	lmo2304	protein_coding	984687	hypothetical protein(lmo2304)
CAD00386	lmo2308	protein_coding	984487	single-stranded DNA-binding protein(lmo2308)
CAD00388	lmo2310	protein_coding	985397	lmo2310(lmo2310)
CAD00409	lmo2331	protein_coding	985570	hypothetical protein(lmo2331)
CAD00417	lmo2339	protein_coding	984799	hypothetical protein(lmo2339)
CAD00421	lmo2343	protein_coding	984458	nitrilotriacetate monooxygenase(lmo2343)
CAD00423	lmo2345	protein_coding	987930	hypothetical protein(lmo2345)
CAD00424	lmo2346	protein_coding	984455	amino acid ABC transporter ATP-binding protein(lmo2346)
CAD00425	lmo2347	protein_coding	984476	amino acid ABC transporter permease(lmo2347)
CAD00426	lmo2348	protein_coding	984447	amino acid ABC transporter permease(lmo2348)
CAD00427	lmo2349	protein_coding	985790	amino acid ABC transporter substrate-binding protein(lmo2349)
CAD00428	lmo2350	protein_coding	984858	hypothetical protein(lmo2350)
CAD00434	lmo2356	protein_coding	984439	lmo2356(lmo2356)
CAD00435	lmo2357	protein_coding	984422	hypothetical protein(lmo2357)
CAD00436	lmo2358	protein_coding	984434	N-acetylglucosamine-6-phosphate isomerase(lmo2358)
CAD00437	lmo2359	protein_coding	984722	hypothetical protein(lmo2359)
CAD00440	lmo2362	protein_coding	984369	amino acid antiporter(lmo2362)
CAD00441	lmo2363	protein_coding	985123	glutamate decarboxylase(lmo2363)
CAD00446	lmo2368	protein_coding	985492	lmo2368(lmo2368)
CAD00448	lmo2370	protein_coding	984540	aminotransferase(lmo2370)
CAD00449	lmo2371	protein_coding	984414	ABC transporter permease(lmo2371)
CAD00450	lmo2372	protein_coding	984413	ABC transporter ATP-binding protein(lmo2372)
CAD00452	lmo2374	protein_coding	984416	aspartate kinase(lmo2374)
CAD00455	lmo2377	protein_coding	987926	multidrug transporter(lmo2377)
CAD00460	lmo2382	protein_coding	984482	monovalent cation/H+ antiporter subunit E(lmo2382)
CAD00463	lmo2385	protein_coding	987552	hypothetical protein(lmo2385)
CAD00464	lmo2386	protein_coding	987551	hypothetical protein(lmo2386)
CAD00465	lmo2387	protein_coding	987550	hypothetical protein(lmo2387)
CAD00467	lmo2389	protein_coding	987546	NADH dehydrogenase(lmo2389)
CAD00468	lmo2390	protein_coding	987545	hypothetical thioredoxine reductase(lmo2390)
CAD00469	lmo2391	protein_coding	987544	hypothetical protein(lmo2391)
CAD00470	lmo2392	protein_coding	987541	hypothetical protein(lmo2392)
CAD00471	lmo2393	protein_coding	987540	hypothetical protein(lmo2393)
CAD00476	ltrC	protein_coding	987501	hypothetical protein(ltrC)
CAD00477	lmo2399	protein_coding	987500	hypothetical protein(lmo2399)
CAD00478	lmo2400	protein_coding	987499	acetyltransferase(lmo2400)
CAD00479	lmo2401	protein_coding	987498	hypothetical protein(lmo2401)
CAD00482	lmo2404	protein_coding	987494	hypothetical protein(lmo2404)
CAD00484	lmo2406	protein_coding	987489	hypothetical protein(lmo2406)

CAD00486	lmo2408	protein_coding	987486	repressor protein(lmo2408)
CAD00487	lmo2409	protein_coding	987484	lmo2409(lmo2409)
CAD00488	lmo2410	protein_coding	987480	lmo2410(lmo2410)
CAD00489	lmo2411	protein_coding	987479	hypothetical protein(lmo2411)
CAD00493	lmo2415	protein_coding	987473	ABC transporter ATP-binding protein(lmo2415)
CAD00494	lmo2416	protein_coding	987472	lmo2416(lmo2416)
CAD00498	lmo2420	protein_coding	987465	lmo2420(lmo2420)
CAD00505	lmo2427	protein_coding	987438	cell division protein FtsW(lmo2427)
CAD00506	lmo2428	protein_coding	987433	cell division protein FtsW(lmo2428)
CAD00507	lmo2429	protein_coding	987431	ferrichrome ABC transporter ATP-binding protein(lmo2429)
CAD00508	lmo2430	protein_coding	987428	ferrichrome ABC transporter permease(lmo2430)
CAD00509	lmo2431	protein_coding	987425	ferrichrome ABC transporter substrate-binding protein(lmo2431)
CAD00512	lmo2434	protein_coding	987419	glutamate decarboxylase(lmo2434)
CAD00514	lmo2436	protein_coding	987417	transcription antiterminator(lmo2436)
CAD00515	lmo2437	protein_coding	987416	lmo2437(lmo2437)
CAD00517	lmo2439	protein_coding	987411	lmo2439(lmo2439)
CAD00520	lmo2442	protein_coding	987407	lmo2442(lmo2442)
CAD00521	lmo2443	protein_coding	987405	lmo2443(lmo2443)
CAD00522	lmo2444	protein_coding	987402	glycosidase(lmo2444)
CAD00523	lmo2445	protein_coding	987394	internalin(lmo2445)
CAD00525	lmo2447	protein_coding	987392	transcriptional regulator(lmo2447)
CAD00526	lmo2448	protein_coding	987391	SsrA-binding protein.(smpB)
CAD00529	lmo2451	protein_coding	987386	preprotein translocase subunit SecG(secG)
CAD00531	lmo2453	protein_coding	987384	epoxide hydrolase(lmo2453)
CAD00532	lmo2454	protein_coding	987383	lmo2454(lmo2454)
CAD00539	sigL	protein_coding	987375	RNA polymerase factor sigma-54(sigL)
CAD00540	lmo2462	protein_coding	987372	dipeptidase(lmo2462)
CAD00541	lmo2463	protein_coding	987371	multidrug transporter(lmo2463)
CAD00542	lmo2464	protein_coding	987370	transcriptional regulator(lmo2464)
CAD00543	lmo2465	protein_coding	987367	lmo2465(lmo2465)
CAD00544	lmo2466	protein_coding	987366	lmo2466(lmo2466)
CAD00545	lmo2467	protein_coding	987365	chitin-binding protein(lmo2467)
CAD00547	lmo2469	protein_coding	987361	amino acid transporter(lmo2469)
CAD00549	lmo2471	protein_coding	987354	NADPH dehydrogenase(lmo2471)
CAD00550	lmo2472	protein_coding	987353	hypothetical protein(lmo2472)
CAD00556	trxB	protein_coding	987338	thioredoxin reductase(trxB)
CAD00557	lmo2479	protein_coding	987336	lmo2479(lmo2479)
CAD00561	lmo2483	protein_coding	987330	HPr kinase/phosphorylase(lmo2483)
CAD00562	lmo2484	protein_coding	987328	hypothetical protein(lmo2484)
CAD00563	lmo2485	protein_coding	987327	hypothetical protein(lmo2485)
CAD00566	uvrA	protein_coding	987320	excinuclease ABC subunit A(uvrA)
CAD00568	lmo2490	protein_coding	987317	CsbA protein(lmo2490)
CAD00569	lmo2491	protein_coding	987316	lmo2491(lmo2491)
CAD00570	lmo2492	protein_coding	987892	lmo2492(lmo2492)
CAD00571	lmo2493	protein_coding	987893	ArsR family transcriptional regulator(lmo2493)
CAD00572	lmo2494	protein_coding	987895	PhoU family transcriptional regulator(lmo2494)
CAD00573	lmo2495	protein_coding	987314	phosphate ABC transporter ATP-binding protein(lmo2495)
CAD00574	lmo2496	protein_coding	987313	phosphate ABC transporter ATP-binding protein(lmo2496)

CAD00575	lmo2497	protein_coding	987312	phosphate ABC transporter permease(lmo2497)
CAD00576	lmo2498	protein_coding	987897	phosphate ABC transporter permease(lmo2498)
CAD00577	lmo2499	protein_coding	987906	phosphate ABC transporter substrate-binding protein(lmo2499)
CAD00581	lmo2503	protein_coding	987903	cardiolipin synthase(lmo2503)
CAD00583	spl	protein_coding	987309	peptidoglycan lytic protein P45(spl)
CAD00585	ftsE	protein_coding	987308	cell division protein FtsE(ftsE)
CAD00586	lmo2508	protein_coding	984634	hypothetical protein(lmo2508)
CAD00592	lmo2514	protein_coding	985904	hypothetical protein(lmo2514)
CAD00594	lmo2516	protein_coding	987299	hypothetical protein(lmo2516)
CAD00595	lmo2517	protein_coding	987297	lmo2517(lmo2517)
CAD00599	lmo2521	protein_coding	984554	polyglycerol phosphate biosynthesis protein TagA(lmo2521)
CAD00600	lmo2522	protein_coding	987898	cell wall-binding protein(lmo2522)
CAD00602	lmo2524	protein_coding	987293	(3R)-hydroxymyristoyl-ACP dehydratase(fabZ)
CAD00603	mbl	protein_coding	986838	rod shape-determining protein MreB(mbl)
CAD00615	lmo2537	protein_coding	987487	UDP-N-acetylglucosamine 2-epimerase(lmo2537)
CAD00616	upp	protein_coding	986484	uracil phosphoribosyltransferase(upp)
CAD00618	lmo2540	protein_coding	987277	phosphatase(lmo2540)
CAD00619	lmo2541	protein_coding	986761	tRNA threonylcarbamoyladenosine biosynthesis protein(lmo2541)
CAD00620	lmo2542	protein_coding	986635	protoporphyrinogen oxidase(lmo2542)
CAD00621	prf1	protein_coding	986736	peptide chain release factor 1(prfA)
CAD00622	lmo2544	protein_coding	986601	thymidine kinase(lmo2544)
CAD00623	thrB	protein_coding	984754	homoserine kinase(thrB)
CAD00624	thrC	protein_coding	986503	threonine synthase(thrC)
CAD00625	hom	protein_coding	987269	homoserine dehydrogenase(hom)
CAD00626	rpmE	protein_coding	987268	50S ribosomal protein L31(rpmE2)
CAD00634	fbaA	protein_coding	986313	fructose-1,6-bisphosphate aldolase(fbaA)
CAD00635	lmo2557	protein_coding	987255	lipid kinase(lmo2557)
CAD00636	ami	protein_coding	987254	autolysin, amidase(ami)
CAD00637	pyrG	protein_coding	987251	CTP synthase(pyrG)
CAD00640	lmo2562	protein_coding	987249	lmo2562(lmo2562)
CAD00643	lmo2565	protein_coding	984565	hypothetical protein(lmo2565)
CAD00644	lmo2566	protein_coding	984810	lmo2566(lmo2566)
CAD00647	lmo2569	protein_coding	987245	peptide ABC transporter substrate-binding protein(lmo2569)
CAD00648	lmo2570	protein_coding	984821	lmo2570(lmo2570)
CAD00649	lmo2571	protein_coding	987244	nicotinamidase(lmo2571)
CAD00650	lmo2572	protein_coding	985849	dihydrofolate reductase subunit A(lmo2572)
CAD00651	lmo2573	protein_coding	987242	zinc-binding dehydrogenase(lmo2573)
CAD00655	lmo2577	protein_coding	987240	hypothetical protein(lmo2577)
CAD00659	lmo2581	protein_coding	985386	hypothetical protein(lmo2581)
CAD00664	lmo2586	protein_coding	987231	formate dehydrogenase subunit alpha(lmo2586)
CAD00665	lmo2587	protein_coding	987227	hypothetical protein(lmo2587)
CAD00666	lmo2588	protein_coding	987224	multidrug transporter(lmo2588)
CAD00667	lmo2589	protein_coding	987223	TetR family transcriptional regulator(lmo2589)
CAD00669	lmo2591	protein_coding	984569	N-acetylmuramoyl-L-alanine amidase(lmo2591)
CAD00670	lmo2592	protein_coding	987219	aldo/keto reductase(lmo2592)
CAD00671	lmo2593	protein_coding	987218	MerR family transcriptional regulator(lmo2593)
CAD00680	lmo2602	protein_coding	987211	hypothetical protein(lmo2602)
CAD00681	lmo2603	protein_coding	987210	lmo2603(lmo2603)

CAD00712	lmo2634	protein_coding	987178	hypothetical protein(lmo2634)
CAD00713	lmo2635	protein_coding	987177	1,4-dihydroxy-2-naphthoate octaprenyltransferase(lmo2635)
CAD00714	lmo2636	protein_coding	987176	hypothetical protein(lmo2636)
CAD00715	lmo2637	protein_coding	987175	hypothetical protein(lmo2637)
CAD00719	lmo2641	protein_coding	986303	heptaprenyl diphosphate synthase subunit II(lmo2641)
CAD00725	gcaD	protein_coding	987026	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase(glmU)
CAD00727	prfA	protein_coding	987031	listeriolysin positive regulatory protein(prfA)
CAD00729	hly	protein_coding	987033	listeriolysin O precursor(hly)
CAD00734	lmo0207	protein_coding	987038	Uncharacterized lipoprotein Lmo0207 precursor.(lmo0207)
CAD00738	ctc	protein_coding	987044	50S ribosomal protein L25(ctc)
CAD00739	lmo0212	protein_coding	987045	lmo0212(lmo0212)
CAD00740	pth	protein_coding	987046	peptidyl-tRNA hydrolase(pth)
CAD00744	lmo0217	protein_coding	987052	DivIC protein(lmo0217)
CAD00745	lmo0218	protein_coding	987053	hypothetical protein(lmo0218)
CAD00748	lmo0221	protein_coding	987060	Type III pantothenate kinase(lmo0221)
CAD00751	sul	protein_coding	987081	dihydropteroate synthases(sul)
CAD00752	folA	protein_coding	987089	dihydroneopterin aldolase(folA)
CAD00753	folK	protein_coding	987097	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase(folK)
CAD00755	lysS	protein_coding	987100	lysyl-tRNA synthetase(lysS)
CAD00758	lmo0231	protein_coding	987202	ATP:guanido phosphotransferase(lmo0231)
CAD00759	clpC	protein_coding	987203	endopeptidase Clp ATP-binding chain C(clpC)
CAD00771	lmo0244	protein_coding	987282	50S ribosomal protein L33 type II(rpmG)
CAD00772	secE	protein_coding	987283	preprotein translocase subunit SecE(secE)
CAD00773	nusG	protein_coding	987288	transcription antitermination protein NusG(nusG)
CAD00779	lmo0252	protein_coding	987321	penicilinase repressor(lmo0252)
CAD00780	lmo0253	protein_coding	987325	penicillinase antirepressor(lmo0253)
CAD00783	lmo0256	protein_coding	987337	hypothetical protein(lmo0256)
CAD00784	lmo0257	protein_coding	987339	hypothetical protein(lmo0257)
CAD00787	lmo0260	protein_coding	987345	hypothetical protein(lmo0260)
CAD00790	inlH	protein_coding	987355	internalin H(inlH)
CAD00792	lmo0265	protein_coding	987360	succinyl-diaminopimelate desuccinylase(lmo0265)
CAD00794	lmo0267	protein_coding	987388	hypothetical protein(lmo0267)
CAD00795	lmo0268	protein_coding	987396	phosphoglycerate mutase(lmo0268)
CAD00796	lmo0269	protein_coding	987397	transporter(lmo0269)
CAD00799	lmo0272	protein_coding	987400	hypothetical protein(lmo0272)
CAD00802	lmo0275	protein_coding	987414	hypothetical protein(lmo0275)
CAD00803	lmo0276	protein_coding	987415	hypothetical protein(lmo0276)
CAD00806	lmo0279	protein_coding	987434	anaerobic ribonucleoside triphosphate reductase(lmo0279)
CAD00807	lmo0280	protein_coding	987436	anaerobic ribonucleotide reductase activator protein(lmo0280)
CAD00810	lmo0283	protein_coding	987440	ABC transporter permease(lmo0283)
CAD00811	lmo0284	protein_coding	987441	ABC transporter ATP-binding protein(lmo0284)
CAD00812	lmo0285	protein_coding	987445	lipoprotein(lmo0285)
CAD00815	lmo0288	protein_coding	987449	two-component sensor histidine kinase(lmo0288)
CAD00816	lmo0289	protein_coding	987451	hypothetical protein(lmo0289)
CAD00818	lmo0291	protein_coding	987454	hypothetical protein(lmo0291)
CAD00819	lmo0292	protein_coding	987455	heat-shock protein htrA serine protease(lmo0292)
CAD00823	lmo0296	protein_coding	987461	lmo0296(lmo0296)

CAD00824	lmo0297	protein_coding	987506	transcriptional antiterminator BglG(lmo0297)
CAD00826	lmo0299	protein_coding	987508	PTS beta-glucoside transporter subunit IIB(lmo0299)
CAD00831	lmo0304	protein_coding	987515	lmo0304(lmo0304)
CAD00833	lmo0306	protein_coding	987520	lmo0306(lmo0306)
CAD00834	lmo0307	protein_coding	987521	lmo0307(lmo0307)
CAD00836	lmo0309	protein_coding	987523	hypothetical protein(lmo0309)
CAD00839	lmo0312	protein_coding	987527	hypothetical protein(lmo0312)
CAD00841	lmo0314	protein_coding	987529	hypothetical protein(lmo0314)
CAD00847	lmo0320	protein_coding	987538	peptidoglycan-bound surface protein(lmo0320)
CAD00848	lmo0321	protein_coding	987539	hypothetical protein(lmo0321)
CAD00849	lmo0322	protein_coding	987554	hypothetical protein(lmo0322)
CAD00850	lmo0323	protein_coding	987557	hypothetical protein(lmo0323)
CAD00852	lmo0325	protein_coding	987559	transcriptional regulator(lmo0325)
CAD00853	lmo0326	protein_coding	987560	transcriptional regulator(lmo0326)
CAD00865	lmo2652	protein_coding	985080	transcriptional antiterminator(lmo2652)
CAD00871	lmo2658	protein_coding	984905	acyltransferase(lmo2658)
CAD00882	lmo2669	protein_coding	987156	lmo2669(lmo2669)
CAD00883	lmo2670	protein_coding	984436	hypothetical protein(lmo2670)
CAD00884	lmo2671	protein_coding	987155	lmo2671(lmo2671)
CAD00885	lmo2672	protein_coding	987154	AraC family transcriptional regulator(lmo2672)
CAD00886	lmo2673	protein_coding	987153	hypothetical protein(lmo2673)
CAD00887	lmo2674	protein_coding	987152	ribose-5-phosphate isomerase B(lmo2674)
CAD00890	lmo2677	protein_coding	984427	esterase(lmo2677)
CAD00893	kdpC	protein_coding	987150	potassium-transporting ATPase subunit C(kdpC)
CAD00894	kdpB	protein_coding	987149	potassium-transporting ATPase subunit B(kdpB)
CAD00895	kdpA	protein_coding	987148	potassium-transporting ATPase subunit A(kdpA)
CAD00899	lmo2686	protein_coding	986869	lmo2686(lmo2686)
CAD00902	lmo2689	protein_coding	987136	magnesium-translocating P-type ATPase(lmo2689)
CAD00904	lmo2691	protein_coding	987132	autolysin(lmo2691)
CAD00908	lmo2695	protein_coding	987129	dihydroxyacetone kinase subunit DhaK(lmo2695)
CAD00909	lmo2696	protein_coding	987127	dihydroxyacetone kinase(lmo2696)
CAD00910	lmo2697	protein_coding	987124	PTS mannose transporter subunit IIA(lmo2697)
CAD00916	lmo2703	protein_coding	987117	hypothetical protein(lmo2703)
CAD00918	lmo2705	protein_coding	984440	lmo2705(lmo2705)
CAD00919	lmo2706	protein_coding	987115	lmo2706(lmo2706)
CAD00923	lmo2710	protein_coding	987111	lmo2710(lmo2710)
CAD00925	lmo2712	protein_coding	987107	gluconate kinase(lmo2712)
CAD00931	cydA	protein_coding	987099	cytochrome D ubiquinol oxidase subunit I(cydA)
CAD00934	lmo2721	protein_coding	984959	6-phosphogluconolactonase(lmo2721)
CAD00935	lmo2722	protein_coding	985237	MerR family transcripitonal regulator(lmo2722)
CAD00937	lmo2724	protein_coding	984922	hypothetical protein(lmo2724)
CAD00938	lmo2725	protein_coding	986997	hypothetical protein(lmo2725)
CAD00939	lmo2726	protein_coding	987090	MarR family transcriptional regulator(lmo2726)
CAD00946	lmo2733	protein_coding	987079	PTS fructose transporter subunit IIABC(lmo2733)
CAD00947	lmo2734	protein_coding	987078	sugar hydrolase(lmo2734)
CAD00948	lmo2735	protein_coding	987075	sucrose phosphorylase(lmo2735)
CAD00949	lmo2736	protein_coding	987073	hypothetical protein(lmo2736)
CAD00952	lmo2739	protein_coding	987067	NAD-dependent deacetylase(lmo2739)

CAD00953	lmo2740	protein_coding	985142	lmo2740(lmo2740)
CAD00954	lmo2741	protein_coding	987061	multidrug transporter(lmo2741)
CAD00955	lmo2742	protein_coding	987057	lmo2742(lmo2742)
CAD00956	lmo2743	protein_coding	987056	translaldolase(lmo2743)
CAD00957	lmo2744	protein_coding	984370	Crp/Fnr family transcriptional regulator(lmo2744)
CAD00959	lmo2746	protein_coding	987030	lmo2746(lmo2746)
CAD00961	lmo2748	protein_coding	984689	hypothetical protein(lmo2748)
CAD00966	lmo2753	protein_coding	984463	lmo2753(lmo2753)
CAD00967	lmo2754	protein_coding	986888	D-alanyl-D-alanine carboxypeptidase(lmo2754)
CAD00968	lmo2755	protein_coding	986886	CoA-transferase(lmo2755)
CAD00970	lmo2757	protein_coding	986884	ATP-dependent DNA helicase(lmo2757)
CAD00971	guaB	protein_coding	986870	inosine-monophosphate dehydrogenase(guaB)
CAD00972	lmo2759	protein_coding	986677	hypothetical protein(lmo2759)
CAD00973	lmo2760	protein_coding	986274	ABC transporter ATP-binding protein(lmo2760)
CAD00979	lmo2766	protein_coding	986816	RpiR family transcriptional regulator(lmo2766)
CAD00980	lmo2767	protein_coding	986810	lmo2767(lmo2767)
CAD00981	lmo2768	protein_coding	986273	hypothetical membrane protein(lmo2768)
CAD00982	lmo2769	protein_coding	986801	ABC transporter ATP-binding protein(lmo2769)
CAD00983	lmo2770	protein_coding	986798	bifunctional glutamate--cysteine ligase/glutathione synthetase(lmo2770)
CAD00985	lmo2772	protein_coding	986779	PTS beta-glucoside transporter subunit IIABC(lmo2772)
CAD00986	lmo2773	protein_coding	986771	transcriptional antiterminator(lmo2773)
CAD00987	lmo2774	protein_coding	986770	ABC transporter ATP-binding protein(lmo2774)
CAD00988	lmo2775	protein_coding	986174	bacteriocin transporter(lmo2775)
CAD00991	lmo2778	protein_coding	986767	lmo2778(lmo2778)
CAD00992	lmo2779	protein_coding	986766	GTP-binding protein EngD(lmo2779)
CAD00996	lmo2783	protein_coding	984856	PTS cellbiose transporter subunit IIC(lmo2783)
CAD00998	kat	protein_coding	984948	catalase(kat)
CAD01001	bvrA	protein_coding	986751	transcription antiterminator(bvrA)
CAD01007	lmo2794	protein_coding	986747	NA-binding protein Spo0J(lmo2794)
CAD01015	gidB	protein_coding	986719	16S rRNA methyltransferase GidB(gidB)
CAD01017	lmo2804	protein_coding	986717	lmo2804(lmo2804)
CAD01018	lmo2805	protein_coding	986900	hypothetical secreted protein(lmo2805)
CAD01019	lmo2806	protein_coding	985133	hypothetical secreted protein(lmo2806)
CAD01020	lmo2807	protein_coding	985340	hypothetical secreted protein(lmo2807)
CAD01024	lmo2811	protein_coding	986680	tRNA modification GTPase TrmE(trmE)
CAD01025	lmo2812	protein_coding	986678	D-alanyl-D-alanine carboxypeptidase(lmo2812)
CAD01027	lmo2814	protein_coding	986681	TetR family transcriptional regulator(lmo2814)
CAD01028	lmo2815	protein_coding	984831	3-ketoacyl-ACP reductase(fabG)
CAD01033	lmo2820	protein_coding	986657	amino-terminal domain-containing protein(lmo2820)
CAD01041	lmo2828	protein_coding	986627	lmo2828(lmo2828)
CAD01042	lmo2829	protein_coding	986896	nitroreductase(lmo2829)
CAD01044	lmo2831	protein_coding	986616	phosphoglucomutase(lmo2831)
CAD01046	lmo2833	protein_coding	986609	maltose phosphorylase(lmo2833)
CAD01047	lmo2834	protein_coding	986600	oxidoreductase(lmo2834)
CAD01048	lmo2835	protein_coding	986592	xylose isomerase(lmo2835)
CAD01049	lmo2836	protein_coding	986578	alcohol dehydrogenase(lmo2836)
CAD01052	lmo2839	protein_coding	987883	sugar ABC transporter substrate-binding protein(lmo2839)
CAD01057	lmo2844	protein_coding	986394	hypothetical protein(lmo2844)

CAD01059	lmo2846	protein_coding	986389	hypothetical protein(lmo2846)
CAD01060	lmo2847	protein_coding	986387	rhamnulose-1-phosphate aldolase(lmo2847)
CAD01061	lmo2848	protein_coding	986386	L-rhamnose isomerase(lmo2848)
CAD01065	lmo2852	protein_coding	986380	lmo2852(lmo2852)
CAD01066	lmo2853	protein_coding	986379	hypothetical protein(lmo2853)
CAD01067	lmo2854	protein_coding	986378	sporulation protein SpoJ(lmo2854)
CAD01068	rnpA	protein_coding	986374	ribonuclease P(rnpA)
CAD01069	rpmH	protein_coding	986371	50S ribosomal protein L34(rpmH)
EBG00000016610	lmo0837	pseudogene		
EBG00000016616	lmo1876	pseudogene		
EBG00000016619	lmo0410	pseudogene		
EBG00000016634	transfert RNA-Asp	tRNA		
EBG00000016636	transfert RNA-Tyr	tRNA		
EBG00000016638	transfert RNA-Glu	tRNA		
EBG00000016639	transfert RNA-Ala	tRNA		
EBG00000016642	transfert RNA-Thr	tRNA		
EBG00000016644	transfert RNA-Arg	tRNA		
EBG00000016648	transfert RNA-Val	tRNA		
EBG00000016650	rRNA-23s	rRNA		
EBG00000016653	transfert RNA-Ala	tRNA		
EBG00000016654	transfert RNA-His	tRNA		
EBG00000016656	rRNA-16s	rRNA		
EBG00000016660	transfert RNA-Thr	tRNA		
EBG00000016661	transfert RNA-Trp	tRNA		
EBG00000016663	transfert RNA-Leu	tRNA		
EBG00000016665	transfert RNA-Pro	tRNA		
EBG00000016668	transfert RNA-Gly	tRNA		
EBG00000016669	transfert RNA-Phe	tRNA		
EBG00000016671	rRNA-23s	rRNA		
EBG00000016674	transfert RNA-Gln	tRNA		
EBG00000016675	transfert RNA-Ser	tRNA		
EBG00000016676	rRNA-16s	rRNA		
EBG00000016677	transfert RNA-Glu	tRNA		
EBG00000016682	rRNA-16s	rRNA		
EBG00000016684	transfert RNA-Arg	tRNA		
EBG00000016689	transfert RNA-His	tRNA		
EBG00000016694	transfert RNA-Asp	tRNA		
EBG00000016695	rRNA-16s	rRNA		
EBG00000016696	transfert RNA-Gly	tRNA		
EBG00000016699	transfert RNA-Gly	tRNA		
EBG00000016701	rRNA-23s	rRNA		

EBG00000016702	rRNA-23s	rRNA
EBG00000016705	transfert RNA-Ala	tRNA
EBG00000016708	transfert RNA-Ser	tRNA
EBG00000016709	rRNA-23s	rRNA
EBG00000016711	rRNA-16s	rRNA
EBG00000016713	transfert RNA-Glu	tRNA
EBG00000016715	rRNA-16s	rRNA
EBG00000016717	transfert RNA-Ala	tRNA

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ENSEMBL gene id	ENSEMBL name	ENSEMBLbiotype	ENTREZ gene id	ENTREZ gene description
CAC98218	lmo0003	protein_coding	984420	hypothetical protein(lmo0003)
CAC98219	lmo0004	protein_coding	984453	hypothetical protein(lmo0004)
CAC98220	RecF	protein_coding	984623	recombination protein F(recF)
CAC98225	lmo0010	protein_coding	984924	mevalonate kinase(lmo0010)
CAC98226	lmo0011	protein_coding	984930	mevalonate diphosphate decarboxylase(lmo0011)
CAC98227	lmo0012	protein_coding	984932	mevalonate kinase(lmo0012)
CAC98231	qoxD	protein_coding	984983	quinol oxidase aa3-600 subunit IV(qoxD)
CAC98234	lmo0019	protein_coding	985005	lmo0019(lmo0019)
CAC98235	lmo0020	protein_coding	985023	GntR family transcriptional regulator(lmo0020)
CAC98236	lmo0021	protein_coding	985040	PTS fructose transporter subunit IIA(lmo0021)
CAC98237	lmo0022	protein_coding	985051	PTS fructose transporter subunit IIB(lmo0022)
CAC98238	lmo0023	protein_coding	985053	PTS fructose transporter subunit IIC(lmo0023)
CAC98239	lmo0024	protein_coding	985058	PTS mannose transporter subunit IID(lmo0024)
CAC98240	lmo0025	protein_coding	985061	phosphoheptose isomerase(lmo0025)
CAC98241	lmo0026	protein_coding	985069	copper homeostasis protein CutC(lmo0026)
CAC98242	lmo0027	protein_coding	985074	PTS beta-glucoside transporter subunit IIABC(lmo0027)
CAC98243	lmo0028	protein_coding	985088	microcin C7 self-immunity protein MccF(lmo0028)
CAC98245	lmo0030	protein_coding	985106	hypothetical protein(lmo0030)
CAC98251	lmo0036	protein_coding	985152	putrescine carbamoyltransferase(lmo0036)
CAC98252	lmo0037	protein_coding	985153	amino acid transporter(lmo0037)
CAC98253	lmo0038	protein_coding	985162	agmatine deiminase 1(lmo0038)
CAC98254	lmo0039	protein_coding	985163	carbamate kinase(lmo0039)
CAC98255	lmo0040	protein_coding	985194	agmatine deiminase(lmo0040)
CAC98256	lmo0041	protein_coding	985277	hypothetical protein(lmo0041)
CAC98258	lmo0043	protein_coding	985417	arginine deiminase(lmo0043)
CAC98259	rpsF	protein_coding	985454	30S ribosomal protein S6(rpsF)
CAC98260	ssb	protein_coding	985468	single-strand binding protein(ssb)
CAC98261	rpsR	protein_coding	985537	30S ribosomal protein S18(rpsR)
CAC98262	lmo0047	protein_coding	985583	lmo0047(lmo0047)
CAC98263	lmo0048	protein_coding	985598	sensor histidine kinase AgrB(lmo0048)
CAC98265	lmo0050	protein_coding	985694	histidine kinase(lmo0050)
CAC98266	lmo0051	protein_coding	985847	response regulator(lmo0051)
CAC98268	rplI	protein_coding	986067	50S ribosomal protein L9(rplI)
CAC98270	purA	protein_coding	986069	adenylosuccinate synthetase(purA)
CAC98292	lmo0077	protein_coding	986552	hypothetical protein(lmo0077)
CAC98293	lmo0078	protein_coding	986565	phosphoglycerate dehydrogenase(lmo0078)
CAC98295	lmo0080	protein_coding	986576	lmo0080(lmo0080)
CAC98296	lmo0081	protein_coding	986577	lmo0081(lmo0081)
CAC98297	lmo0082	protein_coding	986579	lmo0082(lmo0082)
CAC98302	lmo0087	protein_coding	986585	lmo0087(lmo0087)
CAC98304	lmo0089	protein_coding	986587	ATP synthase subunit delta(lmo0089)
CAC98305	lmo0090	protein_coding	986589	ATP synthase F0F1 subunit alpha(lmo0090)
CAC98306	lmo0091	protein_coding	986593	ATP synthase subunit gamma(lmo0091)
CAC98307	lmo0092	protein_coding	986598	ATP synthase F0F1 subunit beta(lmo0092)
CAC98311	lmo0096	protein_coding	986611	PTS mannose transporter subunit IIAB(lmo0096)

CAC98313	lmo0098	protein_coding	986620	PTS mannose transporter subunit IID(lmo0098)
CAC98314	lmo0099	protein_coding	986621	lmo0099(lmo0099)
CAC98315	lmo0100	protein_coding	986623	lmo0100(lmo0100)
CAC98320	lmo0105	protein_coding	986634	chitinase B(lmo0105)
CAC98321	lmo0106	protein_coding	986639	transcriptional regulator(lmo0106)
CAC98322	lmo0107	protein_coding	986644	ABC transporter ATP-binding protein(lmo0107)
CAC98323	lmo0108	protein_coding	986645	ABC transporter ATP-binding protein(lmo0108)
CAC98324	lmo0109	protein_coding	986650	AraC family transcriptional regulator(lmo0109)
CAC98325	lmo0110	protein_coding	986652	lipase(lmo0110)
CAC98328	lmo0113	protein_coding	986656	hypothetical protein(lmo0113)
CAC98329	lmo0114	protein_coding	986659	repressor C1(lmo0114)
CAC98330	lmaD	protein_coding	986665	hypothetical protein(lmaD)
CAC98336	lmo0121	protein_coding	986683	phage tail protein(lmo0121)
CAC98344	lmo0129	protein_coding	986713	N-acetylmuramoyl-L-alanine amidase(lmo0129)
CAC98345	lmo0130	protein_coding	986721	5'-nucleotidase(lmo0130)
CAC98347	lmo0132	protein_coding	986732	inosine 5-monophosphate dehydrogenase(lmo0132)
CAC98348	lmo0133	protein_coding	986735	hypothetical protein(lmo0133)
CAC98349	lmo0134	protein_coding	986737	hypothetical protein(lmo0134)
CAC98355	lmo0140	protein_coding	986783	lmo0140(lmo0140)
CAC98357	lmo0142	protein_coding	986788	lmo0142(lmo0142)
CAC98368	lmo0153	protein_coding	986823	zinc ABC transporter substrate-binding protein(lmo0153)
CAC98369	lmo0154	protein_coding	986826	zinc ABC transporter ATP-binding protein(lmo0154)
CAC98370	lmo0155	protein_coding	986832	zinc ABC transporter permease(lmo0155)
CAC98376	lmo0161	protein_coding	986851	lmo0161(lmo0161)
CAC98377	lmo0162	protein_coding	986854	DNA polymerase III subunit delta'(lmo0162)
CAC98378	lmo0163	protein_coding	986862	lmo0163(lmo0163)
CAC98379	lmo0164	protein_coding	986868	DNA replication intiation control protein YabA(lmo0164)
CAC98380	lmo0165	protein_coding	986872	hypothetical protein(lmo0165)
CAC98382	lmo0167	protein_coding	986880	hypothetical protein(lmo0167)
CAC98384	lmo0169	protein_coding	986890	glucose transporter(lmo0169)
CAC98385	lmo0170	protein_coding	986891	lmo0170(lmo0170)
CAC98391	lmo0176	protein_coding	986935	glucose transporter(lmo0176)
CAC98392	metS	protein_coding	986940	methionyl-tRNA synthetase(metS)
CAC98393	lmo0178	protein_coding	986964	xylose repressor(lmo0178)
CAC98401	lmo0186	protein_coding	987011	hypothetical protein(lmo0186)
CAC98402	lmo0187	protein_coding	987012	hypothetical protein(lmo0187)
CAC98403	ksgA	protein_coding	987014	dimethyladenosine transferase(ksgA)
CAC98407	lmo0192	protein_coding	987018	PurR family transcriptional regulator(lmo0192)
CAC98408	lmo0193	protein_coding	987019	lmo0193(lmo0193)
CAC98410	lmo0195	protein_coding	987022	ABC transporter permease(lmo0195)
CAC98415	lmo0336	protein_coding	987572	lmo0336(lmo0336)
CAC98417	lmo0338	protein_coding	987576	lmo0338(lmo0338)
CAC98418	lmo0339	protein_coding	987577	hypothetical protein(lmo0339)
CAC98419	lmo0340	protein_coding	987578	lmo0340(lmo0340)
CAC98420	lmo0341	protein_coding	987581	lmo0341(lmo0341)
CAC98422	lmo0343	protein_coding	987583	translaldolase(lmo0343)
CAC98423	lmo0344	protein_coding	987585	short chain dehydrogenase(lmo0344)
CAC98424	lmo0345	protein_coding	987586	sugar-phosphate isomerase(lmo0345)

CAC98425	lmo0346	protein_coding	987587	triosephosphate isomerase(lmo0346)
CAC98427	lmo0348	protein_coding	987591	dihydroxyacetone kinase(lmo0348)
CAC98428	lmo0349	protein_coding	987592	lmo0349(lmo0349)
CAC98429	lmo0350	protein_coding	987593	lmo0350(lmo0350)
CAC98431	lmo0352	protein_coding	987595	DeoR family transcriptional regulator(lmo0352)
CAC98432	lmo0353	protein_coding	987596	hypothetical protein(lmo0353)
CAC98433	lmo0354	protein_coding	987600	fatty-acid--CoA ligase(lmo0354)
CAC98434	lmo0355	protein_coding	987602	fumarate reductase subunit A(lmo0355)
CAC98435	lmo0356	protein_coding	987603	oxidoreductase(lmo0356)
CAC98436	lmo0357	protein_coding	987604	PTS sugar transporter subunit IIA(lmo0357)
CAC98438	lmo0359	protein_coding	987607	D-fructose-1,6-biphosphate aldolase(lmo0359)
CAC98439	lmo0360	protein_coding	987608	DeoR family transcriptional regulator(lmo0360)
CAC98440	lmo0361	protein_coding	987609	membrane protein(lmo0361)
CAC98441	lmo0362	protein_coding	987610	hypothetical protein(lmo0362)
CAC98444	lmo0365	protein_coding	987614	hypothetical protein(lmo0365)
CAC98445	lmo0366	protein_coding	987616	hypothetical protein(lmo0366)
CAC98446	lmo0367	protein_coding	987617	hypothetical protein(lmo0367)
CAC98447	lmo0368	protein_coding	987618	hypothetical protein(lmo0368)
CAC98448	lmo0369	protein_coding	987619	hypothetical protein(lmo0369)
CAC98455	lmo0376	protein_coding	987632	transcriptional regulator(lmo0376)
CAC98461	lmo0382	protein_coding	987638	transcriptional regulator(lmo0382)
CAC98462	lmo0383	protein_coding	987639	methylmalonate-semialdehyde dehydrogenase(lmo0383)
CAC98464	lmo0385	protein_coding	987641	IolC protein(lmo0385)
CAC98465	lmo0386	protein_coding	987642	IolD protein(lmo0386)
CAC98466	lmo0387	protein_coding	987643	hypothetical protein(lmo0387)
CAC98468	ltrA	protein_coding	987647	low temperature requirement protein A(ltrA)
CAC98475	lmo0396	protein_coding	987655	pyrroline-5-carboxylate reductase(proC)
CAC98476	lmo0397	protein_coding	987657	hypothetical protein(lmo0397)
CAC98477	lmo0398	protein_coding	987659	PTS sugar transporter subunit IIA(lmo0398)
CAC98478	lmo0399	protein_coding	987673	PTS fructose transporter subunit IIB(lmo0399)
CAC98479	lmo0400	protein_coding	987677	PTS fructose transporter subunit IIC(lmo0400)
CAC98480	lmo0401	protein_coding	987679	alpha-mannosidase(lmo0401)
CAC98482	lmo0403	protein_coding	987752	lmo0403(lmo0403)
CAC98483	lmo0404	protein_coding	987761	lmo0404(lmo0404)
CAC98484	lmo0405	protein_coding	987767	phosphate transporter(lmo0405)
CAC98485	lmo0406	protein_coding	987775	hypothetical protein(lmo0406)
CAC98486	lmo0407	protein_coding	987777	lmo0407(lmo0407)
CAC98487	lmo0408	protein_coding	987782	lmo0408(lmo0408)
CAC98488	lmo0409	protein_coding	987787	internalin(lmo0409)
CAC98490	lmo0411	protein_coding	987794	phosphoenolpyruvate synthase(lmo0411)
CAC98491	lmo0412	protein_coding	987812	lmo0412(lmo0412)
CAC98493	lmo0414	protein_coding	987822	hypothetical protein(lmo0414)
CAC98494	lmo0415	protein_coding	987823	endo-1,4-beta-xylanase(lmo0415)
CAC98500	lmo0421	protein_coding	987848	rod shape-determining protein RodA(lmo0421)
CAC98512	inlA	protein_coding	985151	internalin A(inlA)
CAC98513	inlB	protein_coding	986892	internalin B(inlB)
CAC98514	lmo0435	protein_coding	985154	peptidoglycan binding protein(lmo0435)
CAC98518	lmo0439	protein_coding	985164	hypothetical protein(lmo0439)

CAC98520	lmo0441	protein_coding	985168	D-alanyl-D-alanine carboxypeptidase(lmo0441)
CAC98523	lmo0444	protein_coding	985173	hypothetical protein(lmo0444)
CAC98524	lmo0445	protein_coding	985175	transcripitonal regulator(lmo0445)
CAC98528	lmo0449	protein_coding	985180	lmo0449(lmo0449)
CAC98529	lmo0450	protein_coding	985181	hypothetical protein(lmo0450)
CAC98531	lmo0452	protein_coding	985178	hypothetical protein(lmo0452)
CAC98532	lmo0453	protein_coding	985179	hypothetical protein(lmo0453)
CAC98533	lmo0454	protein_coding	985184	hypothetical protein(lmo0454)
CAC98534	lmo0455	protein_coding	985188	hypothetical protein(lmo0455)
CAC98538	lmo0459	protein_coding	985370	transcriptional regulator(lmo0459)
CAC98541	lmo0462	protein_coding	985196	lmo0462(lmo0462)
CAC98543	lmo0464	protein_coding	985200	transposase(lmo0464)
CAC98545	lmo0466	protein_coding	985199	lmo0466(lmo0466)
CAC98546	lmo0467	protein_coding	985201	lmo0467(lmo0467)
CAC98551	lmo0472	protein_coding	985207	lmo0472(lmo0472)
CAC98553	lmo0474	protein_coding	985208	lmo0474(lmo0474)
CAC98556	lmo0477	protein_coding	985893	secreted protein(lmo0477)
CAC98557	lmo0478	protein_coding	985211	secreted protein(lmo0478)
CAC98558	lmo0479	protein_coding	985210	secreted protein(lmo0479)
CAC98559	lmo0480	protein_coding	985214	transcriptional regulator(lmo0480)
CAC98561	lmo0482	protein_coding	986229	ribosomal RNA large subunit methyltransferase N(lmo0482)
CAC98562	lmo0483	protein_coding	985216	lmo0483(lmo0483)
CAC98573	lmo0494	protein_coding	985230	hypothetical protein(lmo0494)
CAC98574	lmo0495	protein_coding	985247	hypothetical protein(lmo0495)
CAC98575	lmo0496	protein_coding	984435	hypothetical protein(lmo0496)
CAC98580	lmo0501	protein_coding	985244	transcriptional antiterminator BglG(lmo0501)
CAC98588	prs	protein_coding	985257	phosphoribosyl pyrophosphate synthetase(prs)
CAC98594	lmo0515	protein_coding	986558	hypothetical protein(lmo0515)
CAC98596	lmo0517	protein_coding	985270	phosphoglycerate mutase(lmo0517)
CAC98598	lmo0519	protein_coding	985272	multidrug resistance protein(lmo0519)
CAC98599	lmo0520	protein_coding	985284	transcriptional regulator(lmo0520)
CAC98600	lmo0521	protein_coding	985300	6-phospho-beta-glucosidase(lmo0521)
CAC98602	lmo0523	protein_coding	985275	hypothetical protein(lmo0523)
CAC98603	lmo0524	protein_coding	985278	sulfate transporter(lmo0524)
CAC98612	lmo0533	protein_coding	985302	hypothetical protein(lmo0533)
CAC98613	lmo0534	protein_coding	985301	hypothetical protein(lmo0534)
CAC98618	lmo0539	protein_coding	985316	tagatose 1,6-diphosphate aldolase(lmo0539)
CAC98619	lmo0540	protein_coding	985229	penicillin-binding protein(lmo0540)
CAC98620	lmo0541	protein_coding	986277	ABC transporter substrate-binding protein(lmo0541)
CAC98622	lmo0543	protein_coding	984396	PTS sorbitol transporter subunit IIBC(lmo0543)
CAC98625	lmo0546	protein_coding	985462	NAD(P)-dependent oxidoreductase(lmo0546)
CAC98626	lmo0547	protein_coding	984998	DeoR family transcriptional regulator(lmo0547)
CAC98628	lmo0549	protein_coding	984412	internalin(lmo0549)
CAC98630	lmo0551	protein_coding	984417	lmo0551(lmo0551)
CAC98631	lmo0552	protein_coding	986885	hypothetical protein(lmo0552)
CAC98632	lmo0553	protein_coding	984712	lmo0553(lmo0553)
CAC98633	lmo0554	protein_coding	984446	NADH-dependent butanol dehydrogenase(lmo0554)
CAC98634	lmo0555	protein_coding	984577	di-tripeptide transporter(lmo0555)

CAC98636	lmo0557	protein_coding	984617	phosphoglycerate mutase(lmo0557)
CAC98639	lmo0560	protein_coding	986813	glutamate dehydrogenase(lmo0560)
CAC98651	lmo0572	protein_coding	986053	lmo0572(lmo0572)
CAC98652	lmo0573	protein_coding	985853	hypothetical protein(lmo0573)
CAC98653	lmo0574	protein_coding	984589	beta-glucosidase(lmo0574)
CAC98654	lmo0575	protein_coding	986339	GntR family transcriptional regulator(lmo0575)
CAC98656	lmo0577	protein_coding	984939	lmo0577(lmo0577)
CAC98657	lmo0578	protein_coding	984630	hypothetical protein(lmo0578)
CAC98658	lmo0579	protein_coding	986865	hypothetical protein(lmo0579)
CAC98659	lmo0580	protein_coding	986638	hypothetical protein(lmo0580)
CAC98660	lmo0581	protein_coding	984637	hypothetical protein(lmo0581)
CAC98663	lmo0584	protein_coding	984661	hypothetical protein(lmo0584)
CAC98666	lmo0587	protein_coding	986515	secreted protein(lmo0587)
CAC98667	lmo0588	protein_coding	984699	DNA photolyase(lmo0588)
CAC98668	lmo0589	protein_coding	985047	lmo0589(lmo0589)
CAC98669	lmo0590	protein_coding	985311	hypothetical protein(lmo0590)
CAC98670	lmo0591	protein_coding	984755	hypothetical protein(lmo0591)
CAC98671	lmo0592	protein_coding	986217	lmo0592(lmo0592)
CAC98672	lmo0593	protein_coding	984793	formate transporter(lmo0593)
CAC98674	lmo0595	protein_coding	984789	O-acetylhomoserine sulfhydrylase(lmo0595)
CAC98675	lmo0596	protein_coding	985266	hypothetical protein(lmo0596)
CAC98678	lmo0600	protein_coding	985344	lmo0600(lmo0600)
CAC98679	lmo0601	protein_coding	984830	cell surface protein(lmo0601)
CAC98680	lmo0602	protein_coding	984599	transcripitonal regulator(lmo0602)
CAC98682	lmo0604	protein_coding	985855	hypothetical protein(lmo0604)
CAC98683	lmo0605	protein_coding	985094	hypothetical protein(lmo0605)
CAC98684	lmo0606	protein_coding	985290	MarR family transcriptional regulator(lmo0606)
CAC98685	lmo0607	protein_coding	985501	ABC transporter ATP-binding protein(lmo0607)
CAC98686	lmo0608	protein_coding	984780	ABC transporter ATP-binding protein(lmo0608)
CAC98688	lmo0610	protein_coding	985509	internalin(lmo0610)
CAC98690	lmo0612	protein_coding	984912	MarR family transcriptional evidence(lmo0612)
CAC98691	lmo0613	protein_coding	987413	oxidoreductase(lmo0613)
CAC98693	lmo0615	protein_coding	984917	lmo0615(lmo0615)
CAC98702	lmo0624	protein_coding	985292	hypothetical protein(lmo0624)
CAC98703	lmo0625	protein_coding	985881	lmo0625(lmo0625)
CAC98704	lmo0626	protein_coding	985506	hypothetical protein(lmo0626)
CAC98705	lmo0627	protein_coding	984956	pepdidoglycan bound protein(lmo0627)
CAC98706	lmo0628	protein_coding	984963	lmo0628(lmo0628)
CAC98707	lmo0629	protein_coding	984966	lmo0629(lmo0629)
CAC98713	lmo0635	protein_coding	984974	lmo0635(lmo0635)
CAC98715	lmo0637	protein_coding	984971	hypothetical protein(lmo0637)
CAC98717	lmo0639	protein_coding	984972	transcripitonal regulator(lmo0639)
CAC98718	lmo0640	protein_coding	987093	oxidoreductase(lmo0640)
CAC98720	lmo0642	protein_coding	984976	lmo0642(lmo0642)
CAC98721	lmo0643	protein_coding	984977	transaldolase(lmo0643)
CAC98723	lmo0645	protein_coding	984978	amino acid transporter(lmo0645)
CAC98724	lmo0646	protein_coding	984982	hypothetical protein(lmo0646)
CAC98725	lmo0647	protein_coding	985414	lmo0647(lmo0647)

CAC98726	lmo0648	protein_coding	987051	hypothetical protein(lmo0648)
CAC98727	lmo0649	protein_coding	986557	transcriptional regulator(lmo0649)
CAC98728	lmo0650	protein_coding	984986	hypothetical protein(lmo0650)
CAC98729	lmo0651	protein_coding	984985	transcriptional regulator(lmo0651)
CAC98731	lmo0653	protein_coding	985279	lmo0653(lmo0653)
CAC98732	lmo0654	protein_coding	984989	lmo0654(lmo0654)
CAC98733	lmo0655	protein_coding	984992	phosphoprotein phosphatase(lmo0655)
CAC98735	lmo0657	protein_coding	985003	lmo0657(lmo0657)
CAC98736	lmo0658	protein_coding	985006	hypothetical protein(lmo0658)
CAC98738	lmo0660	protein_coding	985017	transposase(lmo0660)
CAC98747	lmo0669	protein_coding	987147	oxidoreductase(lmo0669)
CAC98748	lmo0670	protein_coding	985009	lmo0670(lmo0670)
CAC98752	lmo0674	protein_coding	985015	lmo0674(lmo0674)
CAC98753	lmo0675	protein_coding	987142	lmo0675(lmo0675)
CAC98754	lmo0676	protein_coding	985021	flagellar biosynthesis protein FliP(fliP)
CAC98755	lmo0677	protein_coding	985022	flagellar biosynthesis protein FliQ(fliQ)
CAC98756	lmo0678	protein_coding	985024	flagellar biosynthesis protein FliR(fliR)
CAC98757	lmo0679	protein_coding	986322	flagellar biosynthesis protein FlhB(flhB)
CAC98758	lmo0680	protein_coding	986323	flagellar biosynthesis protein FlhA(flhA)
CAC98759	lmo0681	protein_coding	985019	flagellar biosynthesis regulator FlhF(lmo0681)
CAC98760	lmo0682	protein_coding	985030	flagellar basal body rod protein FlgG(flgG)
CAC98761	lmo0683	protein_coding	985031	chemotaxis protein CheR(lmo0683)
CAC98762	lmo0684	protein_coding	985027	lmo0684(lmo0684)
CAC98763	lmo0685	protein_coding	985036	flagellar motor protein MotA(lmo0685)
CAC98764	motB	protein_coding	986861	flagellar motor rotation MotB(motB)
CAC98765	lmo0687	protein_coding	985029	lmo0687(lmo0687)
CAC98766	lmo0688	protein_coding	986281	hypothetical protein(lmo0688)
CAC98767	lmo0689	protein_coding	987162	chemotaxis protein CheV(lmo0689)
CAC98768	flaA	protein_coding	987167	flagellin(flaA)
CAC98769	cheY	protein_coding	985049	chemotaxis response regulator CheY(cheY)
CAC98770	cheA	protein_coding	985032	two-component sensor histidine kinase CheA(cheA)
CAC98771	lmo0693	protein_coding	985035	flagellar motor switch protein FliY(lmo0693)
CAC98772	lmo0694	protein_coding	985033	lmo0694(lmo0694)
CAC98773	lmo0695	protein_coding	985037	lmo0695(lmo0695)
CAC98774	lmo0696	protein_coding	985038	flagellar basal body rod modification protein(flgD)
CAC98775	lmo0697	protein_coding	985043	flagellar hook protein FlgE(flgE)
CAC98776	lmo0698	protein_coding	985039	flagellar motor switch protein(lmo0698)
CAC98777	lmo0699	protein_coding	987173	flagellar motor switch protein FliM(fliM)
CAC98778	lmo0700	protein_coding	985046	flagellar motor switch protein FliY(lmo0700)
CAC98779	lmo0701	protein_coding	985048	lmo0701(lmo0701)
CAC98780	lmo0702	protein_coding	985034	lmo0702(lmo0702)
CAC98781	lmo0703	protein_coding	985050	lmo0703(lmo0703)
CAC98782	lmo0704	protein_coding	985042	lmo0704(lmo0704)
CAC98783	lmo0705	protein_coding	985054	flagellar hook-associated protein FlgK(flgK)
CAC98784	lmo0706	protein_coding	985052	flagellar hook-associated protein FlgL(flgL)
CAC98785	lmo0707	protein_coding	985041	flagellar capping protein FliD(fliD)
CAC98786	lmo0708	protein_coding	985045	flagellar protein(lmo0708)
CAC98787	lmo0709	protein_coding	985079	lmo0709(lmo0709)

CAC98788	lmo0710	protein_coding	985059	flagellar basal-body rod protein FlgB(flgB)
CAC98789	lmo0711	protein_coding	984818	flagellar basal body rod protein FlgC(flgC)
CAC98790	lmo0712	protein_coding	985062	flagellar hook-basal body protein FliE(fliE)
CAC98791	lmo0713	protein_coding	985064	flagellar MS-ring protein FliF(fliF)
CAC98792	lmo0714	protein_coding	985067	flagellar motor switch protein FliG(fliG)
CAC98793	lmo0715	protein_coding	985068	lmo0715(fliH)
CAC98794	lmo0716	protein_coding	985071	flagellum-specific ATP synthase(fliI)
CAC98795	lmo0717	protein_coding	987208	transglycosylase(lmo0717)
CAC98796	lmo0718	protein_coding	985076	lmo0718(lmo0718)
CAC98797	lmo0719	protein_coding	985078	hypothetical protein(lmo0719)
CAC98798	lmo0720	protein_coding	985065	lmo0720(lmo0720)
CAC98800	lmo0722	protein_coding	986726	pyruvate oxidase(lmo0722)
CAC98801	lmo0723	protein_coding	986712	metyl-accepting chemotaxis protein(lmo0723)
CAC98802	lmo0724	protein_coding	986702	hypothetical protein(lmo0724)
CAC98806	lmo0728	protein_coding	986299	riboflavin kinase / FAD synthase(lmo0728)
CAC98809	lmo0731	protein_coding	986215	lmo0731(lmo0731)
CAC98810	lmo0732	protein_coding	985958	peptidoglycan binding protein(lmo0732)
CAC98811	lmo0733	protein_coding	985919	transcriptional regulator(lmo0733)
CAC98812	lmo0734	protein_coding	985863	LacI family transcriptional regulator(lmo0734)
CAC98813	lmo0735	protein_coding	985578	ribulose-5-phosphate 3-epimerase(lmo0735)
CAC98814	lmo0736	protein_coding	985545	ribose-5-phosphate isomerase B(lmo0736)
CAC98815	lmo0737	protein_coding	985544	lmo0737(lmo0737)
CAC98816	lmo0738	protein_coding	985543	PTS beta-glucoside transporter subunit IIABC(lmo0738)
CAC98817	lmo0739	protein_coding	985542	6-phospho-beta-glucosidase(lmo0739)
CAC98824	lmo0746	protein_coding	985530	hypothetical protein(lmo0746)
CAC98825	lmo0747	protein_coding	985529	lmo0747(lmo0747)
CAC98833	lmo0755	protein_coding	985516	hypothetical protein(lmo0755)
CAC98834	lmo0756	protein_coding	985514	ABC transporter ATP-binding protein(lmo0756)
CAC98835	lmo0757	protein_coding	985511	hypothetical protein(lmo0757)
CAC98836	lmo0758	protein_coding	985508	lmo0758(lmo0758)
CAC98837	lmo0759	protein_coding	985503	lmo0759(lmo0759)
CAC98838	lmo0760	protein_coding	985499	lmo0760(lmo0760)
CAC98839	lmo0761	protein_coding	985498	hypothetical protein(lmo0761)
CAC98840	lmo0762	protein_coding	985496	ATP/GTP-binding protein(lmo0762)
CAC98848	lmo0770	protein_coding	985481	LacI family transcriptional regulator(lmo0770)
CAC98851	lmo0773	protein_coding	985473	alcohol dehydrogenase(lmo0773)
CAC98853	lmo0775	protein_coding	985469	lmo0775(lmo0775)
CAC98855	lmo0777	protein_coding	985466	lmo0777(lmo0777)
CAC98856	lmo0778	protein_coding	985465	lmo0778(lmo0778)
CAC98858	lmo0780	protein_coding	985461	lmo0780(lmo0780)
CAC98859	lmo0781	protein_coding	985460	PTS mannose transporter subunit IID(lmo0781)
CAC98860	lmo0782	protein_coding	985459	PTS mannose transporter subunit IIC(lmo0782)
CAC98861	lmo0783	protein_coding	985458	PTS mannose transporter subunit IIB(lmo0783)
CAC98862	lmo0784	protein_coding	985456	PTS mannose transporter subunit IIB(lmo0784)
CAC98867	lmo0789	protein_coding	985444	hypothetical protein(lmo0789)
CAC98871	lmo0793	protein_coding	985432	hypothetical protein(lmo0793)
CAC98872	lmo0794	protein_coding	985430	hypothetical protein(lmo0794)
CAC98874	lmo0796	protein_coding	985428	hypothetical protein(lmo0796)

CAC98877	lmo0799	protein_coding	985420	lmo0799(lmo0799)
CAC98878	lmo0800	protein_coding	985418	hypothetical protein(lmo0800)
CAC98880	lmo0802	protein_coding	985413	hypothetical protein(lmo0802)
CAC98881	lmo0803	protein_coding	985412	Na+/H+ antiporter(lmo0803)
CAC98884	lmo0806	protein_coding	985404	transcriptional regulator(lmo0806)
CAC98885	lmo0807	protein_coding	985403	spermidine/putrescine ABC transporter ATP-binding protein(lmo0807)
CAC98886	lmo0808	protein_coding	985401	spermidine/putrescine ABC transporter permease(lmo0808)
CAC98888	lmo0810	protein_coding	985395	spermidine/putrescine ABC transporter substrate-binding protein(lmo0810)
CAC98890	lmo0812	protein_coding	985393	lmo0812(lmo0812)
CAC98892	lmo0814	protein_coding	985391	oxidoreductase(lmo0814)
CAC98896	lmo0818	protein_coding	985383	cation-transporting ATPase(lmo0818)
CAC98897	lmo0819	protein_coding	985382	lmo0819(lmo0819)
CAC98898	lmo0820	protein_coding	985380	acetyltransferase(lmo0820)
CAC98900	lmo0822	protein_coding	985376	transcriptional regulator(lmo0822)
CAC98902	lmo0824	protein_coding	985373	lmo0824(lmo0824)
CAC98903	lmo0825	protein_coding	985372	3-hydroxy-3-methylglutaryl-CoA reductase(lmo0825)
CAC98904	lmo0826	protein_coding	985369	transporter(lmo0826)
CAC98907	nifJ	protein_coding	985364	pyruvate-flavodoxin oxidoreductase(nifJ)
CAC98908	fbp	protein_coding	985361	fructose-1,6-bisphosphatase(fbp)
CAC98909	lmo0831	protein_coding	985359	lmo0831(lmo0831)
CAC98910	lmo0832	protein_coding	985355	transposase(lmo0832)
CAC98911	lmo0833	protein_coding	985354	transcriptional regulator(lmo0833)
CAC98912	lmo0834	protein_coding	985353	lmo0834(lmo0834)
CAC98913	lmo0835	protein_coding	985352	peptidoglycan binding protein(lmo0835)
CAC98920	lmo0842	protein_coding	985337	peptidoglycan binding protein(lmo0842)
CAC98921	lmo0843	protein_coding	985333	hypothetical protein(lmo0843)
CAC98924	lmo0846	protein_coding	985329	excinuclease ABC subunit C(lmo0846)
CAC98925	lmo0847	protein_coding	985328	glutamine ABC transporter(lmo0847)
CAC98926	lmo0848	protein_coding	985325	amino acid ABC transporter ATP-binding protein(lmo0848)
CAC98928	lmo0850	protein_coding	985319	hypothetical protein(lmo0850)
CAC98929	lmo0851	protein_coding	985315	lmo0851(lmo0851)
CAC98931	lmo0853	protein_coding	985304	SugE protein(lmo0853)
CAC98933	ddlA	protein_coding	985238	D-alanyl-alanine synthetase A(ddl)
CAC98934	murF	protein_coding	985224	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diamino pimelate-D-alanyl-D-alanyl ligase(murF)
CAC98935	lmo0857	protein_coding	985170	carboxylesterase(lmo0857)
CAC98936	lmo0858	protein_coding	985100	LacI family transcriptional regulator(lmo0858)
CAC98937	lmo0859	protein_coding	985026	sugar ABC transporter substrate-binding protein(lmo0859)
CAC98944	lmo0866	protein_coding	984613	ATP-dependent RNA helicase(lmo0866)
CAC98945	lmo0867	protein_coding	984585	lmo0867(lmo0867)
CAC98946	lmo0868	protein_coding	984573	lmo0868(lmo0868)
CAC98947	lmo0869	protein_coding	984542	lmo0869(lmo0869)
CAC98948	lmo0870	protein_coding	984493	lmo0870(lmo0870)
CAC98949	lmo0871	protein_coding	984472	hypothetical protein(lmo0871)
CAC98950	lmo0872	protein_coding	984428	antibiotic resistance protein(lmo0872)
CAC98958	lmo0880	protein_coding	986636	wall associated protein precursor(lmo0880)
CAC98960	lmo0882	protein_coding	986548	hypothetical protein(lmo0882)
CAC98961	lmo0883	protein_coding	986544	hypothetical protein(lmo0883)

CAC98962	lmo0884	protein_coding	986422	protoporphyrinogen oxidase(lmo0884)
CAC98963	lmo0885	protein_coding	986540	4'-phosphopantetheinyl transferase(acpS)
CAC98966	lmo0888	protein_coding	986538	hypothetical protein(lmo0888)
CAC98968	rsbS	protein_coding	985149	negative regulation of sigma-B activity(rsbS)
CAC98970	rsbU	protein_coding	986534	serine phosphatase(rsbU)
CAC98971	rsbV	protein_coding	986526	anti-anti-sigma factor (antagonist of RsbW)(rsbV)
CAC98974	rsbX	protein_coding	986520	indirect negative regulation of sigma B dependant gene expression (serine phosphatase)(rsbX)
CAC98975	lmo0897	protein_coding	984941	transporter(lmo0897)
CAC98977	lmo0899	protein_coding	987820	hypothetical protein(lmo0899)
CAC98980	lmo0902	protein_coding	986980	GntR family transcriptional regulator(lmo0902)
CAC98982	lmo0904	protein_coding	986917	lmo0904(lmo0904)
CAC98983	lmo0905	protein_coding	986916	lmo0905(lmo0905)
CAC98988	lmo0910	protein_coding	984497	lmo0910(lmo0910)
CAC98989	lmo0911	protein_coding	986500	lmo0911(lmo0911)
CAC98990	lmo0912	protein_coding	986984	formate transporter(lmo0912)
CAC98991	lmo0913	protein_coding	986938	succinate semialdehyde dehydrogenase(lmo0913)
CAC98992	lmo0914	protein_coding	987760	PTS sugar transporter subunit IIB(lmo0914)
CAC98993	lmo0915	protein_coding	987872	PTS sugar transporter subunit IIC(lmo0915)
CAC98994	lmo0916	protein_coding	987774	PTS sugar transporter subunit IIA(lmo0916)
CAC98995	lmo0917	protein_coding	987667	beta-glucosidase(lmo0917)
CAC98996	lmo0918	protein_coding	987658	transcription antiterminator BglG(lmo0918)
CAC98997	lmo0919	protein_coding	986830	antibiotic ABC transporter ATP-binding protein(lmo0919)
CAC98999	lmo0921	protein_coding	986853	hypothetical protein(lmo0921)
CAC99000	lmo0922	protein_coding	986345	pantothenate kinase(lmo0922)
CAC99006	lmo0928	protein_coding	985312	3-methyladenine DNA glycosylase(lmo0928)
CAC99007	lmo0929	protein_coding	986837	sortase(lmo0929)
CAC99008	lmo0930	protein_coding	986560	hypothetical protein(lmo0930)
CAC99010	lmo0932	protein_coding	987846	hypothetical protein(lmo0932)
CAC99012	lmo0934	protein_coding	986642	hypothetical protein(lmo0934)
CAC99013	lmo0935	protein_coding	986554	rRNA methylase(lmo0935)
CAC99014	lmo0936	protein_coding	986658	nitroflavin reductase(lmo0936)
CAC99015	lmo0937	protein_coding	987860	lmo0937(lmo0937)
CAC99021	fri	protein_coding	986847	non-heme iron-binding ferritin(fri)
CAC99022	lmo0944	protein_coding	986825	hypothetical protein(lmo0944)
CAC99031	lmo0953	protein_coding	986396	lmo0953(lmo0953)
CAC99032	lmo0954	protein_coding	986596	lmo0954(lmo0954)
CAC99033	lmo0955	protein_coding	987852	lmo0955(lmo0955)
CAC99034	lmo0956	protein_coding	986776	N-acetylglucosamine-6P-phosphate deacetylase(lmo0956)
CAC99035	lmo0957	protein_coding	986480	glucosamine-6-phosphate isomerase(lmo0957)
CAC99036	lmo0958	protein_coding	986478	GntR family transcirptional regulator(lmo0958)
CAC99038	lmo0960	protein_coding	986469	protease(lmo0960)
CAC99039	lmo0961	protein_coding	986465	protease(lmo0961)
CAC99042	lmo0964	protein_coding	986468	hypothetical protein(lmo0964)
CAC99043	lmo0965	protein_coding	985451	hypothetical protein(lmo0965)
CAC99044	lmo0966	protein_coding	986839	lmo0966(lmo0966)
CAC99045	lmo0967	protein_coding	986471	hypothetical protein(lmo0967)
CAC99048	lmo0970	protein_coding	987821	enoyl-ACP reductase(lmo0970)

CAC99049	dltD	protein_coding	986447	DltD protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid (dltD)
CAC99050	dltC	protein_coding	986460	D-alanine--poly(phosphoribitol) ligase subunit 2(dltC)
CAC99051	dltB	protein_coding	986448	DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid (dltB)
CAC99052	dltA	protein_coding	986449	D-alanine--poly(phosphoribitol) ligase subunit 1(dltA)
CAC99059	lmo0981	protein_coding	986765	transporter(lmo0981)
CAC99060	lmo0982	protein_coding	986804	peptidase(lmo0982)
CAC99061	lmo0983	protein_coding	986438	glutathione peroxidase(lmo0983)
CAC99064	lmo0986	protein_coding	986427	antibiotic ABC transporter ATP-binding protein(lmo0986)
CAC99066	lmo0988	protein_coding	986429	peptide chain release factor 3(prfC)
CAC99069	lmo0991	protein_coding	986787	hypothetical protein(lmo0991)
CAC99070	lmo0992	protein_coding	986459	hypothetical protein(lmo0992)
CAC99071	lmo0993	protein_coding	986421	Na+-transporting ATP synthase subunit J(lmo0993)
CAC99072	lmo0994	protein_coding	986414	lmo0994(lmo0994)
CAC99073	lmo0995	protein_coding	986413	hypothetical protein(lmo0995)
CAC99074	lmo0996	protein_coding	986513	methylated-DNA-protein-cysteine methyltransferase(lmo0996)
CAC99075	clpE	protein_coding	986780	ATP-dependent protease(clpE)
CAC99078	lmo1000	protein_coding	986831	phytoene dehydrogenase(lmo1000)
CAC99079	lmo1001	protein_coding	986350	hypothetical protein(lmo1001)
CAC99081	lmo1003	protein_coding	986170	phosphotransferase system enzyme I(lmo1003)
CAC99083	lmo1005	protein_coding	986400	3-hydroxyisobutyrate dehydrogenase(lmo1005)
CAC99086	lmo1008	protein_coding	986444	hypothetical protein(lmo1008)
CAC99092	gbuA	protein_coding	986360	glycine/betaine ABC transporter ATP-binding protein(gbuA)
CAC99093	gbuB	protein_coding	985002	glycine/betaine ABC transporter permease(gbuB)
CAC99094	gbuC	protein_coding	986358	glycine/betaine ABC transporter substrate-binding protein(gbuC)
CAC99096	lmo1018	protein_coding	986357	copper homeostasis protein CutC(lmo1018)
CAC99097	lmo1019	protein_coding	986368	hypothetical protein(lmo1019)
CAC99101	lmo1023	protein_coding	985239	potassium transporter(lmo1023)
CAC99102	lmo1024	protein_coding	986351	lmo1024(lmo1024)
CAC99107	lmo1029	protein_coding	986340	hypothetical protein(lmo1029)
CAC99116	lmo1038	protein_coding	986325	hypothetical protein(lmo1038)
CAC99120	lmo1042	protein_coding	986318	molybdopterin biosynthesis protein MoeA(lmo1042)
CAC99121	lmo1043	protein_coding	986316	molybdopterin-guanine dinucleotide biosynthesis MobB(lmo1043)
CAC99122	lmo1044	protein_coding	986188	molybdopterin converting factor subunit 2(lmo1044)
CAC99123	lmo1045	protein_coding	985638	molybdopterin converting factor subunit 1(lmo1045)
CAC99124	lmo1046	protein_coding	986305	molybdenum cofactor biosynthesis protein MoaC(moaC)
CAC99125	lmo1047	protein_coding	984816	molybdenum cofactor biosynthesis protein A(moaA)
CAC99126	lmo1048	protein_coding	986817	molybdenum cofactor biosynthesis protein B(lmo1048)
CAC99127	lmo1049	protein_coding	986477	molybdopterin biosynthesis protein MoeB(lmo1049)
CAC99128	lmo1050	protein_coding	986511	hypothetical protein(lmo1050)
CAC99133	PdhD	protein_coding	986542	dihydrolipoamide dehydrogenase(PdhD)
CAC99135	lmo1057	protein_coding	986824	L-lactate dehydrogenase(lmo1057)
CAC99136	lmo1058	protein_coding	986292	hypothetical protein(lmo1058)
CAC99137	lmo1059	protein_coding	984717	lmo1059(lmo1059)
CAC99138	lmo1060	protein_coding	984788	transcriptional regulator(lmo1060)
CAC99139	lmo1061	protein_coding	986289	two-component sensor histidine kinase(lmo1061)
CAC99141	lmo1063	protein_coding	986288	ABC transporter ATP binding protein(lmo1063)
CAC99142	lmo1064	protein_coding	986286	transporter(lmo1064)

CAC99144	lmo1066	protein_coding	986059	myo-inositol-1(or 4)-monophosphatase(lmo1066)
CAC99145	lmo1067	protein_coding	986279	GTP-binding elongation factor(lmo1067)
CAC99146	lmo1068	protein_coding	985811	lmo1068(lmo1068)
CAC99150	pycA	protein_coding	986269	pyruvate carboxylase(pycA)
CAC99151	lmo1073	protein_coding	986508	metal ABC transporter substrate-binding protein(lmo1073)
CAC99153	lmo1075	protein_coding	986506	teichoic acid ABC transporter ATP-binding protein(lmo1075)
CAC99154	lmo1076	protein_coding	986264	autolysin(lmo1076)
CAC99157	lmo1079	protein_coding	986262	hypothetical protein(lmo1079)
CAC99158	lmo1080	protein_coding	986254	teichoic acid biosynthesis protein GgaB(lmo1080)
CAC99159	lmo1081	protein_coding	986258	glucose-1-phosphate thymidyl transferase(lmo1081)
CAC99160	lmo1082	protein_coding	986259	dTDP-sugar epimerase(lmo1082)
CAC99161	lmo1083	protein_coding	986257	dTDP-D-glucose 4,6-dehydratase(lmo1083)
CAC99162	lmo1084	protein_coding	986256	DTDP-L-rhamnose synthetase(lmo1084)
CAC99165	lmo1087	protein_coding	985892	glucitol dehydrogenase(lmo1087)
CAC99166	tagB	protein_coding	986255	teichoic acid biosynthesis protein B(tagB)
CAC99167	tagD	protein_coding	986249	glycerol-3-phosphate cytidylyltransferase(tagD)
CAC99168	lmo1090	protein_coding	986248	glycosyltransferase(lmo1090)
CAC99169	lmo1091	protein_coding	986251	glysosyltransferase(lmo1091)
CAC99174	guaA	protein_coding	986238	GMP synthase(guaA)
CAC99175	lmo1097	protein_coding	986237	integrase(lmo1097)
CAC99183	lmo1105	protein_coding	986240	hypothetical protein(lmo1105)
CAC99190	lmo1112	protein_coding	986216	hypothetical protein(lmo1112)
CAC99191	lmo1113	protein_coding	986214	hypothetical protein(lmo1113)
CAC99192	lmo1114	protein_coding	986213	hypothetical protein(lmo1114)
CAC99194	lmo1116	protein_coding	986570	regulatory protein(lmo1116)
CAC99195	lmo1117	protein_coding	986210	lmo1117(lmo1117)
CAC99198	lmo1120	protein_coding	986206	lmo1120(lmo1120)
CAC99201	lmo1123	protein_coding	986204	lmo1123(lmo1123)
CAC99202	lmo1124	protein_coding	986198	lmo1124(lmo1124)
CAC99208	lmo1130	protein_coding	985135	transcriptional regulator(lmo1130)
CAC99209	lmo1131	protein_coding	986529	ABC transporter ATP-binding protein(lmo1131)
CAC99212	lmo1134	protein_coding	986190	regulatory protein(lmo1134)
CAC99213	lmo1135	protein_coding	986189	lmo1135(lmo1135)
CAC99214	lmo1136	protein_coding	986166	internalin(lmo1136)
CAC99215	lmo1137	protein_coding	986423	lmo1137(lmo1137)
CAC99216	lmo1138	protein_coding	987656	ATP-dependent Clp protease proteolytic subunit(lmo1138)
CAC99218	lmo1140	protein_coding	986180	lmo1140(lmo1140)
CAC99219	lmo1141	protein_coding	986179	uroporphyrin-III C-methyltransferase(lmo1141)
CAC99228	lmo1150	protein_coding	986159	transcriptional regulator PocR(lmo1150)
CAC99247	cobD	protein_coding	986129	threonine-phosphate decarboxylase(cobD)
CAC99248	lmo1170	protein_coding	986128	PduX protein(lmo1170)
CAC99261	lmo1183	protein_coding	986117	lmo1183(lmo1183)
CAC99266	lmo1188	protein_coding	986112	lmo1188(lmo1188)
CAC99286	cbiP	protein_coding	986064	cobyric acid synthase CbiP(cbiP)
CAC99287	lmo1209	protein_coding	986058	hypothetical protein(lmo1209)
CAC99288	lmo1210	protein_coding	986061	hypothetical protein(lmo1210)
CAC99289	lmo1211	protein_coding	986063	hypothetical protein(lmo1211)
CAC99290	lmo1212	protein_coding	986143	hypothetical protein(lmo1212)

CAC99294	lmo1216	protein_coding	986054	N-acetylmuramoyl-L-alanine amidase(lmo1216)
CAC99295	lmo1217	protein_coding	986057	endo-1,4-beta-glucanase and to aminopeptidase(lmo1217)
CAC99296	lmo1218	protein_coding	986185	rRNA methylase(lmo1218)
CAC99299	pheS	protein_coding	986046	phenylalanyl-tRNA synthetase subunit alpha(pheS)
CAC99300	pheT	protein_coding	986682	phenylalanyl-tRNA synthetase subunit beta(pheT)
CAC99302	lmo1224	protein_coding	986043	hypothetical protein(lmo1224)
CAC99304	lmo1226	protein_coding	986040	transporter(lmo1226)
CAC99305	lmo1227	protein_coding	986857	uracil-DNA glycosylase(lmo1227)
CAC99306	rnhC	protein_coding	987663	ribonuclease HIII(rnhC)
CAC99309	lmo1231	protein_coding	986038	DNA polymerase beta(lmo1231)
CAC99310	lmo1232	protein_coding	986039	recombination and DNA strand exchange inhibitor protein(lmo1232)
CAC99313	lmo1235	protein_coding	986030	aspartate kinase(lmo1235)
CAC99315	racE	protein_coding	986027	glutamate racemase(racE)
CAC99316	lmo1238	protein_coding	986029	ribonuclease PH(rph)
CAC99317	lmo1239	protein_coding	986028	nucleoside-triphosphatase(lmo1239)
CAC99318	lmo1240	protein_coding	986025	hypothetical protein(lmo1240)
CAC99319	lmo1241	protein_coding	986024	lmo1241(lmo1241)
CAC99324	lmo1246	protein_coding	986011	ATP-dependent RNA helicase(lmo1246)
CAC99326	lmo1248	protein_coding	986009	hypothetical protein(lmo1248)
CAC99330	lmo1252	protein_coding	986005	hypothetical protein(lmo1252)
CAC99331	lmo1253	protein_coding	984383	GntR family transcriptional regulator(lmo1253)
CAC99332	lmo1254	protein_coding	986004	alpha,alpha-phosphotrehalase(lmo1254)
CAC99333	lmo1255	protein_coding	986002	PTS trehalose transporter subunit IIBC(lmo1255)
CAC99334	lmo1256	protein_coding	985998	lmo1256(lmo1256)
CAC99336	lmo1258	protein_coding	985992	lmo1258(lmo1258)
CAC99337	proA	protein_coding	985995	gamma-glutamyl phosphate reductase(proA)
CAC99338	proB	protein_coding	985996	gamma-glutamyl kinase(proB)
CAC99339	lmo1261	protein_coding	985993	lmo1261(lmo1261)
CAC99341	lmo1263	protein_coding	985085	transcriptional regulator(lmo1263)
CAC99342	lmo1264	protein_coding	985081	lmo1264(lmo1264)
CAC99343	lmo1265	protein_coding	985747	hypothetical protein(lmo1265)
CAC99344	lmo1266	protein_coding	985084	lmo1266(lmo1266)
CAC99345	tig	protein_coding	985096	trigger factor(tig)
CAC99348	lmo1270	protein_coding	985113	type I signal peptidase(lmo1270)
CAC99349	lmo1271	protein_coding	985089	type I signal peptidase(lmo1271)
CAC99350	lmo1272	protein_coding	985097	ribosomal biogenesis GTPase(rbgA)
CAC99351	rnhB	protein_coding	985073	ribonuclease HII(rnhB)
CAC99353	topA	protein_coding	985095	DNA topoisomerase I(topA)
CAC99354	gid	protein_coding	985107	tRNA (uracil-5-)-methyltransferase Gid(gid)
CAC99364	parE	protein_coding	987287	DNA topoisomerase IV subunit B(parE)
CAC99365	parC	protein_coding	985091	DNA topoisomerase IV subunit A(parC)
CAC99366	lmo1288	protein_coding	987285	S-ribosylhomocysteine lyase(lmo1288)
CAC99367	lmo1289	protein_coding	987289	internalin(lmo1289)
CAC99371	glpD	protein_coding	985350	glycerol-3-phosphate dehydrogenase(glpD)
CAC99372	miaA	protein_coding	985128	tRNA delta(2)-isopentenylpyrophosphate transferase(miaA)
CAC99373	lmo1295	protein_coding	985120	host factor-1 protein(lmo1295)
CAC99374	lmo1296	protein_coding	985125	hypothetical protein(lmo1296)
CAC99375	lmo1297	protein_coding	985127	aluminum resistance protein(lmo1297)

CAC99376	glnR	protein_coding	985126	glutamine synthetase repressor(glnR)
CAC99377	glnA	protein_coding	985115	glutamine synthetase(glnA)
CAC99378	lmo1300	protein_coding	985130	arsenic transporter(lmo1300)
CAC99380	lmo1302	protein_coding	985139	LexA family transcriptional regulator(lmo1302)
CAC99383	tkt	protein_coding	987681	transketolase(tkt)
CAC99384	lmo1306	protein_coding	987683	hypothetical protein(lmo1306)
CAC99387	lmo1309	protein_coding	987686	hypothetical protein(lmo1309)
CAC99391	smbA	protein_coding	987690	uridylate kinase(pyrH)
CAC99392	frr	protein_coding	987693	ribosome recycling factor(frr)
CAC99393	lmo1315	protein_coding	987694	UDP pyrophosphate synthase(lmo1315)
CAC99394	cdsA	protein_coding	987695	phosphatidate cytidylyltransferase(cdsA)
CAC99395	lmo1317	protein_coding	987697	1-deoxy-D-xylulose 5-phosphate reductoisomerase(lmo1317)
CAC99396	lmo1318	protein_coding	987698	zinc metalloprotease Lmo1318(lmo1318)
CAC99397	proS	protein_coding	987699	prolyl-tRNA synthetase(proS)
CAC99398	polC	protein_coding	987700	DNA polymerase III PolC(polC)
CAC99399	lmo1321	protein_coding	987701	hypothetical protein(lmo1321)
CAC99400	nusA	protein_coding	987702	transcription elongation factor NusA(nusA)
CAC99401	lmo1323	protein_coding	987703	hypothetical protein(lmo1323)
CAC99402	lmo1324	protein_coding	987705	hypothetical protein(lmo1324)
CAC99403	infB	protein_coding	987704	translation initiation factor IF-2(infB)
CAC99404	lmo1326	protein_coding	987708	hypothetical protein(lmo1326)
CAC99405	rbfA	protein_coding	987713	ribosome-binding factor A(rbfA)
CAC99406	truB	protein_coding	987709	tRNA pseudouridine synthase B(truB)
CAC99408	rpsO	protein_coding	987711	30S ribosomal protein S15(rpsO)
CAC99409	pnpA	protein_coding	987712	polynucleotide phosphorylase(pnpA)
CAC99410	lmo1332	protein_coding	987715	GTPase EngC(lmo1332)
CAC99411	lmo1333	protein_coding	987717	hypothetical protein(lmo1333)
CAC99412	lmo1334	protein_coding	987718	hypothetical protein(lmo1334)
CAC99413	rpmG	protein_coding	987719	50S ribosomal protein L33(rpmG)
CAC99414	lmo1336	protein_coding	987720	5-formyltetrahydrofolate cyclo-ligase(lmo1336)
CAC99415	lmo1337	protein_coding	987722	hypothetical protein(lmo1337)
CAC99417	lmo1339	protein_coding	987723	glucose kinase(lmo1339)
CAC99418	lmo1340	protein_coding	987724	hypothetical protein(lmo1340)
CAC99419	lmo1341	protein_coding	987725	competence protein ComG(lmo1341)
CAC99420	lmo1342	protein_coding	987728	competence protein ComGF(lmo1342)
CAC99422	lmo1344	protein_coding	987731	competence protein ComGD(lmo1344)
CAC99426	lmo1348	protein_coding	987736	glycine cleavage system aminomethyltransferase T(gcvT)
CAC99427	lmo1349	protein_coding	987737	glycine dehydrogenase subunit 1(lmo1349)
CAC99428	lmo1350	protein_coding	987740	glycine dehydrogenase subunit 2(lmo1350)
CAC99429	lmo1351	protein_coding	987739	lmo1351(lmo1351)
CAC99430	lmo1352	protein_coding	987741	lmo1352(lmo1352)
CAC99431	lmo1353	protein_coding	987743	hypothetical protein(lmo1353)
CAC99433	efp	protein_coding	987744	elongation factor P(efp)
CAC99435	lmo1357	protein_coding	987387	acetyl-CoA carboxylase biotin carboxylase subunit(lmo1357)
CAC99437	lmo1359	protein_coding	987880	transcription antitermination protein NusB(nusB)
CAC99439	lmo1361	protein_coding	987878	exodeoxyribonuclease VII large subunit(xseA)
CAC99441	lmo1363	protein_coding	987873	geranyltranstransferase(lmo1363)
CAC99442	cspL	protein_coding	987871	cold-shock protein(cspL)

CAC99444	lmo1366	protein_coding	986969	hypothetical protein(lmo1366)
CAC99446	recN	protein_coding	987672	DNA repair protein(recN)
CAC99447	lmo1369	protein_coding	986887	phosphotransbutyrylase(lmo1369)
CAC99449	lmo1371	protein_coding	987674	dihydrolipoamide dehydrogenase(lmo1371)
CAC99450	lmo1372	protein_coding	987855	branched-chain alpha-keto acid dehydrogenase subunit E1(lmo1372)
CAC99451	lmo1373	protein_coding	987859	branched-chain alpha-keto acid dehydrogenase subunit E1(lmo1373)
CAC99453	lmo1375	protein_coding	987853	aminotripeptidase(lmo1375)
CAC99459	lmo1381	protein_coding	987841	lmo1381(lmo1381)
CAC99463	lmo1385	protein_coding	987832	hypothetical protein(lmo1385)
CAC99464	lmo1386	protein_coding	987830	DNA translocase(lmo1386)
CAC99466	tcsA	protein_coding	984815	CD4+ T cell-stimulating antigen, lipoprotein(tcsA)
CAC99467	lmo1389	protein_coding	984826	sugar ABC transporter ATP-binding protein(lmo1389)
CAC99468	lmo1390	protein_coding	984893	ABC transporter permease(lmo1390)
CAC99469	lmo1391	protein_coding	986482	sugar ABC transporter permease(lmo1391)
CAC99470	lmo1392	protein_coding	986324	peptidase(lmo1392)
CAC99474	lmo1396	protein_coding	985296	phosphatidylglycerophosphate synthase(lmo1396)
CAC99475	cinA	protein_coding	987615	competence damage-inducible protein CinA(cinA)
CAC99477	lmo1399	protein_coding	984906	phosphodiesterase(lmo1399)
CAC99478	lmo1400	protein_coding	986455	N-acetyltransferase(lmo1400)
CAC99479	lmo1401	protein_coding	986807	hypothetical protein(lmo1401)
CAC99481	mutS	protein_coding	985419	DNA mismatch repair protein MutS(mutS)
CAC99483	lmo1405	protein_coding	986841	anti-terminator regulatory protein(lmo1405)
CAC99485	pflC	protein_coding	986485	pyruvate-formate lyase activating enzyme(pflC)
CAC99495	lmo1417	protein_coding	986745	hypothetical protein(lmo1417)
CAC99496	lmo1418	protein_coding	986995	hypothetical protein(lmo1418)
CAC99497	lmo1419	protein_coding	986497	hypothetical protein(lmo1419)
CAC99498	lmo1420	protein_coding	984666	UDP-N-acetylenolpyruvoylglucosamine reductase(murB)
CAC99499	lmo1421	protein_coding	984736	glycine/betaine ABC transporter ATP-binding protein(lmo1421)
CAC99500	lmo1422	protein_coding	986774	glycine/betaine ABC transporter permease(lmo1422)
CAC99501	lmo1423	protein_coding	986759	lmo1423(lmo1423)
CAC99503	opuCD	protein_coding	984750	glycine/betaine ABC transporter permease(opuCD)
CAC99504	opuCC	protein_coding	986463	glycine/betaine ABC transporter substrate-binding protein(opuCC)
CAC99505	opuCB	protein_coding	985838	glycine/betaine ABC transporter permease(opuCB)
CAC99506	opuCA	protein_coding	987882	glycine/betaine ABC transporter ATP-binding protein(opuCA)
CAC99509	lmo1431	protein_coding	986756	ABC transporter ATP-binding protein(lmo1431)
CAC99510	lmo1432	protein_coding	986495	lmo1432(lmo1432)
CAC99511	lmo1433	protein_coding	985502	glutathione reductase(lmo1433)
CAC99513	lmo1435	protein_coding	986494	dihydrodipicolinate synthase(dapA)
CAC99517	sod	protein_coding	986791	superoxide dismutase(sod)
CAC99518	lmo1440	protein_coding	986499	hypothetical protein(lmo1440)
CAC99522	lmo1444	protein_coding	986457	foldase(lmo1444)
CAC99523	zurR	protein_coding	986176	ZurR family transcriptional regulator(zurR)
CAC99524	zurM	protein_coding	986990	metal (zinc) transport protein (ABC transporter, permease)(zurM)
CAC99526	lmo1448	protein_coding	986727	manganese-dependent inorganic pyrophosphatase(lmo1448)
CAC99527	lmo1449	protein_coding	984467	endonuclease IV(lmo1449)
CAC99528	lmo1450	protein_coding	987133	DEAD/DEAH box helicase(lmo1450)
CAC99529	lmo1451	protein_coding	987625	4-hydroxy-3-methylbut-2-enyl diphosphate reductase(ispH)
CAC99532	rpoD	protein_coding	984456	RNA polymerase sigma factor RpoD(rpoD)

CAC99533	dnaG	protein_coding	986564	DNA primase(dnaG)
CAC99534	lmo1456	protein_coding	986822	hypothetical protein(lmo1456)
CAC99536	glyS	protein_coding	987668	glycyl-tRNA synthetase subunit beta(glyS)
CAC99537	glyQ	protein_coding	986742	glycyl-tRNA synthetase subunit alpha(glyQ)
CAC99545	lmo1467	protein_coding	986679	phosphate starvation-induced protein PhoH(lmo1467)
CAC99546	lmo1468	protein_coding	987837	hypothetical protein(lmo1468)
CAC99547	rpsU	protein_coding	987865	30S ribosomal protein S21(rpsU)
CAC99548	lmo1470	protein_coding	986707	16S ribosomal RNA methyltransferase RsmE(lmo1470)
CAC99549	lmo1471	protein_coding	985409	ribosomal protein L11 methyltransferase(prmA)
CAC99550	dnaJ	protein_coding	987063	molecular chaperone DnaJ(dnaJ)
CAC99551	dnaK	protein_coding	986290	molecular chaperone DnaK(dnaK)
CAC99552	grpE	protein_coding	986715	heat shock protein GrpE(grpE)
CAC99553	hrcA	protein_coding	986933	heat-inducible transcription repressor(hrcA)
CAC99557	lepA	protein_coding	986365	GTP-binding protein LepA(lepA)
CAC99558	rpsT	protein_coding	986932	30S ribosomal protein S20(rpsT)
CAC99563	lmo1485	protein_coding	987000	hypothetical protein(lmo1485)
CAC99564	lmo1486	protein_coding	986988	lmo1486(lmo1486)
CAC99565	lmo1487	protein_coding	986903	hypothetical protein(lmo1487)
CAC99566	lmo1488	protein_coding	986963	nicotinic acid mononucleotide adenylyltransferase(nadD)
CAC99568	lmo1490	protein_coding	986965	shikimate 5-dehydrogenase(lmo1490)
CAC99569	lmo1491	protein_coding	986978	GTP-binding protein(lmo1491)
CAC99570	lmo1492	protein_coding	986939	hypothetical protein(lmo1492)
CAC99572	lmo1494	protein_coding	986944	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase(lmo1494)
CAC99575	udk	protein_coding	986986	uridine kinase(udk)
CAC99576	lmo1498	protein_coding	986934	O-methyltransferase(lmo1498)
CAC99581	lmo1503	protein_coding	987746	lmo1503(lmo1503)
CAC99582	alaS	protein_coding	987749	alanyl-tRNA synthetase(alaS)
CAC99583	lmo1505	protein_coding	987751	ABC transporter ATP-binding protein(lmo1505)
CAC99586	lmo1508	protein_coding	987753	histidine kinase(lmo1508)
CAC99592	lmo1514	protein_coding	987768	recombination factor protein RarA(lmo1514)
CAC99594	lmo1516	protein_coding	987771	ammonium transporter NrgA(lmo1516)
CAC99595	lmo1517	protein_coding	987779	nitrogen regulatory PII protein(lmo1517)
CAC99597	aspS	protein_coding	987778	aspartyl-tRNA synthetase(aspS)
CAC99598	hisS	protein_coding	987781	histidyl-tRNA synthetase(hisS)
CAC99602	apt	protein_coding	987786	adenine phosphoribosyltransferase(apt)
CAC99603	lmo1525	protein_coding	987789	recombination protein RecJ(lmo1525)
CAC99604	lmo1526	protein_coding	987791	hypothetical protein(lmo1526)
CAC99605	lmo1527	protein_coding	987793	preprotein translocase SecDF(lmo1527)
CAC99608	lmo1530	protein_coding	987798	queuine tRNA-ribosyltransferase(tgt)
CAC99612	lmo1534	protein_coding	987808	L-lactate dehydrogenase(lmo1534)
CAC99614	lmo1536	protein_coding	987813	prephenate dehydratase(lmo1536)
CAC99615	lmo1537	protein_coding	987811	GTPase ObgE(obgE)
CAC99616	lmo1538	protein_coding	987807	glycerol kinase(glpK)
CAC99617	lmo1539	protein_coding	987817	glycerol transporter(lmo1539)
CAC99618	rpmA	protein_coding	987815	50S ribosomal protein L27(rpmA)
CAC99620	rplU	protein_coding	987770	50S ribosomal protein L21(rplU)
CAC99621	lmo1543	protein_coding	987819	ribonuclease G(lmo1543)
CAC99622	minD	protein_coding	987814	septum formation inhibitor MinD(minD)

CAC99623	minC	protein_coding	987769	septum formation inhibitor MinC(minC)
CAC99625	mreC	protein_coding	986941	rod shape-determining protein MreC(mreC)
CAC99626	mreB	protein_coding	986954	rod shape-determining protein MreB(mreB)
CAC99629	folC	protein_coding	986919	folyl-polyglutamate synthetase(folC)
CAC99630	valS	protein_coding	986904	valyl-tRNA synthetase(valS)
CAC99636	lmo1558	protein_coding	986915	GTP-binding protein EngB(engB)
CAC99637	thrS	protein_coding	986974	threonyl-tRNA synthetase(thrS)
CAC99643	polA	protein_coding	986949	DNA polymerase I(polA)
CAC99645	citZ	protein_coding	986909	citrate synthase(citZ)
CAC99649	pfk	protein_coding	986951	6-phosphofructokinase(pfkA)
CAC99650	accA	protein_coding	986992	acetyl-CoA carboxylase carboxyltransferase subunit alpha(accA)
CAC99651	accD	protein_coding	986998	acetyl-CoA carboxylase subunit beta(accD)
CAC99655	lmo1577	protein_coding	986999	metal-dependent hydrolase(lmo1577)
CAC99656	lmo1578	protein_coding	986985	X-Pro dipeptidase(lmo1578)
CAC99657	lmo1579	protein_coding	986945	alanine dehydrogenase(lmo1579)
CAC99658	lmo1580	protein_coding	986961	hypothetical protein(lmo1580)
CAC99659	ackA	protein_coding	986937	acetate kinase(ackA)
CAC99662	lmo1584	protein_coding	986942	hypothetical protein(lmo1584)
CAC99663	lmo1585	protein_coding	987795	peptidase(lmo1585)
CAC99666	argD	protein_coding	984620	acetylornithine aminotransferase(argD)
CAC99667	argB	protein_coding	987804	acetylglutamate kinase(argB)
CAC99668	argJ	protein_coding	984450	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase(argJ)
CAC99669	argC	protein_coding	984694	N-acetyl-gamma-glutamyl-phosphate reductase(argC)
CAC99670	lmo1592	protein_coding	986418	thiamine biosynthesis protein ThiI(lmo1592)
CAC99671	lmo1593	protein_coding	985205	iron-sulfur cofactor synthesis protein NifS(lmo1593)
CAC99672	lmo1594	protein_coding	986850	septation ring formation regulator EzrA(lmo1594)
CAC99674	rpsD	protein_coding	985744	30S ribosomal protein S4(rpsD)
CAC99675	lmo1597	protein_coding	984705	lmo1597(lmo1597)
CAC99676	tyrS	protein_coding	985752	tyrosyl-tRNA synthetase(tyrS)
CAC99678	aroA	protein_coding	985307	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase(aroA)
CAC99679	lmo1601	protein_coding	985749	general stress protein(lmo1601)
CAC99680	lmo1602	protein_coding	985745	hypothetical protein(lmo1602)
CAC99681	lmo1603	protein_coding	985743	aminopeptidase(lmo1603)
CAC99683	murC	protein_coding	985741	UDP-N-acetylmuramate--L-alanine ligase(murC)
CAC99684	lmo1606	protein_coding	985737	DNA translocase(lmo1606)
CAC99692	lmo1614	protein_coding	985733	hypothetical protein(lmo1614)
CAC99693	lmo1615	protein_coding	985730	tRNA (guanine-N(7)-)-methyltransferase(trmB)
CAC99694	lmo1616	protein_coding	985729	hypothetical protein(lmo1616)
CAC99695	lmo1617	protein_coding	985727	multidrug transporter(lmo1617)
CAC99696	lmo1618	protein_coding	985724	MarR family transcriptional regulator(lmo1618)
CAC99697	daaA	protein_coding	985722	D-amino acid aminotransferase(daaA)
CAC99700	lmo1622	protein_coding	985726	hypothetical protein(lmo1622)
CAC99701	lmo1623	protein_coding	985719	hypothetical protein(lmo1623)
CAC99702	lmo1624	protein_coding	985718	transporter(lmo1624)
CAC99703	lmo1625	protein_coding	985717	transporter(lmo1625)
CAC99704	lmo1626	protein_coding	985552	lmo1626(lmo1626)
CAC99714	lmo1636	protein_coding	985701	ABC transporter ATP-binding protein(lmo1636)
CAC99715	lmo1637	protein_coding	985693	hypothetical protein(lmo1637)

CAC99717	lmo1639	protein_coding	985691	DNA-3-methyladenine glycosidase(lmo1639)
CAC99727	lmo1649	protein_coding	985678	lmo1649(lmo1649)
CAC99728	lmo1650	protein_coding	985591	hypothetical protein(lmo1650)
CAC99730	lmo1652	protein_coding	985675	ABC transporter ATP-binding protein(lmo1652)
CAC99735	tsf	protein_coding	985671	elongation factor Ts(tsf)
CAC99736	rpsB	protein_coding	985326	30S ribosomal protein S2(rpsB)
CAC99738	leuS	protein_coding	985669	leucyl-tRNA synthetase(leuS)
CAC99739	lmo1661	protein_coding	985668	hypothetical protein(lmo1661)
CAC99740	lmo1662	protein_coding	985666	hypothetical protein(lmo1662)
CAC99741	ansB	protein_coding	985663	asparagine synthetase(ansB)
CAC99742	metK	protein_coding	985664	methionine adenosyltransferase(metK)
CAC99744	lmo1666	protein_coding	985661	peptidoglycan-linked protein(lmo1666)
CAC99747	lmo1669	protein_coding	985657	hypothetical protein(lmo1669)
CAC99749	lmo1671	protein_coding	985656	ABC transporter(lmo1671)
CAC99760	lmo1682	protein_coding	985646	transporter(lmo1682)
CAC99762	lmo1684	protein_coding	985633	glycerate dehydrogenase(lmo1684)
CAC99763	gsaB	protein_coding	985629	glutamate-1-semialdehyde aminotransferase(gsaB)
CAC99768	lmo1690	protein_coding	985626	hypothetical protein(lmo1690)
CAC99771	lmo1693	protein_coding	985620	Regulatory protein recX.(recX)
CAC99772	lmo1694	protein_coding	985624	CDP-abequose synthase(lmo1694)
CAC99773	lmo1695	protein_coding	985618	hypothetical protein(lmo1695)
CAC99775	lmo1697	protein_coding	985615	hypothetical protein(lmo1697)
CAC99777	lmo1699	protein_coding	985617	chemotaxis protein(lmo1699)
CAC99778	lmo1700	protein_coding	985611	lmo1700(lmo1700)
CAC99782	lmo1704	protein_coding	985606	hypothetical protein(lmo1704)
CAC99787	lmo1709	protein_coding	985602	methionine aminopeptidase(lmo1709)
CAC99788	lmo1710	protein_coding	985600	flavodoxin(lmo1710)
CAC99789	lmo1711	protein_coding	985599	aminopeptidase(lmo1711)
CAC99790	lmo1712	protein_coding	985590	multidrug resistance protein(lmo1712)
CAC99800	lmo1722	protein_coding	985584	ATP-dependent RNA helicase(lmo1722)
CAC99801	lmo1723	protein_coding	985582	lmo1723(lmo1723)
CAC99802	lmo1724	protein_coding	986662	ABC transporter ATP-binding protein(lmo1724)
CAC99803	lmo1725	protein_coding	985573	GntR family tramscriptional regulator(lmo1725)
CAC99804	lmo1726	protein_coding	985614	hypothetical protein(lmo1726)
CAC99805	lmo1727	protein_coding	986088	LacI family transcriptional regulator(lmo1727)
CAC99806	lmo1728	protein_coding	985695	cellobiose phosphorylase(lmo1728)
CAC99807	lmo1729	protein_coding	985699	beta-glucosidase(lmo1729)
CAC99808	lmo1730	protein_coding	985575	sugar ABC transporter substrate-binding protein(lmo1730)
CAC99809	lmo1731	protein_coding	985577	sugar ABC transporter permease(lmo1731)
CAC99810	lmo1732	protein_coding	985574	sugar ABC transporter permease(lmo1732)
CAC99813	gltC	protein_coding	985367	transcription activator of glutamate synthase operon GltC(gltC)
CAC99814	lmo1736	protein_coding	986571	hypothetical protein(lmo1736)
CAC99815	lmo1737	protein_coding	985567	glycerol dehydrogenase(lmo1737)
CAC99820	adeC	protein_coding	985560	adenine deaminase(adeC)
CAC99822	lmo1744	protein_coding	985378	hypothetical protein(lmo1744)
CAC99825	lmo1747	protein_coding	985559	ABC transporter ATP-binding protein(lmo1747)
CAC99826	lmo1748	protein_coding	986669	lmo1748(lmo1748)
CAC99829	lmo1751	protein_coding	985554	Uncharacterized RNA methyltransferase lmo1751(lmo1751)

CAC99832	gatB	protein_coding	985551	aspartyl/glutamyl-tRNA amidotransferase subunit B(gatB)
CAC99837	pcrA	protein_coding	985986	ATP-dependent DNA helicase(pcrA)
CAC99838	lmo1760	protein_coding	985989	geranylgeranylglyceryl phosphate synthase-like protein(lmo1760)
CAC99839	lmo1761	protein_coding	985984	sodium-dependent transporter(lmo1761)
CAC99842	purD	protein_coding	985980	phosphoribosylamine--glycine ligase(purD)
CAC99843	purH	protein_coding	985977	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/ IMP cyclohydrolase(purH)
CAC99844	purN	protein_coding	985978	phosphoribosylglycinamide formyltransferase(purN)
CAC99845	purM	protein_coding	985975	phosphoribosylaminoimidazole synthetase(purM)
CAC99846	purF	protein_coding	985974	amidophosphoribosyltransferase(purF)
CAC99847	purQ	protein_coding	985972	phosphoribosylformylglycinamidine synthase II(purQ)
CAC99848	purL	protein_coding	985306	phosphoribosylformylglycinamidine synthase I(purL)
CAC99850	purC	protein_coding	985969	phosphoribosylaminoimidazole-succinocarboxamide synthase(purC)
CAC99851	purB	protein_coding	985967	adenylosuccinate lyase(purB)
CAC99853	purE	protein_coding	985964	phosphoribosylaminoimidazole carboxylase catalytic subunit(purE)
CAC99854	lmo1776	protein_coding	985962	hypothetical protein(lmo1776)
CAC99861	rplT	protein_coding	985949	50S ribosomal protein L20(rplT)
CAC99862	rpmI	protein_coding	985946	50S ribosomal protein L35(rpmI)
CAC99863	infC	protein_coding	985947	translation initiation factor IF-3(infC)
CAC99864	inlC	protein_coding	985945	internalin C(inlC)
CAC99865	rplS	protein_coding	985943	50S ribosomal protein L19(rplS)
CAC99866	lmo1788	protein_coding	985948	transcriptional regulator(lmo1788)
CAC99867	lmo1789	protein_coding	985940	hypothetical protein(lmo1789)
CAC99868	lmo1790	protein_coding	985953	hypothetical protein(lmo1790)
CAC99869	lmo1791	protein_coding	985939	lmo1791(lmo1791)
CAC99870	trmD	protein_coding	985936	tRNA (guanine-N(1)-)-methyltransferase(trmD)
CAC99872	lmo1794	protein_coding	985935	hypothetical protein(lmo1794)
CAC99873	lmo1795	protein_coding	985941	hypothetical protein(lmo1795)
CAC99874	lmo1796	protein_coding	985933	hypothetical protein(lmo1796)
CAC99875	rpsP	protein_coding	985931	30S ribosomal protein S16(rpsP)
CAC99876	lmo1798	protein_coding	985932	hypothetical protein(lmo1798)
CAC99878	lmo1800	protein_coding	985934	protein-tyrosine phosphatase(lmo1800)
CAC99881	lmo1803	protein_coding	985925	cell division protein FtsY(lmo1803)
CAC99882	smc	protein_coding	985926	chromosome condensation protein Smc(smc)
CAC99883	rncS	protein_coding	985924	ribonuclease III(rnc)
CAC99884	acpA	protein_coding	986035	acyl carrier protein(acpP)
CAC99885	fabG	protein_coding	985923	3-ketoacyl-ACP reductase(fabG)
CAC99886	fabD	protein_coding	985921	ACP S-malonyltransferase(fabD)
CAC99887	plsX	protein_coding	985913	glycerol-3-phosphate acyltransferase PlsX(plsX)
CAC99888	lmo1810	protein_coding	985918	fatty acid biosynthesis transcriptional regulator(lmo1810)
CAC99892	lmo1814	protein_coding	985909	hypothetical protein(lmo1814)
CAC99894	rpmB	protein_coding	985895	50S ribosomal protein L28(rpmB)
CAC99895	lmo1817	protein_coding	985910	hypothetical protein(lmo1817)
CAC99905	lmo1827	protein_coding	985464	guanylate kinase(gmk)
CAC99906	lmo1828	protein_coding	985886	hypothetical protein(lmo1828)
CAC99908	lmo1830	protein_coding	984389	short-chain dehydrogenase(lmo1830)
CAC99920	lmo1842	protein_coding	985864	hypothetical protein(lmo1842)
CAC99921	lmo1843	protein_coding	985856	hypothetical protein(lmo1843)

CAC99922	lsp	protein_coding	985858	lipoprotein signal peptidase(lspA)
CAC99923	lmo1845	protein_coding	985860	hypothetical protein(lmo1845)
CAC99924	lmo1846	protein_coding	985857	multidrug transporter(lmo1846)
CAC99928	lmo1850	protein_coding	985846	MarR family transcriptional regulator(lmo1850)
CAC99929	lmo1851	protein_coding	985844	carboxy-terminal processing proteinase(lmo1851)
CAC99933	lmo1855	protein_coding	985842	D-alanyl-D-alanine carboxypeptidase(lmo1855)
CAC99934	deoD	protein_coding	985839	purine nucleoside phosphorylase(deoD)
CAC99935	lmo1857	protein_coding	985942	hypothetical protein(lmo1857)
CAC99938	lmo1860	protein_coding	985835	methionine sulfoxide reductase A(lmo1860)
CAC99943	lmo1865	protein_coding	985828	hypothetical protein(lmo1865)
CAC99949	lmo1871	protein_coding	985905	phosphoglucomutase(lmo1871)
CAC99955	lmo1877	protein_coding	985815	formyl-tetrahydrofolate synthetase(lmo1877)
CAC99958	lmo1880	protein_coding	985813	RNase HI(lmo1880)
CAC99959	lmo1881	protein_coding	985812	5'-3' exonuclease(lmo1881)
CAC99960	lmo1882	protein_coding	985810	30S ribosomal protein S14(rpsN)
CAC99961	lmo1883	protein_coding	986008	chitinase(lmo1883)
CAC99963	lmo1885	protein_coding	985807	xanthine phosphoribosyltransferase(lmo1885)
CAC99964	lmo1886	protein_coding	985806	carboxypeptidase(lmo1886)
CAC99965	lmo1887	protein_coding	985805	hypothetical protein(lmo1887)
CAC99968	lmo1890	protein_coding	986335	hypothetical protein(lmo1890)
CAC99970	pbpA	protein_coding	985798	penicillin-binding protein 2A(pbpA)
CAC99976	lmo1898	protein_coding	985789	hypothetical protein(lmo1898)
CAC99979	panC	protein_coding	985788	pantoate--beta-alanine ligase(panC)
CAC99981	lmo1903	protein_coding	985782	thioredoxin(lmo1903)
CAC99988	lmo1910	protein_coding	985775	oxidoreductase(lmo1910)
CAC99990	lmo1912	protein_coding	985772	histidine kinase(lmo1912)
CAC99993	lmo1915	protein_coding	985767	malate dehydrogenase(lmo1915)
CAC99995	pflA	protein_coding	985766	pyruvate formate-lyase(pflA)
CAC99996	lmo1918	protein_coding	985765	hypothetical protein(lmo1918)
CAD00013	lmo1935	protein_coding	984896	protein-tyrosine/serine phosphatase(lmo1935)
CAD00014	gpsA	protein_coding	985475	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase(gpsA)
CAD00015	lmo1937	protein_coding	986528	GTP-binding protein EngA(engA)
CAD00016	lmo1938	protein_coding	987984	30S ribosomal protein S1(rpsA)
CAD00018	lmo1940	protein_coding	987982	asparaginase(lmo1940)
CAD00024	lmo1946	protein_coding	987980	acyl-CoA hydrolase(lmo1946)
CAD00027	lmo1949	protein_coding	984426	hypothetical protein(lmo1949)
CAD00028	lmo1950	protein_coding	985025	hypothetical protein(lmo1950)
CAD00029	lmo1951	protein_coding	987973	segregation and condensation protein A(scpA)
CAD00030	lysA	protein_coding	987983	diaminopimelate decarboxylase(lysA)
CAD00031	pnp	protein_coding	987976	purine nucleoside phosphorylase(pnp)
CAD00032	drm	protein_coding	987977	phosphopentomutase(drm)
CAD00033	lmo1955	protein_coding	987975	integrase/recombinase(lmo1955)
CAD00034	fur	protein_coding	987991	Fur family transcriptional regulator(fur)
CAD00036	fhuB	protein_coding	984897	ferrichrome ABC transporter permease(fhuB)
CAD00044	lmo1966	protein_coding	987970	hypothetical protein(lmo1966)
CAD00045	lmo1967	protein_coding	987886	toxic ion resistance protein(lmo1967)
CAD00046	lmo1968	protein_coding	984877	creatinine amidohydrolase(lmo1968)
CAD00051	lmo1973	protein_coding	987968	PTS sugar transporter subunit IIA(lmo1973)

CAD00053	lmo1975	protein_coding	985427	DNA polymerase IV(lmo1975)
CAD00059	lmo1981	protein_coding	987963	hypothetical protein(lmo1981)
CAD00060	lmo1982	protein_coding	984865	hypothetical protein(lmo1982)
CAD00070	lmo1992	protein_coding	986230	alpha-acetolactate decarboxylase(lmo1992)
CAD00071	pdp	protein_coding	984377	pyrimidine-nucleoside phosphorylase(pdp)
CAD00072	lmo1994	protein_coding	984855	LacI family transcriptional regulator(lmo1994)
CAD00074	lmo1996	protein_coding	984762	DeoR family transcriptional regulator(lmo1996)
CAD00075	lmo1997	protein_coding	984854	PTS mannose transporter subunit IIA(lmo1997)
CAD00076	lmo1998	protein_coding	987959	opine catabolism protein(lmo1998)
CAD00077	lmo1999	protein_coding	984760	hypothetical protein(lmo1999)
CAD00078	lmo2000	protein_coding	984850	PTS mannose transporter subunit IID(lmo2000)
CAD00079	lmo2001	protein_coding	987965	PTS mannose transporter subunit IIC(lmo2001)
CAD00080	lmo2002	protein_coding	984415	PTS mannose transporter subunit IIB(lmo2002)
CAD00081	lmo2003	protein_coding	984849	GntR family transcriptional regulator(lmo2003)
CAD00082	lmo2004	protein_coding	987958	GntR family transcriptional regulator(lmo2004)
CAD00095	lmo2017	protein_coding	987951	hypothetical protein(lmo2017)
CAD00097	ileS	protein_coding	986874	isoleucyl-tRNA synthetase(ileS)
CAD00098	divIVA	protein_coding	984838	chemotaxis protein CheY(divIVA)
CAD00099	lmo2021	protein_coding	984837	hypothetical protein(lmo2021)
CAD00105	lmo2027	protein_coding	987947	cell surface protein, internalin proteins(lmo2027)
CAD00110	ftsZ	protein_coding	987944	cell division protein FtsZ(ftsZ)
CAD00112	divIB	protein_coding	988005	cell division protein FtsQ(divIB)
CAD00113	murG	protein_coding	984828	UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase (murG)
CAD00114	murD	protein_coding	987942	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase(murD)
CAD00115	mraY	protein_coding	984374	phospho-N-acetylmuramoyl-pentapeptide-transferase(mraY)
CAD00116	murE	protein_coding	987940	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase(murE)
CAD00117	pbpB	protein_coding	984823	penicillin-binding protein 2B(pbpB)
CAD00119	lmo2041	protein_coding	984957	S-adenosyl-methyltransferase MraW(mraW)
CAD00122	lmo2044	protein_coding	984734	peptide ABC transporter substrate-binding protein(lmo2044)
CAD00124	lmo2046	protein_coding	986332	2-dehydropantoate 2-reductase(lmo2046)
CAD00125	rpmF	protein_coding	984819	50S ribosomal protein L32(rpmF)
CAD00126	lmo2048	protein_coding	987933	hypothetical protein(lmo2048)
CAD00127	lmo2049	protein_coding	987928	hypothetical protein(lmo2049)
CAD00129	lmo2051	protein_coding	987932	hypothetical protein(lmo2051)
CAD00130	lmo2052	protein_coding	987934	phosphopantetheine adenylyltransferase(coaD)
CAD00133	lmo2055	protein_coding	984919	hypothetical protein(lmo2055)
CAD00134	lmo2056	protein_coding	984807	hypothetical protein(lmo2056)
CAD00135	ctaB	protein_coding	984806	protoheme IX farnesyltransferase(ctaB)
CAD00136	ctaA	protein_coding	984460	heme O oxygenase(ctaA)
CAD00144	lmo2066	protein_coding	984796	lmo2066(lmo2066)
CAD00145	lmo2067	protein_coding	984795	bile acid hydrolase(lmo2067)
CAD00146	groEL	protein_coding	987925	molecular chaperone GroEL(groEL)
CAD00147	groES	protein_coding	985586	co-chaperonin GroES(groES)
CAD00149	lmo2071	protein_coding	985572	lmo2071(lmo2071)
CAD00150	lmo2072	protein_coding	984371	redox-sensing transcriptional repressor Rex(lmo2072)
CAD00155	lmo2077	protein_coding	987921	glycoprotease(lmo2077)
CAD00157	lmo2079	protein_coding	984776	lmo2079(lmo2079)

CAD00158	lmo2080	protein_coding	984774	lmo2080(lmo2080)
CAD00162	lmo2084	protein_coding	984631	lmo2084(lmo2084)
CAD00163	lmo2085	protein_coding	984772	peptidoglycan binding protein(lmo2085)
CAD00167	lmo2089	protein_coding	984766	lipase(lmo2089)
CAD00168	argG	protein_coding	984368	argininosuccinate synthase(argG)
CAD00169	argH	protein_coding	987914	argininosuccinate lyase(argH)
CAD00170	betL	protein_coding	987924	glycine betaine transporter BetL(betL)
CAD00179	lmo2101	protein_coding	984461	pyridoxal biosynthesis lyase PdxS(lmo2101)
CAD00180	lmo2102	protein_coding	984751	lmo2102(lmo2102)
CAD00181	pta	protein_coding	987908	phosphotransacetylase(eutD)
CAD00184	lmo2106	protein_coding	984749	hypothetical protein(lmo2106)
CAD00185	lmo2107	protein_coding	984748	DeoR family transcriptional regulator(lmo2107)
CAD00186	lmo2108	protein_coding	988008	N-acetylglucosamine-6-phosphate deacetylase(lmo2108)
CAD00187	lmo2109	protein_coding	984746	hydrolase(lmo2109)
CAD00189	lmo2111	protein_coding	984745	nitroreductase(lmo2111)
CAD00190	lmo2112	protein_coding	985597	lmo2112(lmo2112)
CAD00191	lmo2113	protein_coding	984744	heme peroxidase(lmo2113)
CAD00192	lmo2114	protein_coding	987889	ABC transporter ATP-binding protein(lmo2114)
CAD00193	lmo2115	protein_coding	987993	ABC transporter permease(lmo2115)
CAD00197	lmo2119	protein_coding	985280	hypothetical protein(lmo2119)
CAD00198	lmo2120	protein_coding	984739	hypothetical protein(lmo2120)
CAD00199	lmo2121	protein_coding	987891	maltose phosphorylase(lmo2121)
CAD00201	lmo2123	protein_coding	984732	sugar ABC transporter permease(lmo2123)
CAD00202	lmo2124	protein_coding	987890	sugar ABC transporter permease(lmo2124)
CAD00203	lmo2125	protein_coding	987894	sugar ABC transporter substrate-binding protein(lmo2125)
CAD00206	lmo2128	protein_coding	987887	LacI family transcriptional regulator(lmo2128)
CAD00208	lmo2130	protein_coding	984779	hypothetical protein(lmo2130)
CAD00209	lmo2131	protein_coding	984721	lmo2131(lmo2131)
CAD00210	lmo2132	protein_coding	985218	lmo2132(lmo2132)
CAD00216	lmo2138	protein_coding	984707	transcriptional regulator(lmo2138)
CAD00217	lmo2139	protein_coding	984576	ABC transporter ATP-binding protein(lmo2139)
CAD00218	lmo2140	protein_coding	988001	ABC transporter permease(lmo2140)
CAD00219	lmo2141	protein_coding	984706	hypothetical protein(lmo2141)
CAD00220	lmo2142	protein_coding	985289	lmo2142(lmo2142)
CAD00221	lmo2143	protein_coding	984703	hypothetical protein(lmo2143)
CAD00223	lmo2145	protein_coding	985144	hypothetical protein(lmo2145)
CAD00224	lmo2146	protein_coding	984701	LysR family transcriptional regulator(lmo2146)
CAD00225	lmo2147	protein_coding	984698	hypothetical protein(lmo2147)
CAD00227	lmo2149	protein_coding	984696	hypothetical protein(lmo2149)
CAD00229	lmo2151	protein_coding	984692	hypothetical protein(lmo2151)
CAD00235	sepA	protein_coding	987998	sepA(sepA)
CAD00236	lmo2158	protein_coding	984441	hypothetical protein(lmo2158)
CAD00252	lmo2174	protein_coding	986302	hypothetical protein(lmo2174)
CAD00253	lmo2175	protein_coding	984669	3-ketoacyl-ACP reductase(fabG)
CAD00254	lmo2176	protein_coding	984665	TetR family transcriptional regulator(lmo2176)
CAD00256	lmo2178	protein_coding	984662	peptidoglycan binding protein(lmo2178)
CAD00258	lmo2180	protein_coding	984657	hypothetical protein(lmo2180)
CAD00259	lmo2181	protein_coding	984655	hypothetical protein(lmo2181)

CAD00260	lmo2182	protein_coding	984654	ferrichrome ABC transporter ATP-binding protein(lmo2182)
CAD00261	lmo2183	protein_coding	984509	ferrichrome ABC transporter permease(lmo2183)
CAD00262	lmo2184	protein_coding	984651	ferrichrome ABC transporter substrate-binding protein(lmo2184)
CAD00263	lmo2185	protein_coding	984803	lmo2185(lmo2185)
CAD00264	lmo2186	protein_coding	984742	lmo2186(lmo2186)
CAD00266	lmo2188	protein_coding	984648	oligoendopeptidase(lmo2188)
CAD00267	lmo2189	protein_coding	988007	competence protein CoiA(lmo2189)
CAD00268	mecA	protein_coding	984925	adaptor protein(mecA)
CAD00269	lmo2191	protein_coding	988006	ArsC family transcriptional regulator(spxA)
CAD00270	lmo2192	protein_coding	984647	peptide ABC transporter ATP-binding protein(lmo2192)
CAD00271	lmo2193	protein_coding	984646	peptide ABC transporter ATP-binding protein(lmo2193)
CAD00272	lmo2194	protein_coding	984644	peptide ABC transporter permease(lmo2194)
CAD00273	lmo2195	protein_coding	984916	peptide ABC transporter permease(lmo2195)
CAD00274	lmo2196	protein_coding	984918	peptide ABC transporter substrate-binding protein(lmo2196)
CAD00276	trpS	protein_coding	984829	tryptophanyl-tRNA synthetase(trpS)
CAD00277	lmo2199	protein_coding	984811	hypothetical protein(lmo2199)
CAD00278	lmo2200	protein_coding	984642	MarR family transcriptional regulator(lmo2200)
CAD00279	lmo2201	protein_coding	985883	3-oxoacyl-ACP synthase(lmo2201)
CAD00280	lmo2202	protein_coding	984640	3-oxoacyl-ACP synthase(lmo2202)
CAD00281	lmo2203	protein_coding	984639	N-acetylmuramoyl-L-alanine amidase(lmo2203)
CAD00283	lmo2205	protein_coding	986282	phosphoglyceromutase(lmo2205)
CAD00284	clpB	protein_coding	985416	Clp protease subunit B(clpB)
CAD00286	lmo2208	protein_coding	984636	hypothetical protein(lmo2208)
CAD00288	lmo2210	protein_coding	984633	lmo2210(lmo2210)
CAD00291	lmo2213	protein_coding	984794	hypothetical protein(lmo2213)
CAD00292	lmo2214	protein_coding	985371	ABC transporter permease(lmo2214)
CAD00293	lmo2215	protein_coding	984629	ABC transporter ATP-binding protein(lmo2215)
CAD00296	lmo2218	protein_coding	985873	lmo2218(lmo2218)
CAD00297	lmo2219	protein_coding	984626	foldase(lmo2219)
CAD00299	lmo2221	protein_coding	984625	hypothetical protein(lmo2221)
CAD00302	lmo2224	protein_coding	985253	hypothetical protein(lmo2224)
CAD00303	citG	protein_coding	987997	fumarate hydratase(fumC)
CAD00308	lmo2230	protein_coding	986212	arsenate reductase(lmo2230)
CAD00309	lmo2231	protein_coding	984616	hypothetical protein(lmo2231)
CAD00310	lmo2232	protein_coding	984442	hypothetical protein(lmo2232)
CAD00311	lmo2233	protein_coding	986617	LysR family transcriptional regulator(lmo2233)
CAD00320	lmo2242	protein_coding	985837	O6-methylguanine-DNA methyltransferase(lmo2242)
CAD00321	lmo2243	protein_coding	984592	AraC family transcriptional regulator(lmo2243)
CAD00322	lmo2244	protein_coding	984802	ribosomal large subunit pseudouridine synthase(lmo2244)
CAD00325	lmo2247	protein_coding	984590	oxidoreductase(lmo2247)
CAD00326	lmo2248	protein_coding	984588	hypothetical protein(lmo2248)
CAD00327	lmo2249	protein_coding	984840	low-affinity inorganic phosphate transporter(lmo2249)
CAD00328	arpJ	protein_coding	984583	amino acid ABC transporter permease(arpJ)
CAD00329	lmo2251	protein_coding	984693	amino acid ABC transporter ATP-binding protein(lmo2251)
CAD00330	lmo2252	protein_coding	984582	aspartate aminotransferase(lmo2252)
CAD00331	lmo2253	protein_coding	984901	phosphoglucomutase(lmo2253)
CAD00332	lmo2254	protein_coding	984903	hypothetical protein(lmo2254)
CAD00336	lmo2258	protein_coding	984575	lmo2258(lmo2258)

CAD00340	lmo2262	protein_coding	984566	hypothetical protein(lmo2262)
CAD00343	lmo2265	protein_coding	984574	hypothetical protein(lmo2265)
CAD00344	lmo2266	protein_coding	984562	hypothetical protein(lmo2266)
CAD00345	lmo2267	protein_coding	985303	ATP-dependent deoxyribonuclease subunit A(lmo2267)
CAD00346	addB	protein_coding	984656	ATP-dependent deoxyribonuclease subunit B(addB)
CAD00347	lmo2269	protein_coding	988009	lmo2269(lmo2269)
CAD00366	lmo2288	protein_coding	984603	protein gp15(lmo2288)
CAD00377	lmo2299	protein_coding	984584	portal protein(lmo2299)
CAD00378	lmo2300	protein_coding	984593	terminase large subunit from bacteriophage A118(lmo2300)
CAD00381	lmo2303	protein_coding	984511	hypothetical protein(lmo2303)
CAD00383	lmo2305	protein_coding	984560	lmo2305(lmo2305)
CAD00402	lmo2324	protein_coding	986505	anti-repressor(lmo2324)
CAD00405	lmo2327	protein_coding	984480	lmo2327(lmo2327)
CAD00408	lmo2330	protein_coding	985317	hypothetical protein(lmo2330)
CAD00410	int	protein_coding	986704	integrase(int)
CAD00413	fruA	protein_coding	984474	PTS fructose transporter subunit IIABC(fruA)
CAD00414	fruB	protein_coding	984473	fructose-1-phosphate kinase(fruB)
CAD00415	lmo2337	protein_coding	986688	DeoR family transcriptional regulator(lmo2337)
CAD00417	lmo2339	protein_coding	984799	hypothetical protein(lmo2339)
CAD00418	lmo2340	protein_coding	984465	hypothetical protein(lmo2340)
CAD00419	lmo2341	protein_coding	984892	sugar kinase(lmo2341)
CAD00424	lmo2346	protein_coding	984455	amino acid ABC transporter ATP-binding protein(lmo2346)
CAD00426	lmo2348	protein_coding	984447	amino acid ABC transporter permease(lmo2348)
CAD00428	lmo2350	protein_coding	984858	hypothetical protein(lmo2350)
CAD00431	lmo2353	protein_coding	984445	Na+/H+ antiporter(lmo2353)
CAD00432	lmo2354	protein_coding	984444	hypothetical protein(lmo2354)
CAD00433	lmo2355	protein_coding	985985	multidrug resistance protein(lmo2355)
CAD00434	lmo2356	protein_coding	984439	lmo2356(lmo2356)
CAD00435	lmo2357	protein_coding	984422	hypothetical protein(lmo2357)
CAD00436	lmo2358	protein_coding	984434	N-acetylglucosamine-6-phosphate isomerase(lmo2358)
CAD00437	lmo2359	protein_coding	984722	hypothetical protein(lmo2359)
CAD00438	lmo2360	protein_coding	984433	transmembrane protein(lmo2360)
CAD00439	lmo2361	protein_coding	984432	hypothetical protein(lmo2361)
CAD00442	lmo2364	protein_coding	984429	hypothetical protein(lmo2364)
CAD00444	lmo2366	protein_coding	984418	DeoR family transcriptional regulator(lmo2366)
CAD00451	lmo2373	protein_coding	984403	PTS beta-glucoside transporter subunit IIB(lmo2373)
CAD00452	lmo2374	protein_coding	984416	aspartate kinase(lmo2374)
CAD00464	lmo2386	protein_coding	987551	hypothetical protein(lmo2386)
CAD00465	lmo2387	protein_coding	987550	hypothetical protein(lmo2387)
CAD00466	lmo2388	protein_coding	987547	hypothetical protein(lmo2388)
CAD00467	lmo2389	protein_coding	987546	NADH dehydrogenase(lmo2389)
CAD00469	lmo2391	protein_coding	987544	hypothetical protein(lmo2391)
CAD00476	ltrC	protein_coding	987501	hypothetical protein(ltrC)
CAD00477	lmo2399	protein_coding	987500	hypothetical protein(lmo2399)
CAD00479	lmo2401	protein_coding	987498	hypothetical protein(lmo2401)
CAD00480	lmo2402	protein_coding	987497	hypothetical protein(lmo2402)
CAD00482	lmo2404	protein_coding	987494	hypothetical protein(lmo2404)
CAD00484	lmo2406	protein_coding	987489	hypothetical protein(lmo2406)

CAD00489	lmo2411	protein_coding	987479	hypothetical protein(lmo2411)
CAD00494	lmo2416	protein_coding	987472	lmo2416(lmo2416)
CAD00503	lmo2425	protein_coding	987446	glycine cleavage system protein H(lmo2425)
CAD00504	lmo2426	protein_coding	987443	hypothetical protein(lmo2426)
CAD00508	lmo2430	protein_coding	987428	ferrichrome ABC transporter permease(lmo2430)
CAD00510	lmo2432	protein_coding	987423	lmo2432(lmo2432)
CAD00512	lmo2434	protein_coding	987419	glutamate decarboxylase(lmo2434)
CAD00514	lmo2436	protein_coding	987417	transcription antiterminator(lmo2436)
CAD00515	lmo2437	protein_coding	987416	lmo2437(lmo2437)
CAD00531	lmo2453	protein_coding	987384	epoxide hydrolase(lmo2453)
CAD00532	lmo2454	protein_coding	987383	lmo2454(lmo2454)
CAD00539	sigL	protein_coding	987375	RNA polymerase factor sigma-54(sigL)
CAD00541	lmo2463	protein_coding	987371	multidrug transporter(lmo2463)
CAD00544	lmo2466	protein_coding	987366	lmo2466(lmo2466)
CAD00546	clpP	protein_coding	987364	ATP-dependent Clp protease proteolytic subunit(clpP)
CAD00547	lmo2469	protein_coding	987361	amino acid transporter(lmo2469)
CAD00549	lmo2471	protein_coding	987354	NADPH dehydrogenase(lmo2471)
CAD00550	lmo2472	protein_coding	987353	hypothetical protein(lmo2472)
CAD00556	trxB	protein_coding	987338	thioredoxin reductase(trxB)
CAD00557	lmo2479	protein_coding	987336	lmo2479(lmo2479)
CAD00558	lmo2480	protein_coding	987334	acetyltransferase(lmo2480)
CAD00560	lgt	protein_coding	987331	prolipoprotein diacylglyceryl transferase(lgt)
CAD00561	lmo2483	protein_coding	987330	HPr kinase/phosphorylase(lmo2483)
CAD00562	lmo2484	protein_coding	987328	hypothetical protein(lmo2484)
CAD00563	lmo2485	protein_coding	987327	hypothetical protein(lmo2485)
CAD00564	lmo2486	protein_coding	987324	lmo2486(lmo2486)
CAD00565	lmo2487	protein_coding	987322	hypothetical protein(lmo2487)
CAD00566	uvrA	protein_coding	987320	excinuclease ABC subunit A(uvrA)
CAD00567	uvrB	protein_coding	987319	excinuclease ABC subunit B(uvrB)
CAD00569	lmo2491	protein_coding	987316	lmo2491(lmo2491)
CAD00570	lmo2492	protein_coding	987892	lmo2492(lmo2492)
CAD00571	lmo2493	protein_coding	987893	ArsR family transcriptional regulator(lmo2493)
CAD00572	lmo2494	protein_coding	987895	PhoU family transcriptional regulator(lmo2494)
CAD00573	lmo2495	protein_coding	987314	phosphate ABC transporter ATP-binding protein(lmo2495)
CAD00574	lmo2496	protein_coding	987313	phosphate ABC transporter ATP-binding protein(lmo2496)
CAD00575	lmo2497	protein_coding	987312	phosphate ABC transporter permease(lmo2497)
CAD00577	lmo2499	protein_coding	987906	phosphate ABC transporter substrate-binding protein(lmo2499)
CAD00580	lmo2502	protein_coding	987905	lmo2502(lmo2502)
CAD00581	lmo2503	protein_coding	987903	cardiolipin synthase(lmo2503)
CAD00582	lmo2504	protein_coding	987901	cell wall-binding protein(lmo2504)
CAD00583	spl	protein_coding	987309	peptidoglycan lytic protein P45(spl)
CAD00586	lmo2508	protein_coding	984634	hypothetical protein(lmo2508)
CAD00589	lmo2511	protein_coding	986743	hypothetical protein(lmo2511)
CAD00592	lmo2514	protein_coding	985904	hypothetical protein(lmo2514)
CAD00593	lmo2515	protein_coding	987300	two-component response regulator DegU(lmo2515)
CAD00594	lmo2516	protein_coding	987299	hypothetical protein(lmo2516)
CAD00595	lmo2517	protein_coding	987297	lmo2517(lmo2517)
CAD00598	lmo2520	protein_coding	987296	O-succinylbenzoate-CoA synthase(lmo2520)

CAD00602	lmo2524	protein_coding	987293	(3R)-hydroxymyristoyl-ACP dehydratase(fabZ)
CAD00603	mbl	protein_coding	986838	rod shape-determining protein MreB(mbl)
CAD00604	murA	protein_coding	984514	UDP-N-acetylglucosamine 1-carboxyvinyltransferase(murA)
CAD00610	atpH	protein_coding	986758	ATP synthase F0F1 subunit delta(atpH)
CAD00611	atpF	protein_coding	987284	ATP synthase F0F1 subunit B(atpF)
CAD00612	atpE	protein_coding	987281	ATP synthase F0F1 subunit C(atpE)
CAD00615	lmo2537	protein_coding	987487	UDP-N-acetylglucosamine 2-epimerase(lmo2537)
CAD00616	upp	protein_coding	986484	uracil phosphoribosyltransferase(upp)
CAD00618	lmo2540	protein_coding	987277	phosphatase(lmo2540)
CAD00619	lmo2541	protein_coding	986761	tRNA threonylcarbamoyladenosine biosynthesis protein(lmo2541)
CAD00620	lmo2542	protein_coding	986635	protoporphyrinogen oxidase(lmo2542)
CAD00621	prf1	protein_coding	986736	peptide chain release factor 1(prfA)
CAD00622	lmo2544	protein_coding	986601	thymidine kinase(lmo2544)
CAD00623	thrB	protein_coding	984754	homoserine kinase(thrB)
CAD00624	thrC	protein_coding	986503	threonine synthase(thrC)
CAD00625	hom	protein_coding	987269	homoserine dehydrogenase(hom)
CAD00628	lmo2550	protein_coding	987266	glycosyl transferase(lmo2550)
CAD00629	rho	protein_coding	987264	transcription termination factor Rho(rho)
CAD00634	fbaA	protein_coding	986313	fructose-1,6-bisphosphate aldolase(fbaA)
CAD00635	lmo2557	protein_coding	987255	lipid kinase(lmo2557)
CAD00636	ami	protein_coding	987254	autolysin, amidase(ami)
CAD00637	pyrG	protein_coding	987251	CTP synthase(pyrG)
CAD00638	lmo2560	protein_coding	987250	DNA-directed RNA polymerase subunit delta(lmo2560)
CAD00639	argS	protein_coding	984764	arginyl-tRNA synthetase(argS)
CAD00645	lmo2567	protein_coding	984546	lmo2567(lmo2567)
CAD00646	lmo2568	protein_coding	987246	lmo2568(lmo2568)
CAD00647	lmo2569	protein_coding	987245	peptide ABC transporter substrate-binding protein(lmo2569)
CAD00648	lmo2570	protein_coding	984821	lmo2570(lmo2570)
CAD00649	lmo2571	protein_coding	987244	nicotinamidase(lmo2571)
CAD00650	lmo2572	protein_coding	985849	dihydrofolate reductase subunit A(lmo2572)
CAD00651	lmo2573	protein_coding	987242	zinc-binding dehydrogenase(lmo2573)
CAD00652	lmo2574	protein_coding	987241	lmo2574(lmo2574)
CAD00653	lmo2575	protein_coding	986612	cation transporter(lmo2575)
CAD00655	lmo2577	protein_coding	987240	hypothetical protein(lmo2577)
CAD00656	lmo2578	protein_coding	987239	lmo2578(lmo2578)
CAD00660	lmo2582	protein_coding	985564	histidine kinase(lmo2582)
CAD00662	lmo2584	protein_coding	987234	formate dehydrogenase accessory protein(lmo2584)
CAD00663	lmo2585	protein_coding	987233	hypothetical protein(lmo2585)
CAD00664	lmo2586	protein_coding	987231	formate dehydrogenase subunit alpha(lmo2586)
CAD00665	lmo2587	protein_coding	987227	hypothetical protein(lmo2587)
CAD00666	lmo2588	protein_coding	987224	multidrug transporter(lmo2588)
CAD00667	lmo2589	protein_coding	987223	TetR family transcriptional regulator(lmo2589)
CAD00669	lmo2591	protein_coding	984569	N-acetylmuramoyl-L-alanine amidase(lmo2591)
CAD00671	lmo2593	protein_coding	987218	MerR family transcriptional regulator(lmo2593)
CAD00673	lmo2595	protein_coding	986306	hypothetical protein(lmo2595)
CAD00674	rpsI	protein_coding	987216	30S ribosomal protein S9(rpsI)
CAD00680	lmo2602	protein_coding	987211	hypothetical protein(lmo2602)
CAD00681	lmo2603	protein_coding	987210	lmo2603(lmo2603)

CAD00683	rplQ	protein_coding	987205	50S ribosomal protein L17(rplQ)
CAD00684	rpoA	protein_coding	984700	DNA-directed RNA polymerase subunit alpha(rpoA)
CAD00685	rpsK	protein_coding	985385	30S ribosomal protein S11(rpsK)
CAD00686	rpsM	protein_coding	984551	30S ribosomal protein S13(rpsM)
CAD00688	infA	protein_coding	984951	translation initiation factor IF-1(infA)
CAD00689	adk	protein_coding	984533	adenylate kinase(adk)
CAD00691	rplO	protein_coding	987200	50S ribosomal protein L15(rplO)
CAD00693	rpsE	protein_coding	987198	30S ribosomal protein S5(rpsE)
CAD00694	rplR	protein_coding	987197	50S ribosomal protein L18(rplR)
CAD00695	rplF	protein_coding	987196	50S ribosomal protein L6(rplF)
CAD00696	rpsH	protein_coding	987195	30S ribosomal protein S8(rpsH)
CAD00697	rpsN	protein_coding	987193	30S ribosomal protein S14(rpsN)
CAD00698	rplE	protein_coding	987192	50S ribosomal protein L5(rplE)
CAD00699	rplX	protein_coding	987191	50S ribosomal protein L24(rplX)
CAD00700	rplN	protein_coding	987190	50S ribosomal protein L14(rplN)
CAD00701	rpsQ	protein_coding	987189	30S ribosomal protein S17(rpsQ)
CAD00702	rpmC	protein_coding	987188	50S ribosomal protein L29(rpmC)
CAD00703	rplP	protein_coding	985437	50S ribosomal protein L16(rplP)
CAD00704	rpsC	protein_coding	987185	30S ribosomal protein S3(rpsC)
CAD00706	rpsS	protein_coding	984385	30S ribosomal protein S19(rpsS)
CAD00707	rplB	protein_coding	985132	50S ribosomal protein L2(rplB)
CAD00708	rplW	protein_coding	984375	50S ribosomal protein L23(rplW)
CAD00709	rplD	protein_coding	987182	50S ribosomal protein L4(rplD)
CAD00710	rplC	protein_coding	987181	50S ribosomal protein L3(rplC)
CAD00711	rpsJ	protein_coding	987179	30S ribosomal protein S10(rpsJ)
CAD00712	lmo2634	protein_coding	987178	hypothetical protein(lmo2634)
CAD00713	lmo2635	protein_coding	987177	1,4-dihydroxy-2-naphthoate octaprenyltransferase(lmo2635)
CAD00714	lmo2636	protein_coding	987176	hypothetical protein(lmo2636)
CAD00716	lmo2638	protein_coding	986300	NADH dehydrogenase(lmo2638)
CAD00720	lmo2642	protein_coding	984410	lmo2642(lmo2642)
CAD00721	lmo2643	protein_coding	985362	lmo2643(lmo2643)
CAD00722	lmo2644	protein_coding	986304	lmo2644(lmo2644)
CAD00725	gcaD	protein_coding	987026	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase(glmU)
CAD00726	prs	protein_coding	987027	ribose-phosphate pyrophosphokinase(prs)
CAD00727	prfA	protein_coding	987031	listeriolysin positive regulatory protein(prfA)
CAD00733	lmo0206	protein_coding	987037	lmo0206(lmo0206)
CAD00734	lmo0207	protein_coding	987038	Uncharacterized lipoprotein Lmo0207 precursor.(lmo0207)
CAD00736	lmo0209	protein_coding	987042	lmo0209(lmo0209)
CAD00737	ldh	protein_coding	987043	L-lactate dehydrogenase(ldh)
CAD00738	ctc	protein_coding	987044	50S ribosomal protein L25(ctc)
CAD00746	lmo0219	protein_coding	987055	hypothetical protein(lmo0219)
CAD00754	lmo0227	protein_coding	987098	hypothetical protein(lmo0227)
CAD00755	lysS	protein_coding	987100	lysyl-tRNA synthetase(lysS)
CAD00756	lmo0229	protein_coding	987186	CtsR family transcriptional regulator(lmo0229)
CAD00757	lmo0230	protein_coding	987194	hypothetical protein(lmo0230)
CAD00758	lmo0231	protein_coding	987202	ATP:guanido phosphotransferase(lmo0231)
CAD00759	clpC	protein_coding	987203	endopeptidase Clp ATP-binding chain C(clpC)

CAD00765	cysE	protein_coding	987230	serine O-acetyltransferase(cysE)
CAD00770	sigH	protein_coding	987276	RNA polymerase factor sigma-70(sigH)
CAD00773	nusG	protein_coding	987288	transcription antitermination protein NusG(nusG)
CAD00774	lmo0247	protein_coding	987292	lmo0247(lmo0247)
CAD00775	rplK	protein_coding	987298	50S ribosomal protein L11(rplK)
CAD00776	rplA	protein_coding	987301	50S ribosomal protein L1(rplA)
CAD00777	rplJ	protein_coding	987306	50S ribosomal protein L10(rplJ)
CAD00778	rplL	protein_coding	987315	50S ribosomal protein L7/L12(rplL)
CAD00779	lmo0252	protein_coding	987321	penicilinase repressor(lmo0252)
CAD00781	lmo0254	protein_coding	987329	lmo0254(lmo0254)
CAD00782	lmo0255	protein_coding	987335	hypothetical protein(lmo0255)
CAD00783	lmo0256	protein_coding	987337	hypothetical protein(lmo0256)
CAD00784	lmo0257	protein_coding	987339	hypothetical protein(lmo0257)
CAD00785	rpoB	protein_coding	987342	DNA-directed RNA polymerase subunit beta(rpoB)
CAD00786	rpoC	protein_coding	987344	DNA-directed RNA polymerase subunit beta'(rpoC)
CAD00787	lmo0260	protein_coding	987345	hypothetical protein(lmo0260)
CAD00788	lmo0261	protein_coding	987346	phospho-beta-glucosidase(lmo0261)
CAD00790	inlH	protein_coding	987355	internalin H(inlH)
CAD00792	lmo0265	protein_coding	987360	succinyl-diaminopimelate desuccinylase(lmo0265)
CAD00793	lmo0266	protein_coding	987368	transcriptional regulator(lmo0266)
CAD00795	lmo0268	protein_coding	987396	phosphoglycerate mutase(lmo0268)
CAD00796	lmo0269	protein_coding	987397	transporter(lmo0269)
CAD00799	lmo0272	protein_coding	987400	hypothetical protein(lmo0272)
CAD00800	lmo0273	protein_coding	987401	lmo0273(lmo0273)
CAD00801	lmo0274	protein_coding	987410	lmo0274(lmo0274)
CAD00802	lmo0275	protein_coding	987414	hypothetical protein(lmo0275)
CAD00804	lmo0277	protein_coding	987427	oxidoreductase(lmo0277)
CAD00808	lmo0281	protein_coding	987437	lmo0281(lmo0281)
CAD00810	lmo0283	protein_coding	987440	ABC transporter permease(lmo0283)
CAD00811	lmo0284	protein_coding	987441	ABC transporter ATP-binding protein(lmo0284)
CAD00812	lmo0285	protein_coding	987445	lipoprotein(lmo0285)
CAD00813	lmo0286	protein_coding	987447	aminotransferase(lmo0286)
CAD00815	lmo0288	protein_coding	987449	two-component sensor histidine kinase(lmo0288)
CAD00816	lmo0289	protein_coding	987451	hypothetical protein(lmo0289)
CAD00817	lmo0290	protein_coding	987453	hypothetical protein(lmo0290)
CAD00818	lmo0291	protein_coding	987454	hypothetical protein(lmo0291)
CAD00819	lmo0292	protein_coding	987455	heat-shock protein htrA serine protease(lmo0292)
CAD00820	lmo0293	protein_coding	987456	rRNA large subunit methyltransferase(lmo0293)
CAD00823	lmo0296	protein_coding	987461	lmo0296(lmo0296)
CAD00833	lmo0306	protein_coding	987520	lmo0306(lmo0306)
CAD00837	lmo0310	protein_coding	987524	lmo0310(lmo0310)
CAD00838	lmo0311	protein_coding	987525	lmo0311(lmo0311)
CAD00840	lmo0313	protein_coding	987528	hypothetical protein(lmo0313)
CAD00843	lmo0316	protein_coding	987532	hydroxyethylthiazole kinase(lmo0316)
CAD00846	lmo0319	protein_coding	987537	phospho-beta-glucosidase(lmo0319)
CAD00848	lmo0321	protein_coding	987539	hypothetical protein(lmo0321)
CAD00849	lmo0322	protein_coding	987554	hypothetical protein(lmo0322)
CAD00850	lmo0323	protein_coding	987557	hypothetical protein(lmo0323)

CAD00852	lmo0325	protein_coding	987559	transcriptional regulator(lmo0325)
CAD00853	lmo0326	protein_coding	987560	transcriptional regulator(lmo0326)
CAD00859	lmo2646	protein_coding	985483	lmo2646(lmo2646)
CAD00861	lmo2648	protein_coding	987171	phosphotriesterase(lmo2648)
CAD00862	lmo2649	protein_coding	987170	PTS system ascorbate transporter subunit IIC(ulaA)
CAD00863	lmo2650	protein_coding	987169	MFS transporter(lmo2650)
CAD00864	lmo2651	protein_coding	984393	PTS mannitol transporter subunit IIA(lmo2651)
CAD00867	fus	protein_coding	986619	elongation factor G(fus)
CAD00875	lmo2662	protein_coding	984684	ribose 5-phosphate epimerase(lmo2662)
CAD00877	lmo2664	protein_coding	987161	sorbitol dehydrogenase(lmo2664)
CAD00881	lmo2668	protein_coding	987157	transcriptional antiterminator BglG(lmo2668)
CAD00883	lmo2670	protein_coding	984436	hypothetical protein(lmo2670)
CAD00884	lmo2671	protein_coding	987155	lmo2671(lmo2671)
CAD00885	lmo2672	protein_coding	987154	AraC family transcriptional regulator(lmo2672)
CAD00886	lmo2673	protein_coding	987153	hypothetical protein(lmo2673)
CAD00887	lmo2674	protein_coding	987152	ribose-5-phosphate isomerase B(lmo2674)
CAD00893	kdpC	protein_coding	987150	potassium-transporting ATPase subunit C(kdpC)
CAD00902	lmo2689	protein_coding	987136	magnesium-translocating P-type ATPase(lmo2689)
CAD00905	lmo2692	protein_coding	984921	lmo2692(lmo2692)
CAD00907	lmo2694	protein_coding	987130	lysine decarboxylase(lmo2694)
CAD00908	lmo2695	protein_coding	987129	dihydroxyacetone kinase subunit DhaK(lmo2695)
CAD00909	lmo2696	protein_coding	987127	dihydroxyacetone kinase(lmo2696)
CAD00910	lmo2697	protein_coding	987124	PTS mannose transporter subunit IIA(lmo2697)
CAD00911	lmo2698	protein_coding	987122	RpiR family transcriptional regulator(lmo2698)
CAD00912	lmo2699	protein_coding	987121	hypothetical protein(lmo2699)
CAD00914	lmo2701	protein_coding	987119	hypothetical protein(lmo2701)
CAD00915	recR	protein_coding	987118	recombination protein RecR(recR)
CAD00917	dnaX	protein_coding	987116	DNA polymerase III subunit gamma/tau(dnaX)
CAD00921	lmo2708	protein_coding	987113	PTS cellbiose transporter subunit IIC(lmo2708)
CAD00928	cydD	protein_coding	984392	ABC transporter ATP-binding protein(cydD)
CAD00929	cydC	protein_coding	986034	ABC transporter(cydC)
CAD00930	cydB	protein_coding	987101	cytochrome D ubiquinol oxidase subunit II(cydB)
CAD00931	cydA	protein_coding	987099	cytochrome D ubiquinol oxidase subunit I(cydA)
CAD00933	lmo2720	protein_coding	987095	acetate-CoA ligase(lmo2720)
CAD00934	lmo2721	protein_coding	984959	6-phosphogluconolactonase(lmo2721)
CAD00937	lmo2724	protein_coding	984922	hypothetical protein(lmo2724)
CAD00938	lmo2725	protein_coding	986997	hypothetical protein(lmo2725)
CAD00939	lmo2726	protein_coding	987090	MarR family transcriptional regulator(lmo2726)
CAD00940	lmo2727	protein_coding	987088	hypothetical protein(lmo2727)
CAD00941	lmo2728	protein_coding	987087	MerR family transcriptional regulator(lmo2728)
CAD00942	lmo2729	protein_coding	987085	hypothetical protein(lmo2729)
CAD00946	lmo2733	protein_coding	987079	PTS fructose transporter subunit IIABC(lmo2733)
CAD00947	lmo2734	protein_coding	987078	sugar hydrolase(lmo2734)
CAD00948	lmo2735	protein_coding	987075	sucrose phosphorylase(lmo2735)
CAD00949	lmo2736	protein_coding	987073	hypothetical protein(lmo2736)
CAD00952	lmo2739	protein_coding	987067	NAD-dependent deacetylase(lmo2739)
CAD00953	lmo2740	protein_coding	985142	lmo2740(lmo2740)
CAD00954	lmo2741	protein_coding	987061	multidrug transporter(lmo2741)

CAD00955	lmo2742	protein_coding	987057	lmo2742(lmo2742)
CAD00956	lmo2743	protein_coding	987056	translaldolase(lmo2743)
CAD00958	lmo2745	protein_coding	987054	ABC transporter ATP-binding protein(lmo2745)
CAD00959	lmo2746	protein_coding	987030	lmo2746(lmo2746)
CAD00960	serS	protein_coding	987010	seryl-tRNA synthetase(serS)
CAD00961	lmo2748	protein_coding	984689	hypothetical protein(lmo2748)
CAD00964	lmo2751	protein_coding	984683	ABC transporter ATP-binding protein(lmo2751)
CAD00965	lmo2752	protein_coding	984457	ABC transporter ATP-binding protein(lmo2752)
CAD00967	lmo2754	protein_coding	986888	D-alanyl-D-alanine carboxypeptidase(lmo2754)
CAD00968	lmo2755	protein_coding	986886	CoA-transferase(lmo2755)
CAD00969	topB	protein_coding	985520	DNA topoisomerase III(topB)
CAD00970	lmo2757	protein_coding	986884	ATP-dependent DNA helicase(lmo2757)
CAD00971	guaB	protein_coding	986870	inosine-monophosphate dehydrogenase(guaB)
CAD00972	lmo2759	protein_coding	986677	hypothetical protein(lmo2759)
CAD00974	lmo2761	protein_coding	986859	beta-glucosidase(lmo2761)
CAD00975	lmo2762	protein_coding	986856	PTS cellbiose transporter subunit IIB(lmo2762)
CAD00976	lmo2763	protein_coding	986739	PTS cellbiose transporter subunit IIC(lmo2763)
CAD00977	lmo2764	protein_coding	986173	ROK family transcriptional regulator(lmo2764)
CAD00978	lmo2765	protein_coding	984518	PTS cellbiose transporter subunit IIA(lmo2765)
CAD00979	lmo2766	protein_coding	986816	RpiR family transcriptional regulator(lmo2766)
CAD00980	lmo2767	protein_coding	986810	lmo2767(lmo2767)
CAD00981	lmo2768	protein_coding	986273	hypothetical membrane protein(lmo2768)
CAD00982	lmo2769	protein_coding	986801	ABC transporter ATP-binding protein(lmo2769)
CAD00983	lmo2770	protein_coding	986798	bifunctional glutamate--cysteine ligase/glutathione synthetase(lmo2770)
CAD00986	lmo2773	protein_coding	986771	transcriptional antiterminator(lmo2773)
CAD00992	lmo2779	protein_coding	986766	GTP-binding protein EngD(lmo2779)
CAD00998	kat	protein_coding	984948	catalase(kat)
CAD00999	bvrC	protein_coding	986755	bvrC(bvrC)
CAD01000	bvrB	protein_coding	986754	beta-glucoside-specific phosphotransferase enzyme II ABC component(bvrB)
CAD01005	lmo2792	protein_coding	986982	lmo2792(lmo2792)
CAD01007	lmo2794	protein_coding	986747	NA-binding protein Spo0J(lmo2794)
CAD01015	gidB	protein_coding	986719	16S rRNA methyltransferase GidB(gidB)
CAD01019	lmo2806	protein_coding	985133	hypothetical secreted protein(lmo2806)
CAD01023	gidA	protein_coding	986685	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA(gidA)
CAD01027	lmo2814	protein_coding	986681	TetR family transcriptional regulator(lmo2814)
CAD01033	lmo2820	protein_coding	986657	amino-terminal domain-containing protein(lmo2820)
CAD01041	lmo2828	protein_coding	986627	lmo2828(lmo2828)
CAD01042	lmo2829	protein_coding	986896	nitroreductase(lmo2829)
CAD01043	lmo2830	protein_coding	984904	thioredoxin(lmo2830)
CAD01044	lmo2831	protein_coding	986616	phosphoglucomutase(lmo2831)
CAD01045	lmo2832	protein_coding	986509	hypothetical protein(lmo2832)
CAD01055	lmo2842	protein_coding	986397	LacI family transcriptional regulator(lmo2842)
CAD01056	lmo2843	protein_coding	986395	lmo2843(lmo2843)
CAD01059	lmo2846	protein_coding	986389	hypothetical protein(lmo2846)
CAD01064	lmo2851	protein_coding	986382	AraC family transcriptional regulator(lmo2851)
CAD01065	lmo2852	protein_coding	986380	lmo2852(lmo2852)
CAD01066	lmo2853	protein_coding	986379	hypothetical protein(lmo2853)
CAD01067	lmo2854	protein_coding	986378	sporulation protein SpoJ(lmo2854)

CAD01068	rnpA	protein_coding	986374	ribonuclease P(rnpA)
CAD01069	rpmH	protein_coding	986371	50S ribosomal protein L34(rpmH)
CAD01070	lmo2857	protein_coding	986370	hypothetical protein(lmo2857)
EBG00000016607	'comK	pseudogene		
EBG00000016610	lmo0837	pseudogene		
EBG00000016616	lmo1876	pseudogene		
EBG00000016619	lmo0410	pseudogene		
EBG00000016634	transfert RNA-Asp	tRNA		
EBG00000016638	transfert RNA-Glu	tRNA		
EBG00000016639	transfert RNA-Ala	tRNA		
EBG00000016641	transfert RNA-Glu	tRNA		
EBG00000016642	transfert RNA-Thr	tRNA		
EBG00000016644	transfert RNA-Arg	tRNA		
EBG00000016646	transfert RNA-Leu	tRNA		
EBG00000016647	transfert RNA-Lys	tRNA		
EBG00000016658	transfert RNA-Lys	tRNA		
EBG00000016665	transfert RNA-Pro	tRNA		
EBG00000016667	transfert RNA-Asn	tRNA		
EBG00000016670	transfert RNA-Gly	tRNA		
EBG00000016674	transfert RNA-Gln	tRNA		
EBG00000016675	transfert RNA-Ser	tRNA		
EBG00000016680	transfert RNA-Ser	tRNA		
EBG00000016687	transfert RNA-Gly	tRNA		
EBG00000016694	transfert RNA-Asp	tRNA		
EBG00000016696	transfert RNA-Gly	tRNA		
EBG00000016698	transfert RNA-Asn	tRNA		
EBG00000016699	transfert RNA-Gly	tRNA		
EBG00000016704	transfert RNA-Leu	tRNA		
EBG00000016709	rRNA-23s	rRNA		
EBG00000016712	transfert RNA-Leu	tRNA		
EBG00000016713	transfert RNA-Glu	tRNA		

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